BOTANY 2025 ABSTRACTS

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Topic: Education and Outreach

A-6

A Discussion on Publishing Botanical Research in the Modern Publishing Landscape

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Academic publishing is going through major transformations, with the shift to open-access (OA) publishing, the rise of aggressive, sometimes predatory journals operating on a for-profit model, and the availability of new computational tools for preparing manuscripts (most notably incorporating artificial intelligence). This is making some aspects of traditional forms of publishing archaic. For example, subscription-based revenue and printed issues are both in decline, while traditional non-profit and society-based botanical journals face strong headwinds from aggressive, profit-oriented competitors. The latter excel at business models focused on open-access revenue and inflated impact metrics, without necessarily raising publication standards that warrant high metrics.

We propose to discuss the role that "traditional" botanical journals have in the future publication landscape, and the steps we are taking to maintain high standards of publication quality, scientific integrity, and manuscript handling—while at the same time, keeping costs down, and ensuring widespread circulation and high-quality coverage of the botanical sciences.

In this short lunchtime event, we will bring attendees up-to-date on the major trends and challenges facing modern academic publishing, and discuss how *American Journal of Botany*, *Applications in Plant Sciences*, and *Annals of Botany* are moving to stay abreast of change.

For our authors, a major consideration is how to cover publication fees when publishers push Article Processing Charges (APCs) to generate sufficient revenue while subscription revenue declines dramatically. This is a particularly sensitive issue for many authors in our journals who may lack access to large research grants to cover APC fees. These may include early-career researchers (ECRs: students and postdocs and new professors), in addition to international and North American researchers of all career stages who often lack sufficient lab funding to cover APCs adequately. In our discussion of publishing costs, we will explain the importance of "read and publish" deals and other sources of funding that may wholly or partly cover APCs—and address the importance of understanding fee structures at journals before submitting manuscripts. We also briefly discuss the role of non-profit and society journals, in contrast to profit-based models, and the aggressive, often predatory tactics found in the profit-based publishing realm.

Students and early career researchers in particular may benefit from the event, as we address how to publish open-access, with minimal or no expense, and how to prepare manuscripts with maximum impact and success for our broadly focussed journals (*AJB*, *APPS*, *AoB*) that serve the botanical community well.

Topic: Phylogenomics

A-8

Phylogenomic Profiles of Whole-Genome Duplications in Poaceae and Landscape of Differential Duplicate Retention and Losses among Major Poaceae Lineages

Author: Taikui Zhang, Hong Ma
Affiliation: Nanjing Forestry University, The Pennsylvania State University

Whole-genome duplications (WGDs) are important for angiosperm genome and gene evolution. Poaceae are the fifth largest plant family with ~12,000 species, including major crops (rice, wheat, and maize) and species with diverse habits and morphologies. Analyses of grass genomes support a WGD called rho shared by all grasses, with proposed contributions to the great Poaceae species diversity, in part through differential contributions of duplicates to various lineages. However, little is known about the evolutionary pattern of the rho-derived duplicates among Poaceae lineages and implications in adaptive evolution. Here we present phylogenomic/phylotranscriptomic analyses of 363 grasses covering all 12 subfamilies and nine previously unknown WGDs. Furthermore, duplications from a single WGD were mapped to multiple nodes on the species phylogeny; a WGD was likely shared by woody bamboos with possible gene flow from herbaceous bamboos; and recent paralogs of a tetraploid *Oryza* are implicated in tolerance of seawater submergence. Moreover, rho duplicates showing differential retention among subfamilies include those with functions in environmental adaptations or morphogenesis, including *ACOT* for aquatic environments (Oryzoideae), *CK2β* for cold responses (Pooideae), *SPIRAL1* for rapid cell elongation (Bambusoideae), and *PAI1* for drought/cold responses (Panicoideae). These findings present a Poaceae WGD profile with evidence for multiple evolutionary mechanisms that contribute to gene retention and losses.

Topic: Comparative Genomics/Transcriptomics

A-9

Phylogenomic and pan-genome evidence for hybridization in angiosperms

Author: Taikui Zhang, Wei Li, Hong Ma
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Polyploid plants are widely spread in nature and often share an origin of allo-polyploidization, especially through ancient hybridization events leading to whole-genome duplications (WGDs) in angiosperms. However, the parental lineages of many well-characterized WGDs are unknown. Poaceae are the fifth largest plant family with ~12,000 species, including major crops and species with diverse habits and morphologies. We identified gene phylogenetic support for a hybridization in the *Oryza*genus, with domesticated and wild rice, for the origin of the tetraploid *Oryza coarctata*, with one parent related to the previously defined F genome in *Oryza* and the other previously unknown genome similar to the ancestor of the A, B, C, and E genomes. We further found support for a WGD shared by woody bamboos and for herbaceous bamboos being related to a parental lineage of woody bamboo. The apple genus, *Malus*, is another interesting woody group, comprising diploid, triploid, and tetraploid species, for exploring the evolutionary genomics of hybridization. Our pan-genome analysis in *Malus*constructed an evolutionary landscape of different genome types and found extensive introgressions contributing to the ploidy diversity. These discoveries underscore the importance of hybridization in shaping the evolutionary trajectories of angiosperms, as revealed by our comprehensive phylogenomic and pan-genome profiling.

Topic: Paleobotany

A-10

Enigmatic Cycad Leaflet Structures

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There are four types of structures of unknown function at the base of the pinnae or on the petiolules in the cycads. These are the colored callous bumps on the acroscopic margin in *Macrozamia*, the raised rim on the abaxial side of the petiolule in *Zamia manicata*, the recurved abaxial flap of tissue on the petiolule of *Z. macrochiera*, and the white to yellow colored area at the juncture of the pinnae and the rachis in developing leaves in *Lepidozamia*, some species of *Encephalartos*, and in *Bowenia* where they are present in

both pinnae and pinnules. The callous bumps in *Macrozamia* vary with species ranging from white, yellow, orange or red during early leaf expansion and they may fade as the leaf ages. The color of the callous does appear to provide synapomorphies because the colors are distributed randomly on latest cladogram for the genus. Instead, the distribution of the colors appears to be geographic in when mapped. The callous bumps and the structures in *Zamia* are comprised of mainly parenchyma with no vasculature. The colored areas in *Bowenia, Encephalartos* and *Lepidozamia* have no distinctive anatomy or morphology other than their distinctive color. These may also be present in *Stangeria*.

Topic: *Systematics & Taxonomy*

A-11

The Mysterious Nesocaryum stylosum (Boraginaceae) is a Cryptantha!

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The classification of *Nesocaryum stylosum* (Boraginaceae) has been a mystery for nearly a century. This species is endemic to Isla San Ambrosio, a small island 900 km due west of the coast of central Chile. Ivan M. Johnston transferred the species from the genus *Heliotropium* to the monotypic *Nesocaryum* in 1927, but acknowledged that despite its quite different and rather unique vegetative, inflorescence, and calyx morphology, its unit fruits (nutlets/eremocarps) resemble those of *Cryptantha*. Here we review the morphology and taxonomic history of *N. stylosum* and provide DNA sequence data that indeed supports its placement in *Cryptantha*, for which we make the new combination, *Cryptantha stylosa*. Our data also supports the placement of this species in the *Maritimae* clade, a monophyletic group of *Cryptantha* species that are phylogenetically separate from the bulk of the genus. We provide both sequence and morphological evidence for an expanded membership of the *Maritimae* clade having up to 14 species: six species (11 minimum rank taxa) from North America, and 12 species (12 minimum rank taxa) from South America, including *Cryptantha stylosa*. We propose a tentative classification of the *Maritimae* clade as subgenus *Maritima*, consisting of series *Maritimae* and series *Muricatae*. We also review the evidence for the biogeographic and evolutionary history of *Cryptantha stylosa*, its probable closest relatives, and the need for additional research in the group.

Topic: *Dryland Floras*

A-12

Deeper bulbs are larger

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Affiliation: Oklahoma State University, University of Pretoria

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Topic: *Symbioses: Plant, Animal, and Microbe Interactions*

A-14

Isolating and Assessing the Plant Growth Promoting Ability of Seed Endophytic Microbes from Weedy and Cultivated (Oryza sativa) Rice

Author: Rachel Tavares
Affiliation: University of Massachusetts Amherst

Weedy rice (Oryza spp.), a close relative of domesticated rice, severely reduces cultivated rice (Oryza sativa) yields due to the competitive traits it has acquired through the process of de-domestication from cultivated rice varieties. Plant competitiveness is closely tied to the plant's microbiome. A healthy, beneficial microbiome can enhance a plant's ability to compete by improving its nutrient uptake, growth, disease resistance, and stress tolerance. As a result, understanding and managing the plant microbiome offers potential strategies for improving agricultural productivity and ecological balance. This study uses a novel culturable approach to isolate the seed endophytic microbiome of several genotypes of weedy and cultivated rice and assess these isolates for four plant-growth promoting (PGP) abilities: nitrogen fixation, phosphate solubilization, iron scavenging, and indole-3-acetic acid production. A total of 70 isolates were cryopreserved in a PGP microbe bank. The PGP ability of isolates from cultivated and weedy rice showed similar levels of performance with some exceptionally high performing isolates. Three high performing microbes were taxonomically identified and used as seed bioinoculants applied to both weedy and cultivated rice varieties. Only weedy rice seedlings showed a significant positive response to the bioinoculants suggesting that plant host identity may have an impact on the plant's ability to form beneficial plant-microbe relationships. The successful use of beneficial biofertilizers in cultivated rice will depend on developing a deeper understanding of the mechanisms that underlie the differential responses of rice plants to plant growth-promoting (PGP) microbes. By elucidating how these microbes interact with the plant, enhance nutrient uptake, and improve resilience, we can tailor biofertilizer applications to maximize their effectiveness and optimize rice growth.

Topic: *Molecular Ecology*

A-22

Less is more in herbarium-inclusive molecular ecology

Author: Yannick Woudstra, Patrick Meirmans, Anne-Sophie Quatela, Tanja Slotte, Barbara Gravendeel, Koen Verhoeven
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Target capture sequencing has enhanced the study of plant evolution and molecular ecology, particularly through the access to degraded DNA from herbarium specimens. A non-trivial consideration is whether to invest time and funds into targeting variable loci (the customised approach) or using a cheaper "off-the-shelf" universal kit with highly conserved targets. There is growing evidence that universal kits can capture considerable intraspecific genetic variation but direct comparisons with customised approaches below the species-level are sparse. This study presents such a comparison at the limits of intraspecific variation using a set of five clonal lineages of the common dandelion (Taraxacum officinale F.H.Wigg.), including up to 93-years-old herbarium specimens. An RNA-bait panel was designed to capture (i) conserved genes from universal kits (Angiosperms-353; Compositae-1061); (ii) variable genes with adaptive potential; (iii) highly variable loci normally obtained with a Genotyping-by-Sequencing (GBS) approach customised for dandelions. For categories (i) and (ii) both introns and exons were captured. The distribution of genetic variation was evaluated for each category through an analysis of molecular variance (AMOVA) and the discrimination between clonal lineages was visualised with a principal component analysis. Gene recovery and clonal lineage identification from herbarium material was comparable to fresh samples. Despite considerably more variation captured with customised approaches, clonal lineage discrimination was not superior to a universal exon target capture. The added value of customised approaches was the capture of relatively more variation within clonal lineages compared to between clonal lineages. However, universal kits can give sufficient resolution to study patterns of intraspecific genetic variation both within and between populations and this approach is therefore recommended to increase the number of samples under budgetary constraints.

Topic: *Ecology*

A-23

The Development of Plant Interaction Networks in a Changing World

Author: Gianalberto Losapio, Nora Khelidj, Bao Tu
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Ecological networks, composed of diverse species interactions, underpin species coexistence and the stability of plant communities. While network ecology has provided key insights into plant–pollinator and plant–soil microbe interactions, the processes driving the development of these networks remain poorly understood. With ongoing climate change, glacier retreat is rapidly reshaping alpine ecosystems, altering species composition and forcing new biotic interactions. Yet, how these emerging networks form, stabilize, and respond to environmental shifts remains an open question. In this presentation, I will synthetize the results of recent studies examining how glacier retreat influences the assembly and dynamics of plant interaction networks. By integrating empirical data and network analyses, I will explore how plant–pollinator interactions shift with glacier retreat and changing plant communities and how plant–soil microbe interactions develop in newly deglaciated landscapes. Sharp changes in the diversity of plant interactions are associated with a shift from plant facilitation and symbiotic soil microorganisms in recently ice-free terrains to shrub encroachment and soil acidification in late stages. We also observed an increase in the frequency of species interactions following glacier retreat, but an ultimate decrease with glacier extinction. These findings highlight how the structure and functional roles of plant interactions networks shift with

glacier retreat and drive biodiversity maintenance. Then, I will conclude with highlighting mechanisms driving the stability of plant interaction networks in rapidly transforming environments. Understanding these dynamics is crucial for predicting biodiversity responses and informing conservation strategies in the face of glacier extinction.

Topic: Comparative Genomics/Transcriptomics

A-25

Conifers concentrate large numbers of NLR immune receptor genes on one Chromosome

Author: Yannick Woudstra, Hayley Tumas, Cyril van Ghelder, Tin Hang (Henry) Hung, John MacKay
Affiliation: Stockholm University, University of British Columbia, INRAE, Université Côte d'Azur, University of Oxford

Nucleotide-binding domain and leucine-rich repeat (NLR) immune receptor genes form a major line of defense in plants, acting in both pathogen recognition and resistance machinery activation. NLRs are reported to form large gene clusters in limber pine (*Pinus flexilis*), but it is unknown how widespread this genomic architecture may be among the extant species of conifers (Pinophyta). We used comparative genomic analyses to assess patterns in the abundance, diversity, and genomic distribution of NLR genes. Chromosome-level whole genome assemblies and high-density linkage maps in the Pinaceae, Cupressaceae, Taxaceae, and other gymnosperms were scanned for NLR genes using existing and customized pipelines. The discovered genes were mapped across chromosomes and linkage groups and analyzed phylogenetically for evolutionary history. Conifer genomes are characterized by dense clusters of NLR genes, highly localized on one chromosome. These clusters are rich in TNL-encoding genes, which seem to have formed through multiple tandem duplication events. In contrast to angiosperms and nonconiferous gymnosperms, genomic clustering of NLR genes is ubiquitous in conifers. NLR-dense genomic regions are likely to influence a large part of the plant's resistance, informing our understanding of adaptation to biotic stress and the development of genetic resources through breeding.

Topic: Graeme P. Berlyn Tribute: Light and Life of Forests from Terrestrial to Subtidal and their Regeneration

A-28

A tribute to Graeme P. Berlyn: A life lived in cadence with the songs of trees from high mountains to coastlines.

Author: Anitra Thorhaug, Dennis Stevenson
Affiliation: Greater Caribbean Energy & ENvironment Foundation, New York Botanical Garden

Forests occupy a space between atmosphere and terrestrial soil, adjusting to light, moisture, soil and temperature with arborescence. These trees' tolerances adjust continually to the changing factors and resultant stress globally creating key ecosystems over time and space. Graeme Berlyn led his students and colleagues in pathways exploring and celebrating this continuum around the world, from high peaks in Alaska into the depths of the marine environment in Sri Lanka. Bill Burch saw "Graeme's life was sustained by and filled with the songs of trees." Graeme's world was also filled with his intense curiosity about how the trees functioned and how they could be kept sustainable for the future. He continually explored new technologies to learn and teach the world of Trees. He was the guru of microtechniques for over 6 decades (his book co-authored by Mischke "Botanical Microtechniques and Cytochemistry" rewritten several times to keep up with pace of techniques coming on line). He encouraged restoration reversing degradation of plant communities anthropogenically stressed. At a period when plant physiology was becoming increasingly molecular, Graeme boldly became more holistic, comprehending forests as massive ecosystems continentally and globally. He plunged into the salty ocean realms where constant moisture and salt occurred, where the saw the "forests of the sea" had need of intense physiological investigations during his last quarter century. Regeneration of forests in regions, that were burned, damaged or overlogged was always of first love. From fire regeneration, through an array of anthropogenic pollutants, Graeme searched for the solutions to reverse the pollutant loss of ecosystems. In Graeme's view was that the societal impact on these plants was held firmly as a factor to be investigated, with solutions to be discovered.

A "gentleman and a scholar" was a description of his approach to scientific Investigation and to teaching. He appreciated the input and thoughts of all his students, and encouraged individual originality in solutions. Many came to his office to ponder the best method to create an answer to their hypothesis, wherever globally their ecosystem was found, or at whatever level of molecular to ecosystem the problem occurred.

A colloquium of appreciation for Graeme P. Berlyn's 60 years of scientific investigation will occur with a series of his former students, and former colleagues describing their joint work in many of the fields of Plant-Environment interaction. They will point out Graeme's guidance and insight as well as his ever wisely interpreting data as to the interaction of environmental effects. Ecosystems from Asia to The Caribbean and North America will be included and a wide array of methodolgies will be explained. All this will pay tribute to the inventiveness, and accumulated wisdom and knowledge given generously to his students, colleagues, and to the world of plant Ecophysiology at large.

Topic: Biodiversity Informatics & Herbarium Digitization

A-32

Spatial diversity and distribution of fern and lycophyte species in karst and non-karst landscapes towards conservation needs

Author: Marjorie delos Angeles, Boniface Ngarega, Harald Schneider, Sirilak Radbouchoom, R. Sedricke Lapuz
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Karst formations are distinguished by their high levels of species diversity and endemism, including ferns and lycophytes. However, the existing data on plant community composition in karst formations remains deficient. Addressing these knowledge gaps is imperative, given the current accelerated rates of species loss, to enhance efforts to conserve biodiversity in these habitats. This study documents and explains patterns of fern and lycophyte species diversity within karst landscapes (KL) and non-karst landscapes (NKL) in the Philippines. Our comprehensive analysis involved aggregating 19,529 occurrence points encompassing 1,024 fern and lycophyte species sourced from field expeditions, voucher records from local herbaria, and online databases. Indices for species richness, weighted endemism, and corrected weighted endemism were then computed across KL and NKL areas to describe spatial diversity and identify fern and lycophyte hotspot areas. Gap analyses were also performed to determine if established protected areas (PAs) were sufficient to cover the identified fern and lycophyte diversity hotspots. Principal Component Analysis (PCA) was conducted to determine potential ecological drivers of distribution between KL and NKL areas. The findings reveal that most fern and lycophyte species were recorded to occur in NKL areas, with 995 (97.16%) species identified, while 676 (66.02%) species were documented to occur in KLs, including 29 (2.83%) exclusive to karsts. Identified hotspots for NKL are within mountain ecosystems which are already under existing legal protection. In contrast, KLs have five areas identified as congruent hotspots but considered gap areas due to their exclusion from current PA boundaries. Existing PAs thus provide less protection to karst habitats and their associated floras. PCA did not reveal any significant environmental predictors suggesting separation of KL and NKL species distributions, possibly due to lack of high-resolution environment data available for karsts. To facilitate the conservation of fern and lycophyte species in karsts, we propose installing and expanding existing PA boundaries, along with conducting more focused surveys in karst regions to better understand their ecological dynamics.

Topic: Conservation Biology

A-33

Cause to conserve - assessing Great Plains endemism in the case of Oklahoma Phlox (Phlox oklahomensis)

Author: Jessica Baughman, James Beck
Affiliation: Wichita State University

Most researchers view the Great Plains' flora as featuring few endemic species. Evaluating potential cases is urgent, due to both basic conservation concern and the chance to identify landscape or historical factors that could produce endemism in this region. Oklahoma Phlox (*Phlox oklahomensis*) is a putative example, known from two eastern and western metapopulations across seven Kansas and Oklahoma counties. Multivariate analysis of morphological measurements from 150 herbarium specimens clearly establishes the morphological distinctiveness of *P. oklahomensis*, and sets

of individual characters allow for a dichotomous key to this and related species. Phylogenetic analysis of both genomic (Angiosperms353) and genetic (nuclear ITS) datasets identify that Oklahoma Phlox is a clear evolutionary lineage, but one that is potentially nested within a more widespread taxon. Results suggest further studies are needed, investigating the potential for gene flow, within-population genetics, and unclear species boundaries. A full understanding of this taxon has the potential to enhance ecological pride in the Great Plains flora.

Topic: *Development and Structure*

A-34

Cell Wall Modification Shapes Twining Internodes in Common Bean Vines: A Xyloglucan Story

Author: Lena Hunt, Angelique Acevedo, Mariane Sousa-Baena, Rosemary Glos, Charles Anderson, Joyce Onyenedum
Affiliation: New York University, Federal University of Rio Grande do Sul, University of Michigan, Penn State

The evolution of climbing or vining growth forms is a key innovation driving the success and diversification of numerous taxonomic groups. Twiners, a subset of vines, climb by wrapping their main stem around a support without relying on tendrils or aerial roots. The rapid spread of many twining species underscores their ecological success. This research explores twining vines through anatomical, morphological, and molecular lenses, with a particular focus on specialized cells called "gelatinous fibers," which possess unique cell wall properties. Common bean (Phaseolus vulgaris) is used as model for twining vines.Twining occurs in the common bean through three phases: elongation, circumnutation to find a support, and gelatinous fiber development in the coiled regions to maintain the twined posture. In this work, we sought to disrupt gelatinous fiber development via exogenous hormone manipulation. Plants were topically treated before twining with either a brassinosteroid (24 epibrassinolide) or a brassinosteroid inhibitor (brassinazole) in lanolin, as these are known to impact gelatinous fibers in woody species. We found all three stages of twining were impacted by the brassinosteroid treatment, leading to 1.) overly elongated internodes that 2.) lacked the structural stability to circumnutate and 3.) showed underdeveloped gelatinous fibers at maturity. RNA was sequenced from the treated stem areas at two timepoints: three days after treatment (when the exaggerated elongation phenotype was emerging) and at maturity. Significant differential gene expression of the XTH gene family was observed between groups at both times. These genes are known to play a role in cell extensibility and make sense to be upregulated during rapid elongation in brassinosteroid treated plants at the first timepoint. However, their significant differential expression at the mature timepoint (after elongation had ceased and gelatinous fibers were maturing) was more intriguing. XTH genes are responsible for modifying xyloglucan, a hemicellulose component of the primary cell wall, with a hotly debated presence in the specialized secondary cell walls of gelatinous fibers. This finding prompted us to investigate whether xyloglucan could be detected in the gelatinous fibers of common bean, and we confirmed its presence through immunolocalization with LM15. Not only was xyloglucan present, but it showed significant differences corresponding to XTH gene expression patterns – lowest in the elongated brassinosteroid-treated gelatinous fibers, and highest in the short, thick gelatinous fibers of plants treated with a brassinosteroid inhibitor. This finding is significant as xyloglucan was once called "the molecular muscle" and thought to be a major contributor to the tension generated in the secondary cell walls of gelatinous fibers. Difficulties detecting xyloglucan in the mature gelatinous fibers of trees has called this theory into question, however, our findings serve as fresh evidence for the presence of xyloglucan in the secondary cell wall in common bean and its potential contribution to the structural support of gelatinous fibers.

Topic: *Pteridology*

A-35

The Search for A Deadbeat Diploid- Clarifying Parentage Of A Substrate Diverse Desert Fern

Author: Ethan Altergott, James Beck
Affiliation: Wichita State University

The genus *Astrolepis* (Pteridaceae) consists of multiple xeric adapted, lithophytic ferns common throughout Mexico and the southwestern U.S. The focus of this project *Astrolepis cochisensis* is of interest because it contains three unique subspecies: *A. cochisensis subsp. chihuahuensis*, a sexual diploid found exclusively on limestone. *A. cochisensis subsp. chochisensis,* a seemingly common asexual triploid also found exclusively on limestone, and *A. cochisensis subsp. arizonica,* a tetraploid that has been reported on a variety of substrates (limestone, granite, rhyolite, etc). The most plausible scenario for the origin of the tetraploid populations involves a diploid parent, which implies the existence of a non-limestone, diploid lineage that is either extinct or undescribed. This project involves the search for evidence of this missing diploid. This evidence could come in the form of an extant population, as an herbarium specimen, or as allelic variation found exclusively in tetraploid populations. Spore number and diameter have been assessed from more than 200 herbarium specimens to establish the geographic range of the cytotypes. Herbarium specimens also create the opportunity to discover a diploid specimen from a non-limestone substrate. A set of highly variable plastid and nuclear genes will be sequenced from select herbarium and field-collected specimens, with a focus on diploids and tetraploids. The discovery of alleles unique to tetraploids would provide evidence of the hypothesized "missing" diploid parent.

Topic: *Floristics*

A-36

Diversity, Distribution, and Conservation of the Annonaceae Family in Nigeria: A Comprehensive Assessment

Author: Sunday Adeniran, Benjamin Ajayi, George Nodza, Kehinde Olawepo, Olumide Bamidele
Affiliation: University of Ilorin Nigeria, Florida State University, University of Lagos, University of Ilorin

The Annonaceae family in Nigeria exhibits remarkable diversity, with a comprehensive checklist documenting 245 specimens across 23 genera and 60 species over eight decades. Genera such as *Annona*, *Monodora, Uvaria*, and *Xylopia* display the highest diversity, whereas *Brieya, Cleistopholis*, and *Enanthia* are sparsely represented, suggesting restricted ecological niches. Widely distributed species like Annona *senegalensis* and *Xylopia aethiopica* thrive across diverse habitats, from rainforests to savannas and mangroves, demonstrating significant environmental adaptability. The dataset, compiled from herbarium records, field surveys, and literature, spans collections from the 1930s to the present, offering historical and contemporary insights. Specimens from national parks and forest reserves, including Okomu, Kashaka Gumti, Kainji Lake, the Mambilla Plateau, and many other parks, underscore the role of protected areas in conserving biodiversity. Conservation assessments indicate that most species are classified as "Least Concern," while vulnerable taxa, such as *Xylopia africana* and *Isolona pleurocarpa*, require urgent conservation action. Additionally, unidentified specimens, potentially representing new taxa, highlight the need for further taxonomic research. This study underscores the importance of systematic botanical documentation, improved conservation strategies, and habitat protection to safeguard Annonaceae diversity in Nigeria. Our findings provide a critical resource for biodiversity conservation, ecological management, and taxonomic resolution in Nigeria and West African floristics.

Topic: *Ecology*

A-40

Transgenerational Plasticity Enhances Offspring Fitness in Competitive Environments Through Epigenetic Mechanisms

Author: Arezoo Fani
Affiliation: University of Kansas

Plants frequently encounter competition for resources, and their ability to respond to such pressures influences ecological interactions and agricultural productivity. Transgenerational plasticity (TGP) is an adaptive mechanism through which parental environmental experiences shape offspring phenotypes, potentially enhancing fitness in predictable conditions. However, the extent to which TGP contributes to adaptive responses in competitive environments, independent of simple provisioning effects, remains unclear. In this study, I investigated the role of TGP in *Mimulus platycalyx*, a species with a strong capacity for vertical growth, to determine whether parental exposure to high-density competition primes offspring for similar conditions.

To test this, I grew 96 parental plants under three competition treatments: (no neighbors), (eight neighbors at the edge of the pot), and (closely packed competitors and edge neighbors). I manually self-pollinated plants and collected seeds to grow the next generation under two offspring treatments: (no neighbors) and (eight surrounding neighbors). Across both generations, I measured key fitness-related traits, including —all associated with biomass accumulation, fecundity and competitive ability.

Results demonstrated that offspring from high-density parents exhibited significantly greater, supporting the hypothesis that. Notably, these effects were not explained by simple maternal provisioning, as there was no correlation between seed mass and offspring traits. Instead, this suggests that epigenetic regulation—rather than differences in resource allocation—plays a key role in transgenerational responses.

These findings have significant implications for both. In natural populations, TGP may contribute to species persistence in dynamic environments by priming offspring for competition, influencing community structure and plant interactions. In agricultural settings, leveraging TGP could improve crop resilience, particularly in high-density planting systems, where enhanced competitive traits could optimize yield without genetic modification. Understanding the epigenetic mechanisms underlying TGP could further inform breeding programs and sustainable farming strategies.

Future research will focus on identifying the molecular basis of these transgenerational effects, including DNA methylation and histone modifications, to investigate how environmental cues trigger heritable phenotypic shifts through epigenetic regulation. This work highlights the ecological and evolutionary significance of TGP and its potential applications in improving plant performance under competitive stress.

Topic: Development and Structure

A-47

Capsella in the big city: investigating the genetic and morphometric mechanisms responsible for Capsella bursa-pastoris leaf shape variation in urban populations.

Author: Asia Hightower, Claudia Colligan, Emily Josephs, Daniel Chitwood
Affiliation: Michigan State University

As urbanization and urban sprawl have become increasingly important and complex issues, the ability to adapt to decreased green space, increased temperature, and increased human disturbance is key for plant survival in these new habitats. One urban weed, *Capsella bursa-pastoris* has been quite successful in thriving in urban habitats and disturbed spaces. However, the mechanisms to *Capsella bursa-pastoris's* urban success are not well understood. A key morphological trait that may contribute to urban success is leaf shape variation. Leaves are more than just photosynthetic organs and leaf shape variation affects many important processes such as water transport, heat dissipation, and frost tolerance. For *Capsella bursa-pastoris* populations, leaf shape is a plastic trait that is known to be affected by increasing temperatures. *Capsella bursa-pastoris* populations are found across the globe and especially throughout the United States. In the U.S., studies have documented significant leaf shape variation within and between populations across a diverse set of climate regions. However, some regions like the Midwest and Mid-Atlantic include significantly less leaf shape variation than populations in the southern regions of the U.S. As such, we do not know if these differences in shape variation are due to environmental, genetic, or a combination of factors. Additionally, to date, the genetic mechanisms for leaf development and shape variation have not been mapped in *Capsella bursa-pastoris*. Therefore, this study will use novel morphometric, dimension reduction, and modeling techniques with genetic analysis to determine the genetic and morphometric/physiological mechanisms for leaf development and variation in *Capsella bursa-pastoris populations* from the Midwest and Mid-Atlantic regions. The results of this study will determine total leaf shape variation and specific leaf area variation. By knowing which parts of the leaf vary most between populations, we can infer how changes in leaf physiology may affect changes in function. Additionally, by determining which genes are related to leaf development, total leaf variation, and specific leaf variation, we can understand the genetic mechanisms that contribute to morphological/physiological variation and the evolution of leaf shape across *Capsella bursa-pastoris populations*. Overall, results from this study will contribute to our understanding of the adaptation strategies urban plants may employ to thrive during increased urbanization and rapid climate change.

Topic: Education and Outreach

A-48

Curing plant blindness one pre-med student at a time

Author: Dianne Anderson
Affiliation: Point Loma Nazarene University

Addressing the lack of interest in plants, particularly in pre-health students, can be a real challenge. Great progress can be made in a one-semester required Organismal Biology course using a combination of 1) outdoor experiences asking students to collect plants, or parts of plants, for further examination in the lab 2) using fresh plant tissues as study specimens in the lab whenever possible 3) highlighting common food plants as examples when teaching concepts and 4) emphasizing the secondary metabolites that plants produce and that humans have found to be useful as medicines.

Topic: Development and Structure

A-49

Morphological and developmental novelties within the intricate androecium of Loasaceae

Author: Andrea Appleton, Yan Gong, Grace Pisano, Elena Kramer
Affiliation: Harvard University, UC Berkeley

While flowers themselves are often considered evolutionary novelties, suites of novel traits have further evolved within flowers that contribute to the morphological diversity across angiosperms, including traits as dramatic as evolution of novel floral organ identities. A surprisingly common example are staminodes, which are stamens that have lost the ability to produce viable pollen. Although some staminodes are retained as vestigial rudiments of stamens, others have evolved an exceptional array of forms in response to selection for alternative functions. Staminode morphological evolution and pollination biology have been well-characterized, but little is known about the genetic underpinnings of these structures despite their potential in illuminating how morphological novelty evolves in a broader context. Loasaceae, the rock nettle family, displays a particularly diverse range of floral morphologies and constitutes an ideal system in which to understand the developmental and genetic basis of multiple novel features, including but not limited to staminodes. Subfamily Loasoideae has evolved extreme androecial complexity: within the androecial whorl, fascicles of fertile stamens alternate with complexes containing two types of staminodes (two inner, free, filamentous staminodes held within an outer, so-called nectar scale comprised of three or more fused staminodes). Further, developmental studies have shown that the entire Loasoideae androecium is derived from a ring of so-called "common" primordia. These are developmentally novel primordia that initiate on the floral meristem as a series of single, large antepetalous units, but then divide into two or more smaller common primordia, which then become subdivided into many individual primordia. We know that common primordia have evolved repeatedly across angiosperms, but their developmental nature is unclear (e.g., are they meristematic?). To summarize, not only do flowers of Loasoideae contain highly modified staminode complexes in addition to stamens (totaling six distinct floral organ identities), but their organization within the flower is unprecedented, with bundles of fertile stamens alternating with complexes of sterile staminodes in the same whorl using novel means of development. We have combined morphological and developmental-genetic approaches, including microscopy, transcriptomics, and gene expression analyses, to understand how common primordia and their staminode derivatives arise in the Loasoid species Aosa rupestris. Our results from this model system will help us understand the evolution of floral morphological diversity in Loasaceae more broadly.

Topic: Ecology

A-50

Carbon Sequestration of Nypa fruticans and Metroxylon sagu in Negros Oriental, Philippines

Author: Sofia Baez, Dave Gauthier, Roy de Leon, Jeanette Mara Sumagaysay, Alicia Gotonero, Chris Bird
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Mangrove forests are highly productive biomes and important for many ecosystem services such as protecting against extreme weather conditions, providing a safe habitat for animals, and sequestering and storing carbon. Understanding carbon sequestration of mangrove systems can aid in understanding their capacity to buffer against climate change. In this study, we investigate the carbon potential of two mangrove palms native to Southeast Asia and Oceania: *Nypa fruticans,* the Nipa Palm, and *Metroxylon sagu, the Sago Palm*. In recent years, Nypa palm populations have declined due to their use in thatched roofing. The objective of this project was to investigate the estimated contribution to carbon budgets by these palms as well as educate and inform the public on the importance of these palms. We hypothesize that *Nypa fruticans* and *Metroxylon sagu* contribute significantly to the carbon sequestration potential of mangrove ecosystems. We collected fronds and soil samples from two study sites in the Philippines within the Central Visayas region. We measured frond length, weight, and number of fronds per individual, as well as organic matter content. The amount of carbon sequestered by

each species was determined from species biomass. Additionally, information on the community structure, topsoil, and carbon content was used to calculate the overall carbon sequestration per hectare.

Topic: Ecology

A-51

Modeling a Murderer: Ecological Requirements of Michigan's Bladderworts (Utricularia)

Author: Alex Risdal
Affiliation: Loyola University Chicago

Carnivorous plants have complex adaptations to low-nutrient environments, making them specialized in attracting and capturing prey. They are often found in threatened habitats like bogs and fens, which have been damaged by spreading invasive species, anthropogenic impacts, and climate change. Utricularia, an understudied genus of carnivorous plants, are widely distributed throughout North American wetlands, with eleven identified species in Michigan. Nine of these species have a coefficient of conservatism (COC) score of 8 or higher, indicating that they are restricted to specialized habitats and have low tolerance for environmental impacts. Utricularia provide food, shelter, and habitat for insects, mammals, and waterfowl. Their ecological importance and habitat requirements are poorly understood due to limited ecological research on the genus. My project aimed to determine the environmental factors influencing Utricularia distribution and develop a Species Distribution Model to predict Utricularia's current distribution in MI. I used data from the Global Biodiversity Information Foundation (GBIF) to select sampling sites based on accessibility and which species were present. In 2024, I collected water quality, plant community, substrate, and water depth data at these sites. Sites were primarily based in the Northern Lower Peninsula of MI. This data was used to conduct model selection using Linear Mixed Effects models to identify important factors in predicting Utricularia distribution. My LME revealed a relationship between two water lily species, Nymphaea odorata and Nuphar variegata, and Utricularia diversity. This discovery will guide a second year of sampling, exploring the influence of Nymphaea and Nuphar on Utricularia diversity, and will inform conservation and restoration efforts for Utricularia and other wetland plants.

Topic: Conservation Biology

A-52

Demographic Structure of Tecate Cypress (Hesperocyparis Forbesii) in the Northern Santa Ana Mountains: Viability in the Face of Fire

Author: Emily Fitzpatrick, Amanda Fisher
Affiliation: California State University, Long Beach, California State Univ Long Beach

Hesperocyparis forbesii is a rare tree found only in southern California and northern Baja. Individuals become capable of reproduction between five and ten years of age, with seed cone production remaining unstable until individuals reach thirty to forty years. Most seed cones do not release seeds until they are exposed to fire. However, the many years required for a canopy seed bank to be established makes increasing wildfire frequency a significant threat to the species, as exposure to multiple fires in a short time period could prevent individuals from reaching reproductive maturity. The northernmost H. forbesii population is found in the Santa Ana Mountains of southern California and partially under the jurisdiction of the Cleveland National Forest Service. Surveys conducted in 2009 found that these stands were made up of relatively few adults. Although adults are valuable due to their reproductive abilities, the overall low number of individuals indicated a high risk of extirpation in the event of fire. This study analyzed the current extirpation risk of the stands by conducting surveys of five H. forbesii stands in 2024 and comparing them to the 2009 surveys. We also assessed the reproductive output of each stand by counting seed cones. We expected that, much like in 2009, the stands would have low demographic heterogeneity and be composed of few adult or mature trees, with a significant risk of extirpation. However, our surveys found that the stands were demographically variable and had increased in size ten-fold, with the population growing from 75 in 2009 to 754 in 2024. This includes the 389 individuals located at a fifth stand that was not documented in the 2009 survey. Stands exhibited a range of reproductive capabilities, with trees in the same age classes differing in the quantity of cones produced. Trees classified as mature should yield the highest number of seed cones, but individual trees were documented as having anywhere from 2 to 2395 cones. This variation was echoed in adult trees, which had anywhere from 1 to 1110 cones. The historic fire return interval also varied more than anticipated, ranging from 15 to 50 years across sites. Three of the H. forbesii stands were found to be more resistant to extirpation than predicted, however, two stands had low numbers of trees and low seed cone production. These stands are at risk of extirpation. The unique characteristics and fire history of each site results in management challenges that require a more individualized approach. We propose using seedbanking to preserve the genetic resources of each stand to protect against extirpation. It would also be useful to develop climate change projections for the study area, which would further inform estimates of extirpation risk for each stand.

Topic: Graeme P. Berlyn Tribute: Light and Life of Forests from Terrestrial to Subtidal and their Regeneration

A-53

Texas Seagrass Restoration: survival from Laguna Madre to Galveston Bay

Author: Anitra Thorhaug, Arthur Schwarz
Affiliation: Greater Caribbean Energy & ENvironment Foundation, Southwestern Adventist University

A century of degrading coastal actions has left Texas estuaries with a low extent of seagrass (Pulich, 1999). The largest seagrass extent is found in Laguna Madre (80,937ha). Very small amounts were present in Matagorda (1.6% or 1550ha) and Galveston Bays (0.1 % or 113.3ha). The total surface area of all estuaries in Texas is 1,092,650 ha (10,926.5 km^2). Less than ten percent of the very shallow estuaries are covered with seagrass. Problems causing seagrass loss include dredging, filling, damming, waste drainage, terrestrial soil runoff, and dust settlement from mining and storage. Meanwhile state funding for coastal ecosystem restoration has focused on salt-marshes, while little funding for seagrass and almost no mangrove restoration has occurred. We report our coastal information from multiple mitigation and some scientific exploratory restorations projects of large-scale and pilot seagrass plantings along the Texas coast. The total spatial area of our planting was 625,126 m^2 with 596,615 Planted Units (PU). Our restoration sites generally expanded into a larger area about quadruple the planted space. Our colleague's (C.B.) planting covered 1,012,777 m^2 with about a million PU. Meanwhile others planted the following: Maristany et al (2018) 108,600 units in over 94,577 m^2 for port mitigation; Sheridan (2004,1997) 10,500 units ; Kennedy (1997) 16,000 units. Thus, 1,732,700 m^2 (173.3 ha) of seagrass has been restored. Various planting methods including sprigs, plugs, sods, and seeds will be discussed. The factors measured for our restoration include light, turbidity, water clarity depth, salinity, sediment type, energetics, fisheries species, endangered species, and stabilization of sediment. We present these variables encountered in the estuaries of Galveston Bay, Matagorda Bay, Mission-Aransas/St Charles, greater Corpus Christi Bay, and Laguna Madre versus their survival. The services we measured include shoreline and underwater resilience, water clarity for bay recreation, fisheries nursery habitat, endangered species food-web habitat, mineral cycling, and stored blue carbon. Of the six species growing in the Texas estuaries, a combination of Halodule wrightii with potentially an understory of Halophila engelmanii has the highest survival after restoration in many sites. Large-scale projects with excellent results will be highlighted. Planning for the future of Texas coastal seagrass restoration will be discussed.

Topic: Ecology

A-54

Modeling a Murderer: Determining the Ecological Requirements of Michigan's Bladderworts

Author: Alex Risdal
Affiliation: Loyola University Chicago

Carnivorous plants have complex adaptations to low-nutrient environments, making them specialized in attracting and capturing prey. Utricularia, considered the largest genus of carnivorous plants, are widely distributed throughout North American wetlands, and are often restricted to specialized habitats, with low tolerance for environmental impacts. Eleven species of Utricularia are present in Michigan, my site of study. Utricularia provide food, shelter, and habitat for insects, mammals, and waterfowl. Their ecological importance and habitat requirements are poorly understood due to limited ecological research on the genus. My project aimed to determine the environmental factors influencing Utricularia distribution and develop a Species Distribution Model to predict Utricularia's current distribution in Michigan. I collected citizen science data from iNaturalist to guide the selection of sampling sites. In the Summer of 2024, I collected data on water quality, plant community, substrate, and water depth at these sites. This data was used to conduct model selection using Linear Mixed Effects

models to identify the most important factors in predicting Utricularia distribution. This LME revealed a relationship between water lily species and Utricularia diversity. This discovery will guide a second year of sampling, exploring the influence of Nymphaea and Nuphar on Utricularia diversity, and will inform conservation and restoration efforts for Utricularia and other wetland plants.

Topic: *Pteridology*

A-56

Putting ferns on the map: global patterns of wide-ranging fern species

Author: Dusty Prater, Jacob Suissa
Affiliation: University of Tennessee, Knoxville, The University of Tennessee

The uneven distribution of species on earth is a fascinating aspect of our planet, which has attracted the attention of biologists for centuries. Of all the possible distribution patterns, those of wide-ranging species are of great interest, as they provide a unique glimpse into various aspects of biology across scales of complexity. Ferns, often thought to be widespread, based on instances of extreme spore dispersal, successful long distance colonization, and inter-continental disjuncts; however there have been no modern analysis of fern distributions at a global scale.

Here we leverage a publicly available dataset to explore the patterns of range size across 5,533 fern species. We find that most species are narrowly distributed, but there is a great diversity of fern distribution patterns across the major clades. Further the variation we see in range size is not largely explained by phylogenetic relationships, suggesting that other factors, such as phylogeographic principles or variable aspects of the fern life cycle, could be causing the trends.

In sum, our work provides a quantitative framework for exploring the underlying dynamics responsible for shaping fern distribution patterns and provides a new context for future work on fern distributions.

Topic: *Ecology*

A-57

Animal consumption on moss sporophytes: Ubiquitous impact and implications for spore dispersal in forest ecosystem

Author: Yume Imada, Ryoei Miyoshi, Yuya Inoue
Affiliation: Kyoto University, Ehime University, NMNS

Mosses primarily reproduce via wind-dispersed spores, but our field assessment reveals that ground-dwelling decomposing insects also play a significant role in their dispersal in forest ecosystems. During our study, we observed frequent foraging of moss sporophytes by some ground-dwelling insects, including camel crickets and earwigs, with their feces retaining some germination ability. Our findings indicate that arthropod-mediated damage on moss sporophyte capsules is widespread and severe across diverse geographical locations and taxonomic groups. Furthermore, we suggest that variations in forms, such as seta and calyptra, among moss sporophytes may influence their susceptibility to animal damage. Additionally, our study has revealed that arthropods feeding on moss sporophytes contribute to spore dispersal through both endozoochory and epizoochory. These findings shed new light on the potential of the zoophilous nature of moss spores.

Topic: *Systematics & Taxonomy*

A-58

Using target capture to resolve species complexes within the genus Aphyllon (Orobanchaceae)

Author: Kiona Leeman, Adam Schneider
Affiliation: University of Wisconsin - La Crosse, University of Wisconsin-La Crosse

Aphyllon is a genus of 27 species in the angiosperm family Orobanchaceae. *Aphyllon* are non-photosynthetic root parasites that attach haustoria to the roots of their hosts to obtain nutrients. The genus *Aphyllon* is composed of two sections: sect. *Aphyllon* and sect. *Nothaphyllon*. Species within sect. *Nothaphyllon* have historically posed significant taxonomic challenges, leading to its members being informally grouped into the *A. californicum*, *A. cooperi*, and *A. ludovicianum* complexes. Previous research suggests that these complexes are the result of a complicated gene history, potentially being confounded by phenomena such as hybridization and/or incomplete lineage sorting (ILS). In this study, we use phylogenomic data to explore the evolutionary history of *Aphyllon*, with special attention to the *A. cooperi* and *A. ludovicianum* complexes, in order to address the taxonomic difficulties within. The Angiosperms353 DNA probe kit was used to perform target capture, HybPiper was used for gene re-assembly in conjunction with the mega353 target file, and ASTRAL was used for phylogenetic inference. ASTRAL uses a multispecies coalescent model and integrates individual gene histories into a species tree, even when the individual gene trees show discordance due to ILS. Here we present our preliminary findings from a pilot study of 25 samples (24 *Aphyllon* and 1 *Orobanche* outgroup). We find that Angiosperms353 works to successfully retrieve genes from *Aphyllon*. We find support for the distinction between the two sections and further validate the previously reported relationships among the five species in section *Aphyllon*. Our results conflict with previous discussion of the informal complexes; the few tested members of the *A. cooperi* complex and the *A. californicum* complex did not form monophyletic groups with their respective complex members. Our research is ongoing; additional samples are currently being collected and processed (with deeper sampling in the *A. cooperi* and *A. ludovicianum* complexes) in order to increase resolution for these complexes. The potential roles of hybridization and ILS in the evolution of *Aphyllon* will also be examined.

Topic: *Phylogenomics*

A-60

Phylogenomic challenges in polyploid-rich lineages: Insights from orthology inference and reticulation methods using the complex genus Packera

Author: Erika Moore-Pollard, Jennifer Mandel, Paige Ellestad
Affiliation: University of Connecticut, University of Memphis, Boise State University

Underlying phylogenomic discordance is common, and resolving it requires more than simply adding additional data. Biological processes such as polyploidy, hybridization, and incomplete lineage sorting are major contributors to discordance and must be accounted for to avoid misleading evolutionary interpretations. To better understand how these processes affect phylogenies, we investigated nuclear discordance in the complex genus *Packera*. With approximately 88 species and varieties—40% of which exhibit polyploidy, aneuploidy, or other cytological complexities—*Packera* presents significant challenges for phylogenetic reconstruction. Given these complexities, we assessed the impact of different published orthology inference methods on the evolutionary relationships and phylogenetic support of this group. We generated multiple nuclear phylogenies using several orthology inference approaches and compared the resulting trees. We then examined three paralog processing methods and evaluated their effects on our understanding of *Packera*'s evolutionary history by constructing a time-calibrated tree, reconstructing historical biogeography, and testing for ancient reticulation. Unsurprisingly, phylogenetic outcomes varied depending on the paralog processing method used, exemplifying the importance of considering paralogy in phylogenomic studies. Our findings highlight the profound impact of orthology inference and paralog processing on phylogenomic analyses, particularly in polyploid-rich groups such as *Packera*. Even so, gaining a robust understanding of *Packera*'s evolutionary history requires more than computational approaches alone. While technological advancements have greatly expanded our ability to analyze genomic data, effective phylogenomic research still relies on strong taxon sampling and detailed species knowledge. Without careful attention to the biological context—such as species boundaries, cytological variation, and ecological interactions—phylogenomic studies risk misinterpreting evolutionary processes. By accounting for these factors, we can begin to improve the accuracy of evolutionary reconstructions and gain deeper insights into the complex history of plant diversification.

Topic: *Paleobotany*

A-66

A fruit of ericaceous affinity from the Paleocene of Wyoming, U.S.A.

Author: Bruce Tiffney, Kaitlyn Krinsky, Steven Manchester, Walter Judd
Affiliation: University of California Santa Barbara, University of Florida, Florida Museum of Natural History, University of Minnesota Herbarium

The Big Sand Draw flora of mid or late Paleocene age includes casts and molds of fruits and seeds encased in iron-cemented sandstones and silts. Examination via reflected light microscopy and micro-CT scanning provides extensive detail of many fruits,

including one of ericaceous affinity. The fruits are 5-carpellate, pedicellate, loculicidal capsules subtended by a pentamerous calyx. The base of each valve is enlarged and contiguous, suggestive of a nectar disk, a common feature in the Ericaceae. Each valve wall is two-layered, the outer of which separates from the inner and degrades more easily. Placentation is axile, with several small, elongate, narrow seeds per locule that are borne beneath the arms of the lobed placenta that occurs at the apex of the central columella. These lobes floor an apical depression that is over-arched by the tips of the surrounding valves.

These characters are consistent with placement in the Ericales, and are most strongly aligned with the Ericaceae. However, the combination of characters does not accord with any single genus within the family, and many of the characters of the fossil are found in more than one tribe and subfamily. Thus, we assign the fossil to an extinct genus. Athough representatives of the Ericales are recognized in the later Cretaceous, extant genera in the Ericaceae do not become common until the later Paleogene and Neogene.

Topic: Paleobotany

A-67

Fruits of a new genus of extinct Fagaceae associated with leaves of Fagopsiphyllum (Heer) Manchester from the Paleocene of Wyoming, U.S.A.

Author: Steven Manchester, Kaitlyn Krinsky, Walter Judd, Bruce Tiffney, Julian Correa
Affiliation: Florida Museum of Natural History, University of Florida, University of Minnesota Herbarium, University of California Santa Barbara

Dispersed pollen and leaves of Fagaceae are widely reported from the Paleocene of the Northern Hemisphere, but fruits have remained elusive. Here we report cupulate fruits found in association with *Fagopsiphyllum groenlandicum* from mid or late Paleocene shales, siltstones and sandstones of the Fort Union Formation at two sites in the Wind River Basin of Wyoming. The pedunculate cupules are borne on a raceme-like inflorscence. Each cupule has four valves and bears three nuts; the lateral nuts are enclosed by two valves and the central nut by all four. The nuts are ovate in lateral view and possess three major and three minor longitudinal ridges, creating a hexagonal cross section towards their base, tapering to a trigonal cross section at the apex. The nuts are topped by a perianth of six tepals in two whorls, the tepals arising from the tips of the six ridges. The cupules are ornamented by irregularly positioned, apically-directed projections.

These features distinguish this fossil from previously described extinct and extant fagaceous taxa.The combination of pedunculate, raceme-like infructescences bearing four-valved cupules containing three flowers and ultimately three nuts is unique within the Fagaceae but combines characters of several taxa in the Quercoideae. The basally hexagonal, apically trigonal nut shape of this fossil is distinct from the generally oval to circular nuts of the Quercoideae, the trigonabalanoid group excepted, and likely reflects a plesiomorphic character of the family. The co-occurrence of these fruiting remains with *Fagopsophyllum* at both Big Sand Draw and Hell's Half Acre is suggestive that the two organs may represent the same plant although they have not been found in attachment. Further research is needed to determine if this fruit morphology co-occurs with *Fagopsiphyllum* where it is found in Greenland, Japan and Scotland.

Topic: Bryology and Lichenology

A-68

Usnea subfloridana as a model for understanding the drivers of the distribution and ecology of imperiled Usnea lichens in the northeastern US

Author: Caroline Witherspoon
Affiliation: SUNY-ESF

Urbanization, global change, and increasing disturbances are altering and eradicating many of our forests and pushing many species out of their historical habitats. We can use indicator species to watch changes occurring in the forests influenced by our management practices, air quality, global warming, and changing climate, to inform conservation efforts. Of various indicators and species being affected, one lichen offers promise as an easily identifiable, historically abundant, and one of the first organisms to react to change within a forested system. Many members of the lichen genus *Usnea* face global declines in population densities and ranges. The prevailing assumption is that this has been caused by air pollution and climate change, but more recent research has begun considering forest management and disturbance as potentially significant influences. This would be a logical factor to investigate, considering several *Usnea* spp. are strongly associated with old-growth and continuous forests. Examinations of these relationships have begun in Europe and the Pacific Northwest but have yet to be explored in the eastern US. This research will aim to answer the question; "What are the drivers of the distribution and ecology of the imperiled *Usnea* lichens in the northeastern US?" by quantifying the decline of *U. subfloridana* in the northeastern US and identifying landscape-scale factors that predict distributions by building historical and modern species distribution models from herbarium records. It will also analyze stand-level environmental factors that may predict their localized presence and abundance through a localized survey at the SUNY-ESF Huntington Wildlife Forest in the New York Adirondacks. Understanding the ecology and decline of *Usnea* spp. can inform our understanding of how global climate change is affecting diverse species populations. If *Usnea* spp. are proven to be restricted to old and/or continuous forests, they can be used to inform the development of more sustainable forest management practices that foster the persistence of numerous forest-dwelling organisms that are likely being affected by global climate change.

Topic: Comparative Genomics/Transcriptomics

A-69

Comparative Genomics in Asterales: Foundations for understanding evolutionary and functional dynamics in Asteraceae

Author: Erika Moore-Pollard, Paige Ellestad, Brannan Cliver, Jakub Baczyński, Matthew Pollard, Zach Meharg, Samantha Drewry, J. Mauricio Bonifacino, Alex Harkess, Zach Nimchuk, John Burke, Daniel Jones, Jennifer Mandel
Affiliation: University of Connecticut, Boise State University, Auburn University, University of Georgia, University of Memphis, HudsonAlpha Institute for Biotechnology, Facultad de Agronomia, Universidad de la Republica, University of North Carolina Chapel Hill

Asteraceae is one of the largest families of angiosperms—with almost 35,000 species—and far surpasses that of related families in the MGCA clade of Asterales, including Menyanthaceae (60 species), Goodeniaceae (430 species), and Calyceraceae (47 species). This remarkable diversity stems from a complex evolutionary history shaped by whole genome duplications (WGD), hybridization, introgression, and shifts in diversification rates. Additionally, one key morphological feature, the capitulum inflorescence, is hypothesized to have contributed to its ecological and evolutionary success. As a result, Asteraceae provides a powerful system for studying the genomic and evolutionary mechanisms driving trait development. To investigate the genomic factors underpinning Asteraceae's diversification and success, we conducted a comparative genomic study within the MGCA clade of Asterales. We generated reference-quality genomes of *Platycodon grandiflorus* (Campanulaceae), *Scaevola aemula* (Goodeniaceae), and *Acicarpha procumbens* (Calyceraceae), and then compared them to five publicly available Asterales genomes. Genome structure analyses revealed extensive variation in genome size, ploidy, repeat content, and synteny. While high repeat content has been a notable characteristic of Asteraceae species, *Acicarpha procumbens* exhibited even higher levels (~90%). Consistent with their deep evolutionary convergence, synteny analyses uncovered widespread rearrangements, including within Asteraceae, and provided evidence of ancient WGDs, which was further supported by synonymous substitution rate analyses. To infer the relative order of WGD events, sub-genomes were generated from one syntenic block from each genome. Sub-genome-aware phylogenies suggested that Asteraceae and Calyceraceae share a WGD event in their evolutionary past, followed by independent duplications in each lineage. Positive selection and gene family expansions and contractions, which may catalyze the neofunctionalization of novel traits, were assessed among the taxa. Within Asteraceae, gene families linked to secondary metabolism and pollen recognition were notably expanded, while multiple genes involved in inflorescence development showed signatures of positive selection. These findings provide critical insights into the genomic innovations that contributed to Asteraceae's ecological success and offer a foundation for future research goals and applications on trait evolution, speciation, and biodiversity.

Topic: *Development and Structure*

A-70

Duplication and subfunctionalization of AGAMOUS genes in the cypress family (Cupressaceae)

Author: Austin Nguyen, Kelly Matsunaga
Affiliation: University of Kansas

Gene duplication can be a source of evolutionary novelty by doubling genetic material on which evolution can act and has been associated with increased morphological diversity and phenotypic innovation. *AGAMOUS* (*AG*) genes are members of the MADS-box gene family that show conserved function in specifying reproductive organ identity in seed plants. While the function, expression, and evolution of these genes has been extensively studied in flowering plants, they remain understudied in conifers. Based on work in Pinaceae and Podocarpaceae, conifer *AG* genes are expressed in the ovules and associated ovule-bearing organ (termed the ovuliferous scale) of the seed cone. However, prior work in Cupressaceae suggested that *AG* expression differs from this expression pattern with little *AG* expression in the ovuliferous scale. Here, we report that Cupressaceae *AG* genes underwent two duplication events prior to the origination of the family over 182 million years ago. Further, we characterize the expression pattern for each resulting *AG* orthogroup in three species, *Metasequoia glyptostroboides*, *Taxodium distichum*, and *Juniperus virginiana* (subfamilies Sequoioideae, Taxodioideae, and Cupressoideae, respectively), using RNAscope-based *in situ* hybridization (ISH). The ISH assays reveal that subfunctionalization likely occurred after *AG* genes duplicated in Cupressaceae: two orthogroups specialized in ovule development while the other orthogroup specialized in development of the ovuliferous scale. This study uncovers convergent patterns of subfunctionalization between Cupressaceae and angiosperms and the ontogenetic underpinnings of the family's vast morphological diversity.

Topic: *Ecology*

A-71

Ectomycorrhizal communities erode as park sizes decrease and urbanization increases.

Author: Sofia Ocampo, Paul-Camilo Zalamea
Affiliation: University of South Florida

Mycorrhizal fungi are mutualistic symbionts that associate with roots of almost every plant species. These fungi provide organic forms of nitrogen and phosphorus to the plant which are otherwise unavailable for plant uptake, while protecting roots from pathogens. Previous studies show that urbanization may cause a decrease in mycorrhizal diversity or shifts in mycorrhizal communities, both of which have implications on urban green spaces. As ecosystems continue to be affected by anthropogenic activities, the need to understand how these activities modify natural patterns of biodiversity increases. Here, we asked how ectomycorrhizal fungi (ECM) vary in abundance and richness along an urbanization gradient, and how does this gradient influence the ECM community structure? We also examined how soil characteristics correlate with ectomycorrhizal diversity patterns. We used *Quercus virginiana* (live oak) as a model tree. This species is widely distributed across the south-east US and can tolerate a range of conditions such as high salinity and urban soils. Urban soil often has heavy metal pollution and unnatural nutrient inputs. We used the Human Footprint Index (Venter et al., 2016) to select the study sites (urban parks), representing all the possible urbanization categories found in the city of Tampa, Florida. The parks fall into four different size categories, and they varied in urbanization level within size category: three small parks (0.081-0.24 km^2), three medium parks (0.25-0.73 km^2), three large parks (0.74-2.59 km^2), and two extra-large parks (4+ km^2). For 99 different trees in 11 different parks, we collected root cores (7.5 cm diameter x 11 cm height; 423.3 cm^3), with soil samples to determine total phosphorus, ammonium, nitrates/nitrites, and pH collected at about half (40) of our study trees. For each root core, we counted the total number of live root tips and the total number of root tips that showed ECM. We then sorted every ECM into morphotypes, which were used for DNA extraction and Sanger sequencing. To rank the effects of park size, human influence (urbanization), and soil conditions on ECM richness, we conducted a random forest analysis. This ranking showed that park size and pH were significantly associated with ECM richness. We found that large parks hosted a higher richness of ECM than smaller parks. The soil pH has a negative relationship with both ECM richness and the total number of root tips. Using a Mantel test, we found that the correlation between ECM community dissimilarly and geographical distance was not significant at the park level (p-value: 0.254) but was significant at the tree level within the parks (p-value: 0.001). This suggests that ECM community structure is likely more influenced by processes or traits occurring at smaller scales but not on the larger scales. This may be due to the nature of urban areas being unfriendly towards fungal dispersion. Our results show that city planning, and the conservation of green spaces can strongly impact ECM communities. Given the ecological importance of ECM, this study has provided insight on community patterns that may influence healthy, self-sustaining urban parks.

Topic: *Biology of mycoheterotrophic and parasitic plants*

A-72

Horizontal gene transfer as emerging markers for host-parasite interaction

Author: Liming Cai
Affiliation: University of Florida

Reconstructing the evolutionary dynamics of biotic interaction has been challenging due to the lack of fossils and insufficient field sampling of extant interactions. This is especially the case for parasitic plants with general host preferences. Using Orobanchaceae as a model system, I show that hundreds of horizontally transferred DNAs in the mitochondrial genome can serve as reliable markers for historical and extant host-parasite interaction. This revealed a fascinating story of concerted range and host shifts in North American broomrapes as well as parallel gene transfers in distantly related, sympatric parasites from their shared hosts. Using comparative genomics and in vivo physiological analyses, I further demonstrate the molecular mechanism and functional impacts of these horizontal gene transfers.

Topic: *Defining forces in fern evolution: Celebrating the contributions of Kathleen Pryer and Michael Windham*

A-73

The globally invasive weed Salvinia molesta is not a pentaploid but a homoploid hybrid

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Few aquatic plants rival Salvinia molesta (Salviniaceae) in invasiveness and global economic impact. Its rapid proliferation forms dense free-floating mats, severely disrupting ecosystems, economies, and human health. The species' remarkable success has been attributed to its hybrid origin, obligate clonal reproduction, and a presumed pentaploid genome (2n=5x=45). However, our recent investigations have revealed an individual with 46 chromosomes, comprising two distinct subgenomes with 22 and 24 chromosomes. These findings imply that S. molesta is not a pentaploid, but rather a homoploid hybrid. Based on these results and further comparative genomic analysis across Salviniales, we propose a new model for genome evolution within the genus Salvinia and the origin of Salvinia molesta.

Topic: *Ecology*

A-75

Population responses of flowering initiation in Linum bienne (Linaceae) to elevational gradients

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Flowering phenology is an important life-history trait in plants that directly affects plant fitness. The onset of flowering is strongly influenced by environmental factors (i.e., climate, photoperiod) but regulated by genetic control. This allows plants to synchronise growth and reproduction with the optimal local growing conditions to maximize fitness. In the last three decades, scientists have observed changes in flowering onset phenology linked to climate change, but it is unclear if these shifts represent a plastic or an adaptive response to new climatic conditions. In this study, we investigate flowering onset variation in *Linum bienne*, an herb growing across Mediterranean and Atlantic regions up to 1850 m in elevation. We used provenance trials along three elevations (low elevation-80, medium elevation-662, high elevation-1885 m.a.s.l.) to measure

plant survival, plant size, flowering onset and reproductive success of 15 populations of *Linum bienne* from the SW of Spain sampled between 50 and 1200 m of elevation, using between 11 and 21 genotypes per population. Our results showed that plant survival substantially declined at the high elevation site compared to the other sites. The number of days to the onset of flowering showed a consistent pattern along the three elevations, depicting a consistent positive association between the number of days to flowering onset and the elevation at the population of origin (i.e., plants from populations at lower elevations flowered earlier than those from higher elevations). This result evidenced genetic differentiation among populations for the onset of flowering, which might reflect past selection and adaptation to local environmental conditions. Finally, we used phenotypic selection analyses on flowering onset and found negative linear selection at the low and medium elevation, indicating that early flowering plants are selected over later flowering plants. In contrast, at the high elevation, we found stabilizing selection, reflecting phenotypes that flowered at an optimal time (adaptive peak) displayed higher fitness. When exposed to contrasting environments, the sign and direction of the adaptive significance of flowering onset varies. These findings highlight the adaptive value of the flowering onset and life history traits to allow shifts in the species distribution along altitudinal gradients, and how they adapt to new environments.

Topic: *Hybrids and Hybridization*

A-76

Clonal invasion: Kalanchoe ×houghtonii, a single genotype conquers the planet

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Invasive alien plant species pose a global challenge, and their impact is amplified by globalisation and the accelerating pace of climate change. In mild-climate regions, drought-tolerant invasive plants showing broad environmental tolerance have a competitive advantage. One example is *Kalanchoe ×houghtonii* (Crassulaceae), popularly known as "mother of millions". It is a hybrid resulting from the interploid cross between *K. daigremontiana* and *K. delagoensis*, both native to Madagascar. *Kalanchoe ×houghtonii*, propagated as an ornamental plant, has emerged as a global invader in less than a century. Four morphotypes of this hybrid have been identified, with different ploidy levels and varying invasive capacities. Here we aim to investigate the genomic variability behind the invasion success of *Kalanchoe ×houghtonii*. We sampled 57 accessions of *Kalanchoe ×houghtonii*, *K. daigremontiana*, *K. delagoensis* and closely related taxa, including old herbarium materials, from all over the world. We analysed genome size, chromosome numbers, sequenced the whole genome, analysed the complete plastome sequence of each accession, and studied the diversity of the ribosomal RNA genes. We also performed a detailed phylogenomic study using nuclear BUSCO genes. Our study reveals the genetic and cytogenetic variability between morphotypes and shows that a single clonal tetraploid genotype (morphotype A) dominates all populations, emerging as the first reported clonal hybrid capable of worldwide colonisation and invasion. Morphotype A shows a striking genetic uniformity, high phenotypic plasticity, and extremely high rates of vegetative reproduction, representing an example of a "general-purpose genotype". The astonishing reproductive capacity, broad adaptability and the speed at which *K. ×houghtonii* is colonising new regions by clonal spread highlight the importance of understanding hybridisation and polyploidy in the invasion of ecosystems. Our findings call for the need for risk assessments before developing new hybrids for ornamental plant breeding that may exhibit invasive characteristics.

Topic: *Ecology*

A-77

Influence of White-tailed Deer herbivory on the Invasion of Callery Pear

Author: Haley Weber, David Gorchov
Affiliation: Miami University

White-tailed deer (*Odocoileus virginianus*) is a generalist herbivore that has become overabundant in much of the United States. Deer herbivory limits the growth of palatable plants, some of which are invasive species. Callery pear (*Pyrus calleryana*) is an ornamental tree species that is invasive in much of the eastern United States, but the effect of deer on this species has not been investigated. This study seeks to understand how deer interact with Callery pear and what influence these interactions have on the invasion of this species. We hypothesize that deer herbivory on Callery pear reduces seedling recruitment in forests.

This study is being conducted in three mature forests with adjacent fruiting Callery pear in southwest Ohio: Mount Airy Forest (MA), Winton Woods (WW), and Harris Benedict Preserve (HBP). We estimated deer density using pellet-based distance sampling. At MA and WW we tagged Callery pear seedlings 0.3-1.7m tall in June 2024; seedlings of this height were absent in HBP. Randomly half of the individuals at each site were caged to protect them from deer browse. Browse damage was tracked for unprotected seedlings. We measured height growth for all seedlings from June-Oct 2024. In summer 2025, we will continue to monitor height growth and browse damage. We will also determine survival, basal diameter growth, age, and aboveground biomass for each seedling at the end of the study in September 2025.

Estimated deer density was highest at MA (16.1 deer/km^2), then HBP (4.4 deer/km^2), and least at WW (2.6 deer/km^2). On average 31-32% of a Callery pear seedling's twigs were browsed by deer at MA and WW. We found significantly more height was lost from unprotected seedlings.

To explain the absence of Callery pear seedlings at HBP we quantified browse intensity and will quantify canopy cover at each of the three sites. Browse intensity was measured as percentage of Amur honeysuckle (*Lonicera maackii*) twigs with browse damage. We found that HBP did have a significantly higher proportion of honeysuckle twigs browsed than the other two sites. Our findings suggest that deer are limiting seedling recruitment of Callery pear. Therefore, we suggest that Callery pear are managed before deer to prevent increase of the populations of this tree in forest systems.

Topic: *Education and Outreach*

A-80

Open-source software integration: A tutorial on species distribution mapping and ecological niche modeling

Author: Zoe Ryan
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Over the last decade, access to global data has become increasingly critical for research, allowing insights into diverse biological, environmental and societal questions at a macro scale. Digitization has greatly enhanced the use of herbarium data in the analysis of species distributions and ecological niche modeling. Yet, sources on modeling and mapping methodology using open-source software is greatly lacking for beginners. We have created a replicable and thorough tutorial to visualize species occurrence data and exploratory analysis that was developed by undergraduates with broad backgrounds and levels of experience. This tutorial integrates the open-source programs QGIS, MaxEnt and R to develop distribution maps, using bryophytes as a case study, to promote the accessibility of open-source software and remote access learning. This tutorial has already set the foundation for further research into distribution modeling of rare Illinois bryophytes to better understand the potential impact of climate change.

Topic: *Development and Structure*

A-81

Stigma and style development genes controlling carpel features relevant to wind pollination

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As the sites of pollination and fertilization, the stigma and style of angiosperm pistils are critical for ensuring reproductive success. Pollination vectors exert great selective pressure on pistil morphology, giving rise to diverse stigma and style structures and functions. However, the genetic mechanisms underlying the development of these diverse reproductive structures remain incompletely understood. *Thalictrum*, a Ranunculid representative of early-diverging eudicots, has undergone multiple independent transitions from insect to wind pollination, with flowers exhibiting pistil adaptations that include long styles and linear or plumose stigmas with feathery extensions. *Thalictrum* flowers have retained ancestral floral traits, such as a spirally arranged apocarpous gynoecium with carpel closure by longitudinal slit. My goal is to provide insight into the genetic mechanisms underlying stigma and style morphology in wind-pollinated flowers, as well as more generally into ancestral eudicot pistil developmental genetic pathways. To that end, I characterized the role of two style development candidate gene families, *STYLISH* (*STY*) and *NGATHA* (*NGA*) in *Thalictrum thalictroides* pistil

development via targeted virus-mediated approaches. Our results suggest that, while the *Thalictrum STY* homologs control adaxial growth and stigmatic development, *NGA* appears to control abaxial growth and style elongation. *NGA* misexpression also results in ectopic stigma formation on anthers and mucronate anthers, another feature associated with wind pollinated species of unknown significance. Thus, we propose that *STY* and *NGA* genes differentially control spatial aspects of apical carpel development in *Thalictrum*. Ongoing *in situ* hybridization analysis will determine spatial expression patterns and provide further evidence for the role of these genes in insect- and wind-pollinated *Thalictrum*.

Topic: Development and Structure

A-82

Investigating the relationships between morphological characters of bulbous species

Author: Morgan Cribelar, Cody Coyotee Howard
Affiliation: Oklahoma State University

Geophytes, herbaceous plants with resting buds situated below the soil surface, come in a wide array of belowground morphologies that are not readily studied. Some commonly known geophytic structures are bulbs, corms, tubers, and rhizomes. These structures not only aid in belowground bud placement but are also the site of resource storage. Of the diverse morphologies found across geophytes, bulbs are unique in that the majority of resources and water are stored in leaf tissue. Bulbs are defined as storage organs with concentric layers of swollen leaf tissue that surround buds attached to a vertically compressed stem. The bulbous habit has evolved ~10 times across the monocots and has also evolved in the eudicot lineage Oxalis (Oxalidales, Oxalidaceae). The convergent evolution of the bulbous habit within the monocots can be capitalized upon to investigate and understand the intricate relationships between structure and function. For example, bulbs are generally similar in appearance from the outside, but the internal morphological components can differ across taxa. One taxon can have a bulb with a few thick scales, whereas another can have many thin scales, yet they have similar overall diameters. We do not yet have a clear understanding of how the individual components of bulbs contribute to diverse morphologies. Specifically, how do stem characteristics, such as shape and size, influence the number of scales and overall bulb size? Here, we quantify the individual components across bulbous taxa to investigate how each contributes to overall bulb morphology. We hypothesize that the shape and diameter of the stem influences overall bulb morphology. We predict that flatter, wider stems will have fewer scales, whereas more conically shaped stems can maintain a greater number of scales.

To quantify bulb morphology across species, we used X-ray micro-computed tomography (microCT). This method uses non-invasive X-ray imaging to create high resolution 2D image stacks ranging from micron to sub-micron scale that enables the construction of detailed 3D models. Plants were scanned at default parameters using a Zeiss Xradia 410 Versa. After scanning, 3D model reconstruction was performed using 3D Slicer and Dragonfly ORS. From the 3-D models, for each bulb for each taxon, we measured five components: 1) perimeter (circumference) at the widest part of the bulb (bulb size), 2) volume of the bulb, 3) perimeter of the basal plate, 4) stem shape, and 5) bulb scale number. Using the 3D Slicer modules Markups and Slicermorph, we performed a geometric morphometric analysis (GMM) on the stem of each sample to quantify stem shape. We find that bulbs with a larger basal plate perimeter have a larger perimeter at the widest point. This suggests that characteristics of the stem drive bulb morphology.

Topic: Systematics & Taxonomy

A-83

A Target-sequence Capture Phylogeny of the Diverse Western North American Genus Heterotheca (Asteraceae: Astereae)

Author: Marisa Szubryt, Abby Moore
Affiliation: University of Oklahoma

The genus *Heterotheca* comprises several dozen species of herbs and subshrubs found throughout North America, several of which are polyploid. Paralogous gene variants would be expected for at least some species of *Heterotheca* when reconstructing evolutionary relationships in the genus. Previous work on nuclear ribosomal loci and plastid genes did not detect numerous paralogs, but these genomic regions exhibit concerted evolution and uniparental inheritance which inherently lack paralogs. These data often provide limited resolution within genera, necessitating the use of high-throughput data to resolve relationships within the genus. Target-capture sequence data were produced for *Heterotheca* and seven closely related genera using the Conserved Ortholog Set for Compositae to capture approximately 1061 non-ribosomal and low-copy nuclear genes. Initial assemblies of the target loci revealed extensive paralogy throughout *Heterotheca*. Different gene copies were manually extracted during the assembly process and then served as revised target loci, successfully parsing out more paralogs. Paralogs were found among all *Heterotheca* samples, including species which are exclusively diploid.

Phylogenies derived from these revised loci indicate that *Heterotheca* comprises three clades and that recent polyploids exclusively belong to the most diverse clade. Support values were generally low throughout the clade that included recent polyploids, but several complexes were consistently recovered. These included separate clades belonging primarily to the California Floristic Province (*H. sessiliflora s.l.*), the southern Great Plains (*H. canescens* and *H. stenophylla s.l.*), and the mountains around Nuevo Leon (*H. gypsophila* and *H. mucronata s.l.*). Site concordance factor values were low to moderate for most relationships in the clade with polyploids, and gene concordance factor values were exceptionally low throughout the genus. PhyParts analyses found that discordance was high, especially for the diverse clade with recent polyploids, even for curated datasets when paralogs were manually removed. These results indicate that incomplete lineage sorting and possibly hybridization are prevalent throughout the dataset, highlighting the need to utilize many independent loci in phylogenetic reconstruction.

Topic: Conservation Biology

A-85

Monitoring California jewelflower (Caulanthus californicus) demography in the context of pollinator networks, plant communities, and a federally endangered herbivore

Author: Isabela Lima Borges, Heather Schneider, Sarah Cusser
Affiliation: Santa Barbara Botanic Garden

California jewelflower (*Caulanthus californicus*) is a federally-listed annual wildflower in the mustard family. In 2022, Santa Barbara Botanic Garden initiated a study in collaboration with the Bureau of Land Management to increase our knowledge of jewelflower demography. We are primarily interested in three remnant jewelflower populations at Carrizo Plain National Monument: whether they are stable, increasing, or decreasing, and the biotic and abiotic factors driving these dynamics. We have collected jewelflower demographic data for three consecutive years, which have spanned a wide gradient of precipitation in California, and will continue to monitor these populations for at least three more growing seasons. Here, we present preliminary results on the effects of local conditions on jewelflower survival and reproduction. We find effects of climate and local plant communities on jewelflower, and we see that herbivory on these plants is widespread, with the primary vertebrate herbivore being the federally endangered giant kangaroo rat (*Dipodomys ingens*). Once plant demographic data collection is complete, we will compile data across years to build an integral projection model to understand how biotic and abiotic factors drive jewelflower population dynamics. Those results will substantially increase our understanding of *Caulanthus californicus* at Carrizo Plain National Monument and point to potential management actions to bolster populations of this endangered plant across its range.

Topic: Ecology

A-86

What drives herbivore communities on hybrid plants?

Author: Mia Stevens, Cathy Rushworth
Affiliation: Utah State University

Hybrid plants often have different assemblages of traits than their parent species. Notably, defense traits are impacted by outcrossing and hybridization, which can influence attraction for herbivores and pollinators. Insect herbivores and pollinators are highly attuned to plant traits; thus hybridization-induced deviations in trait expression can potentially alter the insect visitor community by shifting phenotypes used for attraction, such as floral traits and defenses. Moreover, biotic selection on these hybrid traits remains largely unknown. In my dissertation I am using hybrids between Boechera stricta and B. retrofracta, two native wildflower species that frequently hybridize in the wild. Using these species and hybrids, I ask: What changes do we see in hybrid traits that are under biotic selection? Does insect visitor composition vary between hybrids and parents? How does the interaction between traits and insect communities shape

eco-evolutionary dynamics of hybridization rate in the wild? I have set up seven transects in natural populations in Salmon, ID and collected plant trait and visitation data on 1,122 plants. Here I explore this trait variation and preliminary data on insect community shifts. This research will help elucidate what is driving herbivore and pollinator visitor communities on hybrid plants, with downstream implications for agriculture and crop breeding.

Topic: *Hybrids and Hybridization*

A-87

What drives coexistence in hybrid systems?

Author: Kallol Mozumdar, Cathy Rushworth
Affiliation: Utah State University

Hybridization, the process of mating and producing viable offspring between two divergent lineages, can result in different evolutionary outcomes ranging from long-term coexistence to the extinction of one or both parental species. The genus Boechera in the mustard family (Brassicaceae) is widely distributed across diverse habitats, and exhibits rampant hybridization among the roughly 80 species found in North America. Hybridization and its correlated transition to apomixis are thought to play a crucial role in the morphological diversification of the genus Boechera, and hybrids co-occur with parental taxa in the wild. Mixed parent-hybrid populations provide an intriguing system to think about how closely related species share physical space, compete with one another for resources, and exchange genes. To gain understanding of the mechanism underlying coexistence in hybridizing species, we designed an individual-based simulation model using SLiM. The model is structured to assess how hybridization influences population dynamics, under varying environmental and evolutionary scenarios. Our model illustrates how demographic factors and interspecific interactions govern the stability or decline of hybrid populations within a structured competitive landscape. The results reveal a dynamic interplay between competition, hybrid fitness penalties, and demographic constraints in shaping population trajectories. Our study shows that taking a population-level theoretical approach to study hybridization events can provide significant information about the consequences of gene flow between species and its impacts on species and hybrid coexistence.

Topic: *Ecology*

A-88

Evolutionary diversity of vascular plants and soil-bacterial communities in a protected ecosystem in Central Chile

Author: Diego Arancibia, Rosita Scherson, Constanza Schapheer, Andrés Plaza-Aguilar, Mauricio González
Affiliation: Universidad de Chile

Understanding the relationship between plant communities and soil microorganisms is crucial for addressing conservation challenges, as many ecological processes depend on these two biotic components. The metabarcoding technique allows for the capture of micro-biodiversity in the environment, particularly in soils, and helps establish links between belowground diversity and aboveground communities. However, few studies have explored these relationships in an evolutionary context, and even fewer have focused on forest ecosystems. The divese and highly endemic sclerophyllous forest of central Chile, part of one of the world's 25 biodiversity hotspots, faces varying degrees of degradation due to climate change and human activities. The functionality of these biologically and evolutionarily valuable ecosystems is threatened mainly by biodiversity loss, the expansion of invasive alien species, and intensive livestock grazing. Applying an evolutionary perspective to conservation criteria could optimize decision-making and resource allocation in threatened ecosystems. This research was conducted in La Campana National Park, specifically in the Palmas de Ocoa area, which is located within La Campana–Peñuelas Biosphere Reserve, in the Chilean hotspot. The Ocoa palm grove is a micro-basin with a predominantly northeast-facing exposure, situated on the eastern slopes of the Coastal Mountain Range, with an average annual precipitation of approximately 300 mm and an elevation range of 400–1,400 m a.s.l. This area hosts the largest and best-preserved population of the Chilean endemic monotypic palm (*Jubaea chilensis*) within its entire geographical distribution. Sixteen plots were established across two vegetation units: (1) a xerophytic shrubland dominated by drought-adapted species, and (2) a sclerophyllous forest with greater tree cover. In each plot, we assessed vegetation composition and structure, collected soil samples for environmental variable analyses, extracted environmental DNA (eDNA), and performed metabarcoding targeting bacterial diversity using the V3-V5 domains of the 16S ribosomal RNA gene. We also collected all vascular plant species and built a species-level phylogeny using chloroplast and nuclear genes. Phylogenetic diversity and other biodiversity indices were calculated and compared between the above-and below ground components in the area. Results indicate a clear differentiation between the two vegetation types, particularly in terms of their microbiomes. The bacterial community in the sclerophyllous forest was significantly more diverse in both compositional and evolutionary terms compared to the shrubland. In contrast, vascular plant communities did not exhibit the same degree of differentiation. However, the higher presence of exotic species in the shrubland suggests structural differences and signs of degradation, which align with a lower bacterial diversity. Statistical analyses showed no significant correlation between the phylogenetic diversity (PD) of plants and bacteria. However, we identified potential predictive covariates for plants PD, such as potassium concentration in the soil and degradation level, and for bacterial PD, which appeared to be influenced by soil moisture and pH.

Topic: *Functional Genetics/Genomics*

A-90

Barriers to Hybridization and Genetic Basis of Floral Traits in Asclepias spp.

Author: Brent Lieb, Mason McNair
Affiliation: Michigan State University

Interest in native plants as ornamentals has greatly expanded in recent years. Land development and climate change driven habitat loss emphasize the need to support pollinators by cultivating native plants. *Asclepias* is a large genus of herbaceous perennials, known for their relationship with monarch butterflies (*Danaus plexippus*) and their latex filled sap, giving them the common name, milkweed. This dynamic is perhaps one of the most well characterized symbiotic plant-insect interactions worldwide. While these beloved plants have been of interest for ecology and conservation researchers, little research has been done exploring their pollination biology and interspecific hybridization, potentially limiting its establishment in the horticulture industry. There has been very little horticultural research on *Asclepias*. Several of the traits that make Asclepias a desirable study organism for ecology, botany, and conservation make it undesirable as a landscape plant in spite of the ecological benefits it provides. I will elucidate the pollination biology across multiple species native to Michigan and two model species of temperate *Asclepias* by identifying barriers to interspecific hybridization. I will also identify the genes responsible for multiple floral traits and potential symbiotic microbes which may have an important role in plant health and propagation.

Topic: *Education and Outreach*

A-91

Key Player Approach (KPA) to Teach Difficult Concepts in Plant Biology

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We propose a novel pedagogical method called the "Key Player Approach (KPA)" to enhance student engagement and comprehension of complex botanical concepts. This method addresses the challenge many students face when encountering plant biology cycles and processes, particularly those who are not pursuing biology as their major. Rather than presenting botanical concepts as abstract cycles or diagrams that students often memorize without understanding, our approach identifies a central entity—the "key player"—which serves as a connecting thread weaving through different abstract concepts and processes. Like a narrative thread in a story, the key player creates continuity and coherence across seemingly disconnected botanical phenomena.

The approach functions as an instructional strategy that targets higher-order thinking skills in Bloom's Taxonomy, particularly synthesis, as students must connect multiple concepts and processes to understand the complete journey of the key player. By structuring the learning experience around clearly defined learning objects that follow this central entity, students develop a more integrated understanding that transcends mere memorization. For example, when teaching the life cycle of Bryophytes, we follow the spore as it progresses through meiosis and alternating sporophyte and gametophyte generations, creating discrete learning objects for each stage that build upon each other while maintaining the spore as the connecting thread. This narrative-based approach transforms abstract concepts into coherent stories, making them more accessible and memorable while improving student performance on assessments requiring higher cognitive processes.

Preliminary implementation with 25 first-year community college students with pre and post tests has shown promising results, with noticeable improvements in classroom engagement, concept retention, and assessment outcomes. We are currently developing a comprehensive resource of plant biology concepts and their corresponding key players for educator use, each aligned with specific learning objectives and cognitive levels.

This presentation will demonstrate how the Key Player Approach can revolutionize botanical education by making complex concepts more relatable and understandable for diverse student populations, ultimately promoting botanical literacy within and beyond traditional academic settings.

Topic: Comparative Genomics/Transcriptomics

A-92

Serpentine-adapted populations of Mimulus guttatus reveal large variation in leaf shape, flowering time, and floral patterning

Author: Whitney Murchison-Kastner, Kathleen Ferris, Jessie Lampert
Affiliation: Tulane University

This study aims to investigate phenotypic parallel evolution between two species of Monkeyflowers (Mimulus), granite-adapted M. lacinatus and serpentine rock-adapted M. guttatus. We hypothesize that natural selection and genetic drift have led to the evolution of traits needed in a harsh rocky environment, such as early flowering time, leaf lobing, and floral spotting. Serpentine soils provide unique environmental challenges, including a low calcium-to-magnesium ratio and high levels of heavy metals, elevating potential adaptive evolution (Brady et al. 2005). By employing population genetic analyses like *Fst* estimation, population structure, and gene flow for ten serpentine populations, we aim to determine whether phenotypic traits are shared across multiple populations. Genetic analyses will help to determine whether natural selection or genetic drift has shaped these traits within serpentine populations by looking for specific loci under selection. Preliminary findings indicate significant variation in plant height, leaf lobing, and floral spotting across serpentine populations, with potential evidence of balancing selection maintaining trait diversity.

Topic: Ecology

A-94

Capturing Floral Variation across Baja California using Photogrammetry & landmark-based morphometrics

Author: Emeline Pano, Kelly Ribbey, Nicholas Allsing, Todd Michael, Nico Cellinese
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Arid landscapes are traditionally defined by low precipitation and high temperatures, yet incorporating additional environmental variables can finely distinguish desert systems and reveal the drivers of floral evolution. The Baja California Peninsula has a pronounced gradient from Mediterranean-climate in the north to hyper-arid central deserts and monsoon-influenced southern cape, providing a natural laboratory to test how ecoregional shifts may shape floral forms. Here, we present a photogrammetry study for quantitative 2D and 3D analysis of *Fouquieria splendens* and *F. diguetti* flowers sampled across two principal ecoregions (Gulf coast and Central Desert). Specimens were imaged on a motorized turntable at 8° rotational increments using a macro-equipped DSLR under uniform LED illumination, producing 180 overlapping RAW images per flower. Images were batch-converted, aligned, and modeled in RealityCapture to generate 3D models. We annotated both fixed anatomical landmarks to run a Generalize Procrustes Analysis to capture subtle shape variations. This non-destructive, high-throughput approach leverages 2D and 3D geometric morphometrics to quantify subtle floral shape variations, illuminating how environmental heterogeneity within desert ecoregions may drive evolutionary divergence in *Fouquieria*.

Topic: Comparative Genomics/Transcriptomics

A-95

Towards The Quantitative Study of Genome Architecture

Author: Michael McKibben, Michael Barker
Affiliation: University of Arizona

Genome structural changes can result in reproductive isolation and the linkage of locally adaptive alleles. These processes may drive speciation and long term evolutionary trajectories. However, studying the rate of genome structural change across taxa and through time can be challenging due to the limited availability of quantitative tools. Among current methods, the use of gene collinearity (the conserved order) and synteny (the conserved location) have become widely popular. Although powerful, these approaches require manual interpretation by practitioners, making quantitative comparisons across taxa difficult. Here we present a network theory approach to the study of genome architecture that utilizes GPU acceleration to enable phylogeny wide estimates of genome structural change. In addition, this approach allows us to rapidly identify conserved syntenic regions at different phylogenetic depths. We present this method using over 100 flowering plant references genomes alongside Solanales, Brassicales, Poales, and Fabales specific analyses. Across this work, we find that genome structural change among flowering plants is rapid relative to sequence divergence, but a minority of syntenic blocks can persist for millions of years despite being redistributed throughout the genome. The rate at which these syntenic blocks decay and the rate of overall genome structural change exhibit family specific patterns. The association between this rate heterogeneity and wider patterns of evolution remain unknown, but our work and novel method highlight a need for ongoing research into the study of genome architecture in a quantitatively comparative fashion.

Topic: Floristics

A-96

Incomplete understanding of plant distributions in a biodiversity hotspot: a case study with the vascular and non-vascular flora of the McGee Creek watershed, Mono County, California

Author: Matthew Yamamoto
Affiliation: California Botanic Garden

Conservation efforts, taxonomy, and research in biogeography rely on an accurate understanding of the distribution of plants and plant diversity, but this fundamental data is lacking even in California, a biodiversity hotspot with a rich history of botanical research. By inventorying the vascular and non-vascular plants in a watershed on the eastern slope of the Sierra Nevada over two years, I aim to improve documentation of plant diversity and distributions in this mountain range and demonstrate the degree to which plant diversity in this region of California might be underestimated by existing data. The herbarium specimens and iNaturalist observations from the McGee Creek watershed (26.28 sq. mi) available prior to this study only represented about 25% of over 750 minimum-rank plant taxa documented through voucher specimens during fieldwork in 2024. Moreover, rather than being common species previously known to grow in the general region, the taxa newly documented in the watershed include a number of species outside their known ranges, many rare taxa, and one species that is thought to be undescribed. Given the heterogeneity of the watershed with respect to elevation, climate, slope aspect, and geology, these results indicate that roadside and trailside surveys do not adequately estimate plant diversity in a watershed like this one. Floristic studies like these will continue to be important for the success of research and conservation efforts that rely on accurate data on the distribution of plant diversity.

Topic: Paleobotany

A-97

Anatomically Preserved Eocene Fruits from Vancouver Island, British Columbia

Author: Nova Hodgson, Ruth Stockey, Gar Rothwell
Affiliation: Oregon State University, Ohio University; Oregon State University

Eleven spheroidal, two-loculed dicot fruits with conspicuous idioblasts in the pericarp wall have been identified among the dispersed plant remains that occur at the Eocene (~50 Ma) Appian Way locality on Vancouver Island, British Columbia, Canada. Fruits are preserved in calcium carbonate concretions deposited in a marine environment. Specimens were prepared using the cellulose acetate peel technique. Fruits are

drupaceous, 4-10 mm in diameter, with a prominent septum or axial intrusion with an inflated central region, and were dehiscent. Most fruits are somewhat abraded, but a mesocarp of thin-walled cells, at least 10 cells thick surrounds a zone of prominent idioblasts, some reaching 0.5-1.0 mm in diameter. These cells are underlain by a thin layer of enlarged cells 20 µm in diameter. The endocarp is composed of thick zone of criss cross fibers 10 µm and a distinct locule lining. There are one to two seeds per locule. Seeds appear bitegmic and pachychalazal, with a prominent testa of slightly radially elongated rectangular cells 20 µm in diameter. Within this layer are several layers of thin-walled cells beneath which is a zone of ~10 isodiametric cells, a zone of 4-5 cells that are elongate, and a third zone 5-6 cells layers thick of isodiametric cells. These fruits are compared to several taxa of the Sapindales, Family Burseraceae including, the Canarium and Bursera Alliances, some genera of which also have two-loculed drupaceous fruits with bitegmic ovules.

Topic: *Conservation Biology*

A-98

An integrative study examining the disjunct distribution of Salvia Funerea M.E. Jones (Death Valley Sage, Lamiaceae)

Author: Mia Manfredi
Affiliation: California Botanic Garden/Claremont Graduate University

Salvia funerea M.E. Jones (Death Valley Sage, Lamiaceae) is a drought-deciduous shrub in the mint family that is considered rare in California (California Rare Plant Rank [CRPR] 4.3) and imperiled in Nevada (NatureServe Rank S1). *Salvia funerea* occurs in two disjunct areas in the Mojave Desert; the larger (ca. 16,000 km2) northern portion of its range is centered within Death Valley National Park while the much smaller (ca. 500 km2) southern portion is located in the Bristol, Ship, and Marble mountains of San Bernardino County. I aim to conduct an integrative study that includes population genomics, species distribution modeling, and comparison of morphological and anatomical traits to investigate gene flow and genetic diversity within and between populations of S. funerea and to identify any morphological and ecological differences between the disjunct areas where it occurs. This work will enhance our understanding of the general biology of this rare species and its current conservation status in light of intense climate change in the Mojave Desert. The results will be utilized to update current conservation rankings and to make recommendations for future conservation and management practices.

Topic: *Ecology*

A-99

How heat stress affects bumblebee pollination of zucchini squash (Cucirbita pepo).

Author: Blaire Kleiman
Affiliation: Florida International University

This experiment looks at how rising temperatures may impact squash plants and their bumblebee pollinators. The Southern United States will see a rise of 2°F by 2040 and by 2100 over a 6°F increase. Florida is the number 2 producer of squash in the United States, worth $34 billion dollars annually. Increasing temperatures are *already* having a negative impact on plant-pollinator mutualisms, critical for pollinator dependent squash. This experiment examined heat stress effects on squash and bumblebees warmed using growth chambers under a control, a 1.5°C rise, and 3°C rise in average squash growing season. Mesh arenas were used to see pollination activity of bees. The hottest warming treatment (3°C increase) significantly increased bee visitation to flowers, but reduced flower production compared to control. The 3°C rise treatment had significantly greater nectar volume and sugar content compared to the control. Additionally, warmed zucchini had significantly reduced yield compared to control. Warming increasing nectar sugar volume and content could be a way for plants to compensate as flower production was reduced in the hotter treatments, to ensure that the remaining flowers are still pollinated. This research helps create tools and methods which can be applied to other crops and regions and pushes for a more sustainable future for our growers. It also promotes sustainable agriculture and combats climate change, two ways to improve global food security.

Topic: *Development and Structure*

A-101

LEAFY demonstrates ancestral reproductive functions in the gametophyte and not the sporophyte of the fern Ceratopteris richardii

Author: Hannah McConnell, Jancee Lanclos, Katelynn Willis, Nicholas Gjording, Genevieve Stockman, Julin Maloof, Andrew Plackett, Veronica Di Stilio
Affiliation: University of Washington, University of California, Davis, University of Birmingham, University of Washington, Seattle (WA)

Flowers are a key reproductive innovation of the angiosperms. They evolved as a modification of the ancestral plant life cycle whereby the haploid gamete-producing generation (gametophyte) became enclosed within the diploid, spore-producing generation (sporophyte). The transcription factor *LEAFY* (*LFY*) initiates angiosperm floral development, yet its lineage predates flowers and is found across all land plants. *LFY* function outside angiosperms is known from the moss *Physcomitrium patens*, where they control the first division of the sporophyte, and from the model fern *Ceratopteris richardii*, a vascular plant without seeds or flowers, where *CrLFY1* and *CrLFY2* maintain vegetative meristem activity. However, how *LFY*'s reproductive role evolved remains unclear. Using over-expression, we uncover new roles for *CrLFY1/2* in fern gametophyte reproduction, particularly in sperm cells and in the gametophyte's multicellular notch meristem. No sporophytic reproductive function was detected, but over-expression supports a role in fern frond compounding and a conserved role in the zygote's first division. Our findings highlight an ancestral *LFY* function in fern haploid-stage reproduction, which may have been co-opted into the sporophyte during the origin of the flower.

Topic: *Macroevolution*

A-102

Rapid chromosome number reduction in annual species gives rise to low chromosome numbers in the Machaerantherinae (Asteraceae)

Author: Geoffrey Finch, Michael Barker, Cole Fields
Affiliation: University of Arizona

The chromosome numbers of angiosperm species vary dramatically, from n = 2 to n ~ 320. This variation is driven in part by the frequency of whole genome duplication, typically followed by chromosome number reduction through descending dysploidy, but the ultimate drivers of chromosome number reduction are unknown. The Asteraceae subtribe Machaerantherinae is notable for its exceptionally low chromosome numbers, including one species with only two chromosomes. This subtribe additionally contains a high proportion of annuals (~28%), which has been hypothesized to be one driver of the evolution of low chromosome numbers. However, the association between growth habit and chromosome number remains poorly tested. We explore mechanisms of chromosome number reduction in this clade and conduct a novel test for associations between annual habit and rapid descending dysploidy. We developed a time-calibrated phylogeny of the Machaerantherinae and its closest relatives and tested for shifts in rates of chromosome number evolution using the likelihood framework chromEvol. We additionally tested whether low chromosome numbers could be attributed to an increased rate of descending dysploidy in annual taxa using the model BiChroM. We identified two rate shifts within the phylogeny, one occurring at the base of the Machaerantherinae, and a second occurring within the subtribe Symphyotrichinae. Both clades exhibit elevated rates of descending dysploidy. The Machaerantherinae are distinct from the Symphyotrichinae in also exhibiting low rates of chromosome number increase. Additionally, we estimated a rate of descending dysploidy that is 11.61 times higher in annuals than perennials. The low chromosome numbers found in the Machaerantherinae are the product of rapid descending dysploidy coupled with low rates of chromosome number increase. We show that descending dysploidy is faster in annual taxa, providing additional evidence that chromosome number and life history evolution are linked in angiosperms.

Topic: Ecology

A-103

Investigating the adaptive significance of leaf shape plasticity in a California endemic monkeyflower, Mimulus laciniatus

Author: Jill Love, Kathleen Ferris
Affiliation: Tulane University

Phenotypic plasticity—the ability of a single genotype to produce different phenotypes in response to environmental variation—may play a crucial role in local adaptation, particularly in heterogeneous environments. However, direct evidence for selection on plasticity in natural populations remains limited, because plasticity must be measured across genetic replicates. This study uses recombinant inbred lines to overcome this obstacle and investigates whether phenotypic plasticity in leaf shape is adaptive across an elevational gradient in the Sierra Nevada endemic plant Mimulus laciniatus.

Leaf lobing and its plasticity vary across elevation, with high-elevation populations exhibiting both greater lobing and stronger plastic responses. To test whether these traits confer a fitness advantage in varying environments, I conducted areciprocal transplant experiment in *M. laciniatus'* native granite outcrop environment in Yosemite National Park. Using recombinant inbred lines (RILs) derived from a cross between high- and low-elevation genotypes, my field experiment assessed survival, reproductive success, and trait variation across multiple field sites. By comparing fitness outcomes between RILs with differing levels of plasticity, this study provides insight into whether plasticity enhances adaptation in high-elevation environments where environmental conditions fluctuate more dramatically.

This study leverages a powerful experimental system—inbred replicated genotypes in a natural setting—to directly test the evolutionary significance of plasticity. The results contribute to our understanding of how plasticity influences plant adaptation and persistence under environmental change, with broader implications for evolutionary biology and conservation.

Topic: Development and Structure

A-104

Candidate genes for Tropaeolum nectar spur development revealed through comparative transcriptomics

Author: Sebastian Martinez-Salazar, Yan Gong, Natalia Pabón-Mora, Elena Kramer
Affiliation: Harvard University, Harvard University/UC Berkeley, Universidad de Antioquia

Tropaeolum (nasturtiums), the single genus in the family Tropaeolaceae (Brassicales), encompasses ca. 100 species native from South and Central America. These species display a diversity of morphological traits that are lacking or rare in other families of the order, including the Brassicaceae, to which the model *Arabidopsis thaliana* belongs. In particular, we are interested in understanding the evolution and development of one of these traits: nectar spurs. Nectar spurs are narrow, hollow outgrowths of floral tissue that accumulate nectar. They have evolved multiple times independently in flowering plants, likely facilitating interactions with pollinators. *Tropaeolum* nectar spurs are unique because they represent a modification of the perianth floral tube in bilaterally symmetrical flowers. Currently, we are developing *Tropaeolum majus* as a model species to understand molecular mechanisms responsible for nectar spur development in the genus. Specifically, we aim to characterize molecular mechanisms that 1) determine the position of the flower where nectar spurs will develop; 2) initiate nectar spur outgrowth; and 3) sculpt final morphological traits of nectar spurs. To do so, we have generated a series of transcriptomic libraries to compare expression patterns between spurred and spurless tissue of the *T. majus* floral tube before and after spur initiation. Based on this data, we have identified candidate transcription factors that are consistently overexpressed in spurred tissue at all stages of development. These results, in combination with the analysis of some horticultural mutants that lack nectar spurs, allow us to propose that both floral symmetry and floral organ identity genes are necessary to determine nectar spur development in *Tropaeolum*. Additionally, we have been optimizing virus-induced gene silencing as a technique to study gene function in *T. majus*. We have performed this technique to downregulate a gene required for chlorophyll maintenance (the *PHYTOENE DESATURASE TmPDS*) as a positive control. This technique will allow us to further corroborate the function of our candidate genes for the development of nectar spurs and other morphological traits, and in the long term will allow us to have a better understanding of how these traits have evolved and diversified in the family.

Topic: Ecology

A-105

Radially Symmetric Flowers of Native Plants Drive Pollinator Visitation in Prairie Ecosystems

Author: Amadeu dos Santos Neto, Charles Fenster
Affiliation: South Dakota State University

Floral visitation is shaped by the composition and density of surrounding plant communities, with both native and exotic species influencing pollinator foraging behavior. Exotic plants can alter visitation patterns by attracting or competing for pollinators, potentially affecting native plant reproductive success. Additionally, floral symmetry plays a role in pollinator preferences, as radial (actinomorphic) and bilateral (zygomorphic) flowers often differ in accessibility and pollinator assemblages. In this context, we examined how floral density (native and exotic) affects the chance of insect visitation to native plants. Data was collected over two field seasons (2023 and 2024) across prairies in protected areas of eastern South Dakota. In each sampling event, we randomly selected a native plant as the host plant, then recorded its floral density along with that of all other flowering species within a 3-meter radius. This was followed by a 10-minute pollinator observation, documenting all visitors to the host plant. We used multiple logistic regressions across three models: (1) overall visitation and visitation by functional groups—large bees (LB), large flies (LF), small bees (SB), small flies (SF), beetles (BT), and butterflies (BF)—as responses, with exotic and native floral density as predictors; (2) visitation on radial flowers as the response, with the floral density of radial native, radial exotic, bilateral native, and bilateral exotic plants as predictors; and (3) the same as model 2 but for bilateral flowers. Overall visitation and BT visitation increased with exotic floral density, while LB visitation responded to native floral density. BF and LF were influenced by both native and exotic floral density. For radial flowers, visitation likelihood rose with native radial density, especially for LF, SF, and BT. BT visitation to focal native plants also increased with bilateral exotic density. Focal bilateral flowers and SB had higher visitation with more surrounding bilateral flowers. LF responded positively to exotic radially symmetric floral density, while BT visitation increased with the density of exotic flowers with bilateral symmetry. In summary, insect visitation to native plants increased with the density of exotic flowers, for most functional groups, independent of their symmetry. However, beetles and butterflies were more likely to visit native plants when surrounded by high exotic bilateral flower density. However, the symmetry of surrounding native flowers mattered more, with visitation increasing only in the presence of radially symmetric native flowers. From a conservation perspective, our study demonstrates that radially symmetric native plants are vital for supporting pollinators and maintaining interactions. However, the strong influence of exotic plants on pollinators also highlights the need to consider their role in shaping foraging dynamics. Large, abundant species like *Helianthus maximiliani* and *Rudbeckia hirta* may be key resources in the Northern Great Plains, enhancing visitation and benefiting co-flowering natives.

Topic: Development and Structure

A-106

Morphological Diversity Amongst the Phytoliths of the Gymnosperms—Implications for the Evolution of Phytoliths and Their Paleobotanical Applications

Author: Niall Whalen
Affiliation: Florida State University

Phytoliths are microscopic silica bodies deposited within and between plant tissues. These structures form when silicic acid concentrations reach supersaturation, spontaneously polymerizing into solid silica casts that frequently exhibit taxon-specific morphologies. Phytoliths (depending on their anatomical location, morphology, and abundance) are generally considered to hold functional significance, contributing to plant structural integrity, drought resistance, and temperature tolerance—amongst other roles. Though phytoliths occur near-ubiquitously across plant taxa, the majority of phytolith research has focused on plants that accumulate high silica abundances such as the angiosperm grasses—leaving lower abundance clades like the gymnosperms traditionally overlooked. Gymnosperms however are an incredibly ancient and ecologically diverse clade—cryptic phytolithic diversity may await beyond the relatively few gymnosperm taxa that have been sampled. Here, I analyze and describe the morphologies of gymnosperm foliar phytoliths in a phylogenetic context, systematically sampling

all extant gymnosperm families. Phytoliths were observed and analyzed using optical and scanning electron microscopy resulting in morphological characterizations of each taxon's respective phytolith spectra. These morphotypic datasets were then synthesized with the results of previous studies examining individual gymnosperm taxa to produce the most comprehensive perspective of gymnosperm phytolith production to date. Phytolith production is observed in all sampled taxa and several exhibit unexpectedly high abundances. Characteristic phytolith morphologies are identified and described, and the level of their taxonomic specificity within the greater gymnosperm phylogeny is discussed. This systematic approach generates insights into the evolutionary history of phytolith morphology within the gymnosperm lineage, revealing patterns between taxa such as a trend of increasingly complex phytolith spectra in later-diverging clades. This study's phylogenetically-informed sampling positions gymnosperms as a model group for tracing the structural evolution of phytoliths. The comprehensive morphological descriptions provide critical context for identifying detrital, sedimentary phytoliths—presenting significance for ecological, environmental, stratigraphic, and paleobotanical studies. This new reference material opens numerous avenues for future research, spurring investigations into the ecological and physiological drivers behind phytolith evolution and explorations into these structures' utility in illuminating the ancient ecological contexts that shaped today's plant lineages.

Topic: *Floristics*

A-108

A Flora of the Bighorn Mountains: Sheridan, Big Horn, Johnson, and Washakie Counties, Wyoming

Author: Dan Coles, David Tank, Ben Legler
Affiliation: University of Wyoming, Univeristy of Wyoming

Topic: *Trees, Traits, and Time*

A-109

Adaptations of tropical woody plants to fire: past, present and future perspectives

Author: Marco Chiminazzo
Affiliation: São Paulo State University

Fire is a recurrent disturbance across many tropical ecosystems, driving the diversification of fire-adapted flora and shaping different vegetation types. However, fire is a complex disturbance rather than a single, well-defined environmental factor, making its past, present, and future impacts on terrestrial ecosystems and species highly variable. For instance, the emergence of fire-adapted species in tropical ecosystems ranges from approximately 62 million years ago (Mya) in eucalypt-dominated Australian vegetation to around 8 and 4 Mya in African and Brazilian savannas, respectively. Despite these distinct evolutionary histories, the traits required to withstand fire are largely convergent across tropical ecosystems.

Traits that provide insulation for perennial structures both above and below ground, as well as those that protect meristems, are widespread and enable species to persist after fire consumes their trunks, stems, and branches. However, the relationship between these traits and the various fire regimes encountered by different tropical species varies. Fire regimes differ in frequency, intensity, severity, extent, and seasonality, creating gradients across multiple scales – from individual plants to entire vegetation structures. This suggests that shifts in fire regimes, such as those driven by climate change, may expose species and ecosystems to conditions that differ from those they evolved under or are currently adapted to.

Given the high variability of fire's impacts on different species and vegetation types, this talk will present a framework linking (i) the contexts in which fire adaptations arose across different fire-adapted floras, (ii) the fire regimes species currently experience across various vegetation types, and (iii) the diverse traits species use to cope with contrasting fire regimes. This framework aims to inform predictions about which species, traits, and vegetation types are likely to be favored under changing fire regimes driven by climate change in the tropics.

Topic: *Conservation Biology*

A-110

Grounded in the field, guided by the lab: an integrative approach to protecting Polemonium vanbruntiae

Author: Beth Joslin, Rachel Goad, Cheyenne Moore, Scott Schuette, Chris Martine, Tanisha Williams
Affiliation: University of Georgia, Pennsylvania Natural Heritage Program/Western Pennsylvania Conservancy, Pennsylvania Department of Conservation and Natural Resources, Western Pennsylvania Conservancy, Bucknell University

Maintaining or increasing genetic diversity is an important factor to consider when protecting rare plant species, as it enhances their potential to adapt to environmental shifts. When populations become isolated from their central range, they often experience reduced gene flow and increased inbreeding, leading to lower genetic diversity and reduced population health. *Polemonium vanbruntiae* (bog Jacob's ladder) is a rare wetland species with isolated populations in Pennsylvania near the edge of its southern range. While traditional field-based conservation methods are an essential part of protecting vulnerable species, they do not provide insight into the genetic health of populations or predict habitat shifts under climate change.This study integrates genotyping-by-sequencing (GBS) data and species distribution modeling (SDM) to address these challenges in *P. vanbruntiae*. GBS will be used to analyze genetic variation within and among populations, with a focus on understanding the effects of isolation on the Pennsylvania populations. To assess how habitat suitability may shift under future climate scenarios, we will use ensemble modeling, performed in R. Together, these approaches will provide a comprehensive understanding of *P. vanbruntiae's* conservation needs, including both genetic and ecological perspectives. The findings of this study will be used to update *P. vanbruntiae's* conservation status in Pennsylvania and guide targeted protection plans.

Topic: *Development and Structure*

A-112

SEM Reveals Species-Specific Epidermal Traits in the Carnivorous Genus Heliamphora

Author: Joseph Walston, Jonathan Martin, Luke Larson, Tyler Manzardo, Ken Cameron
Affiliation: University of Wisconsin-Madison

The carnivorous pitcher plant genus *Heliamphora* (Sarraceniaceae) was extensively explored using comparative scanning electron microscopy (SEM) to investigate intra- and inter-specific variation of trichomes, stomata, and extra-floral nectaries and if these characters can be used for species-level identification. Fifty-two specimens grown in cultivation representing all species were investigated, and each specimen was separated into 8 sections for imaging. As a comparison, preliminary analysis suggests that epidermal character traits from herbarium specimens of two species collected in-situ do not significantly differ from specimens grown in cultivation for decades. One species complex, *H. pulchella*, was thoroughly studied with 12 different accessions represented and showed a wide range of epidermal diversity which encourages further investigation into its taxonomy and potential different prey capture techniques. Most stomata were observed on the "outside" of the pitcher which supports the theory that, evolutionarily, the "outside" of the tubular-shaped leaf is the abaxial surface. Comparative micromorphology methodology will continue to be applied to characterize the species-specific character traits of these epidermal structures.

Topic: *Development and Structure*

A-115

Genetic and Developmental Mechanisms Underlying Nectar Spur Evolution in Aquilegia: Insights into Pollinator-Driven Floral Morphology

Author: Teo Cooper
Affiliation: Harvard

Plants represent the largest share of global biodiversity, with angiosperms (flowering plants) showcasing a remarkable diversity of floral morphologies. These morphological traits, particularly those related to floral structures, are thought to have evolved through coevolutionary interactions with pollinators. Among these traits, the structure and shape of nectar spurs have become a focal point in the study of plant-pollinator relationships. The genus Aquilegia (columbine) offers a unique system to explore the genetic

and developmental basis of floral morphology due to its evolutionary radiation and high interfertility across species. Despite its ecological significance, the mechanisms controlling nectar spur formation and evolution remain poorly understood. Specifically, the factors governing the elongation and curvature of nectar spurs, which have adapted to different pollinator groups (bees, hummingbirds, and hawkmoths), have yet to be fully explored.

In this study, we investigate the genetic basis of nectar spur elongation and curvature in Aquilegia, with a particular focus on identifying key genes involved in the development of this iconic floral feature. Using phylogenetic analysis, we identified the closest homologs of the IBH and PRE genes, which are implicated in floral organ development. Existing transcriptomic data from the model species A. coerulea 'Kirigami' allowed us to pinpoint candidate loci associated with spur elongation during Phase II of floral development. This analysis revealed AqPRE2 as a strong candidate for controlling spur elongation and two loci, AqIBL1 and AqIBH3, as candidates for regulating spur shape, particularly in relation to curvature.

To validate these candidates, we employed virus-induced gene silencing (VIGS) to knock down the expression of AqPRE2, AqIBL1, and AqIBH3 in A. coerulea 'Kirigami', a species with straight spurs. We hypothesize that AqPRE2 will promote cell elongation, and its silencing will result in shorter spurs, while silencing AqIBH3 will lead to longer spurs due to its role in inhibiting elongation. Additionally, we will conduct these experiments in A. brevistyla, a species with curved spurs, to further elucidate the role of these genes in curvature.

This study aims to uncover the molecular mechanisms driving nectar spur evolution and to establish a genetic framework for understanding floral diversity. The findings will not only expand our knowledge of plant-pollinator coevolution but also have implications for the breeding of horticultural and agricultural plants, where pollinator attraction is critical. Additionally, this research could provide valuable insights for enhancing floral traits in crops to improve pollination efficiency and ecosystem services.

Topic: *Phylogenomics*

A-116

Inferring ancient tetraploidy and hexaploidy using a machine learning approach

Author: Seongyeon Kang, Michael McKibben, Michael Barker
Affiliation: University of arizona

Inferring the ploidy level of a particular WGD is fundamental to understanding the evolutionary trajectory and the genomic features of many plant lineages. All flowering plants are descended from whole-genome duplication (WGD) events and carry the legacy of duplications from multiple rounds of polyploidy. Genes from ancient WGDs can persist and be lost over time, increasing genetic and phenotypic diversity via processes such as functionalization and reciprocal silencing between lineages. However, duplicated genes fluctuate in copy number over time, with fractionation and diploidization driving gene losses that can complicate the accurate estimation of ancient WGD ploidy levels. Syntenic depth ratio is often used to infer the ploidy level of ancient WGDs, but inferences can sometimes vary depending on the available outgroup, the presence of nested WGDs, and the degree of chromosome reshuffling. Other approaches such as inferences from Ks (synonymous site divergences) distributions are particularly fraught and difficult to interpret when nested WGDs are present. Here, we extend Frackify (Fractionation Classify), a supervised machine learning approach to classify the origins of gene duplications, to assess the ploidal level of ancient WGDs. Frackify classifies genes from a particular WGD as paleologs retained as singletons, duplicates, triplicates, or non-paleologs, successfully separating them from adjacent overlapped WGD. We explored these retention patterns to distinguish ancient tetraploids and hexaploids among 34 ancient WGD events across flowering plants. Consistent with previous inferences, we found that 26 of the WGDs were tetraploidy whereas eight WGDs were hexaploids. Ancient hexaploids had a significantly higher number of genes retained in triplicate than ancient tetraploids if the Ks value is less than 0.95, showing that a ratio of triplicates over duplicates could be an effective indicator to infer ancient ploidal level. The duplicates and triplicates from old WGDs will also help determine the ploidal level because the duplicates and triplicates decrease over time simultaneously and could be well retained for specific species. Based on this cut-off between tetraploidy and hexaploidy, we additionally inferred seven ancient tetraploidies and one ancient hexaploidy that have not been published. Most ancient hexaploids are located in Rosids and Super-Asterids, suggesting that higher ploidal levels may be linked to the high diversification rates and species richness in these clades. Most ancient tetraploids and hexaploids were well-distinguished by paleolog retention numbers inferred with Frackify. Further analyses of ancient ploidal levels across the phylogeny will provide new insight into the polyploid legacies of flowering plants and help answer questions about how different ancient ploidal levels contributed to diversification.

Topic: *Systematics & Taxonomy*

A-117

Phylogeny and taxonomy of Eriogonum subgenus Ganysma with a focus on the Eriogonum deflexum complex (Polygonaceae)

Author: Mahima Dixit, Rebecca Ryvola-Marez, Tada Ryvola-Marez, J. Travis Columbus
Affiliation: Claremont Graduate University, California Botanic Garden

Eriogonum Michx. is a large and diverse flowering-plant genus, with ca. 252 North American species. While most species are xerophytic, they vary in life history and morphology, occurring in a wide range of elevations and habitats. The understudied genus has many narrowly restricted and highly specialized taxa, including those of conservation concern. Furthermore, knowledge of evolutionary relationships within *Eriogonum* is largely incomplete.

We are studying subgenus *Ganysma*, one of eight currently recognized subgenera and comprising 62 mostly annual species. In particular, we are focusing on a subgroup of species known as the *E. deflexum* complex, whose involucres and flowers are oriented upside-down (deflexed). Even within this subgroup, there is great diversity, from floral morphology to habitat type. The overall goal of this study is to utilize phylogenetics, morphology, ecology, ethnobotany, and phytochemistry to uncover the units (species) of diversity, improve the classification, identify any rare taxa, and inform conservation.

Thus far, we have conducted two seasons of fieldwork in the western USA to sample populations of the *E. deflexum* complex and other *Ganysma* species. From these samples, we extracted DNA and prepared and sequenced two ddRADseq libraries. A preliminary phylogenetic tree based on 121 samples representing 27 taxa was estimated under the maximum likelihood criterion. Subgenus *Ganysma* does not resolve as monophyletic because it is nested within perennial species of the large subgenus *Eucycla*. Similarly, the *E. deflexum* complex is not a single lineage as taxa with deflexed flowers resolve in multiple clades separated by taxa without deflexed flowers. The species *E. deflexum* itself is not monophyletic, comprising at least three separate lineages.

Topic: *Floristics*

A-118

A comprehensive, community-powered vascular floristic inventory of the Kootenai National Forest, Northwest Montana

Author: Marguerite Trost, Ben Legler, David Tank
Affiliation: University of Wyoming, Univeristy of Wyoming

Topic: *Development and Structure*

A-119

Capitulum in the making; developmental basis of inflorescence architecture in the Asteraceae

Author: Vandana Gurung, Reid Selby, Sakiyah Jenkins, Jakub Baczyński, Emily Yaklich, John Burke, Daniel Jones
Affiliation: Auburn University, University of Georgia

Transition to reproductive growth in plants is associated with developmental changes in the identity and morphology of the meristem. Variation in the developmental timing, shape, and size of the growing meristem drives architectural diversity among angiosperms. One such unique inflorescence type among angiosperms is a capitulum, a hallmark of Asteraceae, that is comprised of numerous florets arranged on a flat inflorescence receptacle. Despite being considered a key morphological innovation that resulted in the success of Asteraceae, the genetics underlying the evolution and development of a capitulum is largely unknown. A dramatic period of inflorescence meristem expansion prior to floral primordia establishment sets a capitulum apart from most other inflorescence types (for instance, a raceme). Through comparative developmental and genomic analyses of the members of the Asterales clade, our team is building resources to identify suites of genes responsible for the evolution and development of capitula.

In the model system *Lactuca sativa* (lettuce; Asteraceae), we have built reporter lines from orthologs of major shoot meristem maintenance (*SHOOTMERISTEMLESS*) and floral regulatory genes (*APETALA2, UNUSUAL FLORAL ORGANS, LEAFY*) to visualize their expression pattern in time and space in a developing capitulum. We have identified genes such as *ATC* (*ARABIDOPSIS THALIANA CENTRORADIALIS HOMOLOGUE*) and *APETALA2* as promising candidates for altered meristem regulation among Asteraceae. *ATC* has been shown to control inflorescence meristem identity in *Antirrhinum majus.* In *Arabidopsis thaliana,* the closest homologue to *ATC*, *TERMINAL INFLORESCENCE 1* (*TFL1*) represses flower development and maintains indeterminate growth in the inflorescence meristem. We have found that Asteraceae lack *TFL1* orthologs but retain orthologs of *ATC*, indicating that Asteraceae *ATC*/*CEN* orthologs may regulate meristem indeterminacy in place of *TFL1*. This begs the question of *ATC* function during capitulum development in Asteraceae. Additionally, *APETALA2* (*AP2*) regulates reproductive meristem size in Arabidopsis and *ap2* mutants form smaller meristems. Through functional genetics study in lettuce, we aim to discern whether these genes are co-opted into unique regulatory roles during capitulum development. The findings of this study will provide insight on the molecular and developmental underpinnings of capitulum formation.

Topic: *Systematics & Taxonomy*

A-120

Systematics of the Latifolia Clade in Eriogonum, Focusing on Eriogonum nudum

Author: Charles Boissavy, J. Travis Columbus
Affiliation: Claremont Graduate University (California Botanic Garden), California Botanic Garden

Eriogonum (Polygonaceae), or wild buckwheats, constitutes the fourth-largest North American flowering plant genus north of Mexico and second-largest in the floristic hotspot of California. Within *Eriogonum*, an understudied but widespread lineage is the Latifolia clade. Previous phylogenetic study revealed this lineage to comprise five species, but six morphologically similar species were not sampled. By expanding sampling to include these additional species and using a much larger DNA sequence data set, a goal of my project is to elucidate membership and relationships within the Latifolia clade. Within the clade is one species of particular interest, *E. nudum*. *Eriogonum nudum* comprises 15 varieties distributed from Washington through California into Baja California; the species varies appreciably in flower color and occupies a wide range of habitats and substrates throughout its range. I sampled individuals from multiple populations at the species and varietal levels. For each sampled individual, I gathered molecular data using the ddRADseq method. I used IQ-TREE to estimate a phylogeny of the Latifolia clade under the maximum likelihood criterion. Samples from six species and 13 varieties, from throughout California and Oregon, were included. These preliminary results indicate that (1) all of the six species sampled are members of the Latifolia clade, (2) *E. apricum* resolves within *E. nudum*, and (3) *E. latifolium* and *E. nudum* are each non-monophyletic. The unsampled species and varieties are targeted for fieldwork this field season.

Topic: *Paleobotany*

A-121

New Record of Fossil Wood of Goupia from La Venta, Huila: Evolutionary and Paleoecological Implications

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The fossil fauna of La Venta is among the most taxonomically and ecologically diverse. In contrast, the plant fossil record remains largely unexplored, despite the abundance of fossil woods. One of the few reports on the paleoflora of La Venta pertains to Goupiaceae, a small family of flowering plants consisting of a single genus, Goupia, with only two recognized species. Goupiaceae is an understudied family, and its phylogenetic placement remained debated until recently. It is now classified within Clade 1 of the order Malpighiales. Today, this group comprises tree species that grow in lowland forests and can reach heights of 30 to 40 meters. The highest abundance of Goupia is found in the Amazon rainforest, though it also grows along the Magdalena River in riparian environments.

So far, three field expeditions have led to the discovery of ten fossil wood specimens exhibiting anatomical features characteristic of Goupia, such as diffuse porosity, exclusively solitary vessels, scalariform perforation plates, diffuse apotracheal parenchyma, and scanty paratracheal parenchyma. These specimens were collected from the Cerbatana beds (Villavieja Formation), where they had been previously reported, and from San Alfonso (La Victoria Formation).

This study aimed to conduct a phylogenetic analysis focused on Clade 1 of the order Malpighiales to determine the precise phylogenetic placement of Goupiaceae. This, in turn, would allow the integration of fossil specimens into the phylogeny through a combined analysis of molecular and morphological data. Additionally, it is possible that in the past, the center of Goupia's diversity was in the Neotropics, with a broader distribution always associated with the presence of nearby water bodies. Therefore, analyzing the anatomical characteristics of the fossil wood will provide valuable insights into the evolution and ecology of this little-studied family of angiosperms.

One of the key aspects of this discovery is the strong anatomical correspondence between the fossil wood and the extant genus Goupia. This clear relationship allows for a precise identification of the fossil material, providing valuable insights into the Miocene environment of La Venta. By linking a well-defined fossil species with its modern counterpart, we gain a better understanding of past ecosystems.

Topic: *Systematics & Taxonomy*

A-123

Population Genomic Data Refute an Eastern North American Origin for Disjunct Western Cordilleran Populations of Physocarpus opulifolius s.l. (Rosaceae)

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The flora of the Western Cordillera of North America includes numerous examples of Eastern North American (ENA) plant species existing as disjunct western populations. These western populations have been described as "relicts" of an ancestral eastern temperate forest, suggesting that western populations are derived from ENA origins. However, this hypothesis has never been assessed in a systematics framework, and the ENA-Western Cordilleran disjunction remains poorly understood. To evaluate the hypothesis of an ENA origin for the western populations, I sampled populations of Physocarpus opulifolius s.l. (Rosaceae) from across the natural range. I used SNP data generated from ddRAD sequencing to infer maximum likelihood phylogenies and population trees under the multispecies coalescent. geographic structure analyses. Collectively, the evidence does not support an ENA origin for the western populations. Instead, I suggest a more complex biogeographic origin for disjunct populations of "eastern" plants in the Western Cordillera.

Topic: *Systematics & Taxonomy*

A-124

Floristic Survey of Carnivorous Plants in New Jersey (USA)

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This study explores the taxonomic diversity of species in the genus *Utricularia* in New Jersey, based on new field collections and herbarium specimens. Despite over a dozen species of the genus *Utricularia* (bladderworts, Lentibulariaceae) being found in the state, they are understudied and underrepresented in herbaria compared to other genera. To get an updated view of carnivorous plant biodiversity, we conducted field surveys with new collections being made during summer of 2024 at multiple state parks, preserves, and wildlife management areas. Pressed herbarium and liquid-preserved specimens were made; 23 *Utricularia* plant specimens were collected, with identifications comprising 7 out of the 15 species known from New Jersey. Collected specimens were identified to species in the field using local floristic keys, and confirmed in the lab through dissection and compound scopes as needed. For the more difficult to identify *Utricularia sp.*, pictures were taken of their traps, glands, leaf structure, and other morphological features (some using TBO to stain the liquid specimens) studied. The specimens we have not been able to identify to species yet will be used for future projects studying *Utricularia* in New Jersey.

Topic: Ecology

A-125

Revealing and characterizing prokaryotic communities in vitro of Musa spp. through 16S rDNA metabarcoding and culture-dependent approaches

Author: Christopher A. Sambolín-Pérez
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Bananas and plantains belong to the *Musa* genus, recognized as significant food crops globally and often threatened by abiotic (Hurricanes) and biotic (*Fusarium*) factors. Therefore, microbes such as Plant Growth Promoting Bacteria (PGPB) are vital for protecting and enhancing plant growth. However, the effect of Temporary Immersion Bioreactors (TIB) on shaping the microbiomes of *Musa* spp. remains poorly understood. Thus, comprehending the role of TIB in vitro *Musa* spp. microbiome is essential for producing healthier plantlets. We hypothesize that in vitro conditions using TIB for plantain production can shape the microbiome, thereby selecting beneficial bacteria that enhance plant adaptation during ex vitro conditions. To test our hypothesis, we aimed to identify and characterize the overall prokaryotic communities from in vitro *Musa* spp. (Maiden, Dwarf, and Maricongo) pseudostem using culture-independent (16S rDNA-Seq) and culture-dependent approaches to elucidate their diversity and potential functional roles. The results showed the identification of four prokaryotic phyla, primarily dominated by Firmicutes, followed by Proteobacteria, Actinobacteria, and Bacteroides, whereas *Brevibacillus* sp. and *Xylella* sp. were the most dominant bacteria at the genus level. The isolates identified were *Pseudomonas* sp., and *Terribacillus* spp. Consequently, the microbiomes general metabolic pathway included co-factors and amino acid biosynthesis. Together, our findings provided insight into the prokaryotic communities that dominate *Musa* spp. under in vitro conditions, highlighting the ability of artificial conditions to shape the host microbiome. This may help identify specific prokaryotes with potential PGPB characteristics within *Musa* spp., offering an alternative means to protect and enhance *Musa* spp. production.

Topic: Floristics

A-126

Vascular Flora of the Boulder Creek Watershed, Jennie Lakes Wilderness, and Evans Grove Complex, Fresno and Tulare Counties, CA

Author: Garrett Goodrich
Affiliation: California Botanic Garden

The Sierra Nevada in California features globally significant levels of plant diversity; however, floristic sampling within the mountain range has been extremely uneven, and under-sampled areas remain. Floristic inventories in these sampling gaps frequently reveal new rare taxa and range extensions of known taxa. During the 2024 and 2025 field seasons, a floristic inventory of one understudied portion of the range in the vicinity of Big Meadows, Boulder Creek, and the Jennie Lakes Wilderness (Fresno and Tulare counties) is being conducted to search for novel taxa, document range extensions, and provide a comprehensive understanding of the local plant communities. Sampling for this research covers more than 200 km^2 of land and focuses especially on areas with known occurrences of rare species, no historical collections, and unique features associated with endemism. Approximately 1,400 specimens will be collected, identified, and deposited in herbaria to support the resulting voucher-based annotated species checklist and inventory. To date, over 720 specimens have been collected, including at least ten minimum-rank taxa with California rare plant ranks. High-intensity fire, invasive species, recreation, logging, grazing, and climate change all represent significant threats to the plants of this study area; thus, conducting a thorough botanical inventory is essential to conserving plant biodiversity in this understudied portion of California.

Topic: Hybrids and Hybridization

A-127

Hybridization triggered total genome replacement in a Tasmanian endemic eucalypt

Author: Kasey Pham, Rebecca Jones, Arianne Gélinas-Marion, Douglas Soltis, Pamela Soltis, René Vaillancourt, Brad Potts
Affiliation: Case Western Reserve University, University of Tasmania, University of Florida

Hybridization has been proposed as a mechanism for transferring adaptive alleles from one species to another (adaptive introgression), but through the disruption of adaptive allele combinations and genetic incompatibilities, it can also be a huge detriment to fitness. Different genes and regions of the genome are affected heterogeneously by these opposing selective regimes, making it difficult to predict when and where in the genome introgression will be retained. This is especially relevant in taxa with a reputation for hybridization, such as *Eucalyptus*. When hybridization occurs regularly, does it do so as a mechanism for quick adaptation to changing environments, or in spite of negative consequences, leaving few long-term impacts on the genome? With these questions in mind, we used whole genome resequencing and several hybridization analysis approaches to characterize the introgression landscape of two Tasmanian tree species, *Eucalyptus globulus* and *Eucalyptus cordata*. We studied a site where these two species and their hybrids co-occur, with hybrids confirmed by previous work to carry chloroplast and nuclear genomic introgression from *E. cordata*. While we identified a number of small regions thought to be introgressed, the genomes of hybrids were overall indistinguishable from pure *E. globulus*. Thus, in the tens of thousands of years since hybridization occurred at this site, the hybrid lineages underwent a total genome replacement from *E. cordata* to *E. globulus*, possibly because of selection against *E. cordata* alleles. This system serves as a demonstration that even observed hybridization may be of fleeting impact to the genome.

Topic: Ecology

A-128

Negative density dependance and the soil seed bank buffers an endemic plant from a population crash caused by drought

Author: Riley Thoen, Megan DeMarche
Affiliation: University of Georgia

Abiotic and biotic factors drive plant population dynamics, yet their potential interactions are rarely quantified. For example, changing climate conditions can reduce population growth rates of native species, but this effect can be weakened by negative density dependence and/or seed banks. Here, we ask whether population density influences the relationship between precipitation and population growth in an annual granite outcrop endemic plant, *Helianthus porteri*. We measured survival, reproduction, and seed bank dynamics of *H. porteri* at three sites over three transitions. Using demographic models, we assess how population growth is influenced by precipitation and plant density, and we decomposed the effects of precipitation and density on individual vital rates. Population growth was strongly influenced by precipitation. At one site, three consecutive drought years caused a population crash. Yet, the seed bank sustained the population even when vegetative plants experienced widespread mortality. Additionally, population growth was negative density dependent, with low-density patches experiencing booms in favorable precipitation. Our research shows that changing climate can cause population crashes of a short-lived endemic species. However, intrinsic biotic properties of a population may slow that decline. Accounting for intrinsic biotic factors of a population is critical to accurately assess the effects of extrinsic abiotic factors on persistence.

Topic: Population Genetics/Genomics

A-129

Role of suppressed recombination in the adaptive radiation of the Hawaiian Metrosideros

Author: Askhan Shametov, Jae Choi
Affiliation: University of Kansas, The University of Kansas

I will present how variation in recombination rate and inversion affects the genomic architecture of the Hawaiian *Metrosideros* adaptive radiation. Recombination is essential for adaptation and speciation. It provides genetic diversity for populations

and facilitates adaptation by bringing alleles into new combinations. However, breaking down co-adapted alleles associated with local adaptation would hinder adaptation and speciation when diverged populations connected via gen flow. Therefore, recombination suppression mechanisms would be favored to maintain linkage disequilibrium among co-adapted loci and act against homogenizing effects of gene flow. Inversions are well-studied mechanisms that suppress recombination leading to speciation. We thus predicted low recombining regions of the genome are enriched for inversions. The Hawaiian *Metrosideros* (Myrtaceae) is an example adaptive radiation of woody plant species. There are 25 taxa that are found non-randomly across the famously heterogeneous Hawaiian environment. The taxa have distinguishable morphological characteristics (leaf size and shape, pubescence) and reciprocal transplant experiments have shown each taxon are locally adapted to its endogenous environment. Population genomic studies have discovered genomic regions with elevated differentiation and interpret them as candidate regions for the adaptive radiation. We hypothesized genomic regions of elevated differentiation will have low recombination rate compared to background genome and they will be enriched for inversions. To test these two hypotheses, we constructed a genome-wide genetic crossover map for a F2 recombinant population generated from an outbred crossing scheme of two divergent *Metrosideros* taxa (glaberrima × incana) test and establish that suppressed recombination underlies the genomic basis of adaptive radiation in island organisms. We sequenced individuals using PacBio Hi-Fi reads representing the varieties included in the recombination map study, which was used to identify candidate inversions through comparative genomic analysis. Results evaluated the evolutionary role of recombination rate variation and inversions on the maintenance and selection of genetic variants during adaptive radiation.

Topic: Annals of Botany Special Lecture

A-130

The connection between crop pollinator dependence and long-term yield decline: An evidence-based evaluation

Author: Marcelo Aizen
Affiliation: Universidad Nacional del Comahue-CONICET

Pollination deficits often limit fruit and seed production in both wild plants and crops. In recent decades, pollinator diversity has declined due to human-driven factors such as agricultural expansion, land-use change, pesticide use, species invasion, urbanization, and climate change. This decline raises concerns about its impact on plant reproduction and crop yields. Here, I assess whether increasing pollination limitation has led to declines in pollinator-dependent crop yields. While local and regional studies suggest that reduced pollinator abundance and diversity can affect crop yield, a long-term analysis of Food and Agriculture Organization (FAO) data indicates that declines in highly pollinator-dependent crops are primarily due to their being predominantly trees rather than their reliance on pollinators. Further FAO analyses show no evidence of greater yield stagnation or increasing variability linked to pollinator dependence. Surprisingly, a new meta-analysis suggests that pollen limitation in pollinator-dependent crops has decreased over time, likely due to improved pollination management. While humanity has so far mitigated the effects of pollinator decline on crop yields globally, the rapid expansion of pollinator-dependent agriculture and the widespread use of managed pollinators may have contributed to significant habitat destruction and pollinator diversity loss, ultimately threatening wild plant reproduction and biodiversity maintenance.

Topic: Reproductive ecology and evolution of plants in stress-prone environments

A-131

Widespread pollinator-mediated facilitation in the Patagonian Andes

Author: Marcelo Aizen, Sabrina Gavini
Affiliation: Universidad Nacional del Comahue-CONICET

Plant interactions strongly influence species richness across spatial scales. In high-Andean environments, cushion plants act as ecosystem engineers, creating microhabitats that buffer extreme abiotic conditions. We found that their facilitative effects increase with altitude, providing refuge for less stress-tolerant species and significantly enhancing local diversity, which scales up to the regional level. In the Patagonian Andes, such plant-plant facilitation may explain up to 40% of regional species richness. Globally, we also found that plant interactions play a key role in promoting evolutionary diversification in alpine environments. Facilitation can occur through direct mechanisms, such as microclimate amelioration and soil nutrient enrichment, or through biotically mediated processes. We found that flowering plants growing within cushions receive more pollinator visits, experience lower pollen limitation, and achieve greater reproductive success than those outside cushions. At the community level, higher flowering plant diversity enhances conspecific pollen receipt, an effect that strengthens with altitude. Contrary to the prevailing view that plant species compete for pollinators, our findings suggest that pollinator-mediated facilitation is widespread in the Patagonian Andes. This form of indirect biotic facilitation may be a key mechanism for species persistence and biodiversity maintenance in stressful environments.

Topic: Paleobotany

A-132

Paleodendrological analysis of the Jurassic Morrison Formation and Implications for Coniferous Coastal Environments

Author: Clara Abplanalp
Affiliation: University of Idaho

Paleodendrology provides estimations of spatial and temporal climatic parameters as well as indications of water availability in an environment (Gulbranson et al., 2022). This study investigates tree rings from Jurassic Morrison Formation fossil logs to determine the ancient climate in Utah. The manual and digital measurements of tree rings determine parameters such as mean annual precipitation, temperature, and growing season length. Earlywood boundaries can also potentially be indicative of groundwater water sources, as opposed to meteoric water. The validity of using modern dendrochronology programs on ancient fossil wood remains in question, and this study aims to test the use of modern-calibrated programs to ecosystems of the geologic past.

These paleo-estimates can be compared to modern day analogs to better inform our understanding of how plants react to climate change; the climate in the Jurassic Period was, on average, about 2° C (3.6° F) warmer in northeastern Utah than estimates today (Valdes, 1993). With a rapidly warming climate today, a 2-degree change has been determined as the limiting factor for warming before climate change becomes irreversible in terms of CO_2 emissions, natural disasters, and runaway temperatures (IPCC, 2018). By determining the environment in the Jurassic Period, we can understand how our environment will respond if climate warms beyond our projected limit. Preliminary results of this study show tree rings with indistinct boundaries. These boundaries are associated with growth indicative of possible continuous connection to groundwater or riparian zones. Some trees exhibit potential seasonality, which may be indicative of monsoonal climate. This study aims to settle the scientific disagreement (Gee et al., 2019, Parrish et al., 2004) of whether the environment of the Morrison Formation was arid, and the plants had strong ties to groundwater resources, or if the trees lived in a humid, potentially subtropical environment.

Topic: Ecology

A-135

Identifying current and future distributions of the relict fern Christensenia aesculifolia (Marattiaceae) in the Philippines

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Christensenia aesculifolia (Blume) Maxon, a rare fern with limited populations in the Philippines, faces endangerment as a result of ongoing human activities coupled with climate change. This assessed the projected impacts of climate change on the distribution of C. aesculifolia under current and future climate using the maximum entropy modelling approach (MaxEnt). We utilized two Shared Socio-economic Pathways (SSP245 and SSP585) for the future climate periods for 2041–2060 (2050s) and 2061–2080 (2070s). The MaxEnt models demonstrated a high predictive power and accuracy with AUC and TSS, with both values exceeding 0.8. Christensenia aesculifolia distribution was mainly limited by mean temperature of wettest quarter (% contribution and importance = 44.6 and 25.1) and precipitation of the coldest quarter (% contribution and importance = 36.0 and 14.3), and temperature seasonality (% contribution and importance = 7.7 and 38.3). High climatic suitability was observed in Samar, Benguet, Mindoro, Sorsogon, and Agusan del norte, accounting for approximately 39,648 km2 of total Philippines land area. Depending on the climate scenario, future projections of climatically stable areas varied from 53.11% to 70.55%. Range losses for C. aesculifolia were projected to be the highest (46.88%) under the SSP585 scenario for the 2070s,

and lowest (29.45%) under the SSP585 scenario for the 2050s. On the other hand, range gains were observed to be highest (87.06%) and lowest (40.34%) under SSP585 scenario for 2050 and SSP245 scenario for 2050s, respectively. Overall, our results show that the species range will significantly be altered by climate change. However, there is the potential of the current protected areas (PAs) to offer potential sites for conservation in the future. This study marks the first critical evaluation of a threatened fern species across the Philippine archipelago, delivering crucial information for the establishment of targeted conservation management plans as well as strategic identification of potential protected areas suitable for future species reintroduction initiatives.

Topic: Systematics & Taxonomy

A-136

Investigating species delimitation across the Sarracenia rubra species complex to inform future ex situ conservation and reintroductions

Author: Nicholas Chang, Amanda Carmichael, Ethan Baldwin, James Leebens-Mack, Emily Coffey, Lauren Eserman-Campbell
Affiliation: Atlanta Botanical Garden, University of Georgia

Understanding plant species boundaries is critical to informing population size, range extent, and vulnerability to climate and land use change. Despite the ecological importance and conservation status of the Sarracenia rubra species complex, there is no in-depth assessment of species boundaries in this group. The taxonomy of these plants has been contentious (Case and Case, 1976, Rice 2018), and prior work has indicated the presence of cryptic species in this clade (Carstens and Satler, 2013). Furthermore, a phylogenomic study of the genus Sarracenia where multiple individuals were sampled from each species revealed little genetic differentiation among members of the Sarracenia rubra complex from a sample of 199 genetic loci and a portion of the chloroplast genome (Stephens et al., 2015). The Atlanta Botanical Garden is pairing a phylogenomic study using whole-genome sequencing with tests of bioclimatic niche differentiation to test whether named species and subspecies in the Sarracenia rubra species complex correspond to uniquely evolving lineages.

Topic: Floristics

A-137

Revisiting the Flora of Red Rock Canyon State Park, Kern County, California

Author: Mare Nazaire
Affiliation: California Botanic Garden

Floristic studies based on the collection of voucher specimens serve to establish baseline data critical for understanding biodiversity and implementing conservation strategies. As floristic studies represent a snapshot of the plant diversity at a given moment, revisiting historic floras can be valuable in elucidating changes over time, such as community composition, diversity, distribution, and phenological shifts. Red Rock Canyon State Park in Kern County, California, occupies a unique transition zone where the Mojave Desert, Sierra Nevada, and Basin and Range geomorphic provinces meet. Two floristic provinces also intersect here: the California Floristic Province and the Desert Floristic Province. The uniqueness of this area has long been recognized by botanists, and notably, by Ernest C. Twisselmann, who produced a preliminary checklist in 1970 during the time when Red Rock Canyon was being established as a California state park. Yet, there has never been a published flora for the park. This study aims to update the floristic knowledge of the park based on the collection of voucher specimens and to assess floristic change through comparisons with previously unpublished checklists. Red Rock Canyon State Park hosts several rare and endemic plants, including the Red Rock monkey flower (*Erythranthe rhodopetra*) and the Red Rock tarweed (*Deinandra arida*). This study also aims to provide updated information on special status species within the park. As climate change, increased drought, and other impacts pose major threats to California's biodiversity, an updated floristic inventory for Red Rock Canyon State Park will be critical to assess changes in diversity over time and to inform conservation management decisions for this dynamic and significant flora.

Topic: Ecology

A-138

Floristic Diversity of the St. Lawrence River Freshwater Estuary

Author: Simon Pesant, Maurane Bourgouin, Thomas Villeneuve, Olivier Girouard, Étienne Léveillé-Bourret
Affiliation: Institut de recherche en biologie végétale, Université de Montréal, Université de Montréal, Institut de recherche en biologie végétale

The freshwater estuary of the Saint-Lawrence River is the biggest ecosystem of its kind in Eastern North America. The high amplitude of tides, high water turbidity and low salinity make this habitat unique. It houses multiple endemic and endangered taxa like Victorin's water-hemlock (*Cicuta maculata* var. *victorinii*) and Victorin's gentian (*Gentianopsis virgata* subsp. *victorinii*). The estuary of the Saint-Lawrence River, like many others, suffers from anthropogenic perturbations. These include the building of road infrastructure, industrial and residential development, rock walls on the water's edge and marinas. This in turn destroys the habitat of endangered or vulnerable taxa. The expected effects of climate change will also most likely heavily affect habitats of these taxa, especially through erosion of the riverbank due to the rise in water level and increase in extreme hydrological events. It is therefore probable that the health of populations of vulnerable species and species composition have changed since the last large-scale floristic inventory of this estuary done 30 years ago. By replication the transects done in the inventory from decades ago, we will be able to see if any change is visible in plant communities and in the abundance of rare native, endemic and invasive species in the freshwater estuary. We will also be able to see what biotic or abiotic factors influence plant communities and biodiversity in this unique habitat.

Topic: Systematics & Taxonomy

A-140

Taxonomy and evolution of Victorin's water hemlock (Cicuta maculata var. victorinii)

Author: Thomas Villeneuve, Étienne Léveillé-Bourret, Simon Pesant
Affiliation: Institut de recherche en biologie végétale, Institut de Recherche en Biologie Végétale, Université de Montréal

Victorin's water hemlock (Cicuta maculata var. victorinii) is an endemic species of Quebec, considered threatened due to its restricted geographic distribution and the anthropogenic pressures on its small, fragmented populations. The morphological differences between this variety and the nominal variety (Cicuta maculata var. maculata), which is common and abundant in North America, are subtle and difficult to observe in the field. In addition to the weak morphological differentiation between the two varieties, there are presumably morphological intermediates, making it difficult to monitor and assess the decline in Victorin's water hemlock populations. It is therefore essential to clarify the taxonomic status of Victorin's hemlock and to test whether morphological differences are hereditary or due to the environment. The aim of the project is, through morphometric and phylogenetic analyses, to test the hypothesis that Victorin's hemlock does indeed represent one of the four genetically distinct varieties making up the species Cicuta maculata. We also want to revisit the whole genus phylogeny, by sampling herbarium vouchers from all taxa in the *Cicuta* genus.

For the morphometry aspect of the project, we opted for a geometric morphometry approach with the placement of landmarks that enabled us to measure morphological traits of fruit anatomy and compare the shape and size of fruits from the different taxa of the *Cicuta* genus. For the phylogenetic analysis section, we used a RADseq approach for library preparation, with illumina sequencing. For the bio-informatic analysis, we generated trees using the maximum likelihood (IQ-Tree) and parsimony (PAUP) methods.

All *Cicuta* species produce a potent toxin that is present in all organs of the plant. We believe that this chemical compound, called cicutoxin, serves as a defense against herbivores. In a subsequent phase of the project, we will study the chemical defenses of *Cicuta maculata* var. *victorini* by comparing the concentration of cicutoxin with that of *Cicuta maculata* var. *maculata*. The aim will be to determine whether, following its isolation in the estuarine environment, which is subject to very different herbivory pressures, Victorin's water hemlock has modified its investment in chemical defense. Since isolating this type of compound in the laboratory is a major challenge, this part of the project will be carried out in collaboration with Dr. Cory Harris, associate professor at the University of Ottawa and a specialist in plant biochemistry. This will enable us to test the hypothesis that Victorin's water hemlock is in an early phase of ecological speciation and thus displays morphological and ecological differentiation.

Topic: Bryology and Lichenology

A-141

Karinomyces (Pilocarpaceae), a new genus for the Appalachian endemic Schadonia saulskelleyana supported by molecular and phenotypic data

Author: Jeremy Howland
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Recently, a long-recognized, enigmatic crustose lichen from Southern Appalachian conifer forests was formally described as *Schadonia saulskellyana*. It was considered primarily restricted to red spruce-Fraser fir forests and found to be locally abundant in these ecosystems, often dominating bark substrates in humid, low-light forest stands. Phenotypic characters suggested that the species belonged to the arctic-alpine genus *Schadonia*, which occurs in regions far north of the Southern Appalachians. Given the richness of the Pilocarpaceae, relatively few studies have incorporated molecular data to delimit taxa, especially at the ranks commonly used in conservation and biogeography. Moreover, when North American samples have been sequenced, they frequently have been found to represent rare or previously unreported taxa. For this study, we generated multiple sequences from freshly collected specimens to examine its generic placement with respect to other genera of the Pilocarpaceae using phylogenetics. Future projections of the species suitability in the region was also investigated through ecological niche modeling. A new genus is proposed *Karinomyces*to accommodate this unusual and apparently narrowly endemic species.

Topic: Biogeography

A-142

Revisiting Cedrela Biogeography: New Insights into the Southward Dispersal and Diversification Scenario

Author: Viacheslav Shalisko, J. Antonio Vazquez Garcia, Gerardo Hernandez Vera, Alma Rosa Villalobos Arambula, Sergio Gallardo Yobal
Affiliation: University of Guadalajara, Tecnologico Nacional de Mexico

The historical biogeography of *Cedrela* (Meliaceae), a Neotropical tree genus of economic importance, still has aspects to be discovered, as the understanding of its phylogeny has changed over the last two decades. The extant *Cedrela* includes at least 21 species grouped into two well-supported clades: one clade restricted to Central America and Mexico, and another distributed across the Caribbean, Mexico, Central America, and South America.

As evidenced by its fossil record, the modern distribution of *Cedrela* is the result of a complex Cenozoic biogeographic history. This includes a wide-ranging distribution of the genus in North America and Europe from the Eocene to the Late Miocene, southward dispersal in the Americas since the Early Miocene, and local extinctions in Eurasia and northern North America after the Miocene. The dispersal to South America is also suggested to have occurred during the Miocene.

We conducted a phylogenetic analysis using Bayesian inference and maximum likelihood analyses based on nuclear (ITS) and chloroplast (accD, matK, rbcL, trnH-psbA, psbB-T-N, rpl16, rpoB, rpoC1, trnS-G) data, with improved sampling of *Cedrela* from Mexico. To estimate divergence times of evolutionary lineages, we performed a Bayesian analysis using an optimized relaxed molecular clock. The reconstruction of ancestral ranges was conducted using two event-based biogeographical models (S-DIVA and S-DEC) combined with a detailed paleogeographical analysis of area connectivity.

The estimated age for the most recent common ancestor (MRCA) of *Cedrela* is 46.3 million years (Myr), suggesting that the divergence of *Cedrela* into two modern evolutionary lineages may have occurred during the Eocene. Since then, the genus experienced two parallel southward dispersal processes in the Americas. One process involved a Mesoamerican clade (Mexico and Central America) that began diversifying in this region around the Oligocene–Miocene boundary (MRCA estimated at 24.1 Myr).

The other *Cedrela* clade dispersed further south, reaching South America and diversifying there. An early-diverging lineage within the clade is from Central America and Antilles, whereas species with a South American distribution are grouped together in a more derived position. The most probable ancestral distribution of the Oligocene MRCA for this clade was inferred to be Mesoamerica or, alternatively, a broader region including also South America. The estimated mean age for the Miocene MRCA of the South American portion of this clade was 21.5 Myr. Our reconstruction supports a single southward migration scenario at the Oligocene–Miocene boundary from Mesoamerica to South America via the Isthmus of Panama before the complete closure of the Central American Seaway.

The Central American distribution of *C. odorata* s. str. in our results does not require a recent northward dispersal or species re-entry from South America, as the MRCA of this clade was located in Mesoamerica since the Oligocene.

Our results enhance the understanding of *Cedrela* biogeography, supporting a scenario that explains the biogeography of *Cedrela* in a more parsimonious manner than previous studies, without requiring a hypothesis of backward dispersal from South America.

Topic: Systematics & Taxonomy

A-143

Towards a comprehensive phylogeny of North American Delphinium (Ranunculaceae)

Author: Jared Meek, Deren Eaton, Daniel Cook
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Delphinium sect. *Diedropetala* (North American *Delphinium*) comprises 60 described species in the Flora of North America. We present an updated phylogenomic species tree for the western taxa of sect. *Diedropetala*, along with a geographic informed analysis of hybridization, which highlights the need for substantial taxonomic revision in this clade. We generated RAD-seq data for more than 700 samples across 174 populations, and inferred phylogenetic trees using both maximum-likelihood and coalescent-based methods. To investigate putative hybridization within this group, we calculated D-statistics using ABBA-BABA tests, and examined principle component analyses of subclades involving species and populations within three intractable species complexes. While a full sampling of the remaining North American *Delphinium* species is a vital next step for a comprehensive understanding of their evolutionary history, our results offer a significant improvement on the phylogenetic inference of this rapidly radiated clade.

Topic: Population Genetics/Genomics

A-144

Fitness Effect of Adaptive SNPs in a Recently Formed Ranunculus Hybrid Zone

Author: Ziqi Xie, Mitch Cruzan
Affiliation: Portland State University

Hybridization has long been postulated to be an evolutionary stimulus for species to obtain adaptive genetic elements, but the lack of studies in a hybrid zone with ongoing adaptive introgression limits our understanding of this process. This study focuses on assessing the fitness effects of putatively adaptive SNPs (single-nucleotide polymorphisms) in a recently-formed Ranunculus hybrid zone in Southern Oregon, between a wider-range species, Ranunculus Occidentalis, and a range-limited species, Ranunculus austro-oreganus. This hybrid zone is the first one recorded to be demonstrating active adaptive introgression in progress. Preliminary results have revealed geographic clines in the pattern of adaptive introgression from both species into the range of the other for 50 outlier SNPs. Ranunculus seeds were collected from 17 populations and grown in a common garden setting. I measured vegetative and reproductive fitness traits (number of leaves, size of largest leaf, length of longest stem, number of flowers, number of seed produced) of each individual and mapped them onto the presence of outlier SNPs in the individual's mock genome acquire through GBS (genotyping-by-sequencing). To better understand how these putatively adaptive SNPs affect the biogeographical structure of the hybrid zone, the result of this mapping will later be compared to previous estimates based on the speed of adaptive cline movements. This project contributes not only to our current understanding of exchange of adaptive genetic material during hybridization and its evolutionary consequences, but also to conservation ecology, since R. austro-oreganus has been listed as a candidate threatened species, and unique peripheral species are important conservation targets.

Topic: Pteridology

A-146

Phylogeny and Character Evolution in the Fern Clade Elaphoglossum sect. Lepidoglossa (Dryopteridaceae).

Author: Lucia Vargas, Robbin Moran, Alejandra Vasco
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Phylogenetic and taxonomic studies of megadiverse groups are crucial for understanding species distribution, evolutionary history and for supporting conservation efforts, especially as habitat loss and species extinction accelerate. *Elaphoglossum* is one of the world's most diverse fern genera, containing more than 600 species, nearly all of which occur in the tropics, mostly in the Andes. Historically, the genus has represented a taxonomic challenge due to the large number of species and their morphological similarity. Six well-supported and species-rich clades have previously been identified by molecular phylogenetic studies. The most diverse of these clades is *Elaphoglossum* section *Lepidoglossa,* which harbors over 200 species worldwide. This section is characterized by scaly laminae, rhizome and lamina scales typically flat (not subulate), and scale margins with unicellular, acicular, non-glandular cells. Here we present the most comprehensive phylogenetic reconstruction to date for the section. We use the reconstruction to examine distribution patterns and study character evolution within the section. Our phylogenetic hypothesis is based on three chloroplast intergenic spacers: *atpB-rbcL, rps4-trnS,* and *trnL-trnF*. The sampling consisted of 525 accessions representing 144 species, about 70% of the section, capturing the morphological variation across species from both Tropical America and the Paleotropics. We recovered 13 major clades, all of which can be defined morphologically by a suite of characters but not by a single morphological synapomorphy. The best characters to define clades within the section include rhizome architecture, rhizome, petiole and laminae scale morphology, presence of resinous dots or glandular trichomes, lamina apex shape, and habitat. We found much convergent evolution for key characters such as habit, resinous dots, and spore perine micromorphology. We identified several independent long-distance dispersal events from Tropical America to the Paleotropics, as well as species radiations within the Mascarene Islands, Madagascar, and the Andes, contributing to high endemism in these areas. Our study provides new insights into the systematics, distribution, and character evolution of section *Lepidoglossa*. It also delimits several morphologically well-defined subclades suitable for future monographic and detailed evolutionary studies.

Topic: Systematics & Taxonomy

A-147

Phylogenomics and Evolution of Polyploidy in Zanthoxylum (Rutaceae)

Author: Marc Appelhans, Lee Ping Ang, Jun Wen
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Zanthoxylum is a species-rich and economically important genus in Rutaceae and is the only genus of the family with a pantropical distribution. We present a detailed phylogenetic study for the genus with more than 400 accessions representing about 60% of the species and all major areas of the genus' distribution. We employed a hybrid capture approach based on a custom-made bait set for the genus. Ploidy estimations were based on the Illumina sequence data using nQuire, and were complemented with flow cytometry measurements and published chromosome numbers whenever possible. *Zanthoxylum* consists of four major clades and has an Old-World origin that likely dated back to the Paleocene or Eocene. The genus colonized the Americas once, likely via the North Atlantic Land Bridge, and migrated back to eastern Asia likely across the Bering Strait. *Zanthoxylum* also colonized many archipelagos in the Indian and Pacific Oceans. The Hawaiian colonization occurred

independently from the South Pacific colonization(s), in which New Caledonia played a crucial role. Another colonization to the Pacific occurred from South or Central America to the Juan Fernandez Islands. nQuire detected several polyploidization events scattered throughout the genus, and most of them occurred within populations at the species level. For several species, e.g. the economically important Sichuan Pepper species *Z. armatum* and *Z. bungeanum*, nQuire identified diploid and tetraploid individuals, which could be confirmed using Flow Cytometry. Two out of three sampled Hawaiian species were identified as tetraploids, while the third species showed a diploid pattern. This suggests, that the ancestor of the Hawaiian species was a diploid, and that polyploidization occurred on the archipelago. The ploidy screening with nQuire proved to be congruent with our Flow Cytometry measurements and serves as a reliable indicator of polyploidy in taxa for which chromosome counts and / or Flow Cytometric data are lacking or fragmentary.

Topic: Biogeography

A-148

Colonization of Caribbean Gymnosperms

Author: Natalia Ruiz-Vargas, Victor Pérez-Calle, Julissa Roncal
Affiliation: Memorial University of Newfoundland

The assembly of island floras is a complex and dynamic process that results from the interaction of migration, speciation, and extinction. The islands' geomorphological features and geology, as well as natural history components of possible colonizing taxa play a role in migration and successful establishment of island biotas. The Caribbean islands are home to ~ 11,000 indigenous plant taxa of which over 70% are endemic to the region. There are 19 recognized taxa of Gymnosperms on the islands in the genera *Juniperus*, *Microcycas*, *Pinus*, *Podocarpus*, and *Zamia*. In this project we use the R program DAISIE to study the factors that led to the colonization and establishment of Gymnosperms in the Caribbean islands.

Topic: Ecology

A-149

Plant traits explaining aboveground carbon and its proxies in Cerrado tree species

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Understanding plant traits that influence aboveground carbon and biomass (AGC/B) is crucial for managing the Cerrado. This region is impacted by agricultural expansion, leading to CO_2 emissions as land is converted from natural to agricultural use. This study investigates the relationship between functional plant traits and AGC/B in Cerrado tree species. We hypothesized that: (i) conservative traits are positively related to AGC/B and its proxies, plant height and circumference; (ii) AGC/B and proxies vary among dispersal types; and (iii) trait-AGC/B-proxies relationships in the Cerrado align with tropical forests. Using a comprehensive sample from the Cerrado, we analyzed traits such as plant height, leaf and petiole width, seed volume, and wood density. Our findings revealed that plant height negatively correlates with leaf width but positively with petiole width, suggesting adaptations for light and water transport as well as against disturbances. Seed volume and thickness were significant predictors of stem circumference, while fruit dimensions influenced wood density. Anemochorous species exhibited higher wood density than zoochorous species, yet both dispersal types showed similar AGC/B levels. Notably, larger seeds were associated with increased AGC/B, supporting the hypothesis of positive relationships between conservative traits and carbon stocks. This confirms that the relationship is consistent with tropical forests as well as with other terrestrial ecosystems. However, some other relationships are nor consistent with those found in tropical forests. The partial alignment with tropical forest patterns suggests that seeds primarily influence carbon stocks consistently across both the Cerrado and tropical forests.

Topic: Reproductive Processes

A-150

A lover or a fighter? A study on the impacts of climate change on the reproductive biology of Rosa setigera.

Author: Mara Dearth, Kyra Krakos
Affiliation: Maryville University

This study investigates how *Rosa setigera*, Missouri's native climbing rose, responds to climate change through shifts in reproductive and defensive traits—critical for understanding long-term pollination network stability. By comparing historical herbarium samples from 1836 to the present with field data collected during the 2024 growing season at Shaw Nature Reserve in Gray Summit, MO, we assess changes in bloom timing, plant morphology, and pollinator interactions. This research tests the trade-off hypothesis, which suggests that plants must allocate limited resources between reproduction and defense when faced with environmental stress. Morphological traits

such as thorn ratio, flower ratio, and fruit ratio are measured, and pollinator identity is determined through field observations and pollen load analysis. Hand pollination and fluorescent microscopy are used to assess pollen limitation through pollen tube counts. Results show an earlier bloom season in recent decades, likely due to warming trends, and indicate that *R. setigera* continues to prioritize reproductive traits over defensive investment. While *Bombus spp.* remain the dominant pollinators. These findings provide insight into how native species adapt to environmental stress, informing conservation and ecosystem management.

Topic: Systematics & Taxonomy

A-151

Integrative taxonomy informs new boundaries in a clade of Caribbean Pitcairnia (Bromeliaceae)

Author: Natalia Ruiz-Vargas, Robie Mason-Gamer
Affiliation: Memorial University of Newfoundland, University of Illinois at Chicago

Species delimitation seeks to assign boundaries between diverging lineages; a task with important implications for disciplines such as ecology, evolution, and conservation. Although traditionally based on morphology, the incorporation of DNA (especially genomics) has revolutionized the discipline introducing rigor and decreasing the level of arbitrariness often associated with the placement of species boundaries. Recently, there has been a push to incorporate multiple lines of evidence. Here we explore the Caribbean clade of *Pitcairnia*, a terrestrial genus of the family Bromeliaceae, where fifteen taxa are currently recognized based on morphological differences. We used Target Sequence Capture with the Bromaliad1776 Baits kit to produce a phylogeny and perform species delimitation analysis as well as other population genomics tools. We incorporated morphological and environmental data to interpret our results. We present a revised classification for the Caribbean Clade of *Pitcairnia* with a reduced number of species.

Topic: Development and Structure

A-152

"Alles ist Blatt" — The Role of Auxin in Gynoecium Development: Insights from Leaf Patterning Genes

Author: Jaxon Reiter, Elizabeth Schultz
Affiliation: University of California Riverside, University of Lethbridge

As Goethe famously mused, "*Alles ist Blatt* (*All is leaf*)", proposing that unique plant structures arise through gradual transformation from a single, elemental form—the leaf. This concept of transformation and unity in plant structure provides a useful and intriguing framework for understanding plant development, particularly in the context of reproductive organs like the gynoecium. Cellular auxin gradients, crucial for tissue patterning, are established by PIN-FORMED (PIN) proteins, whose plasma-membrane localization is regulated by various genes through complex vesicle transport pathways. Among these genes are members of the *FORKED-LIKE* (*FL*) gene family that are present in multiple copies in vascular plant genomes and are expanded in the angiosperms. The *FL* gene family has previously been implicated in the development of a closed leaf venation pattern typical of most dicot leaves. Like leaf development, the formation of the gynoecium, including the stigma, style, transmitting tract, ovary, ovules, also requires proper auxin gradient establishment. During characterization of leaf development defects in PIN1 localization genes, including members of the *FL* gene family, we also observed severe reductions in seed set in several mutants. Manual pollination, ovule morphology analysis, and *pPIN1:PIN1-GFP* expression revealed that seed set reduction results from gynoecium defects, specifically altered outer integument and nucellus development. These morphological defects are consistent with changes in PIN1 localization during early ovule development. This study suggests that several genes involved in auxin gradient establishment during leaf development, including *FL* gene family members, are similarly crucial for ovule formation. These findings reinforce Goethe's notion that plant structures, from leaf to ovule, may indeed represent some variation on a unifying, fundamental form. This talk will begin with these specific findings and also explore broader insights into the relationships between leaf development and ovule formation, highlighting key similarities and differences, while incorporating recent research on this topic to provide a more comprehensive understanding of how these processes are interconnected through auxin-mediated patterning mechanisms.

Topic: Ethnobotany

A-153

Leafy Companions: Understanding College Students' Love for Houseplants

Author: Keri Maricle
Affiliation: Saginaw Valley State University

Although it is often thought humans seek out solitude, some studies suggest people pursue seemingly nonsocial activities to fulfill a social connection (Gabriel et al., 2016). In recent years (especially during the pandemic), there has been a growing fascination with purchasing houseplants, especially among college students (Behe et al., 2022). However, not much research has focused on the reasons why college students choose to invest time in plant ownership. Therefore, the purpose of this study was to assess whether college students invest resources into taking care of houseplants to satisfy the need for social connections as well as explore other reasons houseplant ownership is popular among college students. College students (N = 82) from three universities who owned one or more houseplants (M = 4) completed a questionnaire regarding their experiences of plant ownership (i.e., relative feelings/behaviors regarding their houseplants, notable events that might have happened in their lives when they first obtained a houseplant, why they named their houseplants). Most participants reportedly spent less than one hour per week interacting with their plants (77%) and spent up to $100 on plant maintenance (86.5%). There was a significant association between the room participants reported spending the most time in and the room with the most plants, $\chi^2(20, N = 82) = 83.36$, $p < .001$. Most students reported learning about houseplants through online resources (82.9%), family and friends (72%), and social media (54.7%). Additionally, various succulents (including cacti and aloe) were among the most common types of houseplants owned by participants. Given the popularity of owning plants among college students, results from this study can be used to better understand why students may invest time and resources into houseplant ownership. Results indicate most college students tie their emotional well-being to their houseplants and may use them as a method of social connection without a large investment of time or money. Specifically, the responses of college students in this study regarding the reasons they invest in houseplants suggest that indoor plants are often actively pursued for their aesthetic qualities but are also obtained during emotionally heightened periods in their life (e.g., moving to college, passing of a loved one). Many participants also personified their houseplants by naming them according to their perceived personality and spent more time in rooms where their plants were located, which further supports the idea that houseplants can be used as a tool for social connection. Overall, this exploratory survey study can provide direction for future experimental studies on how college students may interact with houseplants as well as how houseplants may impact their overall mental well-being.

Topic: Functional Genetics/Genomics

A-154

Ovule Defects in Arabidopsis thaliana PIN Localization Pathway Mutants Lead to Reduced Seed Set

Author: Jaxon Reiter, Elizabeth Schultz
Affiliation: University of California Riverside, University of Lethbridge

The formation of the gynoecium, including the stigma, style, transmitting tract, ovary, ovules, and female gametophytes requires the correct establishment of auxin gradients across a tissue directed by polar transport. PIN-FORMED (PIN) proteins are crucial for establishing local cellular auxin gradients that establish spatially organized auxin maxima and minima. PIN1 vesicle transport is tightly regulated by various genes that play a role in vesicle formation, transport, uncoating, and membrane localization. *SCARFACE/VASCULAR NETWORK DEFECTIVE 3* (*SFC/VAN3*), *FORKED1* (*FKD1*) & *FORKED-LIKE* (*FL*) Group 1 genes, *COTYLEDON VASCULAR PATTERN 2* (*CVP2*) and *CVP2-LIKE 1* (*CVL1*), *PINOID* (*PID*), and *ROTUNDA3* (*RON3*) have all been proposed to be key players in the regulation of PIN1 vesicle trafficking. Mutations to these genes have been shown to disrupt PIN1 localization and lead to developmental defects such as impaired root development and vein formation. However, the role of these genes has not previously characterized in gynoecium development, despite mutants showing severe reductions to seed set. This study examines the underlying causes of the seed set reductions present in *fkd1/fl1-2/fl2/fl3*, *sfc-40*, and *cvp2/cvl1* mutants by analyzing reproductive development. Through manual pollination experiments, observation of pollen tube growth, and the analysis of ovule defects and *pPIN1:PIN1-GFP* expression during ovule development, we identified that reduced seed set in these mutants results from a gynoecium defect. Specifically, reduced seed set involves altered ovule

development, and we suggest that the observed morphological defects are consistent with alterations to PIN1 localization during early ovule development stages (2 *ii-iii*) in these mutants. This study suggests, for the first time, that *SFC*, *FKD1*, *FL1*, *FL2*, *FL3*, *CVP2*, and *CVL1* play an important role in reproduction during ovule development.

Topic: Floristics

A-155

An updated census of the native and non-native plants in Bates County: An under-surveyed region in western Missouri.

Author: Rylan Mason, Neil Snow
Affiliation: Pittsburg State University

Recent studies across much of the USA indicate that many counties are incompletely surveyed for their vascular plant diversity. Data from SEINet and BONAP in 2023 suggested that Bates County, located in western Missouri, was less surveyed than many other counties in the state, and that up to 300 additional taxa might be found with additional fieldwork. Prior to our work, Bates County had 1486 digitally documented collections, including many from prominent early collectors such as E. J. Palmer (1920s-50s) and Julian Steyermark (1930s-50s). That total represents a low collection density compared to many other counties. Moreover, only 369 collections were made for the fifty-year period covering 1970-2019. Our null hypothesis, that Bates County was incompletely known, was corroborated after the first field season (2024), wherein 35 of the first 379 collections (9.2%) represented county records. Among the county novelties were non-native woody species such as Amur honeysuckle (Lonicera maackii) and Autumn olive (Elaeagnus umbellata), whereas herbaceous non-natives included Musk thistle (Carduus nutans) and the Common dandelion (Taraxacum officinale). Many native taxa were among the first occurrences, including Mayapple (Podophyllum peltatum), Buffalograss (Bouteloua dactyloides), Common arrowhead (Sagittaria latifolia) and Missouri ironweed (Vernonia missurica). Our annual collecting involves seven or more day-long collecting trips, which include (with permission) areas managed by the Missouri Department of Conservation. Ongoing floristic surveying is important because the geographical range and local abundance of plant species frequently change. Shifting averages in annual temperatures and precipitation are likely contributing to some changes. The project will continue through the autumn of 2026. An updated tally of vascular plants for Bates County at that time will provide baseline data for future ecological comparisons of flowering times, the presence of invasive species, and monitoring species of conservation concern.

Topic: Bryology and Lichenology

A-156

Beneath the surface: metabolomic profiling and chemical characterization of the yellow basal parts of lichen Flavocetraria nivalis

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Lichens are holobiont-like, self-sustaining entities formed by a dominant fungus in symbiotic association with one or more extracellular photosynthetic partners and an indeterminate assemblage of additional microscopic organisms. They produce a remarkable array of unique compounds, largely absent in higher plants and animals, which can account for up to 10–30% of their dry weight and are believed to confer protection against biotic and abiotic stresses such as herbivory, pathogens, UV irradiation, and desiccation. Lichen metabolites have been historically utilized in traditional medicine, dyes, and perfumes, and continue to attract interest for their potential pharmaceutical applications. Despite over 1,000 substances having been reported in the literature and recent advances in analytical methods nearly doubling this number over the past 15 years, comprehensive chemical profiles of many lichen species remain scarce.

Flavocetraria nivalis (L.) Kärnefelt & Thell, an arctic-alpine species in the *Parmeliaceae* family, is distributed across the Northern Hemisphere. A notable feature of this species is the characteristic yellow to orange coloration of the basal part of its thallus, the biological function and chemical structure of which have remained unclear. To address this gap, we employed advanced analytical techniques by combining high-performance liquid chromatography with diode-array detection and electrospray ionization tandem mass spectrometric (HPLC-DAD-ESI-MS/MS) detection in both low- and high-resolution modes. Specimens were collected from diverse geographic regions, including the Hohe Tauern (Alps), the Scandinavian Mountains and Tarfala (Low Arctic), and the Svalbard Archipelago (High Arctic).

The acetone extracts of the colored basal thallus parts were subjected to heat reflux extraction followed by qualitative analysis using a high-resolution mass spectrometric analyzer (HPLC-Q-Orbitrap-ESI-MS/MS). Selected negative precursor ions were fragmented in a high-energy collision dissociation (HCD) cell, and the resulting MS/MS high-resolution mass spectra were collected.

Our analysis led to the identification of ten metabolites: usnic acid, pinastric acid, pulvinic acid, rugulosin, hypoconstictic acid, cryptostictic acid, hydroxybenzoic acid, strepsilin, lecanoric acid, and atranol. Notably, eight of these compounds were reported for the first time in *F. nivalis*, with four of them being pigments likely contributing to the yellow coloration of the thallus. Additionally, eighteen other metabolites were detected that have not been identified or reported previously and may represent novel compounds.

These findings not only advance current knowledge on the chemical composition of *F. nivalis* but also underscore the utility of HPLC-Q-Orbitrap-ESI-MS/MS as a rapid, effective, and accurate technique for the structural characterization of lichen secondary metabolites. The comprehensive metabolomic fingerprint generated in this study provides a valuable framework for future chemotaxonomic investigations and highlights the potential of lichen-derived compounds for biotechnological and pharmacological applications.

To our knowledge, this study represents not only the first metabolomic profiling of the colored parts of *F. nivalis* thalli using liquid chromatography hyphenated with tandem mass spectrometry but also the first attempt to elucidate the chemical basis underlying the yellow coloration of the basal parts, thereby offering new insights into the species' chemical diversity and paving the way for further research into the biological functions and applications of its secondary metabolites.

Topic: Disabled in Botany: Breaking Barriers in Plant Science Research

A-157

Disabled in the field: navigating nature as a disabled botanist and why orchids are amazing

Author: Kelsey Byers
Affiliation: John Innes Centre

People with disabilities (or disabled people depending on language preference) make up 26% of the population of the US (19% of working age adults in the UK) but only 10.8% of evolutionary biologists (Rushworth et al. 2020 Evolution) and 4.8% of higher education staff in the UK (HESA). This gap is particularly evident in the field-based life sciences, where openly disabled role models for students and early career researchers are in short supply and externally-imposed barriers to full participation are rampant for both students and staff. In this symposium talk, I will discuss my own lived experiences as a multiply-disabled and neurodivergent botanist and provide some suggestions on how to improve inclusion of disabled scientists in academic settings and fieldwork. I'll also discuss some of my group's recent research on orchids and how their amazing diversity is mirrored by the diverse contributions of disabled scientists to STEM fields. By celebrating both the research contributions of disabled scientists as well as equity, diversity, and inclusion efforts made by both disabled scientists and allies, we can increase the visibility of disabled scientists, paving the way for future improved inclusion of the next generation of researchers as well as those already in the field.

Topic: Reproductive ecology and evolution of plants in stress-prone environments

A-158

Linking community structure and function in stress-prone but species-rich plant-pollinator communities

Author: Gerardo Arceo Gomez
Affiliation: East Tennessee State University

Understanding the mechanisms that mediate the assembly of flowering plant communities, particularly of those that exist in stressful but species-rich environments, is central for biodiversity conservation. Pollinators are central in mediating plant-plant interactions that are key for community assembly, but the full complexity of the patterns, underlying drivers and outcomes of these interactions is not fully known. We collected data on pollinator visitation, pollen transport, floral rewards and pollen receipt for over

40 plant species growing in nutrient-poor serpentine plant communities. We then used network tools to uncover patterns and drivers of plant-pollinator interactions at different biological scales and to assess the role of network properties in mediating plant reproductive success. Specifically, we characterized and compared the structure of plant–pollinator interactions at the species and the individual level in order to elucidate how population-level process (niche redundancy and differentiation) help generate the structure of community-wide species interactions. We further evaluated the role that floral reward investment (pollen protein), which is predicted to be limiting in nutrient-poor environments, plays in mediating plant-pollinator interactions and plant reproductive success. We show that investment in pollen protein content significantly affects components of pollen dispersal (male fitness), but not ovule fertilization (female fitness) suggesting the potential for sexual conflicts driven by differential investment in reward quality. Finally, we directly evaluate the link between network structural properties and plant reproductive success in order to advance our understanding of the relationship between network structure and function. Network structural properties differentially affected male and female reproductive functions. Specifically, an increase in specialization increased conspecific pollen dispersal and reduced pollen loss to heterospecific flowers (male reproductive function) but had no effect on fertilization success (female function). This result emphasizes the need to incorporate empirical knowledge on interaction outcomes when making inferences on the importance of interaction network structure. Incorporating fitness components into our understanding of interaction networks has the potential to fundamentally advance our understanding of the role of species interactions for community resilience and stability, particularly in stress-prone environments.

Topic: *Bryology and Lichenology*

A-159

Unveiling sex specific thermal differences in the vegetative thallus of Marchantia inflexa

Author: Hansika Herath, David Nicholas McLetchie
Affiliation: University of Kentucky

Temperature regulation in plants is a key physiological trait influencing ecological adaptability, stress tolerance and survival. In unisexual species, sex specific differences in thermoregulation can impact ecological fitness, however, this aspect remains largely unexplored. This study investigated vegetative thallus temperature in *Marchantia inflexa* to determine whether plants from different sites with differing environments, and sexes exhibits distinct thermal properties. *M. inflexa* is a thalloid liverwort, predominantly found in tropical regions, where it experiences increased heat and water stress during the dry season. Field and controlled environment experiments were conducted to compare the thermal properties. In the field, male and female pairs growing in the shaded conditions on the on the island of Trinidad, Republic of Trinidad & Tobago, were identified. Thallus temperatures were recorded for 20 minutes using thermocouples, alongside measurements of air temperature and relative humidity. The same pairs were then transported to the University of Kentucky (3 days), acclimated in a growth chamber for two nights to reset field conditions (24 to 32 ^{0}C), and monitored for 15 minutes under room temperature (~22 ^{0}C), with air temperature and relative humidity recorded throughout. Our results show that the sexes differed in temperatures in both field and room temperature. In field conditions no one sex was consistently higher in temperature but at room temperature, male plants maintained significantly higher thallus temperatures than female plants. This difference could be attributed to sex specific variations in transpiration rates or metabolic activity. These findings suggest that the sexes are maintaining different thallus temperatures. Understanding the sex specific thermoregulatory mechanisms can provide insights about sex function and the impact of these mechanisms on stress resilience, with implications for species distribution and conservations.

Topic: *Hybrids and Hybridization*

A-160

Evaluating the role progenitor homeolog bias plays in differences in pigment composition in Nicotiana quadrivalvis and N. clevelandii allopolyploids.

Author: Brooke Tillotson, Alyssa Perrino, Elizabeth McCarthy
Affiliation: SUNY Cortland

Polyploids are organisms that receive one or more sets of chromosomes from each of their progenitors. When the sets of chromosomes from each progenitor come together and hybridize, they make new organisms known as allopolyploids. Homeolog bias occurs when expression of one progenitor's gene copies is favored over the other in the hybridized offspring. Hybridization of the progenitor genomes can lead to the development of novel or different flower colors in the offspring. Flower color is important because it attracts a variety of pollinators who all see color differently. A pollinator's perception of color depends on the number of photoreceptors and the spectral range each receptor covers. Most insect pollinators have trichromatic color vision with blue, green and ultraviolet photoreceptors. Ultraviolet light cannot be seen to the human eye, but UV signals can be important for attracting pollinators with UV photoreceptors. Pollinators play a vital role in plant reproduction, making their attraction to different flower colors important for the development and evolution of new species. The flower color of the species used in this study are developed through the Flavonoid Biosynthetic Pathway where numerous enzymes work in a stepwise manner to develop flavonol and anthocyanin pigments. Flavonols such as kaempferol, quercetin, and myricetin are colorless pigments that absorb ultraviolet light, whereas anthocyanins are colorful with pelargonidin, cyanidin, and delphinidin being red, pink, and purple pigments, respectively. Our study focuses on *Nicotiana* section *Polydicliae* which is approximately one million years old and consists of allopolyploids *N. clevelandii* and *N. quadrivalvis* which arose through the hybridization of diploid progenitors *N. attenuata* and *N. obtusifolia*. During our preliminary work, we developed PCR protocols that are effective in differentiating between the progenitor gene copies responsible for creating floral anthocyanins and flavanols in the allopolyploids. In this study, we will use our tested PCR protocols to run droplet digital PCR to quantify the expression of progenitor homeologs of anthocyanin and flavonol genes in *Nicotiana* section *Polydicliae* and their diploid progenitors to investigate if differences in homeolog bias correlate with differences in flower color in the allopolyploids. We hypothesize that *N. quadrivalvis* will have a homeolog bias toward *N. obtusifolia* because both have a colorless phenotype, indicating the presence of flavonol pigments, and that *N. clevelandii* will favor *N. attenuata* since both produce anthocyanins.

Topic: *Systematics & Taxonomy*

A-161

Unique early Texas plant specimens at the Kansas State University Herbarium

Author: Sarah De Groot, Carolyn Ferguson
Affiliation: Kansas State University

The Kansas State University Herbarium (KSC) contains nearly 200,000 specimens of vascular plants and bryophytes, with worldwide holdings but with particular strengths in plants of Kansas and the Great Plains. Surprisingly, the Herbarium also includes over 600 specimens collected in Texas in the mid-1800s by renowned botanists Ferdinand Jacob Lindheimer and Charles Wright. At least 28 of these are taxonomic type specimens. Labels are mostly handwritten and include additional data that in many cases are absent from formal exsiccatae labels and publications, existing nowhere else. All but one of the 64 Wright specimens appear to be unicates, and 11 Lindheimer specimens may not exist elsewhere. We will discuss the importance of these unique historical collections, interesting features, how they likely came to KSC, and access to digital metadata and high-resolution images.

Topic: *Ecology*

A-162

Evaluating success of a community-driven conservation program for an endangered Mexican oak

Author: Dana Barry, Ash Hamilton, Silvia Alvarez-Clare, Sean Hoban
Affiliation: Morton Arboretum, University of Chicago, The Morton Arboretum

The arroyo oak (Quercus brandegeei) is an endangered endemic oak species with significant cultural and ecological significance to Baja California Sur, Mexico. Growth is restricted to seasonally wet streambeds (arroyos) where mature adult trees persist, but regeneration from seed has not been documented in the last century. Since 2019, the Morton Arboretum, local Mexican government agencies, and community leader partners have collaborated to grow approximately 2250 seedlings and "adopt" them out to community areas and ranches. This can be considered an inter situ collection, bridging the gap between in situ and ex situ collections, which is helping safeguard the species and its genetic diversity. We conducted extensive surveys of seedling growth and survival among nursery grown individuals transplanted in a diverse, relatively unmanaged landscape. Using monitoring data collected over 3 years (2022-2024) we quantified seedling survivorship over time to evaluate at what time point most seedlings

are lost. Additionally, using more detailed monitoring data collected during the most recent monitoring effort, we investigated the ecological factors influencing seedling performance among the still living seedlings.

Preliminary survivorship analysis has found that more than 80% of individuals die within the first year of transplanting. We hypothesize that seedlings are often experiencing transplant shock, although it is unclear what specific factors (e.g. improper planting technique, over/under watering post-transplant, soil compaction, etc.) are causing such extensive shock. Using data from the surviving seedlings, we tested if and to what extent light availability, water availability, elevation, slope, and proximity to known wild populations correlate to seedling performance as measured by height and quality. We hypothesize that a combination of ecological and logistical factors influence seedling success.

Community driven conservation is crucial for the future survival of rare trees. Therefore, we hope to use the results of these analyses to not just improve conservation outcomes for Q. brandegeei but also to provide insight in managing community driven conservation projects. For example, we have already recommended the integration of tree planting experts into this conservation project to help identify the cause of transplant shock, and we recommend that any community-driven conservation project should incorporate this type of expertise as early as is feasible to ensure maximal success.

Topic: Systematics & Taxonomy

A-163

Diversification of Hawaiian Cyrtandra (Gesneriaceae): Testing Species Circumscription and Species Relationships with Morphology and Phylogenetics

Author: Destiny Brokaw, Eric Roalson, Warren Wagner
Affiliation: Washington State University, Pullman, Washington State University, Smithsonian Institution

Hawaiian *Cyrtandra* (Gesneriaceae) is a genus of flowering plants distributed among the Hawaiian Islands with about 60 named species and 87 putative hybrids This genus consists of many understory shrubs with white flowers and berries and is the second-largest plant lineage of the Hawaiian Islands with regard to species richness. A comprehensive study of the morphological diversity present within Hawaiian *Cyrtandra* allows for the development of species circumscription hypotheses in which putative hybrids based on morphology may be further revaluated through phylogenetic analyses. A prior study conducted by Kleinkopf et al. (2019) utilized a hyb-seq target enrichment approach on 31 species to hypothesize species relationships and infer possible hybridization events and was determined to be a useful approach, therefore this study will embark on this by including all currently described species of *Cyrtandra* along with a large sampling fraction of putative hybrids found across the archipelago to clarify the taxonomic status of Hawaiian *Cyrtandra* across the islands. This project aims to 1) provide a comprehensive phylogenetic study of all recognized *Cyrtandra* across the Hawaiian Islands and 2) provide insight into the role of hybridization and incomplete lineage sorting in the diversification of the genus. This talk will outline preliminary analyses providing insight into the taxonomic status of *Cyrtandra* across Maui Nui and Kauai in addition to multi-island species.

Topic: Physiology

A-164

Evolution of Leaf Succulence: Examining Photosynthetic Diversity in Zygophyllaceae

Author: Bharti Parihar, Douglas Soltis, Pamela Soltis
Affiliation: University of Florida

Zygophyllaceae, a cosmopolitan clade that includes approximately 285 species, is renowned for its diverse adaptations to arid environments. This diversity provides a unique platform to study the evolution of leaf succulence across C_3, CAM, and C_4 photosynthetic pathways. While succulent plants are generally associated with CAM, based on species so far examined, significant photosynthetic variation exists within Zygophyllaceae, with several members utilizing the C_4 pathway. This research aims to better characterize the diverse photosynthetic pathways in the family, contributing to a broader understanding of the evolution of leaf succulence, independent of the specific pathway employed.Photosynthetic characterization in Zygophyllaceae has largely relied on the carbon-isotope ratio approach. Although powerful, this method has limitations, particularly in detecting weak or facultative CAM and in distinguishing between C_3-CAM intermediates and full CAM pathways due to overlapping $\delta^{13}C$ values. Environmental factors such as light, humidity, CO_2 concentration, and stomatal behavior can influence $\delta^{13}C$ values, potentially leading to the misclassification of photosynthetic pathways under stress conditions.This study utilized direct physiological measurements, including gas exchange data collected with the LiCor 6400XT, to overcome these limitations and provide a more accurate classification of photosynthetic types within the family. Notably, acid-titration tests performed on the three studied species—*Tetraena stapfii*, *Fagonia minutistipula*, and *Tetraena simplex*—revealed no evidence of obligate CAM, suggesting that facultative or weak CAM may be present in these species. This comprehensive approach aims to better understand how different traits related to leaf succulence and adaptive photosynthesis have evolved over time in Zygophyllaceae, offering new insights into plant resilience in arid and semi-arid ecosystems.Ongoing studies will integrate genomic data with these physiological insights; this research will not only elucidate the adaptive strategies of Zygophyllaceae species but will also enhance our understanding of photosynthetic diversity and its role in the evolution of arid-zone flora.

Topic: Paleobotany

A-165

The Diversity of Leaf Mines in the Cenozoic Japan

Author: Kakemu Fujii, Atsushi Yabe, Hirokazu Yukawa, Yume Imada
Affiliation: Kyoto University, NMNS, FPDM

Leaf mining is a feeding strategy of herbivorous insects in which larvae (or adults) inhabit, consume, and develop within the leaf tissues. Their mines provide much of their life history, including the developmental processes (e.g., feeding, defecation, pupation) and outcomes (e.g., larval death, parasitism, or adult emergence). Fossilized leaf mines serve as direct evidence of the specialized modes of plant-insect interactions in deep time. Since the Japanese archipelago is a biodiversity hotspot shaped by complex geologic history, studying these interactions in Japanese plant fossils offers a unique insight into the biogeographical processes underlying biodiversity. However, such interactions remain largely unexplored in Japan's paleobotanical collections, with only two previous records of fossil leaf mines published.

In this study, we investigated the diversity and abundance of mining in fossil leaves of spatiotemporally diverse deposits of Cenozoic Japan. The morphological features of these mines were compared with previous examples using the Damage Type (DT) classification by Labandeira and colleagues, and when possible, we inferred the taxonomic affiliations of the miners. We examined ca. 3,000 fossil specimens from seven deposits in Honshu (mainland of Japan) and one deposit in Hokkaido (northern land of Japan), spanning the Paleocene to Pliocene. These include one Paleocene (64.3-62.5 Ma), four Miocene (20.3–5.5 Ma), and three Pliocene (5.3–3.2 Ma) deposits. The Pliocene deposits are dominated by deciduous trees, especially *Fagus* and *Acer*.

As a result, we discovered over 50 fossil leaves bearing biogenic damage indicative of leaf mining, representing at least 20 DTs, including two potentially novel ones. The mining patterns in some well-preserved specimens exhibited distinctive behaviors characteristic of modern leaf-mining moths. Each DT tended to be specific to a particular plant taxon within a given flora, and the composition of mining DTs varied across time and space. Notably, the diversity and abundance of mining DTs in the Paleocene deposit was comparable to, or potentially higher than, those reported from contemporaneous deposits from Europe and North America.

Our findings highlight the previously overlooked potential of Japanese Cenozoic fossil plants for studying plant-insect interactions and reveal a wealth of highly specific associations from the Paleocene through the Pliocene. Future studies on fossil leaf mines will benefit from taxonomic assignment through comparisons with modern assemblages, which could help reconstruct the intricate evolutionary history leading to Japan's present-day biodiversity.

Topic: Functional Genetics/Genomics

A-166

Phenotypic differences and vulnerability to drought and heat in diploid and autotetraploid Arabidopsis thaliana

Author: Maria Cuervo, Jonathan Spoelhof, Douglas Soltis, Pamela Soltis, William Hammond
Affiliation: University of Florida

Whole-genome duplication (WGD) events, which lead to polyploid formation, are recognized as a major evolutionary force that provides new genetic configurations favoring organismal complexity and speciation. While much attention has focused on allopolyploids (interspecies WGD), autopolyploids (intraspecies WGD) are also prevalent

in nature. Recent studies on synthetic autotetraploids of the model plant *Arabidopsis thaliana* have elucidated the impacts of autopolyploidization, revealing phenotypic variation and an enhanced ability to cope with stressful conditions compared to their diploid counterparts. Although *A. thaliana* synthetic autotetraploids can have greater resistance to drought and other stressors, most research focuses on the effects of extreme events after critical functions have already declined. This has led to a fragmented understanding of the physiological mechanisms driving the differential responses observed across ploidal levels. The present work aims to evaluate the influence of polyploidy on the phenotype and vulnerability to heat and drought in synthetic autopolyploids of *Arabidopsis thaliana*. Plants from isogenic lines with 2*x* and 4*x* ploidal levels were obtained using colchicine treatments on the Columbia wild-type (Col-0). Plants were grown in growth chamber conditions at 22°C under short days. Plants were sampled 24 days after planting for leaf crown mass per area, dry matter content, stomatal density and size determination, and were photographed each week to calculate relative growth rates (RGR). Similarly, 24 days after planting, leaf crowns were subjected to heat treatments using water baths with temperatures ranging from 30 to 60°C for 15 min. To determine vulnerability to heat, thermal limits (*T crit*, *T50*) were calculated with temperature r esponse curves of canopy-level dark-acclimated chlorophyll fluorescence (Fv/Fm). Compared to their diploid counterparts, autotetraploids exhibited larger stomatal cells and reduced stomatal density, but no significant differences were observed in leaf traits associated with resource acquisition. Tetraploids showed lower relative growth rates, consistent with the "high ploidy syndrome," which reflects a tradeoff between DNA content and cell division rates. Contrary to expectations, no differences in thermal limits were observed, suggesting that ploidy does not affect heat dissipation or the vulnerability of the photosynthetic apparatus to rising temperatures. As part of future work, we will assess photosynthetic rates (A), transpiration (E), and water use efficiency (WUE) under both optimal and droughted conditions. Under optimal conditions, we anticipate no significant differences in A, E, and WUE between ploidal levels. However, we expect autotetraploids to show declines in these parameters at lower plant water status compared to diploids. While additional genotypes will be included in the future, this research provides a baseline for further elucidating the physiological mechanisms driving the differential responses to environmental stressors after autopolyploidization events.

Topic: Development and Structure

A-167

Sex determination and flower development in the dioecious Baccharis halimifolia (Asteraceae)

Author: Sarita Munoz-Gomez, Daniel Jones, Leslie Goertzen, Sarah Carey, Alex Harkess
Affiliation: Clemson University, Auburn University, HudsonAlpha Institute for Biotechnology

In plants, how separate sexes evolve and develop within a species is poorly understood. Although common in other groups, dioecy, the presence of unisexual flowers in different individuals of the species, is only found in 6% of known angiosperms (Renner 2014). In addition to its rarity, most dioecious species studied so far are economically important, leaving a gap in our understanding of many unique systems. This is the case of Baccharis halimifolia (Asteraceae), a fall-flowering shrub that presents staminate and pistillate capitula in its unisexual individuals. The species produces a capitulum, an inflorescence characterized by a flattened axis where hundreds of flowers are arranged in specific patterns acting as a single bloom.

The species also presents secondary pollen presentation, another unique family-wide trait that has been poorly studied at the morphological level. To better understand morphological and transcriptomic changes in both capitula-types across development, we collected a succession of developmental stages with the aim to capture the transition between vegetative meristem (VM) and inflorescence meristem (IM), and the stages spanning floret initiation. For this, we collected tissue for confocal imaging and RNAseq, three times a week, from August to October 2024. Additionally, two sex specific transcriptomes were assembled using Trinity (Grabherr et al., 2011). Seven developmental stages were characterized for each capitula type, including VM, IM, floret initiation, and four floret development specific stages.

The transition from VM to floret initiation takes around a month, while the floret development occurs at a faster rate (around 10 days), with staminate florets starting to develop sexual organs first. Both sexes initiate pappus (sepals) and petal primordia first in a similar manner. In pistillate florets, gynoecium primordia then follow, with two small "masses of tissue" extending towards the center to form the pistil, leaving a gap inside where an ovule will develop. However, in staminate florets, anthers expand first, and only a mass of possible placental tissue is visible at the center of the floret where the ovary and pistils should form. However, the ovary and ovules are never formed, and instead, the cells form a pistil (with no connection to a fertile ovary or ovules) that keep growing past the anthers. We propose this structure should be called a "pistilode" due to its homology to the pistil but lack of function in reproduction. This structure is instead used in secondary pollen presentation, and it's the first time it has been characterized to this level in a Baccharis species.

Moving forward, a comparison between both transcriptomes will present additional information on the gene expression differences across developmental stages and different sexes, pointing us toward important genes in anther and pollen development. This data will also inform our genome and sex determination region (SDR) annotation, which represents the first genome of the species and the only one available for a dioecious aster.

This study is the first of its kind in a dioecious species and the starting point in the study of dioecy using genomics, transcriptomics, and developmental biology.

Topic: Development and Structure

A-168

Varileaf: Developing a semi-automatic software for recognizing and quantifying leaf variegation

Author: Liana Gonzalez, Carlos Maya-Lastra
Affiliation: Angelo State University

Leaf variegation commonly occurs due to a genetic mutation, although it can also occur due to a viral infection or as a result of nutrient deficiency. Despite its intriguing nature, research on variegation remains limited due to the labor-intensive and time-consuming process required for accurate measurement. Currently, there are some methods to measure the area of variegation in leaves but they may require training, such as imageJ, or in some cases, researchers need proprietary software, which is less accessible. For this reason, we envisioned a new python program that aims to provide an open source semi-automatic way to quickly and accurately identify and quantify the variegation area present in leaves, enabling more efficient research and deeper insights. To accomplish this, a python package was developed that initially isolates the selected leaf from the background and then uses a variety of algorithms, such as contour detection and edge detection, to identify potential anomalies found within the coloration of the leaf lamina. These spots are then extracted as polygons and organized into dictionaries, of which post-extraction measurements, such as area, can be calculated. The program has the potential to recognize other interesting features present such as large trichomes. It may also use convolution neural networks to help with discriminating various types of variegation such as chlorosis, pathogen attacks, or insect bites. In the future, we plan to develop some algorithms so the program can process images fully automatically. This program is designed as a versatile package that can be seamlessly integrated into other Python scripts and developments, expanding its potential applications.

Topic: Development and Structure

A-169

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This study is the first of its kind in a dioecious species and the starting point in the study of dioecy using genomics, transcriptomics, and developmental biology.

Topic: Ecology

A-170

Multigenerational competitive dynamics between genetically diverse diploid and polyploid populations with and without salt stress

Author: Hannah Rose Assour, Madison Conn, Martin Turcotte, Tia-Lynn Ashman
Affiliation: University of Pittsburgh

Whole-genome duplication, or polyploidy, is a widespread mutational process characterized by an organism possessing more than two sets of chromosomes. Polyploidy stands out as a significant catalyst for evolutionary change in flowering plants, with some ecosystems containing as high as 51% polyploid frequency. Polyploidy can cause many physical and genetic changes, potentially increasing adaptive potential and generally increasing stress tolerance. Through these effects, polyploidy can expand a species range into novel environments. Stress is theorized to facilitate polyploid success, enabling polyploids to outcompete their non-polyploid ancestors. However, most plant studies have been done at the individual level, neglecting how stressors influence population dynamics and competitive interactions. Here using a manipulative, experimental evolutionary field study, we tested 1) the multi-generational, population-level outcomes of competition between genetically diverse populations of diploids and polyploids, and 2) whether competition and community evolution depend on the presence of an environmental stressor. Specifically, we investigated how salt stress affects competition between genetically diverse populations of diploid and triploid populations of the hybrid duckweed (*Lemna japonica). Lemna japonica* is a hybrid duckweed species, with subgenomes from *Lemna minor* ("M" genome) and *Lemna turionifera* ("T" genome). We set up outdoor mesocosms comprised of 1) diploid-only populations, seeded with equal abundances of 3 genotypes of diploid *L. japonica* ("MT" genomic makeup), 2) polyploid-only treatments, also seeded with equal abundances of 3 genotypes of polyploid *Lemna japonica* ("MMT") and 3) competition treatments (diploid and polyploid together), seeded with equal abundances of all 6 genotypes (3 diploid, 3 polyploid, 16.6% of each). All populations were grown both with and without salt contamination. Each treatment was replicated 20 times – high replication is necessary to detect any significant community evolution. Using microsatellite markers, we tracked community evolution through changes in genotypic composition and ploidy composition across a 16-week mesocosm experiments. By analyzing shifts in genotypic frequencies and growth patterns, this research bridges ecological and genetic approaches to enhance our understanding of the ecological establishment patterns and evolutionary dynamics of polyploids. Understanding these dynamics is critical for predicting how polyploidy shapes plant responses to anthropogenic change.

Topic: Biodiversity Informatics & Herbarium Digitization

A-171

Collaborations between herbaria and archives: the Carlquist Extended Specimen Network

Author: Mare Nazaire, Ana Niño, Jason Best, Krishna Shenoy, Sam Ekberg
Affiliation: California Botanic Garden, Botanical Research Institute of Texas

New initiatives in the digitization of herbarium specimens and scientific archives have given rise to the Extended Specimen Network (ESN)–a conceptual framework that places specimens at its center and connects them to disparate types of materials, including field photographs, field notes, maps, and more, to build a vast network of digital resources. Through a National Science Foundation Infrastructure Capacity for Biological Research grant, the Herbarium at California Botanic Garden and the Library at the Botanical Research Institute of Texas have partnered in an effort to preserve and provide physical and digital access to the collections of renowned American botanist and photographer, Sherwin J. Carlquist (1930–2021). Carlquist is best known for his significant contributions to the fields of island biogeography, evolutionary ecology, and wood anatomy.

Carlquist amassed more than 190,000 collection objects during his productive 30+ year career, including herbarium vouchers, wood specimens, specimen material preserved in spirits, microscope anatomy slides, photographs, negatives, slides, index envelopes, and field notebooks. This project, now in year three, aims to (1) curate the comprehensive Carlquist collection for long-term preservation; (2) digitize and mobilize the collection's data; (3) link transcribed collection information, images, and metadata across all plant collections and archival objects; and (4) publish and make linked collection data publicly available through open-access platforms. ESN linkages created through this project have potential to facilitate immediate application to a suite of research areas, including systematics, wood anatomy, ecology, biogeography, island biology, phenology, plant conservation, history of science, plant humanities, digital humanities, and archival theory and practice. The Sherwin Carlquist Collection ESN project represents a unique opportunity for the collaboration of two different but interconnected disciplines to shepherd the way in which herbaria and archive communities envision, implement, and utilize ESNs within and between their collections. Project successes, challenges, and lessons learned during will be highlighted in this talk.

Topic: Defining forces in fern evolution: Celebrating the contributions of Kathleen Pryer and Michael Windham

A-172

Phylogenetic Relationships of Extant Ferns Based on Evidence from Nuclear Sequences

Author: Emily Sessa, Jessie Pelosi, Susan Fawcett, Gordon Burleigh
Affiliation: New York Botanical Garden, University of Arizona, National Tropical Botanical Garden, National Science Foundation

Ferns are the second largest group of vascular land plants, with nearly 12,000, species, and they are critical components of Earth's biodiversity – ferns can be found in nearly every type of ecosystem and habitat, from desert to rainforest. Ferns also occupy a pivotal evolutionary position as sister to the megadiverse seed plants, and they are thus the critical outgroup needed to understand the evolution of key seed plant features. Foundational work was done to resolve phylogenetic relationships within ferns using molecular data starting in the 1990s, with key contributions by Kathleen Pryer that helped lay the groundwork for our modern understanding of relationships between the major lineages of ferns. Since that time, fern phylogenetics has presented researchers with a number of challenges, including recalcitrant nodes along the backbone of the phylogeny that have resisted resolution, conflicting relationships between several key groups in studies using different datasets, and differing dates between studies attempting to determine stem and crown ages of fern families. We will present a phylogenomic approach to fern evolution, using the most highly resolved nuclear dataset to date and with targeted taxonomic sampling that includes nearly all fern families and genera. This dataset allows us to explore a range of outstanding questions in fern phylogenetics, including resolving recalcitrant nodes, and comparing results between our nuclear based trees and other recent large-scale fern phylogenies based on chloroplast loci.

Topic: *Ecophysiology*

A-173

Facing the heat or losing your cool: How does environmental variation drive plant photosynthetic temperature tolerance?

Author: Ria Raut
Affiliation: University of California, Berkeley

Many ecological theories propose that temperature tolerance – the range of temperature at which an organism can survive and thrive – is a product of the interaction between physiological plasticity and environmental variation. For example, Janzen's climate variability hypothesis suggests that species that experience greater climate variation, such as those further from the equator that experience greater annual temperature variation, will likely have a greater thermal tolerance. Plant photosynthetic temperature tolerance range – the range at which carbon assimilation is positive and optimal – is postulated to follow a similar pattern, such as that plants that experience greater temperature variation will be able to actively assimilate carbon at a greater range of temperatures. However, this hypothesis has never been explicitly, robustly addressed; in this project, we address this knwledge gap using carbon assimilation-temperature (AT) performance curves from a globally distributed dataset (248 curves, 91 species) ranging from Canada to New Zealand and almost all Whittaker biome-types. Greater AT curve breadths correspond to greater photosynthetic temperature tolerance. We tested the hypotheses that AT curve breadth varied by H1) absolute latitude, H2) annual growing season temperature variation, or H3) growing season diurnal temperature variation (i.e. the temperature range which may exert the greatest selective force on temperature tolerance as it is when most plants are trying to optimize their photosynthesis). We alternatively tested the hypothesis that photosynthetic thermal tolerance is limited by tradeoffs, and plants can typically maximize either AT curve breadth or the optimal carbon assimilation, but not both. Globally, we found limited support for all 4 hypotheses, suggesting that photosynthetic temperature tolerance ranges are not driven by global macroclimate variation nor photosynthetic trade-offs; this lack of support may be reasonably explained by 2 possible reasons: 1) plants might primarily adapt to microclimate, rather than macroclimate, variation or 2) curve breadth is a complex product of stochasticity, phylogeny, microclimate-based acclimation, and within-individual trait plasticity. Understanding the drivers of photosynthetic temperature tolerance is increasingly significant in the context of climate change, as increasing temperatures may push plants out of their thermal 'comfort' zone, which may have drastic consequences for species persistence, species range, ecosystem dynamics and composition, and global carbon sequestration rates.

Topic: *Lichen and Bryophyte Diversity, Conservation, and Evolution in the Americas*

A-174

Variation in plant-fungal interactions in a tropical liverwort between streamside and roadside populations

Author: Kristen Hillegass, David Nicholas McLetchie
Affiliation: University of Kentucky

Liverworts are the earliest diverging land plants. In order to transition from water to land, plants used fungi to help adapt to the terrestrial environment. Fast forward about 470 million years to today, and most liverwort taxa still form close relationships with fungi. However, this relationship is often overlooked which prevents a more complete understanding of liverwort ecology. Furthermore, studying liverwort-fungal interactions may give us a glimpse into how liverworts transitioned to life on land. To ex mine this relationship, I compared the quantity of fungal associations in the tissue of the thalloid liverwort Marchantia inflexa from four streamsides and three roadsides (human-altered habitat) in Trinidad, the Republic of Trinidad and Tobago. A total of 164 bifurcated thalli from plants at least one meter apart were collected along points of transect s from the seven sites. The plant samples were sent to our lab, where each bifurcated tip was divided with one tip placed on steam sterilized soil to grow in the growth chamber, and the other tip stained for fungus. All 164 plants were stained and preserved on slides, and half of the plants were cross-section ed. We used ImageJ to quantify the amount of fungus in the cross sections, which was primarily located along the midrib of the plant. The percentage of the cross-sectioned midrib area occupied by fungal structures ranged from 0% to 69% with a mean of 29%. As expected, p lants collected from road sides had significantly greater fungal colonization than plants collected from river sit es ($p=0.002$). This finding is consistent with fungi facilitat ing liv erworts' tra nsition to terrestri al envir onme nts, with t he roadsides representing drier land habitat relative to streamsides. Additionally, this study demonstrates that there is variability in pla n t-fungal re lationships among populations of the same plant species. In order to gain a better understanding of this variabil ity, future studies will address how plant fitness and resilience to change is affected by fungal relationships, and if the variability is due to traits of the plant, the fungus, or their interaction. Finally, studying the variability in plant-fungal interactions between natural (streamside) and anthropogenic (roadside) habitats may shed light on how fungi help plants adapt to changing, human-altered environments.

Topic: *Biodiversity Informatics & Herbarium Digitization*

A-176

Digitization and Rapid Specimen Identification: a New Initiative at the Missouri Botanical Garden Herbarium

Author: Jordan Teisher, Matthew Austin, Mike Blomberg, Jeddy Choi, Meredith Woodward, Gunter Fischer
Affiliation: Missouri Botanical Garden, University of Tennessee at Chattanooga

Applications of artificial intelligence (AI) technology to the online mobilization of herbaria have the potential to expedite research and increase curatorial efficiency. This year, the Missouri Botanical Garden (MO) embarked on a major new initiative – coined the *Revolutionizing Species Identification* (RSI) project – that combines digitization and AI to create tools for rapid specimen identification. The RSI project will (1) image and transcribe all 8 million specimens in the MO herbarium, (2) use digitized specimen data and hyperspectral scans to develop models that can automatically predict specimen taxonomy, and (3) establish a curatorial mentorship program to build taxonomic expertise in early career herbarium professionals. This 6-year project will provide MO specimen data and resulting identification tools as online resources for the botanical community. As biodiversity loss continues unabated across the globe, it is vital to expedite the digitization of herbaria, while building taxonomic expertise and tools to ensure these collections remain well curated into the future.

Topic: *Trees, Traits, and Time*

A-177

A genomic portrait of regional introgression in Quercus macrocarpa

Author: Rebekah Mohn, Mira Garner, Laramie Aköbzek, Leah Samuels, Paul Manos, Alan Whittemore, Ian Pearse, Jeannine Cavender-Bares, Peter Kennedy, Heather McCarthy, Alex Harkess, Andrew Hipp
Affiliation: University of Minnesota - Twin Cities, Duke University, Morton Arboretum, US Geological Survey, Harvard University, University of Oklahoma, HudsonAlpha Institute for Biotechnology

Adaptive introgression, the movement of beneficial genes from one species into another species through hybridization and backcrossing, can provide genomic diversity which can be harnessed to identify resilience to both biotic and abiotic factors. The eastern North American white oak syngameon (*Quercus* section *Quercus*) is composed of over a dozen *Quercus* species, many of which co-occur and can interbreed, resulting in viable offspring. This syngameon includes the widespread and morphologically variable *Q. macrocarpa*. We used range-wide genome resequencing data from *Q. macrocarpa* and co-occurring interfertile white oak species to explore the geographical and genomic landscape of introgression and hybridization. We fo und that hybridization is not uniform across the range of *Q. macrocarpa*, but its frequency varies geographically. On the other hand, we found that introgression has occurred across the geographical range and across the genomic landscape. However, introgression disproportionately affects some areas of the genome over others.

Topic: Systematics & Taxonomy

A-178

Species Boundaries of the Rare Menzies' wallflower (Brassicaceae: Erysimum menziesii), an Endemic of the Northern California Coast

Author: Cameron Jones, Oscar Vargas
Affiliation: Cal Poly Humboldt

The California Floristic Province (CFP) is a global biodiversity hotspot, home to 6,143 vascular plant species, 42% of which are endemic. Despite efforts to explain this remarkable diversity, little is known about the microevolutionary processes driving speciation in rare endemics. One such species, *Erysimum menziesii*, is an endangered and federally listed taxon restricted to coastal dune habitats between Monterey and Humboldt counties, California. It coexists with *E. concinnum*, and both are hypothesized to descend from *E. capitatum* due to their shared chromosome count (2n = 18), a rare trait within *Erysimum*. This evolutionary relationship has not been tested phylogenetically, and taxonomic complexity further impedes our understanding of species boundaries, particularly between *E. menziesii* and *E. concinnum*. One particularly ambiguous population, the Tolowa wallflower, is currently classified as *E. concinnum* but shares traits with *E. menziesii*.

To resolve these ambiguities and clarify the mode of speciation, I have sequenced 190 samples of *E. menziesii*, *E. concinnum*, and *E. capitatum* using ddRADseq. This analysis aims to refine species boundaries, identify the progenitor of *E. menziesii*, and uncover the evolutionary forces driving their origin.

Topic: Ecology

A-179

Using Hyperspectral Data to Identify Between Knotweed Species

Author: Addison Gensch, Brett Fredericksen, Alex Crum, Ya Yang
Affiliation: University of Minnesota, University of Wisconsin-Superior, University of Minnesota, Twin Cities

Knotweed describes an invasive species group found throughout the United States, characterized by being difficult to eradicate and control. The species in this group are difficult to identify in a field setting due to high variance in morphology. Three species and one hybrid from this group (Reynoutria sachalinensis, R. japonica, R. compacta, and R. xbohemica) were selected with R. xbohemica being a hybrid of R. japonica and R. sachalinensis. R xbohemica has been noted as the hardest to visually identify, as it may exhibit intermediate morphological traits of its parent species, and is the most invasive amongst the group due to its faster spread, higher capacity for regeneration, and common sexual and asexual reproduction, in comparison to the primary asexual reproduction that is characteristic of the other taxa in the group. This gives the question of how we can use hyperspectral tools to identify between knotweed species, especially this particularly invasive hybrid. These species were sampled from natural populations amongst their invasive ranges in Minnesota and northern Wisconsin and scanned using a photospectrometer to collect hyperspectral reflectance data on both the adaxial (sky-facing) and abaxial (ground-facing) sides of their leaves. Data was analyzed using a partial least squares discriminant analysis (PLS-DA) in an attempt to create models that can discriminate amongst species. This analysis included the creation of models with full separate adaxial and abaxial data (400-2400 nm) alongside separate adaxial and abaxial data with a limited wavelength (400-1000 nm) to mimic that of a more accessible, cheaper photospectrometer. When externally validating both (adaxial and abaxial) full wavelength models, R. compacta and R. xbohemica were correctly classified 73% of the time, R. sachalinensis 80% of the time, and R. japonica 62% of the time, with most common misidentification of R. japonica as R. xbohemica, 26% of the time for the adaxial model and 40% for the abaxial model. Thus, both adaxial and abaxial models were deemed as viable for species identification. Regarding a more accessible model, the limited wavelength abaxial model had 90% correct classification of R. sachalinensis, 81% of R. compacta, 67% of R. xbohemica, and 51% of R. japonica, with a 41% misclassification of R. japonica as R. xbohemica. The abaxial limited wavelength model saw a drop in accuracy, with a 80% correct classification of R. sachalinensis, 70% of R. compacta, 48% of R. xbohemica, and 57% of R. japonica. Based on our findings we found that both adaxial and abaxial models created with 400-2400 nm hyperspectral data can identify between these knotweed species, however there is still difficulty in identifying between R. xbohemica and R. japonica. For limited 400-1000 nm wavelength models, those built on abaxial data have a higher accuracy than adaxial data. This may prove useful in future land management applications, as methods that include remote sensing of hyperspectral data are just in using adaxial data while other hyperspectral methods, such as using a hand-held photospectrometer, may benefit from the collection of abaxial data instead of adaxial.

Topic: Conservation Biology

A-181

Lagged climate effects on the demography of a critically imperiled Astragalus

Author: Sarah Herzog, Noah Dell, Matthew Albrecht
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To protect and conserve species, we must understand not only how a species' environment (e.g., climate) affects species' population growth rates but through what mechanism(s). However, a major challenge in understanding the environmental drivers of rare plant population dynamics is often the absence of long-term data needed to determine the combination of climate variables and temporal windows that affect vital rates and population growth. In this study, we leverage a long-term demographic dataset (15 years) in five naturally occurring populations of a federally endangered perennial forb, *Astragalus bibullatus,* to examine the possible effects of climate on the species' vital rates and population growth rates. We use model selection to examine if and when the climatic windows impact vital rates. We then use vital rate models to examine if there are any corresponding impact of climate on population growth rates using an IPM (integral projection model). Our preliminary analyses indicate that precipitation primarily affects growth (change in size) and probability of survival and that the best climate window for these effects is lagged by one and two years, respectively. Our findings of multiple vital rates exhibiting lagged climate effects emphasizes the need to explicitly examine lagged climate windows, which are often excluded from demographic analyses. Additionally, survival and growth are often the most important vital rates in determining population growth rates for long-lived species, such as *A. bibullatus*. Our results indicate a critically imperiled perennial species' vital rates and population growth rate are likely impacted by climate, a concerning finding given this species' narrow-range species is forecast to be strongly impacted by climate change.

Topic: Ecology

A-182

Conserving Rare and Disjunct Orchid Populations in a Changing American West: Preliminary insights using Spiranthes infernalis (Ash Meadows ladies' tresses) as a case study

Author: Allison Autry
Affiliation: California Botanic Garden

Spiranthes infernalis (Ash Meadows ladies' tresses) is a rare perennial terrestrial orchid that was first described in the late 1980s and was thought to be endemic to Ash Meadows National Wildlife Refuge in Nye County, Nevada. A new population was recently discovered 200 miles northeast in Railroad Valley, Nevada, and a third population in Owens Valley, Inyo County, California is also suspected to belong to the species. Like many groundwater-dependent species, *S. infernalis* is threatened by hydrological extraction and alteration due to agriculture, mining, geothermal development, and industrial scale solar facilities. However, despite its rarity and the high degree of threat, this orchid has yet to be thoroughly studied. The primary aim of this study is to investigate the patterns of population genetic diversity across the range of the species, while also evaluating its conservation needs, such as mechanisms for legal protection and the development of ex situ conservation methods. All three globally known populations of *S. infernalis* were sampled for population genetic analysis in 2024, and censusing and surveying was undertaken as well. In this presentation, I will present the preliminary results from an analysis of ddRadseq data produced from these samples, as well as an overview of the conservation status of *S. infernalis.* The findings of this research will contribute to a growing body of study on threatened desert species in groundwater dependent habitats, and it will improve the understanding of highly disjunct specialist species and associated patterns of genetic diversity.

Topic: *Reproductive ecology and evolution of plants in stress-prone environments*

A-183

Counterintuitive patterns of phenological plasticity in response to climate change

Author: Jill Anderson, Inam Jameel
Affiliation: University of Georgia

Climate change has advanced the seasonal timing of life history events earlier in the year for a diversity of organisms. These phenological shifts appear particularly pronounced for transitions that occur in the spring. In high elevation and high latitude ecosystems, increasing temperatures have reduced winter snowpack and accelerated spring snowmelt, both of which can elicit earlier leaf out, reproduction, and emergence from winter conditions. However, the magnitude of phenological plasticity in response to climate change may not be uniform across the geographic distribution of a species, and environmental stressors could constrain this phenological response to a greater extent in some portions of the range. In this study, we examine plastic phenological responses to the timing of snowmelt in montane ecosystems. We focus our study on the timing of flowering and germination in *Boechera stricta* (Brassicaceae) as a model system. This perennial forb is distributed across broad climatic gradients in western North America. Local populations have adapted to the climatic regime at their home sites. Early snowmelt, especially in low elevation locations, can expose natural populations to spring frosts at sensitive moments in development. Climate change is projected to continue to accelerate the timing of snowmelt and may increase the frequency of duration of spring frosts in some locations.

Phenological shifts in the timing of flowering have been well-documented across time and in many ecosystems. However, these studies often do not contrast patterns across populations that differ climatically. Shifts in the timing of germination are less well studied, owing to the challenges of tracking seeds and seedlings. Nevertheless, seed germination and seedling establishment represent critical life history transitions, which often drive population growth rates. In five field common garden experiments conducted across a decade, early snowmelt delayed germination and reproduction, especially in the lower elevation locations. Selection analyses reveal that these delays could be maladaptive responses to novel stresses. We hypothesized that exposure to freezing temperatures after snowmelt contributes to these reductions in the performance of early life history stages and the failure of plants to track climate change via phenological shifts. To evaluate this hypothesis, we conducted a laboratory experiment in which we subjected seeds and seedlings to freezing temperatures that could occur under climate change. As predicted, low elevation seeds had heightened freezing tolerance compared with their higher elevation counterparts. This genetic cline in freezing tolerance is likely an evolved response to increased spring freezing stress at low elevations. Furthermore, this result suggests that continued climate change could expose mid and high elevation populations to novel freezing conditions to which they are not currently adapted. Even at low elevations, current levels of freezing tolerance may not be sufficient for local populations to persist through novel climates. Advancing snowmelt could limit reproduction and regeneration in future climates.

Topic: *Education and Outreach*

A-184

Showcasing the Biology of Plants Coloring Textbook, an Open Educational Resource for college-level introductory botany

Author: Rachel Jabaily, Madeleine Broadhurst
Affiliation: Colorado College

Open Educational Resources are teaching tools created outside of academic publishing that are often free for students and generally licensed to be modifiable by others. OERs lower the cost of student participation in science and allow for customization by other educators who want to use them in their own classroom. There are few OER options explicitly for botany at the college level. We aimed to create a new OER specific to botany that was customized to the unique block plan structure of Colorado College, with a curriculum covered in 3.5 weeks of concentrated study. Our OER could be incorporated by anyone, especially those who teach college-level introductory botany in shorter timeframes like summer or January terms. The OER is a hybrid of a condensed textbook, laboratory exercises including slide and living specimen observations and experiments, and interactive worksheets and coloring images featuring 30+ original botanical line drawings by the undergraduate artist coauthor. We will discuss our collaborative process developing the project, discuss licensing choices, and showcase our work, focusing on the beautiful illustrations.

Topic: *Biogeography*

A-185

Trait diversity – a novel method for investigating the role of functional traits in community assemblages and biogeography

Author: Israel Borokini, Shawn Laffan, Brent Mishler
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Traits determine species tolerance to abiotic factors and influence the types of biotic interactions, thus affecting community assemblages; moreover, trait evolution has been linked with diversification rates of plant clades. However, the spatial representation of traits has not yet properly incorporated evolutionary information. In this paper, we develop a novel method, trait diversity (TD), which is defined as the sum of phylogenetic branch lengths connecting the taxa present to the base of the phylogeny, where the branch lengths represent evolutionary change in functional traits. Along the same lines, relative trait diversity (RTD) is a ratio comparing TD on the trait-adjusted tree to a comparison tree that has the same topology but equal branch lengths (that is, a cladogram). We tested this new method using native seed plants in Florida (n = 1040 taxa) for which we have occurrence records and complete data for four reproductive and vegetative traits – seed mass, maximum plant height, salt tolerance, and growth form – and a phylogeny. Each functional trait was separately mapped on a cladogram version of the phylogeny using ancestral trait reconstruction to infer a trait phylogram (where branch lengths represent estimated change in the trait). Branch lengths for each of the four traits were then added to produce an ensemble trait phylogram. The four separate trait phylograms and the ensemble phylogram were used with corresponding species occurrence data for spatial phylogenetic analysis to calculate patterns of TD and RTD (and their significance following a randomization) at 25 x 25 km resolution in Biodiverse software. We also calculated phylogenetic diversity (PD) using the original cladogram. Furthermore, we computed functional richness for the four traits using the traditional approach (a multivariate functional diversity; FD), and conducted statistical tests to compare FD and TD. We also produced a composite map comparing FD and TD significance for the seed plants in Florida. Furthermore, we also computed TD for five 100 m^2 plots surveyed at Ordway-Swisher NEON site to investigate TD patterns at the community level. These five sites represent four different vegetative types including woody wetland, mixed forest, deciduous and evergreen forests. Spatial patterns of TD significance show a concentration of taxa with longer branch lengths, i.e., higher rates of trait divergence, in the southern half of Florida, while the northern half of Florida has accumulations of significantly low TD. Raw spatial TD was not correlated with PD ($r = -0.20$, $p = 0.001$), but was positively correlated with FD ($r = 0.52$, $p < 0.001$). At the community level, woody wetland and mixed forest types had the highest and lowest TD values, respectively, but data limitations due to small number of plots and species resulted in low statistical power. Unlike the traditional FD used widely in ecology, which measures contemporaneous similarity among members of a community, TD accounts for the evolutionary history of taxa, including current as well as ghosts of past ecological interactions. Comparing patterns of TD and FD provides deeper understanding of drivers of community assemblages and biogeography.

Topic: *Biodiversity Informatics & Herbarium Digitization*

A-186

Species delimitation in intensively hybridising genera based on herbarium specimens – the CARRARA approach

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Compared with polyploid species formation, the high frequency of homoploid hybridisation among flowering plant species poses an even harder problem for an objective discovery and naming of phytodiversity. The formation of so-called syngameons and of introgressive hybrid swarms are incompatible with the biological species concept (BSC) and urge for additional criteria to delimit species in plant taxonomy. Even greater problems for species delimitation in hybridising plant groups arise when the biological situation is not studied and evaluated in the field, but a taxonomic judgement has to be

based on herbarium specimens due to the deliberate or unavoidable abstinence from additional field work and/or the wilful usage of the rich treasure of plant specimens in museum collections.

The Carrara approach to species delimitation in intensively hybridising plant groups follows the idea of classifying metapopulation systems as infraspecific entities (subspecies) vs. species by discriminating between primary and secondary hybrid zones. By implementing high-throughput molecular techniques based on herbarium material (AFLPseq) in combination with the automated extraction of morphological characters and ecological niche-modelling based on museum material, we aim at the fast discovery and delimitation of evolutionary significant units (species) without the necessity of additional field work. Our approach will be exemplified in three plant groups of the sunflower family (Compositae, Asteraceae) known for their critical taxonomy caused by extensive hybridisation: the *Senecio nemorensis* syngameon (8 species) in Europe, the genus *Rhodanthemum* in north-west Africa (15 species), and the genus *Baccharis* in Chile (14 species).

Topic: Systematics & Taxonomy

A-187

Species boundaries and intraspecific variation of the desert gooseberries (Ribes series microphylla)

Author: Will Pearce
Affiliation: University of Utah

Gooseberries (Ribes subg. Grossularia) are known to be hyperdiverse in the western United States, with 23 species occurring in or west of the rocky mountains. However, many of the species boundaries between these taxa are unclear, which hampers conservation efforts. This issue is exemplified in the desert gooseberries (Ribes series microphylla), a clade which contains many morphologically similar species. Traditionally, keys have primarily relied on floral measurements, in particular the trait of hypanthium length, to distinguish between these taxa. However, a closer examination reveals that there is significant overlap between the observed floral measurements of each species, casting doubt upon the accuracy of the keys and the validity of these species concepts as a whole. Thus, I employed a combination of morphological, geographical, and molecular techniques to reevaluate the species boundaries of this clade. This revealed a strong habitat preference in each species, which creates strong spatial and temporal barriers to gene flow. When morphological and habitat characters are used in combination, species identification can be done reliably. However, areas where the habitat requirements for two taxa overlap may contain hybrids. Furthermore, the extreme intraspecific variation of Ribes velutinum was explored. Plant texture, leaf incision, and flower color forms have varying degrees of geographic coherence, with implications for the infraspecific taxonomy of the species. Molecular results are compared to the morphological results, revealing novel evolutionary relationships in the clade. Future research will examine the Mexican species of the desert gooseberries, explore the relationships between this clade and its sister groups, and include more loci in the genetic analysis.

Topic: Population Genetics/Genomics

A-189

The chromosome-scale reference genome of Pectocarya recurvata, a species with the smallest reported genome size in Boraginaceae

Author: Poppy Northing, Jessie Pelosi, Larry Venable, Katrina Dlugosch
Affiliation: University of Arizona

Pectocarya recurvata(Boraginaceae, subfamily Cynoglossoideae; 2*n* = 24) is a species of desert winter annual native to the Sonoran, Chihuahuan, and Mojave Deserts (North America). *Pectocarya recurvata* and other species in the winter annual plant community are leveraged in a suite of evolutionary and ecological studies to better understand how species adapt to variable environments and subsequently how these environments promote species coexistence. At the same time, there are currently (April 2025) only four available reference genomes in Boraginaceae, which all represent taxa in the Boraginoideae subfamily. Therefore, a high-quality reference genome for *P. recurvata* would be valuable for addressing questions both in the desert winter annual system as well as across broader taxonomic scales. Here, we present a near telomere-to-telomere, chromosome-scale genome and plastid assembly for *Pectocarya recurvata*, the first reference genome in the Cynoglossoideae subfamily of Boraginaceae. We used PacBio HiFi sequencing to assemble the reference genome and annotated the genome with full-length transcripts from an Iso-Seq library. We assessed the completeness of our genome with BUSCO and k-mer analysis, and estimated the genome size of six individuals of *P. recurvata* using flow cytometry. The chromosome-scale genome assembly for *P. recurvata* is 216.0 Mbp long (N50 = 12.1 Mbp). Our assembly includes 12 primary contigs (158.3 Mbp total length) containing 30,655 genes with telomeres assembled at 23/24 chromosome ends. Flow cytometry measurements from the same population include two plants with 1C = 196.9 Mbp, which is the smallest genome size measured for taxa in Boraginaceae. We also measured four individuals with 1C = 385.8 Mbp, consistent with the presence of tetraploidy in this population. The genome and plastome assemblies and annotations are publicly available and can be accessed on NCBI (GCA_046736585.1) and Zenodo (DOI: 10.5281/zenodo.14714947). Ultimately, our annotated *P. recurvata* genome and plastome assemblies provide essential genomic tools for future opportunities to investigate outstanding questions in physiological ecology and phylogenetics.

Topic: Development and Structure

A-190

Laticifers are present in Acalyphoideae after all: new insights from leaf anatomy with implications for the systematics and evolution of Euphorbiaceae

Author: Renata Meira, Clara Mouzella, Ana Sousa, Maria Beatriz Caruzo, Iris Montero-Muñoz, Ricarda Riina
Affiliation: Universidade Federal de Viçosa, UNIFESP, RJB (CSIC)

Euphorbiaceae is among the main angiosperm families with a high number of laticiferous species. Although many of its species remain to be studied in terms of their anatomy, chemistry, and uses, there are some of recognized economic importance due to useful secondary compounds present in the latex. Acalyphoideae, one of the three major subfamilies, has traditionally been distinguished from the rest of Euphorbiaceae by the absence of latex and laticifers. To test this long-standing assumption, we anatomically analyzed 40 species in 10 genera, representing six of the nine subclades of Acalyphoideae *s.s.*, to examine the presence of laticifers using leaf blade and petiole sections. Laticifers were observed in all the studied species and consisted of multinucleate, elongated cells with dense cytoplasm. They were articulated and branched in *Acalypha*, *Bia*, and *Dalechampia*; this was further confirmed by ontogenetic analyses in *Acalypha accedens*, *A. brasiliensis*, and *A. poiretii*. Histochemical tests revealed lipids, proteins, mucilage, and starch in laticifers. Our results demonstrate that laticifers are present and common in Acalyphoideae and thus more widespread in Euphorbiaceae than previously known. The scarcity of detailed anatomical studies, and the often imperceptible latex exudation of most Acalyphoideae, are probably the main reasons that have misled field botanists and systematists in the past.

Topic: Evolutionary history of the Gnetales

A-191

Gnetales: An Enigmatic Clade

Author: Dennis Stevenson
Affiliation: New York Botanical Garden

Gnetales is a small group of seed plants comprised of three genera (*Ephedra* ca 50 spp., *Gnetum* ca. 40 spp. and *Welwitschia mirabilis*). As a group, they have a highly contentious and unresolved phylogenetic affinity. The genera are morphologically divergent with very different ecological situations with *Gnetum* found in mesic tropical habitats in contrast to *Ephedra* in arid temperate to subtropical habitats and *Welwitschia* in a single extreme desert situation. Leaves are highly reduced to scale-like in *Ephedra*, petiolate with a broad net-veined lamina in *Gnetum* and only two persistent, perennial and strap-like leaves with a basal intercalary meristem in *Welwitschia*. Similar disparities a occur in stomatal development, seedling morphology, embryogenesis, secondary growth and vessel element structure. Recent advancements in Evo/Devo present new ways to understand the departures in leaf development including the net venation in *Gnetum* that is different from that in Angiosperms. Similarly, there is the presence of successive cambia in liana *Gnetum* spp. and the taproot of *Welwitschia,* but they have different origins in each as well as other seed plants such as cycads. Similarly, the liana species of *Ephedra* have their own peculiar woos anatomy. understand the basis for these autapomorphies is challenging.

Topic: *Development and Structure*

A-192

An anatomical atlas of angiosperm roots reveal macroevolutionary trends and innovations

Author: Heather Phillips, José Dinneny, Michelle Yang
Affiliation: Stanford University

Shortly after the initial transition of plants to land approximately 500 milion years ago, roots evolved as a means to anchor plants to the soil and enhance water and nutrient uptake. Since the origin of these first roots, plants have evolved to occupy a variety of ecosystems and niches and likewise formed a vast array of unique morphological and anatomical features within their roots. In this study, we aimed to characterize root diversity by growing species with sequenced genomes under common laboratory conditions. Plantlet roots are then anatomically characterized, and images of the root apical meristem as well as cross sections at various stages of development were used to generate an anatomical atlas of flowering plant roots. The resulting atlas allows us to characterize macroevolutionary trends in root anatomy, identify lineage specific innovations, and parse out the effects of life history, phylogenetic signal and climate on root anatomy.

Topic: *Graeme P. Berlyn Tribute: Light and Life of Forests from Terrestrial to Subtidal and their Regeneration*

A-193

Graeme Berlyn: From Microscopy to Ecophysiology—An Eclectic Career.

Author: Dennis Stevenson
Affiliation: New York Botanical Garden

Graeme began his botanical journey at Iowa State University under the aegis of John Sass. Through out this journey, Graeme developed interest multiple botanical subdisciplines including but not limited anatomy and morphology, development, physiology, ecology, microtechnique and microscopy. He had an amazing ability to integrate these interests and apply them to in-depth understanding of plant structure and function in an environmental context. His textbook of Botanical Microtechnique and Cytochemistry is a synthesis of how and why to use the approach as well as establishing a new synthetic and practical approach. As with everything he approached, he brought his skills and knowledge into the classroom. As a result, he was well known as an outstanding teacher and mentor. Importantly, this was not just to students in the classroom, but also to the community at large.

Topic: *Pteridology*

A-194

The genome of the vining fern Lygodium microphyllum highlights genomic and functional differences between life phases of an invasive plant

Author: Jessie Pelosi, Ruth Davenport, Li-Yaung Kuo, Levi Gray, Anthony Dant, Emily Kim, Fay-Wei Li, Katrina Dlugosch, Trevor Krabbenhoft, W. Brad Barbazuk, Emily Sessa
Affiliation: University of Arizona, University of Florida, National Tsing Hua University, University at Buffalo, Boyce Thompson Institute, New York Botanical Garden

Functional and genomic studies on the differences between gametophyte and sporophyte life phases remain scarce, yet unraveling these dynamics is crucial to understanding the biology of plants and the success of each phase under different environments. Here, we provide a novel reference genome for the highly invasive fern *Lygodium microphyllum* and compare the transcriptomic and epigenomic landscapes of the gametophyte and sporophyte life phases. We found differential regulation of developmental genes (homeobox and MADS-box clades) and usage of alternative isoforms that may play a role in the genomic determination of the haploid and diploid life stages. We further generated the first base pair-resolution methylome of a fern gametophyte, and determined that methylation patterns are remarkably similar between vegetative tissues despite their morphological and functional differences. By examining the physiological and transcriptomic responses of gametophytes and sporophytes to freezing stress, the most likely abiotic factor preventing further expansion of this invasive species, we show that life phases and tissues use alternative molecular pathways to respond to this stressor, underscoring the need to incorporate both life phases when developing effective mitigation strategies. These new genomic resources fill a gap in our understanding of fundamental plant biology and inform invasive species research.

Topic: *Development and Structure*

A-195

Assessing the Ontogeny of Floral Fusion and Synorganization Throughout the Zingiberales

Author: Heather Phillips, Chelsea Specht
Affiliation: Stanford University, Cornell University

Floral fusion contributes to the overall synorganization of the Zingiberales flower, and mediates transitions to various pollination syndromes throughout the order. While the morphology of floral fusion phenotypes is well understood at anthesis, the developmental processes defining these phenotypes is poorly understood. Furthermore, developmental landmarks have yet to be defined for these flowers, preventing comparative analyses of the timing and position of floral organ development across the order.

In order to address these gaps in our knowledge, Inflorescence tissue was collected from Zingiberales species in living collections throughout the continental United States, and imaged using a modified version of Sattler's method coupled with epillumination microscopy. Six conserved stages of floral development were identified as "developmental landmarks", which aided in efficiently comparing developmental patterns across species. Fusion processes were found to occur later in development once the floral bauplan was established, and to contribute to the development of several highly synorganized structures found in specific lineages. Our results indicate several, independent origins of floral fusion in the Zingiberales, defined by unique processes and combinations of organs involved. Multiple transitions to perianth adnation were recorded in the banana grade, while a single transition to petaloidy in the ginger families mediated the transition to increased synorganization of the androecial whorl in the Cannaceae and Marantaceae, as well as the development of a fused labellum in the Costaceae and Zingiberaceae.

Topic: *Reproductive ecology and evolution of plants in stress-prone environments*

A-196

Sex Under Stress: Consequences of Sexual Separation in Cylindropuntia

Author: Lluvia Flores-Rentería, Niveditha Ramadoss, Scarlet Steele
Affiliation: San Diego State University

Flowering plants exhibit a wide variety of sexual systems that have ecological and genetic consequences. However, understanding these systems is challenging due to limited species-level data. In this talk, we will explore the genus *Cylindropuntia* (family Cactaceae), focusing on species found in the Sonoran Desert—one of the hottest places on Earth. Despite their diverse sexual systems, this genus remains largely understudied, offering a unique opportunity to understand plant reproduction in extreme environments. Our first goal was to identify its sexual system as plants carrying vestigial reproductive organs can lead to misclassification. For example, species *C. wolfii* was reported anecdotally as gynodioecious while its fruit production resembled that of a dioecious species. Dioecious plants often exhibit sexual dimorphism, which can have ecological effects on pollinator interactions. To study this, we conducted a comprehensive analysis of quantitative and qualitative traits in *C. wolfii* flowers and compared them for statistical differences. Lastly, dioecy has evolutionary consequences such as reduced genetic diversity, so we investigated whether dioecious *Cylindropuntia* species exhibit lower genetic diversity compared to that of hermaphrodites. Our experimental crosses and histological analysis of putative female and bisexual flowers found that *C. wolfii* is functionally dioecious. Our qualitative and quantitative analysis showed that their male flowers are larger and brighter, leading to a greater attraction of pollinators compared to female flowers. We found that dioecious *Cylindropuntia* species maintain genetic diversity levels comparable to those of hermaphrodites. However, overall genetic diversity across all species was low, highlighting the need for conservation efforts. By uncovering the sexual systems' consequences, our study offers insights into reproduction of cacti - an extraordinary but vulnerable group thriving in a stress-prone environment.

Topic: Graeme P. Berlyn Tribute: Light and Life of Forests from Terrestrial to Subtidal and their Regeneration

A-197

Comparison of Blue Carbon Sequestration by Mangroves and Seagrasses among Tropical and Subtropical Ocean Basins.

Author: Anitra Thorhaug, Arthur Schwarz, Graeme Berlyn, Jorge Lopez-Portillo, John Gallagher, Helen Poulos
Affiliation: Greater Caribbean Energy & ENvironment Foundation, Southwestern Adventist University, Yale University, Instituto de Ecología, A.C. (INECOL), University of Tasmania, Wesleyan University

Among tropical and subtropical habitats, mangrove and seagrass communities have among the highest rates of carbon sequestration. The rate of carbon sequestration in these tropical environments is a result of high rates of primary production, low rates of decomposition within sediments due to low oxygen concentrations, and low nutrient concentration in the detritus that sinks out of the water column as the current is slowed by mangrove roots or seagrass blades. Eventually this detritus becomes incorporated into the anoxic sediment. After creating the first basin-wide estimate of Blue Carbon for the Gulf of Mexico, we have expanded our estimates to the Caribbean and then made comparisons to other oceanic areas such as the greater Southeast Asia (Indo-Pacific) and the Indian Ocean (including the east coast of Africa). Tropical and subtropical seagrass and mangrove habitats have high blue carbon values due to long growing seasons, waters that are enriched in dissolved carbon dioxide from equatorial upwellings, and a rich array of habitats that support seagrass and mangroves. The total value of blue carbon from seagrass in the four regions under consideration here is 2,446 Tg, while that of mangroves is substantially greater at 4,391 Tg. Among the four regions there were major differences for seagrass with 1,894 Tg in the Southeast Asian waters, 386 Tg in the Caribbean basin, 184 Tg in the Gulf of Mexico, and 200 Tg in the Indian Ocean. Likewise, for mangroves, the regional blue carbon values are 3,095 Tg in the southeast Asian region, 800 Tg in the Caribbean, 300 Tg in the Indian Ocean, and 196 Tg in the Gulf of Mexico.

The importance of these estimates are to guide international efforts is to protect, enhance and restore these habitats which sequester blue carbon. We have worked for a half century on the physiology, ecology and habitat restoration techniques for these foundation species in the tropics and subtropics. Techniques that we and many others have developed are adequate to restore seagrasses and mangroves on a large scale. Additional ecosystem services afforded by restoration include enhanced fish nursery habitat, endangered species habitat, increased biodiversity, water clarification, and shoreline resilience.

Topic: Graeme P. Berlyn Tribute: Light and Life of Forests from Terrestrial to Subtidal and their Regeneration

A-198

How do seagrasses, higher plants derived from terrestrial plants obtain light in oceans with chiefly Blue and Green light? Blue, green, orange, red light effects on seagrass indicating species, light flux on photosynthetic pathways, pigments, health, and

Author: Anitra Thorhaug, Helen Poulos, Graeme Berlyn
Affiliation: Greater Caribbean Energy & ENvironment Foundation, Wesleyan University, Yale University

Graeme Berlyn boldly leaped from spectral reflectance in terrestrial plants to use it experimentally with marine plants. Clearly testing colored light for seagrass for photosynthetic pathways was needed. In the marine/estuarine realms, light filters through seawater changing the spectral transmission from red to green and blue. Intermediate (10-200m) coastal depths with sedimentary seafloors thus receive only blue and green light. Light color is potentially important in seagrass, a higher plant adapting to marine from terrestrial ancestors minimally 70 million years ago. We tested seagrass using spectral reflectance for the first time blue/green light. Spectral reflectance's analytical power has two fundamental bases: 1.) Einstein's discovery "light consists of particles" (photons); 2.) Feynman's discovery (1985) "light is not really affected by surfaces". As a photon becomes incident on a plant's leaf surface, this photon interacts with electrons throughout the leaf. The photon is then scattered while a new photon is emitted (electrons can absorb one photon and emit another photon). Consequently, the "reflected" light characterizes the signature of the light-absorbing elements of the leaf, the pigments. If light solely struck the leaf surface and bounced off, it would not show this characteristic reflectance spectra. Reflectance spectra have a fundamental identity in a species, but the quality and quantity of the reflectance of a species depends on the physiological state. Indices of spectral reflectance allow scale-able statistical delineation among physiological responses.

Measurements are amenable to remote sensing of community health and species identification. Previously we used spectral reflectance over a variety of types of plants (from vascular alpine to desert and marine phyla), finding pigment responses by this non-intrusive, non-destructive method. Herein light filters of Green, Blue, Orange, Red light for 6 hours incubation on live seagrasses tropical/subtropical species Thalassia testudinum, Halodule wrightii, and Syringodium filiforme and the temperate species, Zostera marina. Light transmissivity was a factor at 10, 23, 40% +full light. We compare normal spectral indices including PRI (photosynthetic efficiency), VAZ (violaxanthin, antheroxanthin, &zeaxanthins), red and green edges, Chl NDI and Chl NDVI (chlorophyll normalized Vegetation Index), plus our new indices created (carotenoid and xanthophyll intensities) and Gitelson's older carotenoid indices compared to spectral reflectance and partial absorption curves. Clearly seen are higher photosynthetic efficiencies at 23% light diminution under all four colors with intense activation of specific pigments below 505nm and far less activation of Chlorophyll. Blue light responses differed greatly from red light responses. Species differed in response to blue light.

Topic: Development and Structure

A-199

Decoding the Cellular and Genetic Basis of Nectary Development in Aquilegia

Author: Yan Gong, Ya Min, Elena Kramer
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Angiosperms are the most speciose and diverse plant lineage, and much of this great diversity is apparent in their floral organ. Many traits of flower development have evolved to facilitate plant-pollinator interactions. The presence of the nectary and its secreted nectar is among these traits. In angiosperms, floral nectaries are thought to have evolved many times independently. While a few core eudicots have been shown to share similar genetic architecture in regulating their floral nectary development, how nectary formation is controlled in other angiosperm lineages is still a mystery. Here, we examined cellular and molecular mechanisms behind nectary development in basal eudicot species *Aquilegia*. In *Aquilegia*, each elaborated petal spur bears a nectary at the tip. Recently, we identified STYLISH transcription factors as novel regulators of *Aquilegia* nectary development, and we employed gene expression profiling methods and RNAi-based gene silencing to probe the genetic pathways downstream of STYLISH. In addition, with imaging approaches at various resolutions, we uncovered the cellular basis behind holocrine secretion in *Aquilegia* nectaries.

Topic: Physiology

A-200

Alleviating physiological dormancy on Trema micrantha seeds

Author: Daniella Fuller, Paul-Camilo Zalamea, Carolina Sarmiento, Gabriela Quesada Avila
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Tropical forests are facing an increase in frequency and intensity of disturbances due to deforestation, land-use change, and climate warming, making the role of pioneer tree species key for ecosystem recovery. *Trema micrantha*, an early successional tree, is widely distributed through the Neotropics and possesses traits that facilitate rapid colonization of degraded environments. However, its strong seed physiological dormancy challenges its use in restoration efforts. Understanding the mechanisms underlying dormancy persistence and germination cues are essential for optimizing seed-based restoration strategies. Here we investigated dormancy-breaking treatments in *T. micrantha* seeds collected from two populations (i.e. Southern Florida and Central Panama). Seed imbibition was also measured to understand optimal imbibition time and seed mass at different time increments (between 0 to 100 hours). To explore dormancy alleviation mechanisms, seeds were mechanically scarified (sanding of the seed coat) and exposed to different concentrations of gibberellic acid (GA_3) under two controlled temperature conditions for germination trials. Zero-inflated mixed effect models were used to determine which factors (GA_3, mechanical scarification, and

temperature regimen) significantly impacted germination proportions across populations. We found that seeds that were mechanically scarified imbibed quicker than seeds that were not scarified, where maximum imbibition of this species was reached at 48 hours. We found inter-population variation in germination response when exposed to the same treatments. While GA_3 enhanced germination success, it is not always equally effective, showing that there are physiological differences among populations. Higher concentrations of GA_3 (from 600ppm to 2000ppm) increased germination success in the Florida population. For the Panama population, germination success peaked at 600ppm, highlighting differences in hormonal sensitivity. Mechanical scarification further increased germination proportions across both populations, but the highest germ proportions were attained when GA_3 was also added. Temperature influences on germination responses on were also population dependent, and difficult to generalize. The observed inter-population differences suggest that restoration protocols should consider population-specific dormancy-breaking treatments to maximize germination success. Given the ecological importance of *Trema micrantha* as a pioneer species, optimizing its germination potential can enhance forest recovery efforts in disturbed tropical landscapes.

Topic: *Pteridology*

A-201

Effective long-distance dispersal of ferns between isolated habitat

Author: James Brock
Affiliation: University of Auckland

Wind is a long-established dispersal vector of fern spore, and isolated populations of ferns are understood to be connected by spore dispersed in the atmosphere. Island biogeography and fern distribution patterns provide robust evidence for the ready dispersal of spore over long distances (> 100 kms) between isolated oceanic islands, but little evidence exists to support wind as the vector underpinning such ready dispersal. Whilst wind is undoubtedly important in the dispersal of fern spore, we can look to the discipline of landscape ecology and evidence of constrained dispersal between fragmented habitat patches to understand the likelihood of wind connecting fern populations across isolated oceanic islands. Combining what is known of anemochorous fern dispersal and modelled dispersal probabilities across fragmented landscapes, I will present an argument that suggests that wind may not be an effective vector for long-distance dispersal of fern spore in scenarios where suitable habitat for ferns is rare in an otherwise hazardous matrix. So, if not wind, what other vectors might there be supporting ready dispersal of fern spore long distances across isolated habitat patches? Prior to the introduction of predatory mammalian pest species onto oceanic islands across the world by European fleets in the 16th and 17th centuries, such islands were connected by significant networks of migratory birds and seabirds. Many surviving seabird colonies today occur in association with dense fern-dominated vegetation and several fern species are known to occur only in association with seabirds. I will present my investigations into the potential of bird dispersal of ferns across oceanic islands including a study examining the correlative relationship between similarity matrices of wind connectivity, bird, and fern communities of islands and continents across the Southern Atlantic, Indian, and Pacific oceans. Findings so far suggest that zoochory may represent an important pathway for fern dispersal between isolated fern populations, in particular where potential animal vectors share similar habitats to the ferns.

Topic: *Trees, Traits, and Time*

A-202

Rethinking stelar evolution

Author: Jacob Suissa, Mihai Tomescu, William Friedman, Karl Niklas
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The primary vascular system of plants (the stele) has attracted interest from paleobotanists, developmental biologists, systematists, and physiologists for nearly two centuries. Ferns, with their diverse stelar morphology, deep evolutionary history, and prominent fossil record, have been a major focus in studies of the stele. To explain the diversity of stelar morphology, past adaptive hypotheses have invoked biomechanics, hydraulics, and drought tolerance as key selection pressures driving the evolution of stelar complexity; but, these hypotheses often isolate the stele from a whole-plant developmental context, ignoring potential covariation between vascular patterning and shoot morphology. Furthermore, incongruence between expected patterns and observed data challenge adaptive hypotheses, precluding a comprehensive explanation of stelar evolution. While ontogeny has been previously recognized as a factor in stelar evolution, it has not been fully integrated into a comprehensive framework. Here we synthesize 150-years of research on stelar morphology, incorporating developmental, physiological, and phylogenetic data and leverage broad scale phylogenetic comparative methods to explore the evolution of stelar morphology. We present the *ontogenetic hypothesis* of stelar evolution. This hypothesis posits that stelar morphology is an integrated feature of whole-plant ontogeny, not a trait shaped by direct selection for adaptive patterns. This shift in perspective provides an updated framework for understanding the determinants of stelar morphology and focusses future efforts to ask more incisive questions about the evolution of primary vascular architecture.

Topic: *Molecular Ecology*

A-203

Demographic origin of a high latitude lineages in Phyllodoce (Ericaceae) and its implication on adaptive divergence

Author: Ryutaro Koda, Hajime Ikeda
Affiliation: The University of Tokyo

Species mainly distributed in extant high-latitude regions are thought to have originated concurrently with climatic cooling during the Pleistocene. Although their phylogenetic relationships have been inferred in several taxa, the evolutionary processes of their divergence remain to be explored. One hypothesis on their evolution is that high-latitude lineages diverged through northward colonization into newly available habitats, in which they acquired adaptive traits to cold environments by positive selection during and/or after the colonization. Alternatively, these lineages may have diverged from ancestral species persisting in the high latitude before climatic cooling; thereby, retaining ancestral adaptive traits. Elucidating the demographic history of high-latitude lineages is essential to examine these evolutionary hypotheses. In this study, we investigated the demographic history and adaptive genes associated with the divergence of high-latitude lineages in *Phyllodoce* (Ericaceae), including *P. aleutica*, *P. caerulea*, and *P. glanduliflora*. Using over 4,000 genes obtained from RNA-seq and genome sequencing, we examined whether high-latitude lineages diverged through northward colonization or originated from pre-existing populations. Our demographic analysis revealed a significant population bottleneck associated with the divergence of the high-latitude lineage, while the mid-latitude lineage maintained a constant population size from its ancestral lineage. This finding supports the hypothesis that the high-latitude lineage was derived from a mid-latitude ancestor. To examine their adaptive divergence, we calculated synonymous and non-synonymous substitution rates to identify genes under positive selection during the evolution of the high-latitude lineages. We found that approximately 600 genes were identified as under positive selection exclusively in high-latitude species. Moreover, gene ontology analysis showed significant enrichment in chloroplast thylakoid membrane-associated genes, particularly genes involved in Photosystem I complex and cyclic electron transport exhibited uniquely fixed amino acid substitutions in the high-latitude lineage. These findings imply that balancing light energy utilization in photosynthesis may be associated with adaptation to cold temperatures in high latitudes during the growing season. Taken together, our study suggests that northward colonization with adaptation in the photosynthetic pathway leads to the divergence of high-latitude species in the Pleistocene.

Topic: *Ecology*

A-204

Combined and interactive effects of deer and invasive ground covers on plants in restoration of a southwest Ohio mesophytic forest

Author: Kathryn Yurek, David Gorchov
Affiliation: University of South Dakota, Miami University

Many forest stands are degraded due to invasive plant species and overabundant deer. We tested the impacts of white-tailed deer (Odocoileus virginianus) and invasive ground cover species on forest floor plants in a Western Mesophytic forest stand in Hamilton County, Ohio. This site has a diverse canopy tree layer, but is depauperate in native plants in the understory and forest floor. The site had been managed for invasive shrubs, but three invasive plant species were common on the forest floor - lesser celandine (Ranunculus ficaria), wintercreeper (Euonymus fortunei), and Japanese stiltgrass (Microstegium vimineum). Deer browse pressure was high based on a browse line in the vegetation, scarcity of species preferred by deer, and browse damage on twigs.

We used a split-plot design to test effects of deer, invasives, and their interaction. We established two deer exclosures and two deer access plots (each 10x10 m) in winter 2022-23. A random half of each plot was assigned to invasive groundcover management. In those half-plots, 2% glyphosate was spot-sprayed on wintercreeper in July and August 2023, and on wintercreeper and lesser celandine in April 2024. Japanese stiltgrass was spot-sprayed with grass-specific herbicide (0.48% fluazifop-P-butyl) in July 2023.

In addition to censusing all plants in sub-plots in each plot, we also tested the effectiveness of enrichment planting. We planted nursery-grown seedlings of two trees characteristic of Western Mesophytic forests - Sugar Maple (Acer saccharum) and American hophornbeam (Ostrya virginianca) - and two perennial herbs with showy flowers - wild geranium (Geranium maculatum) and yellow trout lily (Erythronium americanum) in the dormant season of 2023-24.

Deer density was estimated by distance sampling of fecal pellet piles. Pellets were sparse in summer 2023, suggesting minimal deer use. Buti n Feb.-March 2024 pellets were more common 2024, resulting in an estimate of 29/km2.

Forest floor plants were sampled pre-treatment (spring and summer 2023) and post-treatment (spring and summer 2024). Herbicide treatment significantly reduced cover of lesser celandine and wintercreeper. A month after the Spring 2024 spraying, lesser celandine cover averaged 1% in sprayed plots and 17% in controls; wintercreeper averaged 0.1% cover in sprayed plots and 1.1% in controls. Planted sugar maple seedlings were more likely to lose height (due to browse and transplant shock) than grow, but we found a positive effect of herbicide treatment on growth, supporting our hypothesis that invasive plants negatively impact natives. However, we also found herbicide treatment reduced species richness of native plants and survival of planted wild geranium survival, indicating non-target effects. American hophornbeam and yellow trout lily did not survive in any of the plots.

We attribute the non-target effects of herbicide to application in April when many native plants are in leaf. We did not treat earlier because literature reports that is less effective vs lesser celandine. We've detected few effects of deer on native plants, and no significant deer x invasive plant interactions. However, we are continuing to monitor the survival and growth of the planted species, and the species composition and richness across the

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Topic: Defining forces in fern evolution: Celebrating the contributions of Kathleen Pryer and Michael Windham

A-205

The devil is in the data: Michael Windham and the power of foundational knowledge.

Author: James Beck
Affiliation: Wichita State University

We are now at a time where well-resolved phylogenies can be readily obtained for most plant groups, and where fully sequenced genomes are feasible. As these tools become routine, what increasingly distinguishes research projects are the quality of the study systems- the clarity with which natural experiments provide testable hypotheses. Over the span of a 40-year career, Dr. Michael Windham has been uniquely focused on developing such study systems in a variety of pteridophyte groups. These foundational datasets typically feature multiple data types (morphology, cytology, genetics), a strong link between these data in the form of high-quality voucher specimens, and the aggregation of many specimens into geographically meaningful and taxonomically complete sample sets. This foundational knowledge has been used by Dr. Windham, his many collaborators, and students to answer questions regarding fern relationships, biogeography, cytology, sexuality, hybridization, diversification, and morphological evolution. Here we present three such examples of these foundational datasets and their research legacies.

Topic: Hybrids and Hybridization

A-206

Genetic Diversity, Structure, and Introgression in Quercus Bicolor: Comparing the Range Core and Southern Margin

Author: Jesse Parker, Sean Hoban, Laura Thompson, Scott Schlarbaum
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, but no evidence of introgression from any species in core populations, despite sympatry with closely related congeners. This suggests that hybridization may be more likely to develop into advanced-generation introgression at range margins than cores. These introgressed range edge populations exhibited greater structure and differentiation, even when only including relatively pure *Q. bicolor* individuals, without evidence of increased inbreeding or reduced diversity. Isolation by distance and AMOVA tests support a hypothesis of panmixia, with a combination of local adaptation and introgression potentially driving differentiation at the range edge. Significant correlations between ancestry proportion and heterozygosity, inbreeding coefficients, and population differentiation were found using generalized linear models, indicating that introgression may play a role in stabilizing depauperate marginal populations through the introduction of genetic diversity and adaptive alleles. These findings underscore the possible role of interspecific hybridization in shaping genetic diversity and differentiation at the range edge and highlight the importance of accounting for introgression when testing hypotheses related to the CMH. As conservation efforts increasingly focus on rear-edge populations in response to a changing climate, understanding hybridization, genetic structure, and diversity in these populations is essential for informing interventions such as germplasm conservation, adaptive breeding, and assisted gene flow.

Topic: Phylogenomics

A-207

Resolving discordance along the Asparagaceae phylogenetic backbone

Author: Cody Coyotee Howard, Philip Bentz
Affiliation: Oklahoma State University, HudsonAlpha Institute for Biotechnology

Poorly supported phylogenetic branches are commonly viewed as a nuisance. As a consequence, lineages that contribute to discordance, such as rogue taxa, may be excluded from further analyses. These rogue taxa/lineages may be the result of a rapid radiation, hybridization, and/or incomplete lineage sorting. Therefore, excluding such taxa from analysis narrows our understanding of the complex nature of evolution. The monocot clade Asparagaceae, an ecologically and economically important clade of ~2,500 taxa, has had persistently low resolution along its phylogenetic backbone due to the rogue-like behavior of one monotypic sublineage: Aphyllanthoideae. Establishing robust estimates of the phylogenetic placement of Aphyllanthoideae is critical to understanding trait evolution and historical biogeography across the clade. Using a targeted capture sequencing approach with the Asparagaceae1726 probe set and a generic-level sampling of the clade, we confidently resolve relationships among all seven Asparagaceae sublineages and investigate the underlying causes of discordance across the phylogeny. Specifically, we closely examine the relative phylogenetic placement of Aphyllanthoideae using multiple approaches. Maximum likelihood analysis (IQ-Tree) of concatenated nuclear data placed Aphyllanthoideae sister to all remaining Asparagaceae lineages, but with low support. Coalescent-based analyses (ASTRAL), which can account for high levels of incomplete lineage sorting, placed Aphyllanthoideae sister to a clade of Agavoideae, Scilloideae and Brodiaeoideae with strong support. The ASTRAL relationship aligns more closely with the chloroplast phylogeny, which poorly supported Aphyllanthoideae as sister to Scilloideae and Brodiaeoideae. Considerable discordance was found along the Asparagaceae backbone, which is likely due to historical rapid radiations at the origin of the clade as well as early in the evolution of each sublineage. By resolving the placement Aphyllanthoideae, our work represents great progress towards a more accurate phylogenetic backbone of the Asparagaceae, which will enable more informed studies within each sublineage and increase our understanding of the potential causes of gene tree discordance across the clade.

Topic: Ecology

A-208

Complexity in the city: studying the effects of urban environmental heterogeneity on the life history traits of the annual, invasive forb Centaurea melitensis across California

Author: Anthony Dant
Affiliation: University of Arizona

Over the past 200 years, urbanization has steadily increased around the world. In addition to humans, a variety of life, spanning most groups of taxa, inhabit these new environments. As the number of organisms interacting with urban spaces increases, it is increasingly recognized that biology must include an understanding of how the ecology

and life history of these organisms change in response to urbanization. A central unanswered question is how specific environmental cues within urban areas are responsible for changes in life history traits.

To better understand how urban environmental heterogeneity affects eco-evolutionary variation in traits, I explored the life history traits of the invasive, annual self-pollinating forb *Centaurea melitensis* across the state of California. Specifically, I tested whether the plant economic spectrum, which predicts differences in life history strategies in response to varying environmental conditions, could be applied to *C. melitensis* in urban systems. To test this, I collected seeds from populations of *C. melitensis* across the state of California in locations which varied in environmental conditions including the urban heat island effect, land cover, pollution, and socioeconomics. Seeds were then grown in greenhouse conditions, self pollinated, and grown for a second generation in which a variety of traits were measured such as specific leaf area and root diameter. Associations of traits with environment variables were tested using linear mixed models. Results showed significant associations of traits with multiple urban environmental variables including land cover, urban heat island, and socio-economics. Additionally, traits followed patterns predicted by the plant economics spectrum. For example, specific leaf area was negatively related to an increase of urban heat island, as predicted by the plant economics spectrum.

These results highlight eco-evolutionary change in response to urbanization and particularly the importance of including a wide spectrum of urban environmental heterogeneity in future urban studies. These results also suggest that the plant economic spectrum can be applied to future urban plant studies as a way to understand ecological trade offs when inhabiting urban environments. As urbanization continues to increase across the world, determining which environmental cues lead to eco-evolutionary change will be instrumental in understanding, conserving, and managing species in urban environments.

Topic: *Ethnobotany*

A-209

Narratives of Care: Documenting Plant-Based Abortions and Community Care in Southern California

Author: Guadalupe Maldonado
Affiliation: Cal Poly Pomona

This presented work is an extension of the published work "Andrade[1], G. M., Rueda, D. C., & Ezcurra, E. (2024). Migrant People and Plant Traditions: Cultural Continuity of Abortifacients among Immigrant Michoacán Women in California. *CALIFORNIA GEOGRAPHY*, 29." This collaborative photographic documentation explores the role of plants in abortion practices and community-based accompaniment in Southern California. Developed in partnership with the Los Angeles Abortion Support Collective and French photographer Mahè Elipe from the Mexico City community, the project highlights narratives of care and resistance through visual storytelling. Participants took part in photography and ethnographic sessions, sharing personal experiences and collaboratively creating images inspired by their narratives, incorporating relevant plants and symbolic materials. One photograph from this collaboration was recently featured in the annual selection of Frontline Freelance Mexico. Ultimately, the project foregrounds plant-based knowledge, community solidarity, and the intersection of art, ethnography, and reproductive justice.

Topic: *Reproductive Processes*

A-210

Pollinator-driven divergence and speciation in three Aeschynanthus species

Author: Jing-Yi Lu, Richard Ree
Affiliation: University of Chicago, Field Museum

How does pollinator-driven divergence lead to plant speciation? We examined the role of pollinators in an intriguing case of incipient species in the SE Asian sunbird-pollinated genus *Aeschynanthus*. Previous findings suggested an expansion of pollinator niche breadth led to a shift to mixed vertebrate pollination in the origin of *A. acuminatus*. Its two putatively closest relatives, *A. moningerae* and *A. pedunculatus*, share identical vegetative traits but differ only in key floral traits indicative of sunbird pollination, i.e., their longer corolla tubes and longer peduncles. We first confirmed their sunbird specialized pollination systems, then tested between two specific phylogenetic hypotheses: (1) Reciprocal monophyly - where the two sunbird specialists form a clade sister to *A. acuminatus* (2) Genetic nestness - where the two geographically restricted endemics reflected a budding history with reversal to sunbird pollination from a widespread *A. acuminatus*. Phylogenetic inference based on genome-wide SNPs revealed a combination of two, with *A. moningerae* nested within *A. acuminatus* while *A. pedunculatus* forms a sister lineage with *A. bracteatus*. Morphological analyses on floral traits demonstrated convergence of the two sunbird specialists despite their independent origins. Progenitor-derivative speciation led to a localized reversal to sunbird specialization in *A. moningerae* on geographically isolated Hainan Island. In contrast, sympatric populations of *A. pedunculatus* and *A. acuminatus* in southern Vietnam still partially overlap in flowering phenology and pollinator niche even with pollinator-adapted floral divergence. We detected introgression from *A. pedunculatus* into *A. acuminatus*, resulting in unusually wide floral variation. Together, we demonstrated multiple expansion and contraction of pollinator niche breadths concurrent with the series of speciation events in focal *Aeschynanthus* species. However, pollinator shifts alone did not generate complete reproductive isolation unless complemented with geographic or phenological isolation.

Topic: *Reproductive Processes*

A-211

Selection of pollen heteromorphism in a mixed mating species

Author: Samson Acoca-Pidolle
Affiliation: University of Kansas

The number of pollen apertures is variable in Angiosperms, not only between species but also sometimes between individuals (pollen polymorphism) and even between pollen grains of the same flower (pollen heteromorphism). Pollen heteromorphism in the number of apertures seems to be relatively common in Angiosperms. Apertures are a thinner part of the exine and are a favourable site for exchange between pollen grains and their environment and for pollen germination. Pollen grains with more apertures germinate faster but have a lower survival rate. Therefore, apertures are key to understanding pollen competition and could be under selection. Some models predict that pollen heteromorphism could be stable when pollination is uncertain. However, mixed mating systems have never been included in these models and the evolution of aperture number with the mating system has never been investigated.

Using *Viola arvensis*, a pollen heteromorphic species with mixed mating, and a resurrection approach in natural populations, we tested whether populations with higher selfing rates and evolving a selfing syndrome show changes in pollen heteromorphism. We also tested the effects of pollen heteromorphism on mating patterns through male and female functions in a constant pollination environment. Finally, I have tried to shed some light on the results by constructing a model.

In the model, the selfing rate of the population is positively correlated with the aperture number. However, no change has been detected in natural populations that experienced an increase in selfing rates. Nevertheless, pollen heteromorphism was found to explain mating through male and female functions. Finally, the model helps to understand this apparent contradiction with likely changes in pollination in the natural population which could explain trait stasis.

Topic: *Ecology*

A-212

The impact of climate change on phylogenetic diversity in Rocky Mountain plant communities

Author: Leah Veldhuisen, Jocelyn Navarro, Lorah Seltzer, Brian Enquist, Katrina Dlugosch
Affiliation: University of Arizona, The University of Arizona

As climate change advances, it is imperative to understand its impacts on ecological communities, as well as how individual species are responding to drive community-level change. Globally, nearly 8% of species could be driven extinct by climate change alone. While it is well established that many populations are declining and community composition is changing, the details of which species are lost and their impact on community diversity remains poorly understood in many systems. One promising approach to describe patterns of species' responses to climate change is the variation in evolutionary relationships present in a community. Phylogenetic diversity of communities is linked to ecosystem stability, resilience and resistance to invasion, and is changing with global change. Phylogenetic diversity is predicted to decline with phylogenetically clustered extinction and extinction cascades, as well as homogenization via invasion. However, recent work has shown highly variable responses of phylogenetic diversity to climate change, invasions, extinctions and range-shifting species. Previous work also suggests

that phylogenetic diversity often does not correlate with functional diversity or other traditional community diversity metrics. Here, we assess the impact of climate change on phylogenetic diversity in Rocky Mountain subalpine plant communities, and whether species' responses are phylogenetically conserved. Overall, we evaluate two opposing hypotheses: that species' responses to warming are phylogenetically conserved and phylogeny will predict community and species-level changes under warming, or alternatively, that species' responses to warming are not phylogenetically conserved, and community- and species-level changes will correlate with other variables that are not phylogenetically conserved. We find that, while species richness and Shannon diversity increase with climate warming, phylogenetic diversity does not change, and individual species' percent cover changes in response to climate change do not show phylogenetic signal. However, we also find that range size, a trait without phylogenetic signal in our system, also does not explain species' climate change responses. Our results suggest that phylogenetic diversity does not respond to climate change with similar direction or magnitude as other community diversity metrics, and it remains unclear what may drive species-level responses.

Topic: *Ethnobotany*

A-213

An ethnobotany study of Indonesian Diaspora in the United States

Author: Ester Sinaga
Affiliation: University of California Davis

Numerous studies have documented Indonesia's food and medicinal plant knowledge. Although ethnobotanical practices in Indonesia have been extensively studied, research on the traditional knowledge preserved by the Indonesian diaspora remains scarce. Therefore, this study sets out to understand how these practices are retained or transformed among Indonesians who been dispersed from their home. Data were collected by conducting semi-structured interviews with 49 key informants and a survey with 132 respondents. The Relative Frequency of Citation (RFC) index and principal component analysis (PCA) were utilized to analyze how social and demographic characteristics influence traditional knowledge, practices, and plant use.

We document 131 plant species representing 98 genera and 55 families were cultivated by Indonesian diaspora in the United States. 49 most important plants were selected for the cultural importance analysis and our study found five plant species with the highest utilization were *Citrus hystrix DC., Ocimum basilicum L., Syzygium polyanthum (Wight) Walp, Curcuma longa L. and Manihot esculenta Crantz.* Ethnobotany knowledge of Indonesian diaspora in United States was associated with gender, where woman participants have more knowledge and practices. We also found there is a positive relationship between knowledge and age at the time of migration, where participants who migrated at a younger age retain lower ethnobotanical knowledge. Our analysis shows the importance of age at migration as a key factor in knowledge retention while long-term residence may challenge the continuity of traditional ethnobotanical practices among Indonesian migrants.

Topic: *Population Genetics/Genomics*

A-215

Human colonization history and natural selection shape the North American invasion of white clover

Author: Brandon Hendrickson, Fernando Hernández, Nevada King, Courtney Patterson, Nic Kooyers
Affiliation: University of Louisiana, Lafayette

The ability to leverage herbarium specimens within a population genomics framework is revolutionizing evolutionary biology and defining the impact that anthropogenic activities have on plant populations. A key challenge in invasion biology is dissecting the roles of colonization history, admixture, and selection in facilitating invasion success and shaping contemporary distributions of invasive species. We examine low coverage whole genome sequences from 391 North American herbarium samples collected from 1838-2018 along with contemporary sampling from the native and introduced ranges to recreate an invasion timeline. We ask: Does invasion history closely parallel human colonization history? How have founder events and admixture shaped the invasion? Is there a strong genomic signature of selection? If so, do temporal shifts in allele frequency occur in a protracted or rapid fashion? Individual heterozygosity increases over time before stabilizing at similar levels to those observed within the native range. Thus, despite limited evidence of bottlenecks following introduction using contemporary datasets, there is evidence of founder events and increases in genetic diversity through admixture. Early herbarium samples have ancestry most closely-related to native populations from England and France and there is a consistent increase in ancestry from Spain through time, particularly in lower latitude populations in the introduced range. This signature could reflect range expansion, increased use of warm-adapted cultivars, and/or selection. We identify many loci that exhibit strong signals of selection through time – most exhibit protracted increases in allele frequency in time and heterogeneous signals across space. We discuss regions of the genome that demonstrate rapid allele frequency shifts corresponding to key events including: the development of chemical fertilizer, introduction of modern cultivation lines, and climate change. Our results highlight not only the influence of human colonization and cultivation history on species invasions, but also power of selection to act on ecological timescales across continents.

Topic: *Functional Genetics/Genomics*

A-216

Single-nuclei transcriptomics of a complex photosynthetic system: C4+CAM in Portulaca amilis

Author: Ian Gilman, Robert VanBuren
Affiliation: Michigan State University

Crassulacean acid metabolism (CAM) and C_4 photosynthesis are carbon concentrating mechanisms (CCMs) that have evolved as plant responses to the low CO_2 world of the past 30 million years. Both CCMs have co-opted the same set of ancient metabolic modules to boost the concentration of CO_2 needed for photosynthesis, but have deployed these modules in contrasting ways. C_4 concentrates CO_2 spatially through a two-cell CO_2 pump, while CAM accomplishes CO_2 concentration with temporally coordinated carbon storage and re-release. These adaptations confer C_4 species with the highest rates of plant photosynthesis, characterized by maize and sugarcane, and CAM plants with the highest water use efficiencies, emblematic of cacti, aloes, and agaves. Despite hundreds of independent CCM evolutions, and their shared biochemical components, only a few lineages are known to use both C_4 and CAM (C_4+CAM). *Portulaca*, with multiple independent origins of C_4+CAM, offers unique insights into how multiple CCMs can be integrated to increase the drought tolerance of highly productive C_4 crops and, more broadly, how complex phenotypes arise through modular assembly. Here, we apply a high throughput single-nuclei RNAseq (snRNAseq) platform from Fluent Biosciences to describe photosynthetic transcriptomics in *Portulaca amilis* with cell-type resolution.

Topic: *Pteridology*

A-217

What is the smooth cliff-brake? Testing diversity and biogeographic hypotheses in Pellaea glabella.

Author: James Beck
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The smooth cliff-brake (*Pellaea glabella*) is a familiar and widespread North American fern, found on exposed limestone across much of the U.S. and Canada. However, this seemingly straightforward taxon harbors complexity in the form of sexual, cytotypic, and potential lineage diversity. Both sexual diploids and asexual tetraploids are known, with both forms documented from roughly defined eastern and western portions of the total species range. Some authors have hypothesized that the eastern and western sexual diploids underwent historical lineage divergence prior to the subsequent origin of their asexual tetraploid descendants. This scenario implies specific phylogenetic, biogeographic, sexuality, and cytotypic patterns. Here we test these hypothesis by evaluating key morphological characters and determining sexuality and cytotype in 250 herbarium specimens from throughout the range. We pair these data with analyses of a 2600 bp plastid dataset obtained from select specimens.

Topic: Reproductive Processes

A-218

To buzz or not to buzz: Pollination niche partitioning in urban vs. rural landscapes

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Meadow beauties (*Rhexia*: Melastomataceae) are a genus of angiosperms native throughout the Coastal Plain of the eastern United States. Of the 12 *Rhexia* species, nine are found in North Carolina. These species often co-occur and co-flower, raising the potential for cross-pollination to occur between species, however, hybrids are rare. Some co-flowering genera exhibit prezygotic mating barriers to prevent hybridization through pollinator niche partitioning. This research seeks to explore the possibility of pollinator niche partitioning within *Rhexia* and determine if certain pollinator species exhibit preferences for certain *Rhexia* species. Pollinator activity on *Rhexia* species is being recorded over the course of two field seasons in both urban and rural sites throughout southeastern North Carolina. Data collection is ongoing, and preliminary results from the 2024 observations have yielded interesting insights. We found that meadow beauties are strictly buzz-pollinated by bees, with bumblebees (*Bombus* spp.) being by far the dominant pollinators. All *Rhexia* species share many of the same pollinators, and flower morphology (size and color) appears to influence pollinator activity. Periods of intense heat and heavy rainfall disrupted pollinator activity at all sites, factors that may become exacerbated in upcoming years due to climate change. Rural sites supported more pollinators than urban sites, an especially important finding because urbanization and forest loss are occurring at unprecedented rates in southeastern North Carolina. *Rhexia* and its pollinators contribute to the biodiversity found within the Coastal Plain, as many *Rhexia* species are endemic to the area and some pollinator species are categorized as vulnerable or endangered. The Coastal Plain is a vulnerable ecosystem, experiencing habitat loss and other potential climatic threats. This research serves as a baseline record of local pollination ecology in southeastern North Carolina's Coastal Plain to understand how the *Rhexia*-pollinator system is responding to these impacts. Because many *Rhexia* species rely on pollinators for cross-fertilization, declines in pollinator populations may result in reciprocal repercussions for *Rhexia* populations.

Topic: Ecology

A-219

Altered snowpack depth and timing affects subalpine vegetative phenology, leaf traits, and community composition

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Climate models project reduced winter snowpack depth for many high-elevation, seasonally snow-covered ecosystems over the next century, which will impact subalpine plant communities. These communities are highly sensitive to changes in snow cover, water availability, and soil temperature. The subalpine is a critical ecotone that plays a vital role in regulating ecosystems. Climate change threatens the stability of subalpine plant communities, potentially disrupting biodiversity and impacting global climate. The impacts of reduced snow depth on subalpine plant development and soil processes, especially in relation to changes in snow accumulation timing and winter snow depth, remain poorly understood. To address this, we conducted a one-year experimental snow manipulation study in a subalpine forest in the Front Range of Colorado (elevation 3050 m) to simulate postponed snow accumulation in the fall (October-December) and reduced snow depth during winter (January-May). This study investigated how altered snow pack influences plant phenology, physiological traits, community composition, and soil characteristics (e.g., temperature and moisture). Three treatments were applied: (1) postponed snow cover (PSC), (2) removal, and (3) control, across three blocks, each with three $2m^2$ plots. Our focal species were Achillea millefolium and Fragaria virginiana. Our results indicate that reduced snow depth promoted below freezing soil temperatures and altered vegetative phenology. A. millefolium leaves advanced by 9 days in removal plots while F. virginiana leaves showed no change in timing. Specific leaf area (SLA) and plant height (cm) were unaffected by the treatments. A. millefolium leaf area (LA) marginally increased in response to the removal treatment. The PSC treatment caused a significant decrease in forb cover from 2023 to 2024. These findings suggest that changes in snowpack dynamics can disrupt species interactions and ecosystem function in subalpine environments, highlighting the need for long-term monitoring and further research.

Topic: Biology of mycoheterotrophic and parasitic plants

A-220

Nuclear Phylogenomic Insights Into Relationships, Support, and Conflict Among the Early Diverging Lineages of the Megadiverse Epidendroid Orchids

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Parasites present fascinating examples of evolutionary modification that simultaneously pose challenges for systematics. This is exemplified by mycoheterotrophic orchids, which parasitize fungi, constituting nearly half of all mycoheterotrophic plant species. A large concentration of mycoheterotrophic lineages is found among the eight tribes comprising the base of the megadiverse orchid subfamily Epidendroideae, here referred to as the early diverging Epidendroideae (EDE). To date, relationships among the EDE have been problematic. Previous analyses included sparse taxon sampling, provided low support based on few loci, or were affected by long branch attraction when based on plastid genomes. We conducted the most comprehensive phylogenomic analysis of the EDE to date, using Angiosperms353 loci, coalescent analyses, and deep exploration of support, conflict, saturation, and introgression. Our study is the first to include phylogenomic sampling from all eight EDE tribes, with 22 of 26 EDE genera represented. We took a novel approach selecting best-fit mixture model configurations at the individual locus level, which provided significantly better fit overall and required fewer parameters than all other models, with implications for clades characterized by lineage-specific rate heterogeneity. We recovered strong support for monophyly of all EDE tribes except for Neottieae, which were inferred to be paraphyletic. Information content was generally rich for deep relationships among the EDE tribes, but overall support was weak. We found evidence of saturation and putative introgression, with two inferred reticulation events. We conclude that short internal branches associated with rapid diversification, incomplete lineage sorting, and putative introgression resulted in low concordant signal among EDE tribes, underscoring the continued difficulty in resolving their relationships. Nonetheless, we provide the first strongly supported phylogenetic hypothesis for the five genera of Gastrodieae, representing the largest known radiation of mycoheterotrophic plants. We discuss our findings considering recent phylogenomic studies, taxonomy, morphology, and biogeographic implications.

Topic: Systematics & Taxonomy

A-221

Discovering evolutionary relationships in the economically important plant genus Amaranthus

Author: Andy Cabrera, Josue Magana, Luis Figueroa Hernández, Pankti Chavda, Katherine Waselkov, Danya Sumrein
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Our study focuses on the phylogenetic relationship between the Amaranthus species of the Southwestern US and their relationship with those found in the Galapagos Islands. Previous studies of Amaranthus have primarily focused on either tracing the domestication events or understanding the weedy species' evolution of herbicide resistance. Therefore, there is currently not much known about the non-weedy species of Amaranthus, and there are some unresolved taxonomic and biogeographic questions. The focus on these two groups is based on their similar morphology and some genetic evidence that three different Western North American groups of Amaranthus could potentially have given rise to the three Galapagos natives. Our project adds new species and populations of Southwestern Amaranthus species to the phylogeny, which has helped us better understand how this genus has colonized the Galapagos islands. After extracting DNA, we ran PCR on several nuclear genes (ITS, Waxy, G3PDH) and chloroplast regions (MatK/TrnK, TrnL_C-D). Eurofins Genomics sequenced the purified PCR products, and DNA sequences were aligned using GeneiousPrime software. We obtained DNA sequences from the Galapagos Amaranthus species using NCBI GenBank and used Bayesian methods to reconstruct the relationships within the Amaranthus genus. So far, results have shown that there may be an undescribed species in the area of Tucson, AZ, which could be the closest relative of the Galapagos

endemic A. squamulatus. Improving our evolutionary understanding of species within this group allows us to better study the origin of weeds, crops, and island endemics within the Amaranthus genus.

Topic: Mycology

A-222

Understanding Macroecologial Patterns in the Hyper-Diverse Ectomycorrhizal Genus Inocybe (Agaricales)

Author: Malka Saba
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Inocybe is a monophyletic group estimated to contain some 1500-1800 species worldwide. Species diversity is unevenly distributed across the tree of life. One possible explanations for this heterogeneous diversity pattern is clade age, in which younger clades have had less time to diversify and accumulate species than older clades.

Several biogeographical trait associations have been observed among species of this hyper- diverse ectomycorrhizal genus. However, none of these have been evaluated with phylogenetic correlation tests. In the present study, correlations of different traits with their biogeographical habitats have been proposed including (i) the high prevalence of smooth-spored taxa in Mediterranean habitats of western North America, southern Europe, southwestern Australia, and southeastern Australia; (ii) the high prevalence of nodulose-spored taxa in tropical regions; and (iii) association between species with thick-walled hymenial cystida and occurrence on calcareous soils. In the latter case, it has been suggested that species with thicker walled cystidia cope more efficiently with excess calcium. Given these observations globally, we wish to know if the traits enumerated above are adaptively or functionally linked to biogeographical traits. If yes, then one should expect to see replicated co-distribution or replicated elevated rates of net diversification among species with the paired traits in a given phylogeny. We propose to examine these questions in the context of a 500-taxon tree of *Inocybe* reconstructed from a 6-locus supermatrix. Individual loci are aligned using MAFFT 7.244 and manually adjusted using AliView 1.17.1. Gblocks 0.91b are used to remove ambiguously aligned regions. Individual gene datasets are concatenated using SeaView 4.5.4 after inspection of intergene conflict. Partition Finder 1.0.1 i used to find the best partition strategy and the best models of molecular evolution. Models of discrete trait evolution and continuous trait evolution is applied to resulting phylogenies in R using ape, picante, caper, geiger, corHMM, diversitree, or phylolm. Ultrametic phylogenies of the Agaricineae are calibrated using recently described fossils of Nidulariaceae in BEAST. Models of diversification (as in BAMM 2.50) are applied to a portion of trees sampled from the posterior distribution. To assess robustness of results, multiple methods are explored to detect shifts in net diversification rate. These include BiSSE, FiSSE, BAMM, the gamma statistic, Paradis' diversification test and a species richness contrast test. Detailed results obtained from different models of diversification to understand the global diversification of this genus are presented.

Topic: Reproductive ecology and evolution of plants in stress-prone environments

A-223

Evolutionary responses to historic drought across the range of scarlet monkeyflower

Author: Seema Sheth, Lucas Albano, Charles Blanchard, Emily Cook, Rosalinda Díaz, Xitlaly Gomez-Vega, Katelin Kutella, Mariam Moazed, Macy Patel, Julia Prange, Niveditha Ramadoss, Ashley Regan, Aster Riley, Melissa Rivas Hernandez, Jocelyn Rojas, Marissa Strebler, Aditi Verma, Lindsay Villano, Jordan Waits, Dachuan Wang, Olivia Wilborn-Pilotte, Jeff Diez, Lluvia Flores-Rentería, Jason Sexton, Chris Muir
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Adaptive evolution is a key means for populations to persist under environmental change, yet whether populations across a species' range can adapt quickly enough to keep pace with climate change remains unknown. The breeder's equation predicts the evolutionary change in a trait from one generation to the next as the product of the selection differential and the narrow-sense heritability in that trait. We performed a resurrection study with the scarlet monkeyflower (*Mimulus cardinalis*) to evaluate whether traits associated with drought adaptation have evolved in populations across a species' range in response to extreme drought. We compared differences in phenology and fitness of pre-drought ancestors and post-drought descendants from six populations transplanted into three latitudinally-arrayed common gardens and quantified trait heritabilities and phenotypic selection. Overall, instances of evolutionary responses between ancestors and descendants were few and small in magnitude. Populations with greater trait heritabilities or experiencing more severe drought did not show greater trait evolution. The direction of evolutionary change in populations transplanted southward into warmer, drier environments rarely matched the direction of selection in those environments. Together, these results suggest that the expression of genetic variation, and thus traits, depend on the environment, and that environmental variability in field settings may mask the genetic variation that is often detected in greenhouse environments.

Topic: Pteridology

A-225

The Andes of Colombia & Ecuador as a Barrier to Fern & Lycophyte Species from Mesoamerica

Author: Sarah Morris, Robbin Moran
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We compiled a list of the fern and lycophyte species that occur in Mesoamerica and extend into Colombia and Ecuador, where they are restricted to the western side of the Andes; that is, they occur only west of the crest of the easternmost cordillera and are absent from that cordillera's eastern slope and in adjacent Amazonia. We found 131 species with this Mesoamerican and west-of-the-eastern-cordillera distribution. Those 131 species constitute 7% of the total 1805 fern and lycophyte species that have been recorded west of the crest of the easternmost cordillera in Colombia and Ecuador. All 131 species have elevation ranges with midpoints at low (0–900 m) or middle (900–3000 m) elevations, and none occur above 3000 m. This suggests the cordilleras have acted as elevational barriers. We also investigated the blockage of these 131 species by each of the Andean cordilleras. We found that 75 (57%) of the 131 species were limited eastward by the western cordillera, 15 (11%) by the central cordillera (this cordillera in Colombia only), and 40 (31%) by the eastern cordillera. If estimates of endemics to the western Andean region are considered, then at least 20%–22% of all fern and lycophyte species in the region are restricted west of the crest of the easternmost cordillera. Although usually exhibiting larger geographic distributions compared to angiosperms, fern and lycophyte species may show significant geographic restriction by mountain ranges.

Topic: Systematics & Taxonomy

A-226

Phylogeny and Biogeography history of Tecophilaeaceae (Monocot, Asparagales)

Author: Maria Roman, Gordon Burleigh, Rosita Scherson
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Tecophilaeaceae is a small family of geophyte monocot species belonging to the order Asparagales, with nine genera and 27 species. *Cyanastrum*, *Cyanella, Eremioliron, Kabuyea*, and *Walleria* inhabit tropical areas of Southern Africa. *Odontostomum* is found in Northern California with only one species, and *Conanthera*, *Tecophilaea* and *Zephyra* are endemic to Chile. The most comprehensive published phylogeny of Tecophilaeaceae (Buerki et al., 2013) was inferred from only a few loci, and included seventeen species representing the nine genera. This study found that the origin of Tecophilaeaceae is in sub-tropical Africa, and the breakup of Gondwana drove the deep-level biogeographic patterns. Although this study provides an important initial framework for understanding the evolution of Tecophilaeaceae, there are numerous unresolved questions about the evolution and diversification of this understudied family. In this study, we construct a phylogenetic hypothesis for Tecophilaeaceae using targeted capture data and use it to further elucidate the origins of the Californian and Chilean clades within Tecophilaeaceae and examine the broader biogeographic patterns of diversification across the entire family. Specifically, we generated a targeted capture dataset using the GoFlag angiosperm 408 probe set. Our dataset includes sequences from 24 of the 27 species in the family, with a complete genera sampling and extensive intraspecific sampling for many taxa. We estimated dates of diversification throughout the family with ten fossil records from the most closely related orders as calibration points. We tested whether the resulting biogeographic patterns are a result of the simple breakup of Gondwana or if they reflect more complex dispersal scenarios. Additionally, we discuss the implications of our results on remaining questions concerning the phylogenetic relationships within and between certain species and genera, providing a clearer understanding of evolutionary processes within Tecophilaeaceae.

Topic: *Population Genetics/Genomics*

A-227

AI-Based Modernized Compilation of Pleistocene Glacial Extents of North America for Shapefiles used in Phylogeographic Research

Author: Noah Garland, Ingrid Jordon-Thaden
Affiliation: Murray State University

Our lab group is beginning to focus on studying the effect of climatic fluctuations during the Pleistocene on alpine plant populations in North America. Glaciation cycles of the most recent Ice Ages have resulted in species distributions known as disjunct species as their lineages were split. We seek to compare population genetic dynamics between sites that were unglaciated vs. those that experienced glaciation. As part of this multi-year project, the first step is to identify accessible localities for plant collections of specific alpine tundra species, and to choose these sites we need to understand glacial extents. An important collaboratively compiled map coordinated in 1946 by US Geologist, Richard F. Flint, showcased continental and alpine glaciers covering Canada and parts of North America. Since then, various other updated glaciation maps have been digitized and made available as either smaller shapefiles, images, or projections with variable accuracy. A shape file has been provided by the Paleoglaciers working group, titled, "Western US Paleoglacier Outline" that shows the most up to date glacier outlines, however is still incomplete and accuracy is inconsistent. When locating actual glaciated vs. unglaciated sites on the ground for boots-on-the-ground field work, this resource is useful but needs to be supplemented. For this study, we are comparing these North American glaciation boundaries with Flint's exhaustive 1946 map to find "missing" glaciers in modern data. We are using digitization methods with a trained semantic segmentation AI model to extract all possible glacial data from the Flint map, and supplementing modern data with this older, generalized but viable data. This supplemented shapefile is then used in conjunction with EPA eco region IV zones, USFS roads and trails, satellite imagery, and USFS National Forest boundaries to locate field sites that fulfill logistic, biologic, and geographic criteria.

Topic: *Development and Structure*

A-228

Whole genome duplication enables rapid evolution of male-biased sexual allocation in Galax urceolata

Author: Joe Williams, Alexander Killeffer, Brayan Cavalcante, Cas Bailey, Tonika Birmley
Affiliation: University of Tennessee, University of São Paulo

Sexual allocation in bisexual flowers is thought to evolve to a balance between fitness gains through male and female function. Polyploidy might disrupt such gradually evolved patterns, since whole genome duplication (WGD) is known to cause cell and organ enlargement, but to have less influence on meristic traits. Autotetraploids have larger flowers than their diploid progenitors, and larger floral displays are expected to increase pollinator attraction, which in turn is thought to benefit male more than female fertility. Yet, larger organ sizes increase costs, which may incur stronger size-number trade-offs, and consequently the rapid evolution of fewer flowers, pollen and/or ovules. Thus, "pure" polyploidy might disrupt evolved sexual allocation patterns by itself and/or alter post-WGD selective forces. Here we studied early stages of autotetraploid evolution in *Galax urceolata, a mixed ploidy species native to the* Blue Ridge mountains, USA. We compared floral organ sizes and numbers in four natural diploid progenitor (2n = 2x = 12) and four autotetraploid derivative (4x = 24) populations. Ploidy levels were determined by flow cytometry, using propidium iodide, and the mean 2n genome size (GS) was 2.292 ± 0.017 picograms (pg) and 4.714 ± 0.015 pg for 2x and 4x populations, respectively. Floral organ lengths and pollen and ovule numbers were measured using standard light microscopy. Organ sizes and numbers were compared with a model that included cytotype as a fixed effect, population nested within cytotype as a random effect, and two covariates, pedicel diameter (a proxy for flower size) and flowers per inflorescence (a proxy for inflorescence size). We found that sepals, petals, pistils, anthers and styles were 34-39% longer in autotetraploids, whereas stamens, filaments, and ovary lengths were 22-28% longer. 2x and 4x organ-organ allometries, evaluated by standard major axis regressions, had similar slopes and were generally consistent with isometry. Autotetraploid ovules and anthers were similar in number relative to diploids, whereas 4x ovules were 62% larger in volume and anthers were 167% larger. WGD is known to double pollen volume, but pollen of autotetraploids was only 33% larger, but 87% greater in number, than in diploids. These results extend to the whole-plant level, since both 2x and 4x plants had similar numbers of flowers per inflorescence. We conclude that WGD caused proportional size increases in floral organs, including anthers and ovules, that were retained after WGD. However, organ enlargement generates asymmetric opportunities for gamete number evolution after WGD, since ovules can only produce one egg irrespective of size, whereas pollen number can evolve rapidly by a size-number trade-off that leaves anther size unchanged. Neo-polyploids are thought to face extreme pollen limitation at inception, a situation favoring the evolution of greater pollen production. Yet, doubling of pollen volume by WGD may also generate strong selection for a return to ancestrally smaller sizes, which may result in correlated evolution of greater pollen numbers, since the size and number of pollen precursor cells play a role in determining anther size.

Topic: *Population Genetics/Genomics*

A-229

Uncovering Cryptic Species from Population Genetics Data: a case study in Western North American Draba (Brassicaceae)

Author: Ingrid Jordon-Thaden, Noah Garland
Affiliation: Murray State University

This presentation will summarize a systematics quandary in Brassicaceae in the genus *Draba* where potential cryptic species have been confusing taxonomic identification for many years. For many years the alpine apomictic polyploid, *Draba oligosperma,* has been thought to be an allopolyploid and its potential parents have been hypothesized by experts in the field. This study seeks to explore this possibility with the complex set of data that will be presented. The location of the potential species nomenclature and distribution changes is between the Uinta Mountains of eastern Utah, east of Flaming Gorge in Sweetwater County of Wyoming, and north into the Beartooth Plateau and neighboring Gallatin and Northern Rocky Mountains of Wyoming, Montana, and Alberta. In our larger study of the population genetics of *D. oligosperma*, the sequence results led us to further investigate this geographic area and the taxonomic entities found within. This talk will present how cryptic species, once referred to as subspecies of *D. oligosperma*, were uncovered with population genetics sequence data, what morphological characters led us to investigate further, chromosome counts from cultured plants' root tips, and reproductive mode observations under cultivation.

Topic: *Education and Outreach*

A-230

Identification via DNA barcoding as an embedded research experience in Plant Taxonomy

Author: Adam Schneider
Affiliation: University of Wisconsin-La Crosse

Molecular phylogenetics and DNA sequencing has revolutionized the field of plant systematics, including advancing our understanding of trait evolution, relationships among taxa, and providing new tools for plant identification. In the spring of 2025, I developed a three-part lab that spanned the semester in which students identified an unknown woody plant root that had infiltrated the lining of a water reservoir in the city of La Crosse, Wisconsin via DNA barcoding. Throughout this project, students integrated molecular lab work, bioinformatic analysis of Illumina sequence data, and traditional taxonomic tools such as regional species checklists and morphological analysis to identify the plant by the end of the semester, ultimately providing actionable information to the external client. This also provided an opportunity for students to experience the challenges of interpreting molecular data, including unexpcected patterns of gene tree-species tree conflict, and discuss potential causal mechanisms.

This case-study shows how molecular phylogenetics, DNA barcoding, and bioinformatic analysis can be integrated into an undergraduate Plant Taxonomy course in the form of a course-embedded research experience, all on a modest budget.

Topic: Development and Structure

A-231

Comparative Petiolar and Midvein Anatomy of Members of the Arum Family (ARACEAE)

Author: Charlotte Saltsman, Ingrid Jordon-Thaden
Affiliation: Murray State University

The recent comparative phylogeny concerning the Arum family (Araceae) has grown in number over the past few years, correlating with a rise of their popularity as ornamental houseplants (Haigh et al, 2023). While the anatomical compilation by Richard C. Keating, The Anatomy of Monocotyledons IX (2002) is very comprehensive, the author states there is room for further discovery and comparisons within the family. Additionally, comparative anatomy of the family can now be correlated with the new phylogenetic work of Haigh et al. (2023). Using a horticulturally curated collection at Murray State University, we had the opportunity to sample a significant representation of species across the family. Through harvesting, sectioning, mounting, and observation of leaf anatomical structure via a compound microscope, this study aimed to provide a comparative anatomy of leaf structure across intrafamilial clades, particularly of vascular bundle arrangements and other foliar anatomical features. Following Yeung's protocol to section and observe fresh material (1998), we sectioned fresh leaf material using a simple and inexpensive hand-held microtome, hand-held razor blade, and held the sample with a small piece of carrot. The key areas of study for this project are the leaf midrib and petiole, as well as including longitudinal sections of the leaf tip to describe hydathodes. The sections were then stained using 1% TBO suspended in a pH=4.4 benzoate buffer and mounted in water on slides for observation under light microscopy. Microscope images were then photographed of key structures throughout the sample, including vascular bundles, chlorenchyma, aerenchyma/mucilage ducts, epidermis, and calcium oxalate crystals. This talk will summarize the progress of this study, highlighting the differences in the anatomical tissue structure and arrangement of vascular bundles, mucilage cells, calcium oxalate crystal variation, and other overall anatomical features of different species representing major clades. The goal of this work is to present how structures have changed from more basal to more recent species evolutionarily when comparing the anatomy with the new published phylogeny for the family.

Topic: Physiology

A-232

Identification of Key Factors Affecting In Vitro Plant Callus Storage and Their Optimization Using Response Surface Methodology

Author: Ye-Won Kim, So-Young Park, Han-Sol Lee
Affiliation: Chungbuk National University

In order to maintain plant callus in vitro over extended periods, frequent subculturing is typically required, which not only increases maintenance costs but also elevates the risk of somaclonal variation. In vitro conservation techniques offer a promising alternative by enabling long-term storage, thereby mitigating the labor-intensive nature and potential genetic instability associated with conventional in vitro culture. This study aimed to identify the key factors affecting the viability of callus during long-term in vitro conservation across various plant species. Based on the identified factors, a Response Surface Methodology (RSM) was employed to model and optimize pre-treatment protocols, with the goal of enhancing the efficiency of long-term callus storage. To this end, callus from five plant species — Ligusticum officinale, Centella asiatica, Panax ginseng, Sageretia theezans, and Camellia japonica — were used for experimental analysis. The calli were stored for up to 120 days, during which their viability was assessed. In addition, various physiological characteristics, including antioxidant activity, were analyzed to determine the factors influencing callus survival. Based on this analysis, key factors affecting viability were identified. Sucrose, methyl jasmonate, and citric acid were selected as pre-treatment variables, and RSM was employed to optimize pre-treatment conditions aimed at enhancing antioxidant activity and sugar content — both critical for cell survival. Calli were pre-treated under the optimized conditions for one week, followed by encapsulation and further storage experiments to evaluate the improved preservation efficacy.

Analysis of the characteristics of the five plant callus types revealed that C. asiatica and S. theezans exhibited rapid cell growth, whereas L. officinale, P. ginseng, and C. japonica showed higher antioxidant activity. After 120 days of storage, callus vigor was better maintained in the species with higher antioxidant capacity — namely L. officinale, P. ginseng, and C. japonica. In particular, FRAP (Ferric Reducing Antioxidant Power) values and total phenolic content (TPC) were positively correlated with cell viability. Based on this, the optimal treatment conditions to maximize FRAP, TPC, and sugar content in callus tissues using RSM were determined. FRAP and TPC reached their highest values under treatment with 3% sucrose, 135 μM MeJA, and 20 mg/L chitosan, while the highest sugar content was observed under treatment with 9% sucrose, 200 μM MeJA, and 0 mg/L CTR. Calli were pre-treated for one week under the optimized conditions and subsequently encapsulated using alginate capsules and agarose droplets, resulting in successful long-term preservation. This study demonstrated that antioxidant capacity — specifically FRAP and TPC — is a key factor influencing callus viability during long-term in vitro preservation. By optimizing pre-treatment conditions using RSM, efficient long-term storage of callus was achieved. These findings are expected to be applicable to the preservation of a wide range of plant species.

Topic: Physiology

A-234

Photosynthetic activity in heterotrophic Cuscuta is modulated by phylogeny and ontogeny

Author: Adam Schneider, Jenna Ekwealor, Ingo Ensminger, Saša Stefanović
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Photosynthesis, while central to plant function, has been repeatedly lost within parasitic lineages of angiosperms. Cuscuta species, as a model system for studying parasitism, exhibit varying degrees of plastid functionality and photosynthetic ability, based genomic and ultrastructure studies. However, few direct physiological studies exist, and none that span multiple developmental stages of autotrophic, mixotrophic, and non-photosynthetic species in a phylogenetic framework. We paired photosynthetic activity measurements from Imaging-PAM fluorometry with quantitative analysis of chlorophylls and carotenoids from multiple developmental stages in fourteen Cuscuta species, representing the phylogenetic breadth of the genus, and a closely related autotrophic species. Multivariate data were analyzed using nonparametric hypothesis tests, and comparative phylogenetic patterns were explored through Bayesian model testing. Photosynthetic activity, chlorophyll and carotenoid content were highest in meristematic regions (e.g., shoot tips and developing seeds) and lowest in older stems or haustoria. Neoxanthin, a carotenoid typically highly conserved in plants, appears to have been lost once in Cuscuta and subsequently re-gained in certain lineages. Complex relationships between photosynthetic activity and lutein epoxide concentration suggest differing roles in developmental stages with high and low energetic needs. These findings provide substantial evidence that photosynthesis in Cuscuta is not vestigial but rather modulated based on developmental stage and across phylogenetic history, revealing a dynamic interplay between parasitism and photosynthetic function.

Topic: Conservation Biology

A-235

An accidental biodiversity repository: Investigating genetic diversity of American chestnut (Castanea dentata) planted beyond the historical range in the inland and Pacific Northwest

Author: Christina Riddle, Kelvin Sakyi, Chessa-Grace Foreman, Wendy Harvey, Robert Laport
Affiliation: College of Idaho, The College of Idaho

American chestnut (*Castanea dentata*) occupies a special place in the cultural history of North America stretching back to pre-colonial periods. The rapid functional extinction of *C. dentata* due to the spread of chestnut blight (*Cryphonectria parasitica*) occurred rapidly within the lived memory for many residents of eastern North America, representing a significant biodiversity and cultural loss. While breeding and biotechnology efforts have been successful in generating partially blight-resistant trees, successful restoration of *C. dentata* to eastern forests will require the establishment of genetically diverse, self-sustaining blight-resistant populations of trees. Unfortunately, relatively few reproductive trees remain in the native range, and it is likely that some genetic diversity important for local adaptation was lost during the spread *of C. parasitica* over the last ~100 years. American chestnuts planted in western North America before the advent of chestnut blight, by people who migrated from the east, may represent an important source of genetic variation, and an opportunity to aid restoration efforts by reintroducing pre-blight genetic variants into mature remnant and blight-resistant trees in eastern North America. We located and genetically analyzed specimens from throughout the

inland and Pacific Northwest. Network and phylogenetic analyses of chloroplast DNA suggest the majority of analyzed specimens appear to be genetically related to populations in the northern part of the historical range. With expanded sampling, we aim to better understand genetic diversity and geographic origins of western trees, potentially increasing the genetic diversity available for restoration efforts.

Topic: Systematics & Taxonomy

A-236

Speciation and selection in gypsum edaphic endemics

Author: Kathleen Madsen, Mike Moore, John Schenk
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Edaphic plant communities contain numerous, distantly related species that evolved under similar stressful conditions. The resulting assembly of plants are often rare and are biologically diverse. We are just now beginning to uncover the evolutionary process of edaphic specialization and speciation, but relatively little remains known. We examined species that occur on and off gypsum-edaphic communities to answer two questions: (1) How do diversification rates change for clades where gypsum endemism occur, and (2) has selection favored limited dispersal in two gypsum endemic clades? To answer those questions, we utilized preconstructed cladograms that contained gypsum endemic species. To examine changes in diversification rates of gypsum associated species, four phylogenies were selected, focusing on gypsum communities in the southwestern U.S.A. Phylogenies of Mentzelia L. section Bartonia Torr. & A. Gray (Loasaceae), tribe Helenieae Lindl. in Asteraceae, tribe Onagreae Dumort. in Onagraceae, and the tribe Nyctagineae Horan., Char. Ess. Fam. in Nyctaginaceae, containing common New World gypsum genera, were used. For each clade, a group of seven Binary State Speciation and Extinction models and seven Hidden State Speciation and Extinction models were ran and compared to two character independent models to predict the evolutionary outcomes for species that specialize onto gypsum. Diversification rates in all clades were influenced by specialization onto gypsum with increased speciation rates in endemic lineages. To explore selection for limited dispersal in gypsum endemic species, diaspore material was collected and weighed for species from two clades (Gaillardia Foug. and Mentzelia section Bartonia Torr. & A. Gray). Terminal velocity was measured using a vertical wind tunnel for collected diaspores to assess dispersal ability averaged across each species. A phylogenetic analysis of variance was used to identify selection for limited dispersal in endemic species. A negative relationship was detected between diaspore weight and dispersal, but limited dispersal was not detected in the gypsum endemics of either clade. Overall, the goal of this research was to better understand the evolutionary and ecological consequences of gypsum endemism. Our results show selection towards reduced dispersal ability might not be prevalent in gypsum endemic individuals, but we identified increased speciation rates as species become endemic to gypsum. This work contributes to the growing research on edaphic endemic communities and continues the effort of identifying evolutionary patterns across soil-associated plant-communities.

Topic: Lichen and Bryophyte Diversity, Conservation, and Evolution in the Americas

A-237

Bryophyte conservation in North America: new opportunities and challenges

Author: Mandy Slate, John Atwood, John Brinda, Ben Carter, Amanda Eberly, Wesley Knapp, Scott Schuette, Juan Carlos Villarreal A.
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Tiny in stature, bryophytes are widely distributed across diverse ecosystems including deserts, forests, and tundra, where they play a crucial role in enhancing biodiversity and supporting essential ecosystem functions. Bryophytes affect terrestrial water, carbon, phosphorus and nitrogen cycling and create a unique microhabitat known to support diverse communities of bacteria, cyanobacteria, fungi, algae, micro and meso invertebrates. Given their vital ecological roles, bryophytes are key contributors to ecosystem stability and resilience, underscoring the need for their conservation and study. Despite the importance of bryophytes in natural environments, of the 2,100 North American bryophyte species, only one is federally listed under the Endangered Species Act. The newly formed Bryophyte Conservation Alliance (BCA) seeks to advance North American bryophyte conservation by providing sound scientific support for bryophyte conservation efforts, galvanizing individuals to take action and advocate for bryophyte conservation, and fostering a conservation-focused research agenda for bryophytes. To further advance our agenda, we have three main objectives: 1) Increase general knowledge and appreciation of bryophytes in North America, 2) Create a clearinghouse for information on bryophyte conservation, and 3) Develop and implement bryophyte conservation-related research and long-term strategies. BCA will expand bryophyte conservation efforts internationally through a budding collaboration with the Moss and Lichen Specialist Subcommittee of COSEWIC (Canada), Société Québécoise de Bryologie (Canada), the European Committee for Conservation of Bryophytes of the IUCN, and the International Association of Bryologists. In this talk, we present our initiative and aim at motivating conservationists and evolutionary biologists to contribute and recognize the importance of these inconspicuous yet essential organisms on which our planet depends.

Topic: Phylogenomics

A-238

Soils are like onions—they have layers: investigating the role of preadaptation in North American Allium soil specialization

Author: Emily Humphreys, Carrie Tribble
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Plants have evolved to thrive across an incredible breadth of soils including ultramafic serpentine soils high in heavy metals, calcareous soils high in pH, and gypseous soils high in sulfur. While the significance of plant adaptations to such specialist soils has long been recognized, plants on each soil type have been studied largely independently (e.g. serpentinophiles, calciphiles, gypsophiles). However, some lineages appear to repeatedly specialize onto a variety of stressful soil types. This motivates the question: do some clades possess preadaptations, that underly their success across multiple distinct stressful substrates? I am investigating this question using the North American clade of *Allium* subgenus *Amerallium,* a group of ~100 species known for their geophytic habit and high levels of sulfur-containing compounds. North American *Amerallium* species occur on ultramafic, calcareous, and gypseous soils, among others. To test my hypothesis that preadaptation has facilitated diverse substrate tolerances, I will construct an updated species-level phylogeny of the group and develop and implement structured Markov models of trait evolution. I will complement this work with tissue and soil analyses to directly examine plant-soil interactions and explore the potential for hyperaccumulation of soil-specific elements and comparative transcriptomics to investigate the genetic mechanisms of soil tolerance. In undertaking these analyses, I aim to inform foundational science on the globally important genus *Allium* and provide further insight into patterns of preadaptive trait evolution and stress tolerance.

Topic: Bryology and Lichenology

A-239

LiDAR Remote Sensing and Unsupervised Machine Learning for Vegetation Characterization

Author: Michael Kerr, David Burchfield
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Characterizing vegetation into functional groups is costly, both in terms of time and money. However, research suggests that data on functional group presence and abundance is needed for land management decisions and livestock forage estimation. Combining remote sensing and machine learning offers the potential for more efficient large-scale vegetation surveys. One type of remote sensing, LiDAR, gives researchers the ability to use both structure and visible light spectrum data to characterize vegetation in a given area. Similarly, unsupervised machine learning models offer relatively quick data annotation to aid in future work. We hypothesized that LiDAR imaging and unsupervised machine learning can together form a useful workflow for vegetation characterization. After using LiDAR from a small unmanned aerial system (sUAS) to image a sagebrush steppe landscape—habitat for the endangered Idaho grouse pellet lichen—we analyzed the imagery using three different unsupervised machine learning models. Performance was assessed relative to each other model and to field validations. Preliminary results suggest that LiDAR and unsupervised models have the potential to increase efficiency in vegetation characterization surveys. This workflow may also allow for medium-scale characterization of lichen habitat and the further understanding of endangered lichen ecology.

Topic: *Ecology*

A-240

Population trends, demography, and seed ecology of Florida scrub endemic Chrysopsis highlandsensis (Asteraceae: Astereae)

Author: Aaron David, Stephanie Koontz, Sterling Herron, Steve Orzell, Eric Menges
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TITLE: Population trends, demography, and seed ecology of Florida scrub endemic *Chrysopsis highlandsensis* (Asteraceae: Astereae)

AUTHORS: Aaron S. David, Stephanie M. Koontz, Sterling A. Herron, Steve Orzell, Eric S. Menges

Chrysopsis highlandsensis DeLaney & Wunderlin (Highlands Goldenaster; Asteraceae) is a Florida state endangered herbaceous perennial found primarily within pyrogenic scrub communities in south-central Florida. Little is known about its ecology, including population trends, demography, response to fire, and seed ecology. Here, we report on the first detailed demographic study of *C. highlandsensis* over 24 yrs of field monitoring across ten populations (6,456 plants) as well as supplemental surveys and experiments to investigate (1) population trends and vital rates in scrub and roadside habitat, (2) the seed ecology, and (3) rangewide population trends. Seedling recruitment occurred year-round, primarily during the winter dry season following flowering (Dec – Mar), and large recruitment events were not associated with fire or mechanical disturbances. Although burning reduced survival, 39% of individuals (>1 yr old) that experienced fire survived, indicating a capacity for surviving fire. Roadside vegetative plants transitioned to reproductive adults at smaller sizes (rosette diameter) than did those in the scrub. Reproductive individuals lived 4.3 yr (max. 12 yr). Mortality occurred following the first reproductive event in 87% of individuals, indicative of a largely monocarpic life cycle. Viability of intact seeds was estimated at 20%. Across five field germination experiments, germination ranged from 1.0-8.6%, and the maximum observed seed bank duration was 5 yrs. Seed predation by vertebrates accounted for a 23% decline in seed numbers. Rangewide surveys showed significant declines in 5 of 7 sites from 2005-2020. Together, these findings indicate that populations are generally declining, and that several factors, particularly low reproductive output and seedling recruitment, likely limit population growth.

Topic: *Dryland Floras*

A-241

Hidden biodiversity: Whole genome duplication shapes cryptic interspecific interactions in a dominant desert shrub

Author: Robert Laport, Shelly Gaynor, Benjamin Gerstner, Jacob Landis, Tim O'Connor
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The North American creosotebush (*Larrea tridentata*; Zygophyllaceae) is one of the most iconic species of the North American warm deserts comprising recently formed diploids, autotetraploids, and autohexaploids. The genus is amphitropically distributed, with closely-related species distributed in arid regions of South America. Molecular studies suggest *L. tridentata* is a relatively recent (≤1mya) arrival to North American desert ecosystems, yet this ecologically dominant desert shrub now hosts an extraordinarily diverse assemblage of insect pollinators and herbivores. Integrative studies over the last two decades suggest the cytotypes of *L. tridentata* act as cryptic units of biodiversity with whole genome duplication having profound and multifaceted effects on interspecific interactions and the structuring of biotic communities. For example, pollinators exhibit biases in pollen collection from sympatric *L. tridentata* cytotypes, contributing to appreciable assortative mating. The distributions of diploid, and polyploid *L. tridentata* also structure specialist galling insect distributions, with several closely-related species galling their preferred host cytotype even when the cytotypes occur sympatrically. Recent studies also suggest that the cytotypes experience cryptic plant-soil feedbacks and microbially-mediated niche differentiation that may facilitate the persistence of mixed-cytotype populations. Here, I will discuss the implications of these cryptic dimensions of biodiversity and how acknowledging the contemporary importance of genome duplication to evolutionary trajectories and global patterns of biodiversity may offer new insights into the formation and structuring of dryland floras.

Topic: *Systematics & Taxonomy*

A-242

An exploration of ancient hybridisation in Narcissus L.

Author: Zoe Dennehy-Carr, Alastair Culham, Kálman Könyves, John David, Chris Yesson
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The taxonomy and evolutionary relationships of the Mediterranean geophytic genus *Narcissus* are unclear, with the number of sections ranging between 10 – 14 and the number of widely accepted species between 30 – 90. Whilst previous phylogenetic research has consistently resolved the genus and both subgenera (*Hermione* and *Narcissus*) as monophyletic, the relationships between sections have remained unresolved. This has been attributed to hybridisation and polyploidy across the genus, which has led to discrepancies between morphological classifications and discordance between molecular phylogenies. Using whole plastomes and 261 low-copy nuclear genes, we present a genus-wide phylogeny of *Narcissus* and investigate cytonuclear discordance using phylogenetic network methods.

All phylogenetic analyses resolve *Narcissus* and both subgenera as monophyletic, however, high levels of cytonuclear discordance were recovered, and some sections are para- or polyphyletic. Our nuclear coalescent phylogeny recovered section *Jonquillae* and subsection *Pseudonarcissi* as monophyletic concurring for the first time with current sectional classifications, which are primarily based on morphology.Thehigh levels of cytonuclear discordance recovered were attributed to several ancient hybridisation events across the genus including the origin of sections *Bulbocodii*, *Dubii*, *Ganymedes* and *Nevadensis*. These ancient hybridisation events explain the polyphyly of section *Jonquillae* and subsection *Pseudonarcissi* in plastome phylogenies, with members of these groups identified as maternal lineages. These results highlight the importance of considering reticulation when conducting taxonomic revisions for groups with high levels of hybridisation and introgression, particularly for groups where discrepancies between morphological treatments and molecular phylogenies exist.

Topic: *Ecology*

A-243

Post-Wildfire Resprouting and Survival of Yucca Jaegeriana and Yucca Baccata Var. Baccata after the 2020 Dome Fire, Mojave National Preserve CA

Author: Melanie Davis, Lynn Sweet, Scott Heacox, Danelle Baronia, Clay Noss, Tasha La Doux, Joseph McAuliffe, Megan Korte
Affiliation: University of California, Riverside, Desert Botanical Garden

Understanding post-fire survivorship of key desert plant species is critical to effective response to post-fire conservation and management. Fire frequency and extent in North American deserts has increased throughout the last century, causing dramatic shifts in shrubland composition at mid-elevations. The Mojave National Preserve, located in the Mojave Desert in San Bernardino Co., CA, protects unique ecosystems, including eastern Joshua tree woodlands, and the preserve has experienced two major wildfires in the past five years. This study covers the impacts of the 2020 Cima Dome fire, in which over 43,000 acres and an estimated 1.3 million eastern Joshua trees were burned. Both eastern Joshua tree (*Yucca jaegeriana (McKelvey) L.W. Lenz*) and banana yucca (*Yucca baccata Torr. var. baccata*) exhibit root-crown sprouting, an important mechanism for post-fire recovery where successful seedling establishment is less probable due to climate variability and decrease of vegetation on the landscape. We collected field data to produce empirical estimates of *Yucca jaegeriana* and *Yucca baccata var. baccata* survivorship after the 2020 fire two (2022), two and a half (2023), and four and a half (2025) years post-fire. We used a long-term repeat photography dataset to produce a publicly-available web resource for conservation and science communication. Using both pre- and post-fire photography and data from 18 sites spread across the burned area, we documented post-fire survivorship and growth metrics for the *Yucca jaegeriana* and *Yucca baccata var. baccata* in 2022, 2023, and 2025. We used vegetation mapping data to select and survey 11 local unburned control sites that matched burn sites in classified vegetation type, shrub and tree community cover and composition, elevation and aspect. Overall we observed variable natural survivorship of eastern Joshua trees and banana yucca in our plots across the Dome Fire burn area, and we found a significantly higher survival in *Yucca baccata var. baccata* (66%) than in the *Yucca jaegeriana* (18%), 2.5 years post-fire. We also found an annual decrease of approximately 5% of

Joshua trees surviving during the year prior to the 2023 survey. These results further our understanding of *Yucca* recovery post-fire and are timely for the application of pre- and post-fire management of *Yucca jaegeriana* stands.

Topic: Biogeography

A-244

The Central Indo-Pacific is the center for modern seagrass biodiversity.

Author: Joseph Kesler, Collin Gross, Barnabas Daru
Affiliation: Stanford University

Biodiversity patterns are underpinned by multiple processes including dispersal, speciation, and extinction. However, the processes structuring marine diversity compared to terrestrial organisms remain poorly understood. In this study, we combined phylogenetic and species distribution data to inform six ancestral state reconstruction models to estimate the ancestral range evolution of extant seagrass biodiversity over the past 120 million years. The models were calibrated using dispersal multiplier matrices based on tectonic plate reconstructions to account for shifts in historic dispersal rates across marine regions. Of these six models, the Dispersal, Extinction, and Cladogenesis + Jump dispersal model (DEC+J) emerged as the best fit and was the basis for the following results. We found that the Central Indo-Pacific has been the dominant source of seagrass biodiversity over the past 120 million years. Mean values derived from 50 biogeographic stochastic maps estimate that 31.72 out of 77.06 (41%) dispersal events across nine globally encompassing marine biogeographic realms originated out of the Central Indo-Pacific. The Central Indo Pacific is also by far the largest source for in-situ speciation with 49.66 out of 87.24 (57%) events across all nine realms. Meanwhile, the adjacent Central Pacific region acts as the largest sink for biodiversity, with it being the recipient of 14.64 out of 77.06 (19%) dispersal events. Overall, this analysis makes it clear that the Central Indo-Pacific is the center for seagrass biodiversity, both in terms of in-situ speciation, and as a source for adjacent regional diversity, reinforcing the region's importance as a marine conservation priority. These findings support the Center of Origin hypothesis as an explanation for the coral triangle of the Indo-Pacific as the center of marine biodiversity.

Topic: Plant phenology in an era of rapid global change: new perspectives and frontiers

A-245

Recent trends in phenology observed across the United States through the USA National Phenology Network

Author: Janet Prevéy, Theresa Crimmins, Erin Posthumus, Erin Zylstra, Ellen Denny
Affiliation: U.S. Geological Survey, University of Arizona, USA National Phenology Network

Observers with The USA National Phenology Network's Nature's Notebook platform have been collecting phenology observations on plants across the USA starting as early as 2009. After over 15 years of operation, a large number of detailed phenological measurements have been collected through this platform, and this data presents an unparalleled opportunity to examine how phenology has changed over the recent past across a large spatial scale. Here, we focused on these data from locations with nine or more years of observations to ask two questions: (1) Does the strength or direction of phenological trends or phenological sensitivity to climate conditions vary by plant phenophase or region? (2) Do we see overall shifts in important aspects of phenology, such as the length of the growing season, in this dataset? We calculated a proxy for growing season length as the number of days between leaf out and leaf senescence for individual plants that had observations for both leaf out and leaf senescence phenophases.

Preliminary results show that across all plant species with nine or more years of observations, leaf out and fruit ripening have advanced an average of one day per year earlier, while flowering and leaf senescence have not significantly changed over the recent past. The timing of all plant phenophases occurred significantly earlier in years with warmer temperatures, and leaf out, flowering, and fruit ripening phenophases were more sensitive to changes in temperatures than leaf senescence phenophases. We found that the total number of days between leaf out and leaf senescence was significantly greater in years with warmer springs and summers across the entire dataset. We also found a significant interaction between site latitude and year and latitude and spring and summer temperatures on growing season length – with leaf seasons becoming longer over time and in warmer years at higher latitude sites than lower latitude sites. This study offers invaluable insights in plant response to rapidly changing climate conditions, encompassing observations from many species across the entire U.S. and for all seasonal events over the entirety of the growing season.

Topic: Conservation Biology

A-246

Status of Research And Conservation of Five Rare Endemic Plant Species of the Coachella Valley, California

Author: Lynn Sweet, Melanie Davis, Scott Heacox, Hector Zumbado-Ulate, Remy Vincent
Affiliation: University of California, Riverside

The Coachella Valley, in the Colorado Desert portion of the Sonoran Desert is among the hottest and driest areas in North America. The surrounding area encompasses a range of habitats from the valley floor containing saline wetlands and bottomlands and near the Salton Sea, active sand dunes across the valley floor, dry wash woodlands within the alluvial fans of the surrounding mountain foothills, and the desert scrub, chaparral and woodlands of the surrounding transitional uplands. The valley is surrounded by the Little San Bernardino Mountains (Joshua Tree National Park) to the north, Santa Rosa and San Jacinto mountains to the south, and the Mecca Hills, and the Orocopia Mountains to the east. The aridity and unique hydrologic and geologic history of this region, among other factors, has created an environment supporting many species of locally-adapted plants and animals. In the past half-century, the human population of the Coachella Valley has grown exponentially, leaving these specialized endemic species vulnerable to habitat fragmentation and destruction, and the effects of climate change. Here we present our long term research that supports the applied conservation of ecosystem functions and habitats of five endemic plant species to the Coachella Valley region. We synthesize results from range-wide inventories, demographic studies, habitat condition assessments, and habitat suitability models. The five local species we will focus on are *Astragalus lentiginosus* Douglas var. *coachellae* Barneby (Fabaceae - Federally Endangered), *Astragalus tricarinatus* A. Gray (Fabaceae - Federally Endangered), *Linanthus maculatus* (Parish) Milliken subsp. *maculatus* (Polemoniaceae), *Salvia greatae* Brandegee (Lamiaceae), and *Xylorhiza cognata* (H.M. Hall) T.J. Watson (Asteraceae).

Topic: Lichen and Bryophyte Diversity, Conservation, and Evolution in the Americas

A-247

The bryophyte community of a second-order stream in a tropical forest in Puerto Rico

Author: Amelia Merced, Cecilia Sahnow
Affiliation: University of Puerto Rico, Mayagüez

Streams are important ecosystems that harbor high diversity of plant species including bryophytes. Studies suggest that in spite of disturbances, streams can act as refugia and/or corridors to buffer the effects of disturbances. In this study, we sampled within 5 sites in a second-order stream in the Luquillo Experimental Forest in Puerto Rico. We described the riparian bryophyte community composition in conjunction with the physical structure of the stream to understand what environmental factors influence bryophyte composition in the stream. We identified 57 bryophytes, 34 liverworts and 23 mosses; we recorded cyanobacteria associated with over half of the species of bryophytes. Rocks were the most frequent substrate and had the greatest richness followed by decomposing logs. Community composition and species diversity was similar among sites. Although stream width varied between sites, all of the other environmental variables measured (canopy cover, temperature, humidity, elevation) were similar. Bryophyte community composition was most influenced by the location in the stream from edge to center, and substrates occupied. We found that similar types of substrates such as branches, trunks, logs and vines, have more species in common. These results will allow subsequent research to understand the response of bryophytes to increased disturbances and a changing climate.

Topic: *Biodiversity Informatics & Herbarium Digitization*

A-248

Seeds in a Second: A Python Script for Rapid and Accurate Seed Phenotyping

Author: Benjamin Sims
Affiliation: University of California, Berkeley

Quantifying phenotypes is essential in nearly every field of biology. In plants, measuring seed size can reveal trade-offs between viability and quantity, provide insight into maternal environmental stress, or indicate embryo ploidy. However, for species bearing numerous or small seeds, this phenotype is prohibitively tedious to measure. Mimulus (syn. Erythranthe) seeds, for example, measure fractions of a millimeter in their largest dimension and number in the hundreds to thousands per a single fruit. Manually counting and measuring them is impractical, even for a large team. To circumvent this issue, I wrote a script using the OpenCV library in Python that can analyze an image of thousands of seeds in less than a second. The script measures the maximum and minimum dimensions along with the cross-sectional area of each seed, provides the total seed count, and then outputs these data to a spreadsheet. Images are corrected for perspective skew, so you can image seeds quickly with a handheld camera or smartphone. The program has high accuracy and repeatability and can measure seeds of any size as long as they're imaged on a plain background within a printed square of known size. Image analysis is not computationally intensive, so you can quickly process hundreds of images in a few minutes on a standard laptop computer. To demonstrate the utility of this script, I measured over 100,000 Mimulus seeds spread across 20 populations. I have made this script publicly available on github: github.com/adequate-soup/seed-measurer. This script's efficiency and ease of use script makes measuring seeds easily accessible to future studies, opening the door to new insights about plant adaptation, trade offs, and genetics.

Topic: *Biodiversity Informatics & Herbarium Digitization*

A-249

The Andropogoneae Extended Specimen Project: background and rationale

Author: Jordan Teisher, Paul Smock, Taylor AuBuchon-Elder, Elizabeth Kellogg
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e Systematic research produces large amounts of data tied to individual specimens, including measurements, images, chromosome number, and DNA sequences, among many others. Traditionally, these data have been aggregated into monographs, in which species descriptions summarize the results, but the direct connection between any given data point and a specimen is often lost or, at best, hard to find. Monographs are also often long-term efforts, generally taking years, if not decades. In the meantime, the data associated with the specimen – the extended specimen - are scattered and not always easily accessible. While the ideas of extended specimens and modern monographs have both received much thoughtful discussion, near-term solutions – i.e., what repositories and approaches can be implemented now – have received less attention. We faced a specific need, in the form of extended data for over 1500 specimens for a large clade of grasses, the tribe Andropogoneae. For most specimens, we had images of the herbarium sheet, close-up images of spikelets (both intact and dissected), basic morphometric trait data from the same spikelets, genome sizes, whole genome sequences (short-read and long-read assemblies) and assembled chloroplast genomes, in addition to the metadata on a standard herbarium label. We placed a high value on immediacy, making the data accessible as rapidly and efficiently as possible. In particular, we chose to minimize additional tool development. Where new tools were needed, we aimed to create a structure that was general enough to be modified for other taxonomic groups but not one that required re-collecting or re-interpreting the data. In addition, we aimed to minimize reliance on hyperlinks, placing as much of the data as possible in an archival database. We used a controlled vocabulary for the morphological trait data but did not attempt to create an ontology, nor did we try to use terms that would suggest homologies with plant groups outside the grasses. Following our goal of immediate data release, we used existing resources and personnel to create a prototype for an extended specimen database. For the Andropogoneae project, the Missouri Botanical Garden database, Tropicos (tropicos.org), already held all the specimen records and corresponding taxonomic information, including records from K as well as MO, plus images of herbarium specimens and dissected spikelets. A new field was created to hold hyperlinks to Genbank sequences. For the morphometric traits, we used an existing Tropicos module known as Projects, which limits cross-project data sharing but greatly simplifies data entry. We then created the Andropogoneae Extended Specimen Project (legacy.tropicos.org/Project/Andropogoneae) to aggregate the project specimen records and their associated data in one location. While far more elaborate structures can be envisioned, we show that it is possible to develop a basic extended specimen project immediately, without needing to wait for realization of additional resources. This provides rapid public release of data, while permitting future migration to other database types. We suggest that making the data available can proceed at the same time as additional databases and interfaces are under development. See also companion poster.

Topic: *Population Genetics/Genomics*

A-250

Following sunflower domestication through space and time with ancient DNA

Author: Benjamin Blackman
Affiliation: University of California, Berkeley

Where and how many times crop plants were domesticated, the speed and depth to which genetic diversity is lost during domestication, and how polygenic evolutionary change yields integrated syndomes of domestication traits over time are all questions of active research and frequent debate. My group has been researching these problems with modern and archaeological DNA approaches in the common sunflower, *Helianthus annuus*. Beginning ~5000 years before present, Native American farmers began the process of transforming the common sunflower from a bushy, branchy wild plant with many small disks bearing many small seeds into a staple oilseed crop that often sports just a single large head filled with large oil-rich seeds on an unbranched stalk. To reveal how this domestication process has altered sunflower genetic diversity through time, we have assembled a time series of 69 archaeological samples spanning from ~3800 to ~400 years before present, and then we obtained endogenous DNA sequences from these samples through whole-genome sequencing and sequence capture approaches, Our analyses of these data help resolve a controversy about where and how many times sunflower was domesticated, and they also suggest that the multiple genetic bottlenecks and gene flow reflect how agricultural practices underwent major shifts over the course of sunflower's cultivation history. Finally, through targeted resequencing of ~425 candidate domestication genes we defined through population genomics and transcriptomics approaches with extant germplasm, our archaeological times series is allowing us to order which selective sweeps happened when over time and thus gain deeper understanding into how the sunflower domestication syndrome was assembled by Native American farmers through time.

Topic: *Phytochemical*

A-251

Comparison of Phenolic Compound Concentrations in Utah Native species of Populus (Salicaceae)

Author: Abbigale Baum, Michael Rotter
Affiliation: Utah Valley University, Utah Valley Univeristy

Members of the genus *Populus* (Salicaceae) produce phenolic compounds that are used as defence mechanisms and in response to damage. *Populus* can be found in a wide range of elevations and landscapes, with variations in phytochemicals throughout; the factors that influence concentrations of these compounds are a complicated mosaic. To better understand the landscape mosaic of phenolic compounds, we sampled four Utah native *Populus* species (*P. fremontii, P. angustifolia, P. tremuloides*, and *P. x accuminata*) and a non-native *Salix* (*Salix fragilis*). We collected branches of each species and evaluated them for visual health of the individual and noted their elevations. We then calculated total phenolic concentration for each individual. We found that differences in the convention of phenolics between species were significant, and a pairwise analysis test showed that *P. x accuminata* differed from *P. alba*, and *P. fremontii*. *Populus angustifolia* differed from *P. alba* and *P. fremontii*. Further, there was no significant relationship between elevation and phenolic content, which was true for each species compared. Lastly, visible damage or illness did not have a significant relationship with phenolic content. Our work gives insight on how phenolic compounds differ between *Populus* species in different ecological contexts. Additional studies may include comparisons of specific phenolic compounds, different organs of the plants, or seasonality.

Topic: Dryland Floras

A-252

Life on the dry side: exploring the genomic and ecological dimensions of desiccation tolerance

Author: Rose Marks
Affiliation: University of Illinois

Understanding how plants survive extreme water limitation will improve predictions of dryland ecosystems under climate change. My research focuses on the convergent evolution of desiccation tolerance across diverse plant lineages, with an emphasis on integrating comparative genomics, population-level variation, and ecological contexts. Through large-scale field sampling in South Africa my team is assembling datasets of desiccation-tolerant species to understand how resilience traits have evolved repeatedly across phylogenetically distinct lineages.

We use genome sequencing, transcriptomics, and physiological measurements to identify shared and lineage-specific mechanisms of desiccation tolerance, revealing both deep conservation and noteworthy novelty in stress response networks. Our work also explores how local adaptation and polyploidy shape desiccation tolerance within species, and how these dynamics intersect with biogeographic patterns in dryland floras. By bridging scales—from cells to ecosystems—we aim to build a more integrated framework for understanding how plants survive in extreme conditions, and what these strategies can teach us about resilience in an increasingly arid world.

Topic: Macroevolution

A-253

Detecting whole genome duplication in the present and the past

Author: Shelly Gaynor, Keyi Feng, Douglas Soltis, Pamela Soltis, Stephen Smith
Affiliation: University of Michigan, University of Florida

Whole genome duplication, or polyploidy, is a major evolutionary force known to occur throughout the tree of life. Polyploids are often classified as auto- or allopolyploids. Following one method of classification, autopolyploids contain genome copies inherited from the same species; these could be from one individual or different individuals from the same or different populations. In contrast, allopolyploids have genome copies from two distinct species (typically congeners). These classifications represent the ends of a continuum, where we expect autopolyploids to contain additional alleles (compared to the parents) that undergo tetrasomic inheritance and allopolyploids to contain additional gene copies, each with disomic inheritance, due to the combination of two distinct genomes. Here, we evaluate commonly used methodology for detecting and classifying whole genome duplication events in shallow and deep evolutionary times. We also unravel the biological implications of the limitations of these detection methods. Overall, we find that commonly implemented approaches cannot detect both gene copies and allele copies.

Topic: Ecophysiology

A-254

CAM photosynthesis in the carnivorous plant genus Pinguicula (Lentibulariaceae)

Author: Daniel Mok, Robert VanBuren, Kadeem Gilbert
Affiliation: Michigan State University

Most plants use C_3 photosynthesis and balance a fundamental trade-off between carbon gain and water conservation. Open stomata during the day allow CO_2 uptake, but is accompanied by transpirational water loss, posing a challenge in arid or seasonally arid environments when water becomes a limiting resource. Crassulacean acid metabolism (CAM) is an adaptation to these conditions enabling high water-use efficiency by shifting CO_2 uptake activity to the nighttime when the pressures of potential transpirational water loss are reduced. CAM is convergently evolved, with over 60 predicted origins across the plant tree of life. The carnivorous plant genus Pinguicula (Lentibulariaceae) offers an intriguing and understudied system for researching CAM. This presentation will introduce Pinguicula as a novel CAM lineage, and highlights its potential for advancing our understanding of CAM evolution

Topic: Ecophysiology

A-255

Comparing the Effects of Early Spring Warming and False Spring on Trees Along a Coastal to Inland Gradient

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Climate change may have differential effects on seasonal development and carbon gain in trees according to proximity to coastal environments. With warmer temperatures, trees with higher phenological plasticity will respond by breaking dormancy earlier and extending their growing seasons. This may benefit trees if more seasonal carbon may be gained through photosynthesis and carbon assimilation. However, trees with advanced spring phenology in response to earlier warming may experience increased risk of false spring, where a late spring freeze causes damage to vegetative and/or reproductive tissue. False springs present a potential cost where damaged leaf tissue decreases the total leaf area able to photosynthesize and reduces seasonal carbon gain. Where the costs of false spring outweigh the benefits of extended growing seasons, downstream effects on survival and reproduction may impact the resiliency of some trees under future climate conditions. This impact of climate change may vary depending on where trees grow and local adaptation. Coastal tree phenology and growth may be impacted by the influence of a large body of water, which can moderate temperature. In Duluth, MN, USA we have a strong climatic gradient extending from the coast of Lake Superior to approximately thirty miles inland. This area spans three USDA hardiness zones, from 4a (inland) to 5a (coastal). Data from a five-year phenological study through the Superior Phenology Network surveying three sites across this gradient shows differences in the timing of leaf out between coastal and inland trees of the same species. With this research, we aim to assess the costs and benefits of earlier spring warming and false springs on phenology, growth, and seasonal carbon gain along a coastal to inland gradient. A randomized block design of seedlings from five species of temperate deciduous trees with maternal lines from three sites along a coastal to inland gradient have been exposed to three different warming treatments simulating early spring warming conditions. One block has also been exposed to a freeze treatment simulating a typical spring freeze event for this region. Exposure to a freeze treatment occurs once a tree's terminal leaves unfold and reflex. Data was collected on the timing and progression through phenophases, plant growth, including shoot elongation, basal diameter and leaf area, and environmental conditions of temperature and light. To develop a model for estimating seasonal carbon gain, we measured photosynthetic light response curves using a portable gas exchange system (6800, LI-COR, Lincoln, NE). Estimates for carbon gain were made by calculating the photosynthetic capacity for an individual leaf at two stages, immature and mature, and then multiplying it by the leaf area for the whole plant. We then include measurements of day and season length to estimate the total seasonal carbon gain. Measurements of phenology, growth, and carbon gain are being compared for seedlings with origins along the coastal to inland gradient to observe possible differences in the effects of early spring warming and false spring on these different species of trees.

Topic: Comparative Genomics/Transcriptomics

A-256

Phylogenomics and genome assembly reveal polyploid history of the Geraniaceae

Author: Summer Blanco, James Leebens-Mack, Shu-Mei Chang
Affiliation: University of Georgia

Polyploidy has occurred repeatedly in land plant evolution and has likely played a key role in the diversification of angiosperms. Polyploids are typically categorized as either (1) autopolyploids, derived from genome duplication within one species, or (2) allopolyploids, derived from two or more complete sets of chromosomes from different species. Both allo- and auto- polyploidy have been observed across major plant lineages. Previous phylogenetic evidence suggests that several N. American Geranium species are of allopolyploid origin (i.e., derived from 2 diploid progenitor lineage). Here, we reconstructed phylogenetic relationships for 50 species using the Angiosperms353 probe set to investigate the nature of polyploidy in the genus. Further, we generated haplotype-resolved genome assembly for the gynodioecious, putative allopolyploid, G. maculatum. Synteny and Ks analyses implicate multiple rounds of whole genome duplication (WGD) over the evolutionary history of Geraniales. In alignment with previous work, preliminary phylogenomic results suggest that the most recent WGD seen in the G. maculatum genome was an allopolyploidy event.

Topic: *Biogeography*

A-257

Using ecological niche models to predict the Pleistocene distribution of the conifers Torreya taxifolia, Taxus floridana, and their associated refugial species

Author: Tyler Radtke, Makenzie Mabry, Pamela Soltis, Douglas Soltis
Affiliation: University of Florida

Torreya taxifolia and *Taxus floridana* are two species of conifers found only on the north-facing side of ravines in the Apalachicola River area, on the border of Florida and Georgia. They are often purported to be "glacial relicts", meaning that their distribution shifted south into refugia during the last glacial period in response to cooling temperatures farther north. To predict potential current and historical distributions of *T. taxifolia* and *T. floridana*, ecological niche models (ENMs) were generated. Comparable analyses of other cool-adapted plant species found in the Apalachicola ravines were conducted to better assess the niche dynamics of plants in this community. Species' occurrence records were correlated with environmental variables using machine learning algorithms, generating a model explaining the relationship between known species locations and environmental variables. Climate models for the Pleistocene epoch (c. 22 kya and 120-140 kya) were then used to generate a prediction of where these species occurred during and before the last glacial maximum. By comparing species with similar habitat preferences but different ecological niches, the objective was to test whether *T. taxifolia* and *T. floridana* may have other ecological barriers that have prevented them from dispersing and establishing new populations further north at the end of the last glacial period. The past climate projections were largely unreliable for most species analyzed; they were often unable to predict suitable habitat during historical climatic periods and failed to provide meaningful insights into historical range shifts. Our results suggest that suitable present-day habitat for *T. taxifolia* and *T. floridana* may exist beyond the Apalachicola region, and dispersal limitations could have played a key role in restricting the two species to their current small geographic ranges. Additional research is needed to refine modeling approaches and investigate the ecological and environmental factors, including potential biotic interactions, that may be limiting the distributions of these two conifers.

Topic: *Pteridology*

A-258

Investigating the bioactive properties of the genus Lygodium through phytochemical composition analysis

Author: Sasha Carrasco, Sally Chambers
Affiliation: Eastern Kentucky University

Many of the secondary metabolites produced by plants serve as a chemical defense mechanism against herbivory, some of which have been utilized by humans for medicine (Kusari et al., 2014, Facchini and De Luca, 2008). While many phytochemicals have been identified in angiosperms, other major land plant lineages have received less attention despite their taxonomic diversity and putative utility. For instance, some fern species are used medicinally by indigenous cultures to treat various ailments (Wong et al., 2018). Of focus in this manuscript is the genus, *Lygodium* (Sw.) which is comprised of climbing ferns exhibiting worldwide distribution. Previous studies on *Lygodium venustum* and *Lygodium flexuosum* indicate medicinal usage in Mesoamerica and India (Morais-Braga et al., 2012, Achari et al., 1986). We investigated the bioactive compounds in two North American species, the native *Lygodium palmatum* and the invasive *Lygodium japonicum*. Metabolites were identified using acetonitrile and hydrochloric acid extracts from fresh and herbarium tissue samples and analyzed through liquid chromatography-mass spectrometry (LC-MS). Our results identified two flavonoids; quercetin and kaempferol in *L. palmatum*, and the absence of kaempferol in the herbarium samples of *L. japonicum*. We found that kaempferol production can vary significantly among individuals from different populations, which may be correlated with the biosynthesis of phenylalanine as a result of differing environmental stressors (Kumari et al., 2023). Future work should include other *Lygodium* species, such as *L. microphyllum* and *L. venustum*, with the goal of constructing a chemical phylogeny to better understand the evolution of secondary metabolism in the genus.

Topic: *Pteridology*

A-259

The effect of applied electric field on the germination of Lygodium palmatum, Asplenium trichomanes, and Polystichum acrostichoides

Author: Sasha Carrasco, James Britt, Sally Chambers, Jason Fry
Affiliation: Eastern Kentucky University

This study aims to explore the effect of an applied electric field on the germination of spores from various species within the Monilophyte (ferns) lineage. External electric stimulation can increase the transmembrane potential and conductivity of the cell membrane through the formation of micropores, enhancing its ability to absorb nutrients from the environment and promoting germination (Qin et al, 2023). Previous studies provide evidence that a positive relationship exists between high voltage, germination and vitality rates (Hou et al, 2023). Investigation of this relationship would expand on what is currently reported in the literature, as previous studies primarily focus on flowering plants and fungi (Gamage et al, 2018; Rezaei-Zarchi et al, 2012). We selected three species native to eastern North America for this study - *Lygodium palmatum*, *Asplenium trichomanes*, and *Polystichum acrostichoides*. Spores were surface sterilized and resuspended in DI water and 100uL of the spore solution was then placed in a drop of water on agarose media. Following this, media plates containing spores were exposed to constant electric field strengths ranging from 0, 2, 5 and 8 kV for 30 minutes daily over the course of 2 weeks. While not in the electrical field apparatus, plates were maintained in a seedling flat with a humidity dome under a grow light. Plates were checked for germination every two-three days via a dissecting microscope. Results of this study may offer novel tools for the conservation and cultivation of ferns and provide new knowledge regarding the physiological behavior of fern spore germination.

Topic: *Ecology*

A-260

Drivers of woody encroachment in the Great Plains: modeling the spread of Eastern redcedar

Author: Aleah Querns, Allison Louthan
Affiliation: Kansas State University

Temperate grasslands are currently considered to be one of the most threatened ecosystems worldwide due to land use changes, climate change, and species invasions. One type of invasion occurring in grassland systems is woody encroachment, or the displacement of grasses with woody plants. Eastern red cedar (*Juniperus virginiana*; hereafter, ERC) is an evergreen tree species native to the eastern and central regions North America which has encroached at a rapid rate in the Great Plains region over the last several decades. While human plantings, loss of megaherbivores, changes in fire regimes, and climate change have all been seen as reasons for observed high rates of encroachment, little is known about the relative impacts of each driver, as well as their interactions, on rates of encroachment in the Great Plains region. Our project utilizes a mathematical model parameterized by field-collected data to estimate the relative response of ERC invasion speed (i.e., shifts in the location of waves of invasion over time) to changes in fires, grazing, and climate. This model has two main components: first, a population model that predicts ERC demographic performance as a function of climate, fire frequency, and grazer presence; and second, dispersal estimates which, in combination with our population model, allow us to simulate waves of invasion. Preliminary results indicate that ERC population growth is most sensitive to changes in fire regimes, with weaker effects from climate and cattle grazing, though interactions among these drivers also shape growth patterns. These findings suggest that fire management is the most effective tool for controlling ERC encroachment. Our work provides clear management recommendations, highlighting the life stages most responsive to intervention, with the goal of slowing encroachment and preserving Great Plains grasslands under future climate scenarios.

Topic: Ecology

A-261

Ecological Niche Models Reveal Climate Threats to Florida's Hardwood Forest Biodiversity

Author: Sydney Barfus, Makenzie Mabry, (JT) Jared Miller, Pamela Soltis, Douglas Soltis
Affiliation: University of Florida

Florida hardwood forests are important ecosystems that support diverse temperate plant species at their southernmostdistributions within the North American Coastal Plain biodiversity hotspot. These forests are increasingly threatened by human activities, including deforestation, changes in land use, and the challenges induced by climate change, necessitating the development of ecological niche models to predict the putative distributions of key hardwood forest species in the future and inform conservation strategies. Using occurrence data collected from global biodiversity databases GBIF and iDigBio, we compiled, cleaned, and filtered thousands of records for native hardwood forest species. Environmental variables were used to map current suitable niche distributions and then to estimate potential future habitat availability under various climate scenarios. These ecological niche models provide important insights into the potential impacts of climate change on species distributions, enabling a deeper understanding of how the species comprising these hardwood forest ecosystems may shift in the future. Our findings can help guide conservation efforts to protect Florida's hardwood forests, ensuring the preservation of biodiversity and ecosystem function amidst ongoing environmental changes.

Topic: Functional Genetics/Genomics

A-262

Genes-at-Extremes: An Ecological Multi-Omics Approach to Uncover Climate Change Relevant Stress Resilience Genes

Author: Lauren Audi
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Climate change is projected to threaten global food systems with a projected 17% increase in global desertification of the total land surface. Over 50% of the yield of major crops are lost due to exposure to drought, salinity, and extreme temperatures. Studying plants adapted to extreme environments, such as the Atacama Desert in Chile, reveals underlying mechanisms involved in stress resilience and informs the development of agricultural solutions to food insecurity. The Atacama Desert is the driest, non-polar region on earth. It is characterized by hyper-arid conditions, high UV irradiance levels and extremely low soil nitrogen content, yet over 60 plant species grow there. One such species, *Solanum chilense*, is a drought tolerant tomato relative. Using comparative phylogenomics and systems biology approaches, we identify genes under convergent positive selection for low nitrogen and drought tolerance in five major plant lineages and validate them via transient expression assays and generation of transgenic drought tolerance lines in *Arabidopsis thaliana* to inform stress resilient crop breeding.

Transcriptome data was collected for 28 Atacama species, as well as from closely related species of each Atacama plant (sister species) in two comparative ecosystems—California Xeric, (drought tolerant, not nitrogen deficient) and California Mesic (not drought-adapted). Using this triplet species framework, we investigate adaptation to abiotic stress across 84 species and a range of drought and nitrogen. Our phylogenomic approach identifies shared adaptive processes, genes, and metabolites associated with major plant lineages that have evolved to enable them to thrive in extreme environments.

Within the agriculturally-relevant Lamiid clade (tomato), we identified 67 Positively Selected Ortholog Groups (PSOGs) for specific adaptation to the Atacama, while 276 PSOGs were globally adapted to drought (Atacama and CA Xeric). Some of these PSOGs are orthologs to Arabidopsis genes with functional relevance to stress tolerance, including transcription factors (TFs). Three TFs under positive selection with known drought function were validated via the plant cell-based TF perturbation assay, TARGET (Transient Assay Reporting Genome-wide Effects of Transcription factor) to compare regulation of the drought version of the TF from *S. chilense* to Arabidopsis. Identification of differentially regulated drought and low nitrogen direct target genes of candidate *S. chilense* TFs validates functional relevance. Moreover, differential expression analysis using high coverage whole RNA sequencing from multiple tissues, cross validates phylogenomic and systems biology methods. Another important outcome of this research is the production of high coverage whole RNA transcriptomes for 84 non-model organisms, including *S. chilense*, allowing for the identification of novel genes and pathways.

Our novel system employs a comparative phylogenomic approach that integrates large transcriptomic datasets to identify genes that evolved in the wild to varying levels of drought and nitrogen stress across major plant families and validates them for application to sustainable crop engineering.

Topic: Comparative Genomics/Transcriptomics

A-263

Conservation of a key CAM gene triplication in a hybrid Yucca species

Author: Anna Pardo, Karolina Heyduk
Affiliation: University of Connecticut

Photosynthesis serves as green plants' primary form of carbon acquisition, but is inhibited by abiotic stresses such as water limitation due to the dual function of stomata in carbon intake and transpiration. Furthermore, carbon must compete with oxygen for the active site of rubisco, the primary carbon-fixing enzyme in C3 photosynthesis; this reduces photosynthetic efficiency. Crassulacean acid metabolism (CAM) is a form of photosynthesis in which stomata are opened only at night, when temperature is reduced, thus reducing transpiration and increasing the plant's water use efficiency. During the night, CAM plants use phosphoenolpyruvate carboxylase (PPC) as the primary carboxylating enzyme, rather than rubisco, and store acquired carbon as malate until the day, when the CO_2 is decarboxylating. This carbon concentrating mechanism results in high CO_2 concentrations around rubisco and serves to increase photosynthetic efficiency. Most CAM plants use PPC1 as the primary carbon-fixing enzyme, but a few, including those in the genus Yucca, use PPC2, which share sequence similarity to bacterial PPCs.

The genus Yucca (Asparagaceae, Agavoideae) contains both C3 species, such as Y. filamentosa, and strong CAM species, such as Y. aloifolia. A third species, Y. gloriosa, arose from hybridization between Y. filamentosa and Y. aloifolia, and has varying levels of facultative CAM activity upon drought treatment. Recently, CAM Y. aloifolia was found to contain a tandem triplication of PPC2, whereas Y. filamentosa (C3) contains only a single copy of this gene. Here, we investigate the characteristics of the PPC2 region in the hybrid Y. gloriosa, as well as the relation of PPC2 to CAM and drought response in all three species.

Topic: Defining forces in fern evolution: Celebrating the contributions of Kathleen Pryer and Michael Windham

A-266

What is Polypodium vulgare? Discerning disparate origins of an iconic fern in Europe and Asia

Author: Jonas Mendez-Reneau, Christopher Haufler, Erin Sigel
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Few fern taxa are as readily recognized and iconic as *Polypodium vulgare*, the type species of *Polypodium*, the namesake genus of the largest fern family, Polypodiaceae. Characterized by pinnatifid leaves with round sori and creeping rhizomes, *P. vulgare* was originally described by Linnaeus in *Species Plantarum* and was once considered a single a circumboreal species exhibiting subtle morphological variation. Generations of researchers have revealed that *P. vulgare* comprises a complex of mainly northern temperate diploid and allopolyploid species. Although among the best studied fern reticulate groups, the *P. vulgare* complex continues to yield novel taxonomic diversity including an Asian segregate that was tentatively named '*Polypodium okiense'* by Drs. Christopher Haufler and Michael Windham based on isozyme markers. Here we apply expanded sampling, maternally inherited plastome sequences, and bi-parentally inherited nuclear target capture datasets to demonstrate that *P. vulgare* is only European, whereas '*P. okiense*' is restricted to Asia and of distinct parentage. While both are of Pleistocene origin, our divergence dating estimates suggest that '*P. okiense'* likely formed prior to *P. vulgare* and support the hypothesis that *P. vulgare* is a progenitor of the European allohexaploid *Polypodium interjectum*. In addition, we advocate for the formal recognition of '*P. okiense',* infer the taxonomic identity of an enigmatic population from South Africa, and address implications for conservation and pharmaceutical applications of these often confused taxa.

Topic: Biodiversity Informatics & Herbarium Digitization

A-267

Deconstructing a Biodiversity Hotspot: Diversity and Rarity in the North American Coastal Plain

Author: Taliesin Kinser, Julie Allen, Narayani Barve, Pamela Soltis, Douglas Soltis, Robert Guralnick
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The North American Coastal Plain (NACP) is one of the world's biodiversity hotspots of critical conservation concern, representing a substantial and unique portion of Earth's threatened biodiversity. Despite its low topographic relief, the NACP harbors many endemic and vulnerable species. Thus, identifying the factors that build its high diversity and endemism can inform more strategic conservation. In this study, we assess three key facets of biodiversity in this region: 1) the distribution of angiosperm diversity overall, 2) the accumulation of rare taxa into certain areas (total rarity), and 3) areas in which species tend to be rare (relative rarity). We apply a phylogeny and modeled distributions of the regional species pool along with spatial statistics of temperature, precipitation, and edaphic predictor variables. With this approach, we analyze lineage turnover across environmental gradients, environmental factors linked to potential speciation, and factors related to lineage persistence or filtering. We assemble these analyses into structural equation models to explain patterns of phylogenetic diversity, rarity, and relative rarity. Minimum temperatures and precipitation seasons are the primary gradients separating lineages across the region, and soil nutrients define interior geographic zones where there is high lineage overlap. Young species concentrate into nutrient-poor soils of these interior zones, while areas with stable temperatures contain many older species. Reduced precipitation and low minimum temperatures filter out lineages in western and northern parts of the region, respectively (where species "cluster" into fewer lineages); and certain zones of potential speciation also produce lineage clustering patterns. Phylogenetic diversity is high in sandy soils of lower elevations, especially where there is lineage overlap from limited lineage filtration and novel diversity. There are three main centers of rarity: the East Gulf, Florida peninsula, and mid-Atlantic. Rarity is closely associated with diversity, but rare taxa oversaturate lineage diversity in very sandy and rainy parts of the high-diversity, high-rarity East Gulf. Diversity is lower in the peninsula, but it has high relative rarity linked to its stable temperatures and highly seasonal rainfall (droughtier winters). Overall, aspects of the soil, including restrictive conditions, support high densities of taxa or spur novel diversity, while water supply and favorable temperatures retain lineages or old species. Geographic differentiation of these conditions and lineages produces various diversity and/or rarity centers that build regional biodiversity and endemism, which can inform comprehensive conservation action for this hotspot.

Topic: Systematics & Taxonomy

A-268

Phylogenomics and macroevolution of a florally diverse Neotropical plant clade (Hillieae)

Author: Laymon Ball, Ana Maria Bedoya, Charlotte Taylor, Laura Lagomarsino
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The remarkable diversity of Neotropical flowering plants has been shaped by a complex interplay of abiotic and biotic factors, including mountain uplift, ecological niche evolution, and shifts between pollinator groups. Yet few studies integrate these drivers across spatial and evolutionary scales within a single clade. Hillieae (Rubiaceae) is a diverse Neotropical tribe comprising ~30 epiphytic species that exhibit spectacular variation in floral morphology, including adaptations to hawkmoth, hummingbird, and bat pollination. While most species occur in low- to mid-elevation wet forests and species richness peaks in southern Central America, the group as a whole occupies a broad range of habitats and abiotic niches. To understand how biogeography, plant-pollinator interactions, and ecological divergence have shaped Hillieae diversification, we integrate target enrichment data, ancestral biogeography and pollination syndrome reconstruction, ecological niche modeling, and multivariate trait analysis. A phylogenetic framework based on ~1000 loci supports multiple shifts in pollination syndromes and a Southern Central American origin ~19 million years ago. Biogeographic reconstructions reveal a history of dispersal and vicariance across geologically complex regions, with pollinator shifts often occurring in distinct geographic and climatic contexts. Zooming in on Hillia subg. Hillia —a clade of nine long-tubed, hawkmoth-pollinated species occurring in diverse habitats along the eastern Andean slopes—we investigate patterns of recent radiation (~5 Mya) and cryptic diversity to understand how mechanisms beyond pollinator-driven selection, which has been common in other subclades, contribute to diversification. Several species overlap in environmental niche and geographic range, and one member of the subgenus, Hillia parasitica, is particularly widespread—occurring not only in the Andes but also in the Atlantic Forest of eastern South America and throughout the Caribbean—and exhibits notable intraspecific morphological variation. Phylogenetic analysis reveals that H. parasitica is non-monophyletic with respect to other members of the subgenus, raising questions about species boundaries. To better resolve population structure and delimit species across this subgenus, we integrate SNP data, model-based clustering, species delimitation under varying assumptions of admixture, and analyses of floral and vegetative traits. Despite high floral similarity, SNP-based clustering suggests the existence of multiple ecologically and geographically structured lineages. Collectively, this work underscores the value of integrative approaches in understanding plant diversification and sheds new light on the processes generating biodiversity in the Neotropics.

Topic: Ecology

A-269

Floral frenemies: How pollinators and seed predators shape female advantage in a gynodioecious plant

Author: Brooklyn Richards, Thomas Kaye, Susan Waters, Andy Jones
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Gynodioecy, the coexistence of females and hermaphrodites, is a plant sexual system that may represent a transitional stage in the evolutionary pathway from hermaphrodism to dioecy, but it can also persist as an evolutionary stable state. In order for gynodioecy to be maintained, females must have a fitness advantage in offspring quality and/or quantity. While considerable theoretical work has modeled the conditions under which gynodioecious systems could evolve, empirical research on the ecological factors influencing this system remains relatively limited. Sex-biased ecological interactions that influence plant reproductive success have the potential to help or hinder female advantage, thereby playing a role in the maintenance of gynodioecy. Hermaphrodites typically have larger floral displays than females. In addition to sexual size dimorphism, differences in reward type, nectar properties, scent, flower florescence patterns, and chemical defense are expected to shape ecological interactions such as pollination and pre-dispersal seed predation.

We measured differences in pollinator and seed predator dynamics between female and hermaphroditic plants in *Sidalcea campestris* to evaluate the role of pollinators and pre-dispersal seed predators in maintaining gynodioecy. Despite receiving less than half as many pollinator visits as hermaphrodites, average female seed set was nearly double that of hermaphrodites. Furthermore, pre-dispersal seed predation by a specialist weevil, *Macrorhoptus sidalceae, was approximately 34% higher in hermaphrodites than in females.* Taken together, the effects of pollinators and pre-dispersal seed predators on *S. campestris* reproductive success indicate that females achieve the necessary reproductive advantage to persist. By incorporating both mutualistic and antagonistic interactions across multiple reproductive stages, this study broadens our understanding of how multispecies ecological interactions shape the evolution and persistence of dimorphic sexual systems.

Topic: Systematics & Taxonomy

A-270

Development of Species Webpages and Interactive Key for Mexican Lobelia (Campanulaceae)

Author: Isabel Andrade-Muñoz, Mariola Barrera, Arturo Castro-Castro, Edward Gilbert, Miguel Perez Perez, Tina Ayers
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The genus *Lobelia* (Campanulaceae) is species-rich with centers of diversity in Mexico and Africa. Most of the ca 100 Mexican species occur in the pine-oak forests of the five major mountain ranges called the Mexican Transition Zone. About 80 of these species are narrow endemics and many are poorly known. One of the goals of the Mexican *Lobelia* project is to delineate these species and create updated morphological descriptions of taxa, as well as publish an accessible, interactive key to Mexican Lobelias. This process involves using mounted specimens from herbaria across the US and Mexico to record diagnostic morphological characters. We also referenced original plant descriptions, field photos, and digitized types from JSTOR Global Plants along with the results of genomic sequencing to verify differences in especially difficult species complexes.

Morphological characters were coded as character states into a Symbiota web interface using the Southwestern Environmental Information Network (SEINet) portal to create an interactive key. The morphology was also used to develop short comparative descriptions of each species in both English and Spanish that are electronically published on individual species web pages generated by SEINet tools. Each species page also includes habitat, elevation, distribution, and notes on endemism, whether the species is known only from the type locality, and how to separate it from morphologically similar species. Each web page also includes an interactive map based on specimen data, photos of herbarium specimens, and field photos if available. During this process we discovered three species new to science, which we illustrated and wrote detailed descriptions.

Topic: Phylogenomics

A-271

Phylogenomics and ecomorphological evolution in Deuterocohnia (Bromeliaceae: Pitcairnioideae)

Author: Bing Li, Nicole Schütz, Kurt Weising, Georg Zizka, Jacob Landis, Thomas Givnish
Affiliation:, University of Kassel, Cornell University, University of Wisconsin-Madison

Deuterocohnia (17 spp.) shows extraordinary variation in elevation (0-3900 m), diverse growth forms, and narrow species distributions in the central Andes and the Peru-Chile coast. Previous research using few plastid and nuclear loci failed to produce well-resolved or supported phylogenies for this genus. Here we sequence 1815 single-copy nuclear genes and whole plastomes to infer relationships, screen for reticulation, reconstruct evolution of vegetative and floral characters, and evaluate species groups and their ties to geography. We developed the Bromeliad1815 bait set to capture low-copy nuclear genes across Bromeliaceae, producing nuclear and plastome phylogenies for *Deuterocohnia* and outgroups in six bromeliad subfamilies using maximum likelihood, ASTRAL, and network analyses; test for cytonuclear conflict and its potential causes; and evaluate the evolution of morphological characters in relation to each other and elevation using phylogenetic PCA and phylogenetic regression. We produced fully resolved, strongly supported nuclear and plastome phylogenies for *Deuterocohnia*, with crown ages of 5.5 and 8.0 Mya, respectively. Cytonuclear conflict appears driven mainly by hybridization/introgression, consistent with several species co-occurring in small areas. Vegetative organs and growth form become increasingly compact with elevation, reflecting adaptation to greater desiccation, wind exposure, and cold soils. Some floral traits remain consistent across elevations, perhaps shaped more by pollinators. Our results imply rapid adaptive divergence (e.g., in *strobilifera-chrysantha*), convergent evolution (two origins of the cushion growth-form), and phylogeny consistent with form in some cases (e.g., *seramisiana-brevispicata-meziana*) and recurrent effects of the Rio Pilcomayo barrier on speciation and chloroplast capture.

Topic: Ecology

A-272

How much of pollinator visitation rate and diversity can be inferred from pollen receipt and pollen tubes?

Author: Javier Valverde, Mónica Medrano, Esmeralda López-Perea, Conchita Alonso
Affiliation: Sevilla University, Estación Biológica de Doñana

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Topic: Molecular Ecology

A-273

A dynamic perspective on above- and below-ground epigenetic regulation: phenotypic and molecular responses to seed demethylation in *Erodium cicutarium*

Author: Conchita Alonso, Rubén Martín-Blázquez, Mónica Medrano
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Epigenetic regulation has emerged as a significant element in adaptation to heterogeneous and stressful environments, with modifications in DNA methylation being particularly relevant in plants. In non-model plants, DNA methylation inhibitors have been used to investigate the relationship between DNA methylation and plant phenotypes, with particular emphasis in leaf DNA and aboveground traits. Root DNA methylation remains, however, virtually unexplored, despite both root DNA methylation and traits could be at least equally relevant for plant adaptation to challenging environments. Here, we investigate the relationships between above and below-ground DNA methylation along individual lifetime and analyze the phenotypic and transcriptomic effects of seed exposure to 5-azacytidine in leaves and roots of *Erodium cicutarium*, an annual plant native to Mediterranean Basin, that has become invasive in several regions worldwide.

Different experiments were conducted to analyze the effects of 5-azacytidine in individual and organ phenotypes, global DNA methylation and transcriptomes at juvenile and adult stages. To do so, scarified seeds were soaked for 48 h in either water or a 500 µM solution of 5-azacytidine before sowing and emerged plants were grown under common conditions. DNA and RNA were extracted form leaf and root tissues were collected at juvenile and adult stages.

We found that global DNA methylation varied between leaf and root tissues and increased from juvenile to adult stage, difference with age being stronger in root tissue. Further, 5-azacytidine significantly reduced DNA methylation in leaf and root tissues. Moreover, 5-azacytidine slowed plant development and tended to up-regulate gene expression. In particular, it up-regulated two gene copies of chromomethylase *CMT1* across all study samples, and the domain rearranged DNA methyltransferase *DRM2* in juvenile roots. Furthermore, at adult stage, leaves of individuals treated with 5-azacytidine exhibited up-regulation of genes involved in seed dormancy release, photoinhibition, and osmotic stress. Altogether, this study illustrates how experimental seed demethylation help to understand the highly dynamic association between epigenetics and phenotype.

Topic: Floristics

A-274

Hundreds of atlas records confirm a Wallacean Shortfall for vascular plants and support the need for targeted collecting

Author: Neil Snow
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Over twenty years ago Prather et al. (2004: Syst. Bot. 29: 15–38) discussed the general and rapid decline of plant collecting in the USA after the 1970s, including the reasons and implications for the steep decline. Yet the Wallacean Shortfall – our collective acknowledgement that species' distributions remain imperfectly known – remains significant. Curatorial and (mostly) collecting activities in the Sperry Herbarium the past eleven years have documented 707 atlas records (= first vouchered occurrences at the state or county level), representing 72 state and 635 county records. Records were determined by whether a vouchered specimen could be found at the time on SEINet or the current beta version of BONAP. The novelties represent 9 states, with most from ID, KS, MO and OK, where recent field activities have focused. Among the 77 counties represented, the top 6 comprised ca. 58% of the total. Of the 580 (82%) collections made by students, many derived from 3 MS theses (2 in KS, 1 in ID) and an ongoing project in Missouri by an undergraduate student. Other records were by undergraduates for classes in Plant Taxonomy, Grass Taxonomy and Wetland Plants. Opportunistic collecting of the author contributed 12% and the remaining 6% were discovered among existing herbarium specimens. Taxa native to North America comprised 67% and non-native taxa 33% of the discoveries. The average across the eleven-year period is 64.3 new atlas records annually. This level of novelties coming from an herbarium of 53K specimens after 150+ years of botanical collecting in North America was unexpected. Counties are the smallest levels of geographic resolution normally indicated on distribution maps in taxonomic revisions and should be fully surveyed because they typically include a wide variety of habitats. However, the results indicate that the Wallacean Shortfall for vascular plants at the county level in the USA is more pronounced than generally realized. New occurrence records have implications for early detection/rapid response approaches to mitigation of weeds, conservation and effective land use management, ecosystem processes, and are critical for ecological niche modeling. Targeted collecting at the county level to reduce the Wallacean Shortfall further is advisable and will keep herbaria active locally. Moreover, the continued documentation of distribution records upholds the relevance of herbaria regionally and may engender continued administrative support, especially if students are actively involved in collecting and curating.

Topic: Paleobotany

A-275

Return to Form: Pipeline for 3D reconstruction of plant fossil image-series datasets using free software

Author: Robert Menning, Brian Atkinson, Kelly Matsunaga
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Three-dimensional models of fossil plants are a data type that is increasingly becoming essential for studying fossil specimens and making inferences on plant evolution and diversity across macroevolutionary time scales. These data are often produced from X-ray microcomputed tomography or image stacks made from a series of physical sections (e.g., cellulose acetate peels). Here, we discuss a pipeline for 3D reconstruction of these plant fossil datasets using software that is freely available to academic institutions and thus accessible to a wide range of users. Although developed for use with paleobotanical datasets, the pipelines can be applied to other study systems that use similar types of tomographic data. The 3D reconstructions are fully manipulatable and are valuable for clarifying morphology that is difficult to discern from 2D images. The models can also be used to generate animations and 3D prints for communicating results with scientific audiences and the public and can be uploaded to online repositories (e.g. Morphosource) along with other specimen data.

Topic: Hybrids and Hybridization

A-276

Reproductive isolation and introgression in monkeyflowers (Mimulus)

Author: Jennifer Coughlan, Megan Frayer, Hagar Soliman, Pia Schwarz
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The age of genomics has revealed the ubiquity of introgression across diverse eukayotic taxa. Despite its commonality, determining the dynamics and evolutionary consequences of introgression is an active area of research. Although considered quite rare, the origin of a new species is one potential outcome of introgression. Typically, such incidences of homoploid hybrid speciation arise when introgression causes novel combinations of adaptive traits, allowing for hybrids to inhabit a new environment. Yet, a growing body of work has revealed the role of intragenomic conflicts in speciation, and moreover hypothesized that alleles evolving via conflict may easily invade new populations due to their selfish evolution. Here, we provide a putative example of homoploid hybrid speciation via conflict in monkeyflowers. We describe complex patterns of reproductive isolation via hybrid seed inviability, which is thought to evolve via conflict between parental interests in resource allocation to offspring. We then show that hybrid seed inviability has evolved rapidly and repeated in this group. Moreover, we find that parallel patterns of hybrid seed inviability also have a shared genetic basis. Lastly, we apply rangewide whole genome sequencing to show that species with shared patterns of reproductive isolation also exhibit a significant history of introgression. In total, this work suggests that introgression may transfer incompatibility alleles across taxa and has implications for how old genetic variants are re-parceled into new species.

Topic: Biodiversity Informatics & Herbarium Digitization

A-277

Small Features, Big Picture: What 2 Million Leaves Reveal About Plant Evolution

Author: Will Weaver, Stephen Smith
Affiliation: University of Michigan

Combining leaf outline shapes with large-scale phylogenetic analyses remains challenging using traditional metrics. Basic descriptors like area, perimeter, and circularity fail to capture outline complexity, while advanced methods such as procrustean geometric morphometrics and elliptical Fourier descriptor analysis require homologous features, limiting their application to similar shapes and closely related taxa. We apply the Euler characteristic transform (ECT), a topology-based method that captures shape information by measuring connectivity patterns across all directions and scales. ECT generates continuous distribution curves that comprehensively represent leaf outlines without requiring homologous landmarks. Using these distributions, we perform ancestral character reconstruction to trace evolutionary trajectories and identify nodes where significant shape changes occurred. To test our methods, we analyzed five morphologically distinct clades using LeafMachine2, extracting over 2 million leaf outlines from 150,000+ specimens across 450 herbaria.

Topic: Symbioses: Plant, Animal, and Microbe Interactions

A-278

Dynamic DNA (de)methylation underpins parasitic Cuscuta-host plant communication

Author: Megan Adler, Allison Vanek, Paula Ralph, Saima Shahid
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Parasitic flowering plants have evolved sophisticated mechanisms to recognize and attach to diverse hosts through specialized feeding structures called haustoria, stealing valuable water and nutrients. Aggressive parasitic plants feeding on economically important hosts can cause significant yield loss. Previous work demonstrated that *Cuscuta campestris*, a generalist parasitic vine with a broad host range, uses microRNAs to silence host defense genes via interspecies RNA interference. *Cuscuta* also induces transposable element (TE)-derived small RNAs at the haustoria. In plants, TE-derived small RNAs function in the maintenance and *de novo* DNA methylation of targeted TEs that result in long-term epigenetic silencing. Whether *Cuscuta* haustoria-induced small RNAs trigger DNA methylation changes and epigenetic memory for host/parasite adaptation remains unknown. Using whole-genome enzymatic methylation sequencing, we identified host and parasite-specific DNA methylation changes in haustorial and non-haustorial tissues from *Cuscuta-Arabidopsis* associations. Our results demonstrate that *Cuscuta* parasitism triggers global DNA demethylation in both host and parasite genomes, affecting thousands of TE, genic and intergenic regions. Host DNA demethylation targets include several well-characterized defense genes, which is consistent with the known role of DNA demethylation in immunity response against other plant pathogens and herbivory damage. Surprisingly, the parasite genome also gains *de novo* methylation at many regions, suggesting epigenomic plasticity may facilitate parasite establishment. Findings from this work could direct future development of epigenetically engineered crops with broad-spectrum resistance to multiple plant parasites.

Topic: Biodiversity Informatics & Herbarium Digitization

A-279

High-Throughput Digitization of the Asian Collections in the Missouri Botanical Garden Herbarium: A Case Study of Automating Transcriptions at Scale

Author: Matthew Austin, Carmen Puglisi, Jordan Teisher
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The Missouri Botanical Garden (MBG) has been conducting research on tropical plants since its founding in 1859. Its herbarium is among the largest in the world, with nearly 8M specimens, and is consulted extensively for its rich collections from the Neotropics, Africa, and Madagascar. Its collections from Asia are less frequently highlighted, despite MBG having strong historical connections to the region, both as the international headquarters for the *Flora of China* project (since 1988) as well as through collaborative programs in Vietnam (1993-2012), Indonesia (2012-2013), and the Himalayas (2005-present).

A digitization grant through the National Science Foundation is making the Garden's unique collections of Asian specimens available globally through Tropicos, MBG's in-house botanical database, as well as through aggregators like GBIF and iDigBio. To date, digitization staff at the MBG Herbarium have used high-speed, single-user photostations to image approximately 500,000 specimens. However, non-English labels on many of these specimens and the time required for manual transcriptions pose obstacles to efficiently transcribing this collection. To address this challenge, we developed a pipeline that harnesses OCR, Google Cloud Translation, and the large language model (LLM) ChatGPT to automate label transcriptions. All automated transcriptions were edited and verified for accuracy by digitization staff prior to being made publically available on Tropicos. This pipeline successfully transcribed all tested fields a majority of the time, with many common specimen-related variables achieving accuracies >76%. Implementing this pipeline reduced the time digitization staff invested in transcriptions by 12% and the transcription cost by 10%. This case study provides valuable lessons for implementing automated transcription pipelines in large-scale digitization projects, and demonstrates the value of these pipelines for digitization at scale.

Topic: *Phylogenomics*

A-280

Phylogenomics disentangles the evolutionary and biogeographic uncertainty in Apocissus (Vitaceae)

Author: Alberto J. Coello, Gabriel Johnson, Betsy R. Jackes, Jun Wen
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Apocissus is one of the most intriguing genera in the grape family (Vitaceae). For decades, the morphological differentiation of some Australasian *Cissus* led to the assignment of a few species from Australasia in several groups, e.g., *Nothocissus*, *Cissus* or *"Austrocissus"*. Subsequent phylogenetic studies showed the polyphyly of *Cissus*, with an early diverged clade sister to the core *Cissus* clade. The analyses designated the early diverged clade initially as the *Cissus* II clade and included one Neotropical species. The *Cissus* II clade was sometimes informally known as the *"Austrocissus"* group, which shows a tropical disjunction between Australasia and the montane areas of the Neotropics. However, the phylogenetic position of this group showed controversies, with the latest reconstructions placed this group as sister to *Cissus*. In 2023, the genus *Apocissus* was described based on morphological characters, but evolutionary relationships remain poorly understood. In this study we explore, for the first time, the phylogenetic and biogeographic patterns of *Apocissus* through a phylogenomic approach. In particular, we used the Vitaceae specific Hyb-Seq bait set (1,013 nuclear loci). Additionally, to compare nuclear and plastid data, we used the complete plastome of *Cissus quadrangularis* as a reference to extract plastid information. We performed nuclear and plastid phylogenetic reconstructions and biogeographic reconstructions to understand the evolutionary history of *Apocissus*. Additionally, because of the high degree of hybridization in some lineages of the grape family, we performed hybridization analysis. Our phylogenetic reconstruction strongly supports the identity of *Apocissus* as an independent genus sister to *Cissus*. The *Cissus* lineage was inferred to have originated during the late Cretaceous, but its diversification began much later in the Oligocene in Australasia. This huge difference in time suggests early extinctions during the evolutionary history of the *Apocissus* – *Cissus* clade, resulting in the low biodiversity observed nowadays in *Apocissus*. Also, despite of what was expected, hybridization was not supported to have played an important role during the evolution of *Apocissus*. Finally, our plastome analysis suggested that *C. penninervis* is grouped with the rest of *Apocissus*, a pattern already observed considering its seed morphology. We hence propose transferring *Cissus penninervis* into *Apocissus*. Our results shed light into the evolutionary and biogeographic history of *Apocissus*, and they highlight the potential of genomic approaches as a tool to solve complex evolutionary histories.

Topic: *Biogeography*

A-281

Boreotropical origin and expansion across Neotropical America explain the evolution of the amphi-Pacific tropical genus Dendropanax (Araliaceae)

Author: Angelica Gallego-Narbón, Gabriel Johnson, Pedro Fiaschi, Pedro Acevedo-Rodríguez, Jun Wen
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Intercontinental disjunctions can be a result of vicariance due to continental fragmentation, long distance dispersal (LDD) events, or a combination of both. Despite the extensive contribution of tropical areas to global biodiversity, the factors explaining the origin of intercontinental disjunctions in tropical lineages have been underexplored in contrast with those of temperate lineages. Here, we explore the origin of the amphi-Pacific biogeographic disjunction in *Dendropanax* Decne. & Planch. (Araliaceae), including 93 accepted species distributed across tropical and subtropical areas in eastern Asia (18 species) and America (75 species). Previous research based on limited species and genetic sampling supports two geographic clades (Asian and Neotropical) and provides two alternative hypotheses: (i) that the divergence of *Dendropanax* occurred in eastern Asia with subsequent colonization of the Neotropics; and (ii) that *Dendropanax* had a boreotropical origin. To test these hypotheses, we sequenced c. 60% of *Dendropanax* species and additional representative specimens of closely related genera using an Araliaceae specific Hyb-Seq bait set (936 nuclear loci) and obtained highly resolved nuclear and plastid phylogenies. Our nuclear phylogeny was time-calibrated based on the fossil record and used to perform ancestral biogeographic reconstruction. Given the relevance of hybridization in the evolution of other Araliaceae lineages, we performed hybridization analyses. Both nuclear and plastid phylogenies supported five geographic clades in Asia (I), Central America and Mexico (II and IV), the Caribbean (III) and South America (V). In addition, we did not detect hybridization events between clades and hybridization within each clade was scarce. The biogeographic reconstruction supported that *Dendropanax* diverged during the mid Eocene and was distributed across eastern Asia and Central America during its early evolution, with crown ages of current Asian and Neotropical clades dating to the Eocene-Oligocene transition. The Neotropical *Dendropanax* clade originated in Central America, from where it colonized the Caribbean and South America during the Miocene. Our results support the boreotropical origin of *Dendropanax* and provide evidence that geographic isolation is the main driver of evolution in the genus. This underscores the importance of colonization events across Neotropical Americas for the evolutionary diversification of the genus.

Topic: *Pteridology*

A-282

A global survey of non-native ferns: insights into ecology, genomics, and phylogeny

Author: Jessie Pelosi, Agustina Yañez, Leah Veldhuisen, Anthony Dant, Poppy Northing, Rebecca Bland, Weston Testo, Katrina Dlugosch
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Non-native taxa are now ubiquitous members of the world's flora, and those that form established, self-sustaining populations can have substantial economic and ecological impacts. Ferns are the second largest group of vascular plants with >12,000 recognized species, yet are typically overlooked in non-native floras, despite having profound impacts on the communities to which they are introduced. To address this fundamental gap, we compiled a global checklist of non-native ferns and use this to 1) assess geographic and phylogenetic distributions, 2) examine rapid evolution in the ecological niche, and 3) analyze the association of polyploidy and genome size with invasiveness of non-native ferns. Our checklist is compiled from a variety of published resources and occurrence information in both the native and introduced ranges and was validated using a combination of floras and expert-verified observations. We then classified each taxon following a scheme that recognizes casual/adventive, naturalized, and invasive categories along a continuum by searching the primary literature. The final list contains 80 fern taxa: 16 casual/adventive, 35 naturalized, and 29 invasive. This resource allows us to explore patterns of ecological traits, genomic traits, and phylogeny of non-native ferns from a global perspective.

Topic: *Ecophysiology*

A-283

Plasticity and Ontogenetic Variability of Joshua Tree Common Garden Study

Author: Lizzy Doan, Sara Sciulla, Jeremy Yoder, Christopher Smith, Todd Esque, Lesley DeFalco, Karolina Heyduk
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Joshua trees (Yucca brevifolia and Yucca jaegeriana) are an iconic hallmark of the Mojave desert. Due to anthropogenic pressures, both species are experiencing reductions in suitable habitat in addition to hotter, dryer environments. To better understand the species' physiological response to these pressures, we planted three common gardens with seedlings collected across the species' ranges, representing 15 source populations of Joshua tree. Seedlings were measured across three years (2022-2024) for physiological and photosynthetic traits, including the strength of CAM photosynthesis. We assessed gas exchange, titratable acidity, relative water content, and obtained carbon isotope ratios. We compare the populations between gardens to better understand the extent of Joshua trees' plasticity vs. adaptation under variable environmental conditions represented by the different common gardens across the Mojave. In addition, we compare the differences of two gardens planted in different years in the same location, analyzing how age impacts physiological response. Our analyses suggest a high degree of plasticity across individuals of Joshua tree, with similar responses to environmental conditions regardless of the individual's home environment. We further show ontogenetic differences between age cohorts and demonstrate seasonal variability in CAM use.

Topic: Biogeography

A-284

Spatial phylogenetics of Iberian ferns: unravelling centres of paleo- and neoendemism

Author: Sonia Molino, Ignacio Ramos-Gutiérrez, Alberto J. Coello, Mario Mairal, Llorenç Sáez, Mario Fernández-Mazuecos
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Spatial phylogenetics, investigating the geographical distribution of phylogenetic diversity and endemism, provides novel insights into biogeographic patterns and conservation priorities in an evolutionary framework. A recent study of the Iberian angiosperm flora identified distinct centres of neo- and superendemism, but a limited presence of paleoendemism areas. However, a global study of fern spatial phylogenetics revealed that southern Europe, including the Iberian Peninsula, represents a significant paleoendemism area, suggesting that ferns and angiosperms display divergent spatial phylogenetic patterns. Here we conducted a spatial phylogenetic analysis of Iberian ferns to delve into their phylogenetic diversity and endemism patterns at a finer scale.

We constructed the first comprehensive phylogeny of all Iberian ferns (class Polypodiopsida), based on plastid DNA sequences. Distribution data were obtained from the AFLIBER database, with some taxonomic and chorological updates. Spatial phylogenetic patterns were analysed using the R package canaper. Phylogenetic diversity and endemism were mapped, and categorical analysis of neo- and paleo-endemism (CANAPE) was conducted.

Results show that phylogenetic diversity is concentrated in southern Cádiz and along the Atlantic and Cantabrian coasts. Neoendemism areas concentrate in the Balearic Islands (driven by species of *Asplenium* and *Dryopteris*) and, to a lesser extent, the Baetic Mountains, the Algarve and the Pyrenees. Meanwhile, the main paleoendemism areas are found in southern Cádiz, the Cantabrian region, and northeastern Catalonia. Paleoendemism in southern Cádiz and the Cantabrian region is driven by species such as *Psilotum nudum, Culcita macrocarpa, Woodwardia radicans, Diplazium caudatum* and members of the Hymenophyllaceae. Meanwhile, paleoendemism in northeastern Catalonia depends on whether *Salvinia natans* is classified as native. This study highlights critical areas of evolutionary significance for Iberian ferns and underscores the importance of integrating spatial phylogenetics into conservation strategies.

Topic: Overcoming the barriers to on-going Castilleja research: From botanical enigma toward an emerging model system

A-285

Herding Castilleja's: Integrating genomic, phenotypic, and ecological data to understand divergence in a lineage that doesn't play by the rules

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Conflicting phenotypic and genomic patterns of divergence are increasingly recognized as common, especially for young, rapidly-diversifying lineages. These lineages are often marked by taxonomic uncertainty, such as in species complexes, in which assigning individuals into discrete species is challenging. Attempts to reconcile complexes by incorporating multiple lines of evidence are important with respect to utility, but they may also reveal additional layers of discordance (eg, between phenotypes, genomics, geography, and ecology) that can illuminate how evolutionary processes operate at early stages of divergence. In Castilleja, overlapping distributions of morphological traits, fuzzy species boundaries, and conflicting signals of genomic differentiation challenge assumptions about the nature of species, affording opportunities to investigate unresolved questions. The core members of the *Castilleja pilosa* species complex occur widely across the Intermountain West of the United States and pose challenges to traditional species assignment, due to continuous diagnostic characters and taxonomy that is largely based on distribution and/or habitat preferences. Here, we investigate multiple lines of evidence to assess patterns of divergence and the nature of species in the *C. pilosa* species complex. Based on phenotypic, ecological and genomic traits, we examine whether and how datasets align with each other, and what this can reveal about the patterns and processes shaping early divergence.

Topic: Macroevolution

A-286

The role of leaf morphology, elevation, soil and climate in Mimosa L. (Leguminosae) diversification

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Variation in species diversity among lineages is often linked to differences in ecological opportunity across their evolution. However, distinct diversification histories may arise from the interaction between intrinsic factors, such as morphological traits, and extrinsic factors, like environmental conditions. Here, we conducted a preliminary analysis of how leaf morphology, elevation, soil, and climate relate to diversification dynamics in *Mimosa* L. (Leguminosae, Caesalpinioideae, Mimoseae), a megadiverse genus of mostly Neotropical plants. Using Bayesian Analysis of Macroevolutionary Mixtures (BAMM), we estimated diversification rates and summarized soil, climate, and leaf morphological data through ordination methods. Correlations between diversification and ecological/morphological variables were tested using the structured permutation method (STRAPP). Results support a scenario with four diversification rate shifts, but we found no significant correlation between diversification and either niche or leaf morphology via STRAPP. Still, visual inspection of the data suggests that some rate shifts may be linked to changes in elevation. Notably, occupation of high-altitude environments—such as the Campos Rupestres, a key region of *Mimosa* diversity—may contribute to diversification in the genus. While our findings suggest that elevation may have influenced specific diversification events, further analyses are needed to determine whether the evolutionary history of *Mimosa* supports the hypothesis that mountains are important drivers of plant diversification.

Topic: Systematics & Taxonomy

A-288

Evolution of functional traits across parallel global climatic transitions in the buckwheat family (Polygonaceae)

Author: Aaron Lee, Jin Oong, Lauren Vander Esch, Kyle DuVal, Brett Fredericksen, Timothy Whitfeld, José Meireles, Jeannine Cavender-Bares, Ya Yang
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The buckwheat family, Polygonaceae, consists of approximately 1,100 species that occur in a variety of environments, from lowland moist tropical forests to temperate woodlands and wetlands, and from rocky desert outcrops and sandy flats to exposed alpine slopes and the Arctic tundra. Polygonaceae can be divided into two major clades corresponding to geography: one originated in tropical South America and dispersed throughout the New World, and the second originated in Southeast Asia and dispersed towards and across higher latitudes worldwide. Thus, there appears to be parallel diversification towards increasingly dry and cool environments between these two clades. We hypothesize that similar climatic pressures have shaped parallel transitions in functional trait evolution between these two clades. We have developed a nondestructive approach to acquire functional traits at scale, from 382 species representing all major genera and about ¼ of the species-level diversity in Polygonaceae. To do this, we use hyperspectral reflectance spectra collected from 1,300 herbarium specimens. Reflectance spectra are integrative measures of leaf physiology, biochemistry, morphology, and evolutionary history, and these traits have been accurately recovered from spectra collected from both fresh and pressed-and-dried leaf tissue. We have trained trait prediction models to estimate leaf mass per area (LMA), nitrogen, carbon, mineral nutrients, and fiber content, and are evaluating how the relationships between these traits change across the Polygonaceae phylogeny. Our work will show how trait syndromes evolve in this family, and spotlight key trait transitions that facilitate adaptations to changing environments. We also demonstrate how reflectance spectra can be used to mobilize data from herbarium collections in eco-evolutionary studies.

Topic: *Molecular Ecology*

A-289

The genetic architecture of parallel life-history divergence: a non-repeatable pattern among perennial taxa within the Mimulus guttatus species complex

Author: Hongfei Chen, Jennifer Coughlan
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Understanding the repeatability of evolution is a central question in evolutionary biology, as it informs how predictably organisms respond to similar selection pressures. However, the extent to which the genetic architecture of adaptive traits is shared across populations remains poorly understood. The recurrent evolution of similar phenotypes in high-elevation populations, relative to their low-elevation counterparts, offers an ideal model for testing the repeatability of adaptation at the genetic level. In this study, we investigate the genetic architecture of life-history trait divergence across perennial taxa within the *Mimulus guttatus* species complex that occupy contrasting elevational habitats. We found that the genetic architecture underlying each life-history trait is largely non-repeatable across populations, with rhizome traits exhibiting particularly low repeatability despite their relatively simple genetic basis. Moreover, while phenological and stolon traits consistently do not form evolutionary modules in any population examined, floral, size-related, and rhizome traits appear to form repeatable modules across populations. These findings suggest that evolution may proceed through distinct genetic pathways while repeatedly converging on functionally integrated trait modules—flexible yet stable units of adaptation to heterogeneous environments. Overall, our results provide important insights into the genetic architecture of life-history divergence among closely related perennial taxa and advance our understanding of evolutionary repeatability in natural systems.

Topic: *Phylogenomics*

A-290

TreeHouse: Blazing Fast Phylogenetic Tree Viewer and Editor

Author: Karolis Ramanauskas, Joseph Walker, Jarrad Hampton-Marcell
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The emergence of mega-phylogenies and phylogenomics have altered the landscape of phylogenetics. Datasets are now often comprised of thousands of taxa or thousands of genes, and sometimes both. Although many tree viewers exist, they usually do not scale well for these large datasets. Here, I present TreeHouse, a phylogenetic tree viewer specifically designed for large phylogenetic pursuits. The current project has basic implementations of commonly used features for tree viewers, with the goal that, through community feedback, TreeHouse can continue to be expanded to meet the needs of the community.

Topic: *Mycology*

A-291

Genome-wide Association of Growth-virulence tradeoffs in Botrytis cinerea

Author: Peter Eludini, Jaisy Huang, Minh Tran, Daniel Kliebenstein, Jordan Dowell
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To successfully invade the host immunity, pathogens invest in virulence mechanisms. However, the energetic investments in virulence may come at the expense of growth and proliferation. Pathogens incorporate virulence mechanisms like cellulases that break down their hosts' cells, providing nutrients, and making the potential virulence-growth trade-off more complicated. For generalist pathogens, the disease outcome is dependent on the genetic variation in the pathogen and the host. Leading to a limitation on the number of pairwise interactions that can be assessed. Therefore, we posit that genes associated with growth variation are potential virulence genes. To identify genes association with growth variation in a generalist pathogen, we conducted a genome-wide association study (GWAS) using 96 isolates of *B. cinerea* (a necrotrophic generalist pathogen of most eudicots) in *in-vitro* conditions. Most genes associated with variation in growth in our study are previously validated virulence mechanisms across a wide array of hosts from *Arabidopsis* to tomato. This work furthers the importance of maintaining collections of natural variants of pathogens and their utility in identifying virulence mechanisms independent of the host, saving time, money, and resources.

Topic: *Systematics & Taxonomy*

A-292

Malus (Rosaceae) systematics and diversification: insights from a RAD-seq phylogeny

Author: Lindsey Worcester, Eric Roalson, Andrew Hipp
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Malus (Rosaceae)—the apples and crabapples—are a genus of 25 to 55 flowering tree species renowned for their taxonomic complexity. Hybridization, apomixis, and polyploidy work together to confound both species circumscription and phylogenetic inference in the genus. We present the most comprehensive phylogenetic sampling of species and infraspecies, and hybrids to date, using analysis of RAD-seq data to (1) identify major clades within the genus, (2) place previously unsampled taxa onto the phylogeny, and give a brief overview of a proposed classification.

Topic: *Hybrids and Hybridization*

A-293

"From Past to Present: Evidence of Ancient and Contemporary Hybridization in Andean Weinmannia

Author: Eduardo Aguirre-Mazzi, Christy Edwards, J. Tello, Alexander Linan, Alfredo Fuentes, Ricardo Segovia, Juan Penagos Zuluaga
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Hybridization can influence population genetic structure and shape lineage evolution, yet its prevalence among Neotropical plant lineages and contributions to plant evolution and diversification remain unclear. Weinmannia is a genus of ecologically important trees and shrubs abundant in diverse mountain ecosystems throughout the Neotropics, particularly in the Andes. While morphological studies suggested hybridization among multiple coexisting Neotropical Weinmannia species, no molecular study has confirmed hybridization or evaluated its extent and evolutionary consequences. Here, we used RAD-seq to examine hybridization and introgression among 10 common Weinmannia species co-occurring on the eastern slopes of the central Andes in Bolivia and southern Peru. Using population genomics and phylogenomic approaches, we found strong evidence of ongoing hybridization and introgression. Hybrids were identified in 31 of 45 possible species pairs, with all 10 species forming hybrids with 3-9 other species. In total, 169 of 470 genotyped individuals (36%) showed hybridization signatures. Using a newly developed machine learning-based approach coupled with hybrid index estimates, hybrids were classified into F1/F2 and backcross categories. Generalized linear model analysis showed that hybridization probability is strongly reduced by pairwise genetic distance between species, whereas geographic distance and elevational distribution dissimilarity play minor roles in preventing hybridization between coexisting species. Finally, f-branch statistics, phylogenetic networks, and admixture graphs constructed from non-admixed individuals revealed varying historical scenarios but supported recurrent introgression over evolutionary time, consistent with reticulate evolution. Despite widespread historical and contemporary gene flow, genomic evidence indicates that species maintain morphological and genetic distinctiveness, suggesting syngameon-like dynamics in the genus evolution. Further studies are needed to assess whether such patterns are consistent across other Andean centers of endemism. Our results underscore the importance of investigating hybridization and reticulate evolution in Neotropical lineages, with broad implications for conservation, taxonomy, and understanding evolutionary processes shaping species-rich floras.

Topic: Paleobotany

A-294

Fossil infructescence from Antarctica shed light on the Cretaceous diversification of Fagales in the Southern Hemisphere

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Topic: Conservation Biology

A-295

Collaborative plant conservation across islands: the California Island Biodiversity Information System

Author: Isabela Lima Borges, Heather Schneider, Benjamin Brandt, Denise Knapp, Sean Carson
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The 18 islands in the Pacific Ocean off the coast of California and Baja California are home to more than 1,200 native plant taxa, many of which are endemic to the islands. The islands are connected by geography, ecology and a shared history of human impacts. A variety of dedicated island stakeholders work to protect and restore these islands, including agencies in both the U.S. and Mexico governments, universities, and non-profit organizations. These stakeholders often have common conservation goals, though their activities, protocols, and data management differ. In order to maximize conservation efforts across the archipelago, knowledge-sharing has become a priority. In 2014, collaborators began meeting regularly to discuss shared challenges and opportunities, eventually formalizing the Islands of the Californias Botanical Collaborative (ICBC; aka Islas de Californias: Colaboración Botánica). From there, the California Islands Biodiversity Information System (Cal-IBIS) was born. Developed to first house basic information about all taxa on the islands, the database consists of aggregated georeferenced data from across the archipelago and represents the most complete information about the distribution of various taxa across the islands. We are now in the process of developing the next node of Cal-IBIS, which will include detailed occurrence and survey data for rare plants across the archipelago. ICBC partners have developed a standardized data collection system for rare plant mapping, streamlining the curation and analysis of complex island-wide datasets and allowing island owner-managers to benefit from each other's work and knowledge. By not only sharing data, but also standardizing collection practices, we are moving toward more effective conservation across these unique and vulnerable islands. Our system provides a blueprint for information-sharing across other areas of conservation concern.

Topic: Ecology

A-296

Defense traits vary across leaf ages in the thistles (Cardueae)

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Much of plant phenotypic diversity has been directly attributed to coevolution between plants and herbivores. Plants produce a wide variety of both physical and chemical defenses to deter herbivores, and covariation between defense traits has been reported at every scale of biological organization. Here, we investigate the range of physical and chemical defenses in the thistles (Cardueae, Asteraceae). We collected data on physical (spines, trichomes, and leaf toughness) and chemical traits (using an untargeted metabolomics approach) for leaves of different ages from seven thistle species. We supplemented these data with chemical traits from 21 species collected from herbarium specimens and spine presence/absence data for 79 species from the literature. Among our seven focal species, young leaves generally had similar defense profiles (long spines, dense trichomes), but species diverge in the defenses they produce in their older leaves. Chemical defenses tend to be more diverse in older leaves, with considerable variation between species. Previous studies have described syndromes of defense traits across species associated with distinct strategies for reducing herbivory, but instead of syndromes of traits we find continuous variation along the axis of unarmed (both chemically and physically, e.g., Arctium lappa) to heavily armed (with both physical and chemical defenses, e.g., Cirsium vulgare). Across Cardueae, leaf spines evolved multiple times independently, and species with and without spines differ chemically even when accounting for phylogeny. Overall, thistles employ a diversity of approaches to defense but do not fall into the classic defense syndromes reported from other clades.

Topic: Ecology

A-297

Climate drives early flowering of native species: analysis of a 36-year phenology dataset

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Long-term phenology records are an important tool to understand plant community responses to rapidly changing climate. Here, we present results from a 36-year flowering phenology dataset recorded at Cuivre River State Park, covering 355 native Missouri species. Flowering was monitored in 10-day intervals, documenting flower emergence and presence for each species throughout the growing season. Using linear mixed effect models, we asked whether date of first flowering changed during the period observed (1978 – 2015) and whether these phenological changes are correlated with environmental drivers. We find that mean first flowering date is occurring earlier across our dataset, though there is variation in species responses throughout the record period. Additionally, we found a significant interaction between year and annual mean temperature; where increasing temperatures further accelerated flowering. We also found a significant interaction between year and growing season precipitation, as measured by the Standardized Precipitation Evapotranspiration Index (SPEI), with higher precipitation driving later flowering. To disentangle the variation in species responses over time, we tested whether species seasonality of flowering time impacts the direction and strength of phenological change. We find that species that flower later in the year (e.g. during summer and fall) respond more strongly than spring-flowering species. That is, that they are experiencing a greater shift in first flowering date. Our results suggest that native species flowering phenology is sensitive to changing climate, and that these effects are likely increasing over time.

Topic: Paleobotany

A-298

A window into the Cretaceous bryosphere: An exceptionally preserved fossil sheds light on the evolution of moss-cyanobacteria symbiotic associations

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The bryosphere is the nexus of living and dead moss tissue that hosts diverse microbial communities including fungi and N-fixing diazotrophs, such as cyanobacteria. Symbiotic associations between epiphytic cyanobacteria and mosses are a critical gateway for bio-available nitrogen, an essential compound to all life, to enter the nutrient cycle in a variety of terrestrial ecosystems. Well over 50% of N input may be derived from moss-cyanobacteria associations in boreal ecosystems, which potentially has major consequences on a global scale. Precisely when moss-cyanobacteria symbioses evolved is poorly understood. Here we report an exceptionally preserved bryophyte from the Late Cretaceous of Antarctica that represents the first fossil evidence of a cyanobacteria-moss symbiotic association, which provides a minimum yet ancient age for this important ecological relationship. The moss was identified in a calcium carbonate concretion that was recovered from the Baculites Hill locality on James Ross Island. Upper Cretaceous deposits exposed at this locality belong to the Beta member of the Santa Marta Formation which is early to mid-Campanian in age (82-80 Ma). The fossil was sectioned using the cellulose acetate peel technique and studied with light microscopy. The moss is represented by a dioecious gametophyte with a single unbranched stem bearing helically arranged leaves. The stem is terminated by a perichaetium that contains several archegonia and abundant paraphyses. There is one archegonium containing an intact ovum with a nucleus and one with a possible developing embryo. Cyanobacteria filaments are present in the leaf axils and within the perichaetium. There are two distinct cyanobacterial morphotypes: filaments with spheroidal cells and those with barrel-shaped cells. Both morphotypes have structures that appear to be heterocysts which are larger than vegetative cells, double walled, and spheroidal. While these filaments could represent other microbes, their morphology, including the presence of heterocyst-like cells, and positions on the moss is most consistent with cyanobacteria,

especially Nostocales. In addition, septate hyphae of a possible bryophilous fungus were found colonizing the surface of a leaf. The delicate and ephemeral reproductive structures including several archegonia preserved in remarkable detail, suggests that this specimen experienced relatively little to no decay prior to permineralization. Therefore, this moss was likely a host to a mutualistic or commensal microbiota rather than substrate for necrotrophs and saprotrophs. Our findings suggest that moss-cyanobacteria symbiotic associations may have played an important role in the N cycle in potentially resource limited polar forests during the terminal phase of Gondwana when such ecosystems experienced dramatic changes in vegetational turnover in the wake of the Cretaceous diversification of angiosperms.

Topic: Systematics & Taxonomy

A-299

Phylogenetics, Biogeography and Conservation of the genus Dasylirion (Asparagaceae)

Author: Sara Ruiz Flores, Sara Fuentes-Soriano
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Dasylirion part of the Asparagaceae, includes 23 species that hold both ecological and cultural importance. In Northern Mexico, several species are traditionally used to produce sotol, a distilled spirit with a protected designation of origin. However, the increasing harvesting and industrialization of sotol has raised significant concerns about the sustainability of wild populations. Despite growing awareness of the potential extinction risk, only two species are included in the IUCN red list as Least Concern (LC), highlight ing a critical gap in our understanding and underscores the urgent need for comprehensive research into the conservation status and sustainable management of the entire genus.

This study aims to reconstruct the evolutionary history of all 23 species of *Dasylirion* using Target Sequencing techniques. Our goal is to build a strong phylogenetic framework to test biogeographic hypotheses and guide effective and sustainable conservation efforts for the genus. While previous phylogenetic studies using chloroplast markers (*mat* K and *rbc* L) exist they offer limited resolution and weak phylogenetic support.

To improve upon this, we present preliminary results related to the selection of suitable genetic markers and describe the methods planned for future phylogenetic analyses. We chose the Hybseq (hybridization -based target enrichment) method as a reliable strategy to analyze hundreds of genes simultaneously. To guide our sampling, we compiled data from 1,818 herbarium specimens, integrating morphological, ecological, locality data and GIS-based distribution maps. This dataset ensures coverage of the genus's full range of morphological, ecological and geographic diversity as well as taxonomic and sympatric patterns. Additionally, we ran *in silico* experiment to assess bait efficiency by comparing two probe sets – Angiosperm353 and Asparagaceae1726 probes – using an existing Asparagaceae dataset. Results showed that the Asparagaceae1726 probe set is the most effective for close related genera of *Dasylirion*. It recovers significantly more genes (1716 vs 206), detected fewer paralogs (8% vs 41%) and provided a higher supported phylogenetic resolution.

Our findings also reveladed that *Dasylirion* most frequently inhabits xeric shrublands in ecotones with coniferous and *Quercus* forests. The greatest species diversity is concentrated in the Sierra Madre Oriental, especially in areas transitioning into the Chihuahuan Desert. Within this region, two zones were identified as centers of high species richness and endemism. These findings support the hypothesis that this ecoregion may represent a center hotspot of diversification within the group.

Topic: Ecology

A-300

An Assessment of Carbon Sequestration and Carbon Storage Within Forested Conservation Easements in Northeastern Oklahoma

Author: Kaitlin Branson, Lizz Waring
Affiliation: Northeastern State University

Carbon dioxide is being discharged into the atmosphere by the burning of oil and coal for industrial purposes and by large scale deforestation efforts. This flux of anthropogenic carbon dioxide emissions has created a unique and potentially complicated issue, because the intricacies of the natural global carbon cycle are not entirely understood. It is known that forests serve as one of the greatest and most valuable forms of terrestrial carbon sinks. Individual trees within forests extract carbon dioxide from the atmosphere and utilize it for their maintenance and growth. It is incredibly important that forests, and the individual trees that compose those forests, can be quickly assessed in order to determine their carbon sequestration potential, their carbon storage potential, and their subsequent economic value. This project sought to quantify the amount of carbon being sequestered within specific trees within four Grand River Dam Authority conservation easements using general forestry methodology and the U.S. Forest Service I-Tree Design software. Using the I-Tree Design software allowed for the determination of the economic value of the specific trees that were assessed. Once this was done, satellite images of the same four easements were evaluated using the U.S. Forest Service I-Tree Canopy software. This was done to determine the amount of carbon sequestered and stored within all of the trees within the four conservation easements. This also allowed for the economic value of all of the trees within the forests of the four conservation easements to be determined. Lastly, satellite images of all seventy-three GRDA conservation easements are being assessed using the U.S. Forest Service I-Tree Canopy software in order to determine how much canopy cover of each plot was assessed. The use of the I-Tree Canopy software will also provide the economic value of all seventy-three conservation easements.

Topic: Ecology

A-301

The Legacy Effect of Past Disturbance on the Population Dynamics of Venus Flytrap

Author: Zheng Yao
Affiliation: Kansas State University

Venus flytrap (Dionaea muscipula, VFT) is an iconic yet vulnerable species native to the wet sandy soils of the longleaf pine savannahs in the Carolinas. In this ecosystem, fire disturbance is key in maintaining the open savannahs in which VFT is found: regular fires reduce shrub density and prevent tree establishment into the canopy. Like many other savannahs, fire suppression is common in longleaf pine ecosystems; because fire suppression results in the loss of open savannah habitats, VFT and other species of concern may suffer. To conserve VFT in their native habitats, we need to understand how current fires and histories of fire suppression might impact VFT population dynamics. Previous work has shown strong effects of time since the most recent fire (TSF) on VFT population dynamics, but TSF does not faithfully represent long-term fire histories. In this study, we explicitly incorporate both TSF and long-term fire history into our population model and quantify their effects on VFT vital rates (survival, growth, fruiting, and recruitment). Starting in 2015, we have collected demographic data on 8 VFT populations in North Carolina that vary in both TSF and in an integrated metric of long-term fire history, time between the last two fires (TBF). We verified field-based fire occurrence data with Landsat multispectral reflectance data to get accurate fire histories for each population. Our results show that both TSF and TBF affected VFT vital rates. In addition, our results suggest [something about the interaction term]. Thus, our results suggest that both current fires and fire histories are important to VFT population dynamics. Population models incorporating both TSF and TBF are likely to more accurately reflect VFT population growth than models incporating only TSF. Our work suggests that for future demographic studies of VFT, and for the conservation of at-risk, threatened, or endangered plants in disturbance-maintained ecosystems, it is important to consider the legacy effects of past disturbance regimes to accurately predict changes in population sizes. Considering both current and historical disturbance regimes will allow us to design more effective and site-specific management strategies.

Topic: Ecology

A-302

Investigating the spatial distribution and symptomology of Tubakia californica

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Tubakia californica (Tubakia leaf spot), a recently described species, is a foliar disease that mainly infects oaks, tanoak, and chinquapin. The pathogen initially causes small lesions on the underside of leaves and spreads until leaves are brown and dry, with blackened veins. While the disease is primarily cosmetic, it can cause significant leaf drop, which impacts tree crown health and can make them more vulnerable to other diseases. While observations support the inference that trees in certain terrain are more susceptible, no research has been done to further examine the relationship between

landscape and infection. Transects were installed at several sites in Humboldt County, CA to assess T. californica symptoms in tanoak and oak using a rating system based on percentage of crown dead, affected live crown, symptom severity of affected crown, and overall crown vigor. Several samples were also collected along each transect to confirm constant association between pathogen and symptoms. Samples were observed under compound and fluorescent microscopes to investigate hyphal presence within plant tissues. Data was used to establish a spatial distribution of symptomatic trees, and to uncover the relationship between site factors and pathogenicity. The discovered relationship may help in modeling infection risk on the landscape as well as in monitoring host tree health. Microscopy findings expand insight on the degree of pathogenicity within host tree material.

Topic: Development and Structure

A-303

Complex petal development and evolution across Ranunculaceae

Author: Grace Pisano, Andrea Appleton, Yan Gong, Elena Kramer
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Ranunculaceae is a large, morphologically diverse clade of basal eudicots with cosmopolitan distribution, occupying diverse habitats from tropical wetland to xerophytic and alpine environments, and is an ideal system in which to study the developmental basis of evolutionary change. One especially variable aspect of the Ranunculaceae flowers is the perianth, which is markedly diverse in morphology and function. Common perianth features of flowers spanning the Ranunculaceae include petaloid sepals, specialized, nectiferous petals, and petal loss. When petals are present, they often have a unique suite of features, such as adaxial nectaries, reduced size, staminiform morphology, and three-dimensional elaboration, and bear developmental and morphological similarities to stamens. These petals have often been given special names, such as honigblätter ("honey-leaves"), nectaries, nectar leaves, or staminodes reflecting the specialized function of the organs, and have historically been regarded as independently evolved, but the shared developmental genetics of the petals and ancestral character reconstruction support the homology of petals in Ranunculaceae with repeated, independent loss. Using literature review, developmental study, ancestral character state reconstruction of several petal traits, and gene expression analysis, we argue that the complex morphology of Ranunculaceae petals is directed by activation of partial stamen identity in the petals. Stamen identity is translated into polarity rearrangement in the developing petal and this activation of peltate growth is intrinsic to the three-dimensional elaboration of the petals of the family.

Topic: Plant phenology in an era of rapid global change: new perspectives and frontiers

A-304

Phenotypic and phenological shifts in reproductive traits of polyploids depend on their mode of origin

Author: Nathalia Susin Streher, Tia-Lynn Ashman
Affiliation: University of Pittsburgh

Topic: Biodiversity Informatics & Herbarium Digitization

A-305

The Andropogoneae Extended Specimen Project: implementation

Author: Taylor AuBuchon-Elder, Paul Smock, Elizabeth Kellogg, Jordan Teisher
Affiliation: Missouri Botanical Garden, Donald Danforth Plant Science Center

Natural history collections are becoming more and more accessible, as specimens and their metadata are digitized and added to museum databases. However, additional specimen-based data, such as measurements, images, chromosome numbers, and DNA sequences are scattered, sometimes to be found in supplemental data of various publications, but often only on lab hard drives or as a pile of papers in a desk drawer. Connections to specimens are lost to all but the original researcher. One consequence of this distributed model is that updates or additions to data on specimens (e.g., name changes, addition of DNA sequences) are rarely available to users of the derived data.

In recent years we have produced extended data for over 1500 specimens representing a little over half of the 1200 species in the grass tribe Andropogoneae. In addition to the standard image of the herbarium sheet and data from its label, we have in hand close-up images of spikelets, morphometric trait data from the same spikelets, genome sizes, whole genome sequences and assembled chloroplast genomes. This extensive collection of data and data types was initially neither aggregated nor publicly available. We therefore aimed to build a set of extended specimens, with the goal of releasing the data as rapidly and efficiently as possible.

The Tropicos database at the Missouri Botanical Garden already held all the specimen records and corresponding taxonomic information plus specimen and spikelet images. Accordingly, we built on the resources that already existed. Names, specimens, authors, publications, types, institutions, and other data types are already fully integrated in Tropicos and supported by images and external links in a highly curated, publicly accessible system. In addition, the website receives tens of millions of hits per year and shares specimen data with major aggregators like GBIF, Symbiota portals, and JSTOR.

To accommodate our substantial set of sequence data (ca. 550 Illumina sequences and about three dozen long-read, chromosome-scale genomes), a new field, Genbank data, was added to the existing specimen pages to hold hyperlinks to as many Genbank sequences as desired.

Morphological trait data are particularly difficult for current taxonomic databases to accommodate. We therefore created the Andropogoneae Extended Specimen Project. A Project established within Tropicos has its own data environment, distinct from the core specimen data. In our case, quantitative and qualitative trait data captured from the spikelet images already in the database were uploaded as a.csv file or entered by hand using the Project data entry interface. For each specimen, the measurements are then displayed on the main specimen page. The entire dataset (currently over 1500 unique specimen IDs) can also be downloaded as tab delimited text.

By using existing data structures, the Andropogoneae Extended Specimen Project was completed within about 6 months for a modest budget. While we can envision many future improvements, we have reached a near-term goal of making a large amount of specimen-based data readily accessible to the community. For additional details, see the companion talk on this project.

Topic: Education and Outreach

A-306

Assessing use of open access digitized natural history collections databases for course-based undergraduate research experiences

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Course-based undergraduate research experiences (CUREs) increase student learning and self-efficacy but are often difficult to implement across a variety of class types and institutions. CUREs built using digital Natural History Collection (dNHC) data are more accessible as they do not require expensive equipment or wet lab resources. Four CUREs recently developed by the Biological Collections for Ecology and Evolution Network (BCEENET) provide students with research experience employing open access digitized natural history collection data and have been implemented at 42 institutions serving over 4000 students. BCEENET published the curriculum for these CUREs open-access and provides assistance to instructors implementing these CUREs through resources for implementation and opportunities to participate in assessment activities. During these CUREs, students gain experience with a variety of advanced data handling and analysis skills, including data management, georeferencing, GIS, and data analysis. However, these CUREs differ from more traditional wet lab-based CUREs in that students do not design and carry out data collection procedures. We seek to explore whether these digital data CUREs provide the same gains in student self-efficacy and content knowledge as more expensive laboratory CUREs. We developed novel concept inventories to measure students' data science and geospatial reasoning skills, which we think students will gain during these CUREs. We administered these measures, along with measures of self-efficacy and science identity to students pre- and post-CURE at 26 institutions over 5 semesters (n=2,320). We assess evidence of validity for the concept inventories and have made iterative revisions to the inventories. Our preliminary results suggest that students gain self-efficacy, science identity, and data science skills through

participating in these CUREs. Our results demonstrate proof-of-concept that students can gain benefits associated with traditional CUREs through these high-flexible, scalable, and accessible CUREs that use open access data sources.

Topic: Population Genetics/Genomics

A-307

A Population Genetics Approach to Characterizing the Styrax platanifolius Subspecies

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Styrax platanifolius, a rare plant species primarily from Central and West Texas as well as Coahuila, Mexico, has long been subject to taxonomic debate. The species is currently considered to contain five subspecies which are primarily distinguished by their pubescence. Genotyping *Styrax platanifolius* subspecies *platanifolius*, *stellatus*, and *texanus* (currently limited sampling of *mollis* and *youngiae*) using microsatellite loci will facilitate analysis of many aspects of their biology. Mainly, we will discover interbreeding (or lack thereof) between the subspecies, levels of inbreeding within populations, and whether the variation across the complex can be attributed to a geographic cline as opposed to a clear taxonomic distinction between subspecies. These preliminary results (and future morphometric and cross pollination experiments) will inform conservation of these rare plants in central Texas.

Topic: Systematics & Taxonomy

A-308

Taxonomic synopsis for the genus Albizia Durazz in Nigeria (Fabaceae) based on morphology and molecular data

Author: Uhunwa Igho-Osagie, Ya Yang, Emmanuel Shokefun
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The genus Albizia Durazz (Fabaceae) is economically important for livestock fodder, soil stabilization, nitrogen fixation, timber production, and medicine. However, species identification within the genus has been complicated due to overlapping morphological traits. This study aimed to revise Albizia species in Nigeria, clarify their taxonomic relationships, and provide additional characters for species identification using morphological and molecular data. Vegetative and reproductive traits were examined from living and herbarium specimens from the Forest Herbarium Ibadan and the University of Ibadan Herbarium. Principal Component Analysis (PCA) assessed the morphological variation among Albizia species in Nigeria. Key characters such as terminal leaflet lengths and widths effectively distinguished Albizia species into two groups. Molecular data for Albizia species were obtained from the National Center for Biotechnology Information (NCBI) GenBank database, focusing on the matK, rbcl, and ITS gene regions to determine species relationships and further validate our morphological groupings. Phylogenetic analysis using Maximum Likelihood (ML) further supported the morphological groupings. However, our study exposed the limitation in the reliability of obtaining data from public sequence databases. A BLAST result for an Albizia ITS sequence returned a match with Lycopersicum (tomato), highlighting issues related to depositing unverified and contaminated metabarcoding data in GenBank. Our study revealed that combining morphological and molecular data improves our understanding of species relationships within the genus and aids species identification. This study also provides a revision of the genus and an accessible dichotomous key for the genus in Nigeria.

Topic: Biodiversity Informatics & Herbarium Digitization

A-309

Digitization and Enrichment of U.S. Herbarium Data from Tropical Africa to Enable Urgent Quantitative Conservation Assessments

Author: Heidi Schmidt, Alexander Linan, Alex Asase, Israel Borokini, Alison Colwell, Charles Davis, Nico Franz, Peter Fritsch, Edward Gilbert, Bonnie Isaac, Robert Johnson, Beth Kaplin, Rebecca Kartzinel, Lucia Kawasaki, Jonathan Kennedy, Jennifer Kluse, Elena Kramer, Laura Lagomarsino, Tatyana Livshultz, Michelle McMahon, Brent Mishler, Tiwonge Mzumara, Mare Nazaire, Nestor Obiang, Sylvia Orli, Katie Pearson, A. Townsend A. Townsend, Daniel Potter, Mitchell Power, Tiana Rehman, Michaela Schmull, Eric Schuettpelz, D. Simmons, Chelsea Smith, Neil Snow, Patrick Sweeney, Nicole Tarnowsky, Jordan Teisher, George Weiblen, Timothy Whitfeld, John Wieczorek, Paula Zermoglio
Affiliation: Missouri Botanical Garden, University of Ghana, Montana State University Bozeman, University of California Davis, Harvard University, Biodiversity Institute, University of Kansas, Fort Worth Botanic Garden, Arizona State University, Carnegie Museum of Natural History, Bringham and Young University, Univeristy of Rwanda, Brown University, Field Museum of Natural History, Louisiana State University, Drexel University, University of Arizona, University of California Berkeley, Malawi University of Science and Technology, California Botanic Garden, National Herbarium of Gabon

Herbarium specimens represent the primary source of data on plant diversity. These rich sources of knowledge however, too often remain in analog format only, and have not been digitized and "enabled" in the service of science. This project aims to digitize, enrich, and share openly the rich data resources held in 21 U.S. herbaria that correspond to plants of tropical Africa. Imaging and data capture is being carried out at each of the herbaria, and data are then aggregated for efficient georeferencing. Currently, the project has imaged 558,577 specimens, of which 251,991 have data captured with georeferencing being conducted by plant scientists in Gabon, Ghana, Malawi, and Rwanda. Recent advances in Large Language Models (LLMs) have allowed more efficient data capture from images such that technicians now verify, and correct LLM derived data records read from images. Finally, project data is openly available to the scientific community via a dedicated "African Plants" portal on Symbiota (african-plants.org/portal/index.php), as well as integration into biodiversity data portals such as iDigBio and GBIF. The project has thus created a broad, international, intercontinental network of scientists and students interested in and experienced with management and analysis of data about African plant distributions. These rich data resources will be used to understand the conservation status of African plant species in much greater detail than has been possible to date.

Topic: Overcoming the barriers to on-going Castilleja research: From botanical enigma toward an emerging model system

A-311

Pollinators of the Castilleja pilosa species complex: how pollinators differ among complex members and across geography

Author: Isabel Dalton, Katie Wenzell, Anahí Espíndola, Sarah Jacobs
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Different types of pollinators can drive differing evolutionary pressures on floral traits. Divergent selection on floral traits can lead to phenotypic differentiation in flowers, with potential for reproductive isolation and speciation in some cases. Investigating variation in floral traits and pollinators among closely related taxa can help improve our understanding of mating patterns and the potential for reproductive isolation, and thus divergence, within and among diversifying lineages. Based on current taxonomy, the members of the *Castilleja pilosa* species complex have limited morphological variation between them (but considerable floral variation overall), and geographic distributions largely determine species identification, warranting study of pollinator interactions and the potential for pollinator-mediated isolation in this group. This study aimed to 1) document which pollinators visit the members of the *C. pilosa* species complex, 2) determine what pollinator identifications are feasible using non-lethal sampling, and 3) investigate whether or not there is variation in floral visitation among taxa or between populations. We recorded 2,005 floral visits to 17 populations of *C. pilosa* complex spanning over 165,000 square miles. Floral visitors were diverse, including chiefly bumble bees (*Bombus* sp.), solitary bees (e.g., *Osmia* sp., Anthidiini, *Anthophora*, and *Lasioglossum* (*Dialictus*) sp.), butterflies and moths (Lepidoptera), flies (Diptera), wasps

(Hymenoptera), and beetles (Coleoptera). For certain taxa, non-lethal sampling (e.g., photographs) of pollinators could be used to identify them down to the species, whereas other taxa required higher magnification for identification, likely requiring collection of specimens. This research established a baseline of floral visitors to the *C. pilosa* species complex, which provides valuable data on the natural history of this group. These results suggest that observed variation in pollinator visitation among members of the complex is likely not due to chance, but does not strictly align with current taxonomy. This study provides a foundation for further exploration of ecological and evolutionary dynamics within the *C. pilosa* species complex.

Topic: *Ecophysiology*

A-313

Construction costs and tradeoffs in carnivorous pitcher plant leaves: towards a pitcher leaf economic spectrum

Author: Kadeem Gilbert, David Armitage, Ulrike Bauer, Kenji Fukushima, Laurence Gaume, Qianshi Lin, Sukuan Liu, Sylvie Martin-Ebehardt, Jonathan Millett, Tanya Renner, Mathias Scharmann, Chris Thorogood
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Leaf economic theory holds that physiological constraints to photosynthesis have a role in the coordinated evolution of multiple leaf traits, an idea that can be extended to carnivorous plants occupying a particular trait space that is constrained by key costs and benefits. Pitcher traps are modified leaves that may face steep photosynthetic costs: a high-volume, three-dimensional tubular structure may be less efficient than a flat lamina. While past research has investigated the photosynthetic costs of pitchers, the exact suite of constraints shaping pitcher trait variation remain under-explored—including constraints to carnivorous function. In this review, we describe various constraints arising from the dual photosynthetic and carnivorous functions of pitchers arising from developmental, functional, budgetary, and environmental factors. In addition, we identify the data required to establish the leaf economic spectrum (LES) for carnivorous pitcher plants (CPPs), and — owing to the multifunctional roles of pitcher leaves — discuss difficulties in placing pitchers onto existing frameworks. Because pitcher traps serve multiple functions, both photosynthesis and nutrient acquisition (carnivory), they are difficult to place in the context of the LES, especially in light of a current lack of trait data. We describe a spectrum across the independent CPP lineages in approaches to balancing carnivory-photosynthesis tradeoffs. Future efforts to collect relevant data can clarify the forces that shape observed pitcher trait variation, and increase understanding of principles that may be ultimately generalized to other plants.

Topic: *Bryology and Lichenology*

A-315

Life in Oil: Exploring the Role of Symbiotic Bacteria in Liverwort Oil Bodies

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For nearly two centuries, the biological function of liverwort oil body organelles has remained an open question. Our novel discovery of endophytic bacteria residing within the oil bodies of liverworts points toward a previously unrecognized function of this organelle, compartmentalization of symbionts. Using confocal microscopy with the fluorescent nucleic acid stain SYTO-13 and the peptidoglycan-binding stain RADA, we found populations of bacteria confined to the oil body stroma of two distantly related liverwort species, *Marchantia polymorpha* (Marchantiopsida) and *Radula complanata* (Jungermanniopsida). In both taxa, bacterial cells were consistently located within the stroma between the oil body membrane and the central droplet of terpenoids and aromatics, the same site associated with the biosynthesis of the organelle's secondary metabolites. We also performed Gram staining on additional liverwort species representing diverse phylogenetic lineages. Putative oil body-associated bacteria were observed in multiple species representing seven orders throughout the liverworts, suggesting that the presence of oil body bacteria is widespread and possibly ancestral to the group. Our observations of meristematic regions in several species show that intracellular bacteria are present preceding oil body development and may represent a source population from which developing liverwort oil bodies are inoculated. The metabolic interaction between the oil body bacteria and their host liverworts is unknown, but the localization of bacteria to the site of terpenoid biosynthesis suggests they may play a role in the production of secondary metabolites, which is supported by the fact that liverworts possess many terpene synthase genes of bacterial origin. Additionally, our observations of oil bodies under diphenylamine staining suggest that the bacteria may provide nitrogenous compounds to the plant. Many of the antibacterial compounds in oil bodies degrade bacterial cell walls, which is an important component of extracting nitrogenous nutrients from intracellular bacterial symbionts in the Rhizobium-Legume symbiosis. These results propose a fundamental shift in how we understand liverwort oil bodies: not merely as chemical storage compartments, but as active symbiont-hosting organelles. If this microbial association is conserved across liverworts, it may represent one of the earliest still extant examples of intracellular bacterial symbiosis in land plants. Further genomic work is required to identify the bacterial taxa involved, elucidate their metabolic interactions with the host, and determine the ecological and evolutionary implications of this relationship.

Topic: *Paleobotany*

A-316

MADS about Yew: C-class genes in conifer evolution

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The homology and evolutionary origins of conifer seed cones have been the subject of debate in the plant morphology literature for well over a century. Although seed cones are broadly considered to be compound, in which the ovule-bearing structure is a highly modified shoot termed the ovuliferous scale, the lack of differentiation between bract and ovuliferous scale in many extant taxa calls this interpretation into question. This problem is most acute in the Cupressaceae. In addition to seeds being subtended by a single organ in most subfamilies (Taxodioideae being an exception), seeds are also axillary or even axial in many species (Cupressoideae and Callitroideae), suggesting loss of the ovuliferous scale entirely. Historically, the ovuliferous scale is thought to be congenitally fused to the bract in such taxa, but this does not explain the position of ovules. Previous evo-devo studies have focused on C-class MADS-box genes, which pattern ovuliferous scale development in Pinaceae and reproductive organs of seed plants more broadly. Expression patterns of C-class genes have supported the hypothesis that the ovuliferous scale has been lost in Cupressaceae, including in Taxodioideae. At this meeting we report new data on the evolution and expression of C-class genes in conifers (for full details, see talk presented by Austin Nguyen in Development and Structure, "Duplication and subfunctionalization of *AGAMOUS* genes in the cypress family (Cupressaceae)"). We show that the conifer C-class gene *AGAMOUS* underwent two ancient duplication events, leading to three C-class copies in Cupressaceae. Expression patterns support the presence of an ovuliferous scale in Cupressaceae. The three copies further exhibit a pattern of subfunctionalization within developing seed cones, with two specialized in the development of the ovules and the third specialized in development of the ovuliferous scale. These results suggest that patterning of the ovuliferous scale and ovule may have been developmentally decoupled in Cupressaceae via the duplication and subfunctionalization of a key regulator of reproductive development, leading to greater developmental modularity. This process may help to explain some of the morphological diversity of Cupressaceae seed cones and features of their development that have puzzled plant morphologists. We discuss the implications of these novel findings in the context of the evolution of conifer reproductive systems.

Topic: *Development and Structure*

A-317

Phylogenomics and evolution of vascular variants in the neotropical Paullinieae vines

Author: Israel Cunha Neto, Zachary Kozma, Isaac Lichter-Marck, Pedro Acevedo-Rodríguez, Joyce Onyenedum
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Woody vines from the maple family, Sapindaceae, form a monophyletic tribe known as Paullinieae. This lineage represents one of the major groups of climbing plants that structure ecological communities across various biomes in the Neotropics. Insights from molecular data have significantly reshaped our understanding of the phylogenetic relationships in Paullinieae, while also revealing the recurring evolution of complex vascular architectures, also called vascular variants. In addition to creating complex functional forms, these vascular variants serve as informative characteristics for the systematics of the group. However, current phylogenetic studies in Paullinieae encompass fewer than a quarter of the species in the tribe, hindering our ability to investigate the evolutionary history of key morpho-anatomical traits such as vascular variants. Here, we implemented a phylogenomic approach to elucidate the relationship

between the taxa of Paullinieae and phylogenetic comparative methods to illuminate the evolutionary processes shaping the diversification of stem vasculatures in the tribe. Our phylogenetic analysis included the most extensive taxonomic sampling of Paullinieae species to date (including all currently recognized genera). Furthermore, we used sequences of 351 genes captured with the Angiosperm353 probe kit to produce a time-calibrated phylogeny, assess species diversification drivers, and test the evolution of development of vascular variants in the tribe. We obtained a well-resolved phylogeny with seven major clades that confirm most of the known phylogenetic relationships in Paullinieae. This tree confirms the polyphyly of some traditionally recognized genera (e.g., *Cardiospermum*) and corroborates the circumscription of a newly described genus (i.e., *Acevedoa*). It also indicates taxonomic conflicts in other lineages (e.g., *Urvillea*), suggesting diversification processes that a single phylogeny cannot yet resolve. Most species of Paullinieae radiated during the Miocene, an event confirmed as one of the shifts in diversification rates in the lineage. Vascular variants have been present in Paullinieae species since the Miocene, with six major *patterns* recognized in extant species. We demonstrate that these complex vascular variants evolved convergently in four of the seven genera, with multiple transitions to different variants and reversions to the typical form. Evidence suggests that the evolution of some patterns of vascular variants is correlated with the arrangement of vascular bundles in early developmental stages. Our findings also indicate a combination of evolutionary developmental mechanisms driving the emergence of these novel patterns. However, transitions from typical growth to vascular variants or trees/shrubs to woody vines likely do not explain species diversification dynamics in this lineage. Our new Paullinieae phylogeny greatly improved our understanding of the group's systematics and enabled the application of interdisciplinary approaches that clarified the evolutionary history of one of nature's most intricate vascular architectures.

Topic: Ecophysiology

A-318

Effects of Increased CO_2 on Stomata and Water Use Efficiency in Guadalupe Mountains National Park

Author: Jazlyn Salazar, Madison Bullock, Gwendolyn Wagner, Nicholas Smith, Matt Johnson, Zachary Bailey
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Plant gas exchange is a key process shaping global hydrological and carbon cycles and is often characterized by plant water use efficiency. Plants can balance CO_2 intake with water loss by regulating the stomatal pore aperture via guard cell signaling, which is controlled by environmental factors and plant hormones. Together, stomatal density and size contribute to determining the maximum leaf conductance of CO_2. Plant fossil records suggest that plant adaptation to changing atmospheric CO_2 has a correlated evolution in stomatal density and size. Herbarium specimens can provide unique temporal information on ecosystem form and function but are often collected haphazardly and sparsely. In contrast, the Guadalupe Mountains National Park collection housed in the E.L. Reed Herbarium at Texas Tech University represents an extensive floristic survey conducted over 50 years ago with over 2000 specimens. Using stomatal impressions imaged with Leica software, we measured stomatal density and size on specimens from the 1960s and 1970s compared to modern collections from the 2020s and collections from the 1920s at New York Botanical Garden, matched by species, elevation, and ecoregion. We expect the increased atmospheric CO_2 will result in a decrease in stomatal conductance and could mean increased photosynthetic efficiency, and when combined with the higher water-use efficiency, we predict decreased stomatal area over the past 100 years. Our results leverage a look into the past in floristic biological diversity to predict how plant communities will respond to future climate changes.

Topic: Ecology

A-319

Herbarium specimens reveal changes in plant-pollinator-microbe interactions across time, taxa, and geographic space

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Adaptive phenotypic plasticity of fitness-related traits has enabled some species to persist and respond rapidly to disturbances. The plasticity of attractive and rewarding floral traits in response to altered plant-pollinator interaction networks can enhance the likelihood of pollinator visits and successful plant reproduction. Consequently, understanding shifts in floral trait diversity over space and time is crucial. Nectar is one of the most essential floral traits for mediating pollinator visitation and ensuring successful pollination. The quality of floral nectar–as determined by its nutritional content, microbial community, and effectiveness in attracting pollinators–is directly connected to successful plant reproduction. Here, I present ongoing work with historical herbarium specimens to analyze changes in nectar microbial communities (i.e., diversity, abundance, and distribution) and nectar organic composition including carbohydrates, amino acids, and secondary metabolites, to investigate how nectar quality and plant-pollinator-microbe interactions have changed during the Anthropocene, the era of profound human impact on the planet.

Topic: Population Genetics/Genomics

A-320

Getting SNPpy: A new Python workflow for the analysis of microhaplotypes from targeted plant sequences

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The evolution of high-throughput targeted sequencing using universal markers has allowed for the generation of substantial sequence data pools from non-model organisms at cost-effective rates. These methods target areas of interest such as highly conserved regions and functional genes under the assumption of containing enough genetic variability to differentiate between species or even individuals. Recent population genomic research using Angiosperms353, a universal probe set targeting 353 protein-coding genes found in flowering plants, found little gene recovery bias based on taxon, high recovery in segregating sites representing both between- and within-species distinction, and hitchhiking recovery of flanking non-coding regions. It is therefore possible to genotype multiple SNPs occurring in both coding and their flanking non-coding regions together as a multi-allelic "microhaplotype" for use in relationship inference of individuals and populations. Using microhaplotypes allows us to retain more genetic variability per locus through linked information when compared to single nucleotide polymorphisms alone. Previous studies have had success using microhaplotypes for relationship inference in models such as malaria-causing Plasmodium, the rabies virus, multiple species of fish, and even humans. To our knowledge, however, only one study utilized microhaplotypes in a plant model (cycads) through restriction site-associated DNA sequencing rather than a targeted DNA sequencing approach. Here, we propose a new microhaplotype bioinformatics workflow for population genomics analysis using target-capture sequencing of plant DNA. We provide evidence from two case studies of two congeneric species pairs with a special focus on core vs. edge range and widespread vs. endemic population demographics.

Topic: Systematics & Taxonomy

A-321

Phylogenomic Analysis of Xanthisma (Asteraceae) And Assessment of Ploidy Variation Using Herbarium Specimens

Author: Oluwaseun Shodipo, Matt Johnson
Affiliation: Texas Tech University

Accurate species delimitation is fundamental to biodiversity assessment and conservation, particularly in taxonomically complex plant groups such as the Asteraceae. Within the Astereae tribe, genera like Xanthisma, Machaeranthera, and Haplopappus are taxonomically challenging due to rapid evolutionary radiation, frequent polyploidy, and high morphological convergence. Among them, Xanthisma—a genus native to Texas—has experienced significant taxonomic reorganization, yet its monophyly and species boundaries remain poorly resolved. This research aims to clarify the evolutionary relationships within Xanthisma by integrating high-throughput targeted DNA sequencing (Angiosperms353 and Compositae1061), cytogenetic analyses, and morphological assessments. Preliminary phylogenomic data suggest Xanthisma may be monophyletic with distinct subclades, but weak species-level resolution points to ongoing gene flow and insufficient reproductive isolation. To address this, the study will incorporate field-based population sampling across overlapping species distributions, experimental hybridization to assess reproductive barriers, and chromosome staining to investigate the role of ploidy in species divergence. Historical herbarium specimens, including those collected by R.C. Jackson in the mid-20th century, will be reexamined and compared with newly collected material to detect morphological changes over time. Species tree inference (IQTREE, ASTRAL), PCA, and admixture analyses will be used to

evaluate whether genetic, morphological, and chromosomal variation align across lineages. By leveraging genomic tools and herbarium resources, this study will generate a refined phylogenetic framework for Xanthisma, support taxonomic reclassification, and provide broader insights into the evolutionary dynamics of polyploid-rich lineages in Asteraceae. The outcomes will contribute to more effective biodiversity monitoring and conservation strategies across the genus's native range.

Topic: Ethnobotany

A-322

Mapping Cultural Heritage: Comanche Ethnobotany and Species Distribution Modeling

Author: Anna DesHotels, Matt Johnson, Michael Jordan
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Ethnobotanical knowledge of the Comanche Nation is an understudied subject, and contemporary Comanche people express deep sadness at the loss of their traditional ecological knowledge (TEK). This process began during the cultural erasure enforced by boarding schools and allotments in the late 19th to mid-20th century. Ethnographers began documenting TEK of many tribes in Oklahoma in the early 1900s, believing the cultures would soon be completely eradicated. Despite centuries of genocide and attempts to force assimilation, the Comanche Nation remains alive today and members continue to practice many aspects of their culture, including the use of many medicinal, edible and ceremonial plants. However, the number of traditional knowledge holders diminishes every year, and the need to document and preserve their knowledge as well as educate the youth has been vehemently expressed by many tribal members. Our work seeks to bring together archival and historic ethnobotanical information, knowledge from contemporary elders, and species distribution modeling to aid in tribal education, food sovereignty, and plant harvesting initiatives. We intend to integrate TEK from over 100 years of informants with known and potential plant harvesting locations. We aim to utilize archival research, ethnographic interviews, visit sites of cultural significance with elders, and create an ethnobotanical database and species distribution model that integrates cultural variables. This data will also inform interpretive materials for regional state parks, who plan to incorporate indigenous perspectives in educational materials and resource management at Texas State Parks, in collaboration with the Comanche Nation. We intend to honor the voices of Comanche elders and to contribute to a broader movement of cultural resilience, helping sustain the deep-rooted plant knowledge for the next generation of knowledge keepers.

Topic: Symbioses: Plant, Animal, and Microbe Interactions

A-323

Characterizing Temporal Changes in Microbial Diversity in Herbarium Specimens from Guadalupe Mountains National Park

Author: Mara Hosaka, Matt Johnson, Madison Bullock, Sherese Price
Affiliation: Texas Tech University

Arbuscular mycorrhizal fungi (AMF) are endophytes that are understood to play a significant role in the ecology of their plant hosts. However, some studies suggest a loss in phylogenetic diversity of AMF in response to changing environmental factors, though few trends have shown conclusive evidence. Now, the diversity of microbes can be routinely quantified with DNA sequencing, but there is little historical data with which to compare modern findings. Herbarium specimens can provide a historical record of fungal endophyte communities, allowing for study of how AMF communities may have changed over time. In this study, we analyzed changes in endophyte biodiversity over the past 50 years in the Guadalupe Mountains, a biodiversity hotspot in Texas spanning seven ecoregions. We sampled roots and leaves of herbarium specimens from several species collected from Guadalupe Mountains National Park, pairing old (1973-1977) and new (2022-2023) specimens from the same species. We extracted and sequenced 18S fungal DNA from herbarium specimens and analyzed data using QIIME2. Our characterization of AMF species richness and phylogenetic relatedness provides proof of concept for characterizing changes in AMF diversity over time using herbarium specimens. Our results will contribute to modeling the change in composition of AMF communities as they respond to climate change.

Topic: Phylogenomics

A-324

Fun Sized Library Prep: Cost-Effective Target Capture Sequencing with Miniaturization

Author: Rylee Creek, Matt Johnson, Mohamed Fokar, Madison Bullock
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Target capture sequencing is a commonly used method for the study of specific genomic regions, greatly reducing the per-sample cost for phylogenetics and conservation genomics analysis. One advancement that has reduced costs to produce high-throughput DNA sequencing libraries is miniaturization, made possible with precise liquid handling robots. Specifically, the SPT LabTech Mosquito and Dragonfly allow library preparations at one-tenth the normal volume. However, we observed a tradeoff, where insert sizes were reduced to 200-300 bp on the Mosquito, limiting effectiveness of paired-end sequencing on the NovaSeq 6000 SP 2x250 flow cells. This especially impacts target enrichment studies within species, which benefit from larger flanking regions. This study investigates the impact of adjusting parameters on the Mosquito, increasing insert size and efficiency while reducing sequencing costs. Our aim is to develop best practices that produce longer DNA fragments, closer to a 500 bp insert size. Specific adjustments include reagent handling, DNA fragmentation, and hybridization conditions to maximize the size of the captured sequence without compromising target specificity or library complexity. We evaluated the impact of these parameters using fluorometry, automated electrophoresis, and qPCR prior to and after target enrichment. Generating larger insert sizes will recover greater flanking regions containing polymorphisms, aiding conservation genomic studies while potentially lowering sequencing costs.

Topic: Education and Outreach

A-325

Plant Education Walk Learning Model: Broadening impact of community engagement through a community-partnered, project-based service-learning community

Author: Ashley Egan
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Learning communities (LCs) are a designated high-impact practice (HIP) defined as "a group of people who share common academic goals and attitudes and meet semi-regularly to collaborate on classwork" – a shared goal unites members. In higher ed, LCs are often presented as cohort-based, inter-disciplinary learning experiences, such as first-year learning communities, where the student membership defines the community. Here, I propose that an LC can be defined by a community-partnered, project-based service-learning endeavor that broadens the impact of community engagement by bringing together a diverse set of students, professors, courses, and community members to produce lasting social impact via a large-scale deliverable. Here, I present a case study centered around my "Plant Education Walk Learning Model" that showcases a 1.5-year partnership with Orem City to create a public, interactive learning space within the Orem City Arboretum geared towards promoting public engagement and education of science, botany, and environmental stewardship. This LC brings together students and professors across multiple courses in Biology, Botany, and Digital Media, and community partners with such diverse titles as city project manager, communications manager, urban forester, and marketing. In this presentation, you will hear the "community amplified voices" of student, professor, partner, and the public via first-person accounts (written, recorded, in-person) of how this LC broadens the impact of community engagement from the perspective of stakeholder representatives. We discuss how this case study crosscuts across HIPs, impacts on students, community, and the public, and the challenges, triumphs, and logistics that come with such an endeavor.

Topic: *Ecology*

A-326

Seed functional traits underlie a tradeoff between temporal and spatial dispersal across an aridity and variability gradient

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In variable and extreme environments, many organisms employ dispersal strategies to either seek favorable conditions or spread the risk of encountering unfavorable ones. These dispersal strategies can entail movement through space as well as movement through time, via dormancy, diapause, or hibernation. Because these two types of dispersal can achieve similar population dynamic functions and can be subject to resource allocation and biophysical tradeoffs, theory has generally predicted a negative correlation, or tradeoff, between dispersal through space and time. However, empirical tests of theory have been limited, in part because of the inherent challenges of quantifying these types of dispersal in natural environments, and have often been limited to smaller numbers of taxa or locations. Here we leverage hidden Markov models, long-term community abundance data from five sites along an aridity and variability gradient, and detailed functional seed trait measurements on 277 species to explore relationships among dispersal strategies, how they vary across the gradient, and identify traits that underlie these patterns. We find that, across our gradient, spatial and temporal dispersal indeed demonstrate a tradeoff, but that temporal dispersal is more prevalent among species in systems with higher aridity. Moreover, seed traits, specifically shape, size, and dispersal distance class drive this trade-off with smaller, rounder seeds with unassisted dispersal showing higher temporal dispersal and lower spatial dispersal. More arid sites had higher community weighted means of traits associated with temporal dispersal, and had both lower functional richness and dispersion, highlighting convergence towards seeds specialized for temporal dispersal as aridity increases. Together this work presents a strong test of theory across multiple communities along an aridity and variability gradient, is one of the first studies to provide critical links between seed functional traits and realized dispersal strategies, and provides valuable insight into functional and life history traits in dynamic and changing environments.

Topic: *Biogeography*

A-327

The effects of missing taxa and phylogenetic imputation on spatial phylogenetic studies

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Identifying patterns of biodiversity and finding centers of endemism draws information from a wide range of disciplines such as biogeography and conservation management. Biodiversity can be characterized using multiple facets beyond taxonomic richness, including phylogenetic history and geographical distribution. Spatial phylogenetics adds an evolutionary and geographically explicit framework to biodiversity studies.

Although phylogenetic trees have become more comprehensive, phylogenetic diversity (PD) and associated metrics are estimated on datasets containing a fraction of the known terminals in a biota. Although sampling is necessary in science, and not objectionable per se, biased sampling may well affect results and warrants close attention. To attempt to improve sampling, missing taxa are sometimes imputed into a backbone phylogeny using taxonomic classification, but assumptions are needed to do this which may themselves affect results.

Thus we evaluated the effects of both incomplete taxon sampling and phylogenetic imputation on the quantitative and spatial patterns of phylodiversity, using a previously published data set on Japanese ferns. We ran sensitivity analyses for a set of phylodiversity indices using sets of trees with: (1) an increasing proportion of tips pruned and (2) those tips phylogenetically re-imputed using taxonomic classification. Tips were pruned at random as well as through two methods mimicking biased phylogenetic sampling based on a simulated quantitative trait. Then, we compared the estimates between full, pruned, and imputed data using regression and mapping tools.

We found that incomplete taxon sampling decreases the estimates' precision while moderately affecting accuracy (i.e., match to results with full data). Further, sampling fractions below 70% increase the estimates' uncertainty by threefold with stronger effects on relative phylogenetic diversity (RPD) and endemism (RPE). While variance increases, with extreme deviations in the randomized RPD and RPE, accuracy is relatively robust up to 20% missing taxa. Even though taxonomically-based imputation performs better than random tip imputation, it does not outperform incomplete sampling (i.e., simply leaving the missing taxa out). Taxonomic imputation tends to be inaccurate in all metrics and less precise (i.e., increased uncertainty) as compared to incomplete sampling. Our work suggests using caution when carrying out spatial phylogenetic analyses in cases of limited taxon sampling (including presence of suspected cryptic taxa) and discourages taxonomic imputation as a workaround.

Topic: *Biogeography*

A-328

Tracing the Past, Projecting the Future: An Integrated Approach to Species Distribution Modeling.

Author: Antonio Castilla, Sarah Naughtin, Allan Strand, Adam Smith, Andria Dawson, John Robinson
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Climate change poses a significant threat to biodiversity, and it remains uncertain whether species can adapt or shift their ranges rapidly enough to track suitable habitats. Hindcast species distribution models (SDMs) offer valuable insights by reconstructing past range shifts, but discrepancies among modeling algorithms and climate reconstructions often lead to conflicting outcomes. This highlights a critical need for approaches that integrate independent data to evaluate SDM performance, improve biogeographic inferences, and enhance predictions of future distributions.

We applied an integrative distributional, demographic, and coalescent (iDDC) modeling framework to reconstruct post-glacial range shifts in Fraxinus pennsylvanica, a widespread North American tree. We developed 24 SDMs using combinations of two climate reconstructions, three calibration regions, and four modeling algorithms. These SDMs informed spatially explicit demographic models, which we used to simulate genomic data through coalescent modeling—yielding a total of 1.2 million simulations. Model comparisons were performed using Approximate Bayesian Computation (ABC) to assess concordance between simulated and empirical genomic data.

Our results consistently favored SDMs based on the CCSM climate reconstruction. Leave-one-out cross-validation demonstrated stronger discriminatory power among SDMs based on climate models than those differing by algorithm. Using the best-supported SDM, we inferred the locations of glacial refugia for F. pennsylvanica and projected its potential range shifts under 21st-century climate change scenarios. This study underscores how alternative SDMs can lead to divergent biogeographic interpretations and highlights the utility of genomic data for evaluating competing models. Despite its computational demands, the iDDC framework offers a powerful tool for integrating ecological and genetic data to improve reconstructions of past distributions and forecasts of future species responses to climate change.

Topic: *Population Genetics/Genomics*

A-329

Investigating Local Adaptation in Quercus havardii

Author: Ryan Silver, Antonio Castilla
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Climate change presents a range of existential threats to plant species, from rising temperatures to shifting precipitation patterns. In response to these rapidly changing conditions, some species may persist by dispersing offspring into newly available, climatically suitable regions. While species with strong dispersal mechanisms may succeed in this strategy, many others have limited dispersal capacity, making it difficult for them to colonize all available habitats within their expansion range. For these species, the pressure to adapt to changing environmental conditions is likely to intensify, increasing the risk of extinction if adaptation does not occur. An example of this selective pressure could be plant species with edaphic specialization (i.e, species with distributions limited to particular soil conditions). These species can only colonize a subset of climatically suitable habitats that also meet their specific edaphic requirements.

Quercus havardii, an arid-adapted oak specializing in sandy soils, is a keystone species in the sand-shinnery ecosystem that provides critical habitat and resources for wildlife, including a number of threatened species. Previous studies have shown substantial phenotypic variation among populations and a significant correlation between genetic diversity and precipitation seasonality, suggesting potential for local adaptation.

However, the extent to which this species exhibits local adaptation across its environmental range remains unknown. Understanding the genetic basis of adaptation in Q. havardii is essential for assessing species' evolutionary potential and resilience to environmental change. This information is critical for developing conservation and management plans to preserve populations of the species.

I will present the conceptual framework and planned methods for my PhD dissertation, which aims to assess local adaptation in Quercus havardii. To capture the species' full environmental range, I will sample populations across its entire distribution and analyze genetic structure using whole-genome sequencing. This genomic data, combined with phenotypic traits and environmental variables will also be used to conduct genome-environment association (GEA) and genome-wide association (GWAS) analyses. Additionally, my research will involve experimental work, where seedlings from different populations will be exposed to varying temperature and water availability scenarios to assess adaptive response. Results of my research will help to inform conservation strategies by identifying conservation units within the species.

Topic: Disabled in Botany: Breaking Barriers in Plant Science Research

A-330

Defying expectations: resolving the Forest Fragmentation Paradox… while navigating physical disability

Author: Ash Hamilton, Sean Hoban
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Genetic diversity facilitates population persistence, by enabling adaptation and resilience during environmental change. Unfortunately, habitat fragmentation can reduce the genetic diversity of populations. However, extensive research has found that forest trees often do not exhibit this expected genetic diversity decline in response to fragmentation, a phenomenon dubbed the Forest Fragmentation Paradox. This paradox remains unresolved. One potential resolution lies in the unique suite of life history traits that characterizes trees. I aim to test if and to what extent one particular life history trait–many consecutive reproductive opportunities–buffers tree populations against genetic diversity loss. To do this, I will conduct genetic analysis on offspring from three consecutive years of a tree species which has experienced long-term fragmentation, *Quercus brandegeei*. I will then determine if and how different progeny cohorts exhibit differing levels of genetic diversity. If diversity is higher when progeny cohorts are aggregated, it would point toward the reproductive strategy of trees indeed contributing to the apparent paradox. This project involves intensive field and lab work components which I, a physically disabled person, am often unable to conduct on my own. While my disability could be perceived as barrier to my science, I will explain how it instead has broadened the impact of this project. My science is only made possible through teamwork and community building. So, I have spent time focusing on strengthening inter-institutional collaborations and fostering scientific opportunities for students, particularly those of underrepresented backgrounds. My disability has therefore pushed me to become a better mentor, team leader, and scientist, and has made my science better by the incorporation of a diversity of perspectives.

Topic: Common gardens in the 21st Century: the intersection between evolution and ecology, science and management

A-331

Plastic responses to drought in Mimulus cardinalis vary among traits and populations

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Plant persistence in heterogeneous environments is influenced by phenotypic plasticity—the ability of one genotype to express alternate phenotypes in different environments. Plasticity can be adaptive if it provides a fitness advantage, and in the face of climate change, understanding whether plasticity may buffer fitness is increasingly important for range edge populations experiencing increased environmental variability. Yet it remains unclear whether increased plasticity will consistently benefit edge populations in plant systems. A leading hypothesis to predict where in a species range we might expect plasticity to be adaptive is the Climate Variability Hypothesis (CVH), which posits that highly variable environments could select for increased plasticity, due to an increase in fitness when individuals alter their phenotype in the direction of selection. However, empirical tests of this hypothesis in the field remain rare, especially across species' ranges.

Using Mimulus (Erythranthe) cardinalis, we evaluated how baseline plasticity in drought-associated traits may differ due to environmental variation across a species' range (explicitly testing the CVH), and whether plasticity is adaptive in response to an extreme drought. We specifically tested whether plasticity in flowering time, specific leaf area, and leaf dry matter content were selected for across the species' range. We conducted a resurrection experiment, transplanting pre-drought ancestors and post-drought descendants from 6 populations into three diverse common gardens spanning the species' latitudinal range.

We found significant plasticity in all traits. Flowering time and leaf dry matter content showed greater plasticity in southern and central populations than in northern populations, consistent with spatial predictions based on the CVH. In some cases, plasticity increased in descendants but this did not always result in higher fitness. Within descendants, one southern population displayed a clear fitness advantage with increased flowering time plasticity, but plasticity in both leaf traits in some southern populations displayed a negative relationship with fitness.

These results highlight that adaptive plasticity is both trait and population-specific, and underscore the importance of considering spatial variation across species' ranges when examining selection on plasticity.

Topic: Bryology and Lichenology

A-332

California bryophytes: evolution and conservation in a biodiversity hotspot using novel continuous metrics for spatial phylogenetics

Author: Brent Mishler, Matthew Kling, Ixchel González-Ramírez, Ben Carter, Israel Borokini
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The developing field of spatial phylogenetics adds a phylogenetic dimension to biodiversity assessment and thus gives evolutionary depth to spatial inferences about diversity, endemism, and their causes. In addition to its academic uses, the field also contributes significantly to applied conservation assessments. Spatial phylogenetics is premised on the idea that species are not discrete categorical entities but instead lie on a hierarchical evolutionary continuum that contains rich biological information valuable for quantifying spatial biodiversity patterns. Yet while current approaches use quantitative information to represent phylogenetic patterns, most have continued to rely on methods that discard valuable information about spatial patterns by converting continuous variables into binary categories. This includes representing geographic ranges using binary presence-absence data, classifying statistical significance into categories, and quantifying biogeographic gradients into discrete regions. Here we demonstrate how a full suite of spatial phylogenetic analyses, including analyses of alpha and beta diversity, neo- and paleo-endemism, biogeographic hypothesis testing, and spatial conservation prioritization, can be implemented with "smooth" methods that never remove information content by categorizing continuous data.

Our analysis focused on the bryophytes of California, an understudied group in a global plant biodiversity hotspot. Using a time-calibrated phylogeny and species distribution models (SDMs) for 548 species of mosses and liverworts, we profiled the evolutionary diversity, compositional turnover, and conservation value of bryophyte communities across the state. The SDMs were fitted with maximum entropy, using bioclimatic variables at 810 m resolution and 10,000 background points. Predicted geographical ranges were constrained by known location using half Gaussian distance-decay function and by land intactness. The modeled ranges were combined with the phylogeny to calculate phylogenetic diversity (PD), phylogenetic endemism (PE), relative phylogenetic diversity (RPD), and relative phylogenetic endemism (RPE) with significance tests based on a spatial randomization that maintains the original richness of each cell and the original range-size of each species. In addition we looked at turnover using pairwise phyloSorensen's dissimilarity and conducted a standard categorical analysis of neo- and paleo-endemism (CANAPE). These CANAPE results were compared with a novel method that uses continuous values (Smooth Neo- And Paleo-Endemism analysis; SNAPE).

Our results highlight important patterns in the diversity of this key plant group and important conservation implications. Additionally, the novel SNAPE method uncovered more nuances in phylodiversity patterns than the traditional CANAPE, thus,

underscoring the information lost when discretizing continuous data. This new method can serve as a model for future studies seeking to maximize the information content of spatial phylogenetic analyses.

Topic: Biodiversity Informatics & Herbarium Digitization

A-333

Revitalizing the Sacramento State Herbarium: Decontamination, Digitization, and Discovery

Author: Mel Weber, Marina LaForgia
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The Sacramento State Herbarium, which contains over 20,000 dried plant specimens, has sat in disarray for decades, oversaturated with paradichlorobenzene, a pesticide fumigant. Only 10% of specimen metadata was available online and lacked images, making these data inaccessible to other researchers. Over the Summer of 2024, we set out to change this. I, along with a small team of undergraduates, helped to decontaminate half of the herbarium cabinets and place thousands of specimens in fume hoods to aid in off-gassing of the pesticide. With the contaminant finally dealt with, we turned to specimen digitization. During the past 6 months, we obtained imaging equipment and I developed our digitization workflow with help from the Consortium of California Herbaria and the UC Davis Center for Plant Diversity. As of today, I have helped image 5520 specimens and helped transcribe nearly 1000 specimens. Our collection of digitized specimens covers 69 families and 709 species, with over 2000 specimens from Poaceae alone. While specimen collection dates range between 1870 and 2013, ~60% of specimens were collected between 1975 and 1984. Most specimens (1480) were collected in Placer County, California. A group of knowledgeable volunteers are helping to speed up the process of digitizing this historic collection, allowing it to grow and connect with local and global communities of scientists, universities, and collections. Sac State's online collection offers high resolution images and metadata from associated labels; data regarding species of interest can thus be more efficiently searched for and analyzed, helping to streamline future research.

Topic: Phylogenomics

A-335

MissMap: A pipeline for visualizing sequence data availability in plant clades.

Author: Linda Mansour, Joseph Walker, Karolis Ramanauskas
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A major challenge in plant phylogenetics is resolving contentious taxonomic relationships that arise from whole genome duplications, rapid diversification, or errors in inference and analysis. MissMap is a pipeline in development that aims to help address this taxonomic conflict within large phylogenies by maximizing the data collected from NCBI GenBank. The pipeline is being developed to identify all publicly available NCBI GenBank genetic data (i.e. chloroplasts, mitochondria, nuclear, transcriptomic, rad-seq, and barcoding genes) for a user's clade of interest. MissMap's novelty comes from its ability to account for a wide range of sequence types, as opposed to other methods that often rely on just two or three genetic markers. MissMap outputs a matrix of values, with each species labeled on one axis and the availability of each type of data for those species on the other axis, visualizing information gaps in the genetic database. This aids in portraying the availability of sequence types that the user is looking for. The current consensus for taxonomic decisions relies on phylogeny, so we aim to improve the underlying methods of phylogenetic tree inference by providing a user-friendly way to obtain the maximum genetic data available for a given species. This information then enables researchers to refine these relationships and resolve contentious regions, providing a more accurate foundation for analyzing plant taxonomy.

Topic: Biodiversity Informatics & Herbarium Digitization

A-336

Digitisation and Metadata Harvesting for Herbaria Collections: Strategies for Transcribers and Curators to Assess Taxonomic and Geospatial Data.

Author: Frank Owen
Affiliation: Max Communications

The digitisation of the entire herbarium collection at the Royal Botanic Gardens Kew and the integration of the specimen sheets into a browser based mass transcription tool has allowed a large team of transcribers working remotely to harvest the metadata from over 6 Million specimen sheets.

However the taxonomic data gathered still needs to be quality controlled by curators with the knowledge to identify anonymlies and anachronisms in the original transcribed labels.

Further for specimens with no GPS location a latitude and longitude needs to be arrived upon using any locality descriptions which in many cases require specific geographical knowledge.

AI-driven metadata extraction has been successfully integrated into the digitisation and metadata workflows of several other herbaria collections. While this advancement has significantly improved efficiency, AI-generated metadata, like human-transcribed data, still requires validation and enhancement by subject matter experts to ensure the accuracy of taxonomic and geospatial information.

This presentation will explore strategies, considerations and solutions used in extracting metadata from over eight million herbarium specimens across five institutions worldwide. The presentation will focus on key aspects workflows:

- Capturing Taxonomic Hierarchy during Imaging: Methods for imaging staff to efficiently register the existing taxonomic structure in the physical collection i.e. boxes, folders and sub folders.
- Integration of Institutional Authority Lists: Allowing transcribers to select from taxon, location and collector lists. Allowing curators to add to those lists.
- Validation and Quality Assurance: Implementing scalable methods to track, monitor, and support large teams of transcribers and quality assurance staff in validating and enriching transcribed metadata.
- Expert Engagement and Data Presentation: Designing interfaces that organise metadata by taxon, collector, and geography, enabling subject matter specialists to refine and enhance AI-generated records.
- Sourcing Expertise: Strategies for identifying and engaging taxonomic experts and individuals with specialized geographical knowledge, ensuring institutions of all sizes can leverage the best available expertise.

This presentation has a focus on Themis, Max Communications' bespoke in-house browser based software. Currently deployed in four herbaria imaging and metadata harvesting projects, while Themis serves as a case study, the strategies and methodologies presented are broadly applicable to any metadata harvesting workflow.

Topic: Ecophysiology

A-337

Biodiversity comparison between restored and natural subtropical and tropical Seagrass: Texas and Florida Halodule and Thalassia communities.

Author: Anitra Thorhaug, Arthur Schwarz
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Biodiversity in seagrass ecosystems is known to be high globally. The tropical biodiversity of southeast Asian seagrass meadows has been shown to contain one of the global peak richness of number of marine species for both flora and fauna. Not only are the number of tropical associated plant species significant (including macro-algae, epiphytic microalgae and Submerged Aquatic Vascular plants), but a wide variety of invertebrates and fish are associated with seagrass along with select shorebirds, marine mammals and marine reptiles (sea turtles). The biodiversity richness differs between tropical regions. in the face of global degradation of seagrasses globally the question examined, "Is it possible to restore the full biodiversity of seagrasses through restoring the same seagrass species and density in the degraded area after the degrading event is

removed?" A comprehensive understanding of how fish and invertebrate communities respond to seagrass restoration is necessary to quantify the biodiversity of ecosystem services in restored areas. We have had decades of restoration investigations in multiple sites. In Biscayne Bay Florida we found that restored seagrass duplicated faunal and floral biodiversity. The biodiversity baseline occurred from a 7 year, 30 station monthly monitoring of invertebrate plus fish in the far southwestern coastal area of Biscayne Bay plus Card Sound, an adjacent estuary shared with Key Largo (Florida Keys), the results were the following: 1.) Seagrass of 2 dominant species grew 12 months/yr with blade densities varying seasonally demonstrating spring and fall peaks when temperatures were around 26-28.5C ; 2.) macro-algae dominated by Laurencia obtusa was higher density in months below 26C; 3.) Invertebrate fauna was rich were dominated by Thor floridanus, grass shrimp, with seasonal cycles related with temperature. Then the first large-scale global restoration occurred restoring Thalassia testudinum in August, 1973 at Turkey Point, Biscayne Bay. In the 4th year, a detailed study of the invertebrates and fish results showed equal amounts of biodiversity richness of species and abundance within the restored bed versus the naturally-occurring, proximate seagrass meadows, while both biodiversity richness and abundance were significantly different from proximate barren sediment (McLaughlin, Lamaitre et al., 1983). From this investigation, Shrimp species richness and abundance in restored seagrass was greater than naturally-occurring proximate seagrass meadows. Following this, 20 pilots including 6 large-scale plantings occurred in northern Biscayne Bay From the early 1990's onward restoration at pilot and large-scale occurred in damaged areas in estuarine Texas wherein Halodule wrightii was the dominant seagrass ecosystem. Biodiversity was measured only within the ability of the funding, so necessarily only key species were traced. These showed large scale recolonization of crab and shrimps immediately after densities began to return to 500-700 blades/m2, which was in 3-4 months. Additionally, final restoration results included endangered species feeding on the restored seagrass ecosystems such as Whooping cranes, sea turtles, and brown pelicans. Comparisons of 20 multiple restored seagrass areas in the Texas estuaries with the 20 areas in Florida Biscayne Bay will be discussed as to species richness, abundance, endangered species, infauna, epifauna, and sediment

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Topic: Biodiversity Informatics & Herbarium Digitization

A-339

A Deep Learning Framework for Trait Extraction from Digitized Herbarium Collections

Author: Oluwatobi Oso, Erika Edwards
Affiliation: Yale University

Over the past decade, large-scale herbarium digitization has transformed centuries-old plant collections into a valuable global resource. At the same time, the application of machine learning in science gained momentumand recent advances in artificial intelligence (AI) create new opportunities to explore botanical research. Currently, the integration of deep learning into herbarium informatics for large-scale trait extraction is still underexplored.

In this work, we present the first AI-driven framework for extracting leaf margin traits from digitized herbarium specimens, applied to over 80,000 woody angiosperm species. Using a convolutional neural network trained via Roboflow, we classify leaf margins into a binary categorization from high-resolution specimen images sourced from iDigBio. The trained model achieves high predictive accuracy and is deployed in a fully automated pipeline that includes leaf identification, margin classification, metadata filtering, georeferencing, and reproducible trait assignment.

Our results significantly expand margin trait coverage beyond what is available through existing databases (e.g., TRY, GIFT), particularly across underrepresented taxa and regions. This approach transforms herbarium sheets into a high-throughput source of trait data, and allows for advanced research into trait evolution, climate adaptation, and global biodiversity patterns. We applied this new dataset to examine a centuries-old question about the distribution of leaf margin types in different biomes, shedding new light on the higher prevalence of entire margins in tropical regions and nonentire margins in temperate zones.

Topic: Phylogenomics

A-340

PhyloMod: A Whole-Genome Duplication Aware Approach to Reducing Artificial Gene Tree Conflict

Author: Juan Naasko, Keyi Feng
Affiliation: University of Michigan

Phylogenetic research can often be complicated due to gene tree conflict arising from ancient whole genome duplications (WGD). Like Yang and Smith (2014), most current pipelines detect gene duplication events when duplicated taxa are present within the same homolog tree. However, datasets with limited sampling and sequencing limitations can lead to artificial gene tree conflict and incorrect phylogenetic relationships being drawn that do not represent the true species tree topology. A further complication of this problem is that angiosperms can experience heavy gene loss after a WGD. Even with more recent methods of inferring ortholog trees, such as Orthofinder (Emms and Kelly, 2019) and ASTRAL-pro (Zhang et al., 2020), the issues caused by WGDs persist. PhyloMod is a new package that aims to reduce artificial gene tree conflict caused by WGDs. It reduces artificial gene tree conflict by collapsing relationships susceptible to these kinds of errors near WGDs. To assess the efficacy of PhyloMod in finding and reducing artificial gene tree conflict, PhyloMod is applied to a transcriptome data set of sixty-six Caryophyllaceae species and five outgroup species. The resultant species tree is then evaluated against current consensus-agreed-upon species trees and relationships. Providing evidence of PhyloMod, a WGD-aware pipeline that collapses potentially error-prone relationships, in producing more accurate phylogenetic inference and reduced artificial gene tree conflict. Proving it as a useful and reliable tool for future phylogenetic studies.

Topic: Biogeography

A-341

Range-weighted branch length difference (RWiBaLD), a new method for distinguishing meso-endemism from neo-endemism and paleo-endemism

Author: Brent Mishler, Nunzio Knerr, Joseph Miller, Andrew Thornhill, Shawn Laffan
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There is a continued need for method development in the field of spatial phylogenetics, to support uses in academic studies of ecology and biogeography as well as in practical applications for conservation. Our goal here is to enhance understanding of phylogenetic endemism (PE), which is studied using a range-weighted phylogenetic tree (i.e., with each branch down-weighted proportionally to the size of its range, thus emphasizing the contribution of range restricted branches).

We present a new method called *ange eghted rnch engthifference* (RWiBaLD), which is based on the difference between the length of a branch on a range-weighted observed tree and its length on the corresponding range-weighted comparison tree (i.e., a tree with the same topology as the observed tree but with branches adjusted to be of equal length before range-weighting). The goal of this method is to detect the branches of the phylogeny that contribute most to PE, and to distinguish among neo-endemism, paleo-endemism, and a novel category: meso-endemism. The latter is a heretofore missing category in the study of endemism referring to a highly range-restricted lineage that is not particularly short (neo-) or long (paleo-).

Application of this approach is illustrated using the plant genus *Acacia* across the continent of Australia, using previously published spatial data and phylogeny. We show the properties of RWiBaLD, and how to apply it by: (1) mapping it on a phylogeny, thus for the first time enabling PE to be scored for use in existing phylogenetic comparative methods, and (2) dissecting the composition of concentrations of PE on the landscape that are detected by the previously published *Categorical Analysis of Neo- And Paleo-Endemism* (CANAPE) method.

Whereas CANAPE identifies geographic concentrations of high PE, and gives a summary classification of the type of endemism dominating in a location, RWiBaLD identifies the specific branches that contribute the most to PE, and what type of endemism they represent. Thus the two methods are mutually supportive and should be used together to advance the study of endemism.

RWiBaLD enables novel studies of the evolutionary and ecological causes of endemism, and can be applied to any group of organisms, including microbes. It will be useful to researchers studying eco-evolutionary processes, biogeographers assessing the spatial distribution of biodiversity, and conservation biologists setting priorities on the landscape.

Topic: Conservation Biology

A-342

Rethinking Lawns: Exploring native plant species as lawn alternatives to meet urban sustainability and conservation goals in Chicago

Author: Becky Barak, Rebecca Tonietto, Lauren Umek, Liz Anna Kozik, Natalie Love, Nadav Mouallem
Affiliation: Chicago Botanic Garden, University of Michigan, Flint, Chicago Park District

Lawns are important landscapes in cities, but not all are actively used. Converting non-recreational lawns to native landscapes can help cities meet sustainability and conservation goals by improving ecosystem function and providing ecosystem services that benefit both people and organisms that call cities home. However, transforming lawns via full-scale ecological restorations that re-create reference ecosystems, like native tallgrass prairie, is not always feasible, appropriate or accepted in urban contexts. In Chicago, we are exploring native lawn alternatives: landscape installations that are short and lawn-like in appearance but include native plants that are hypothesized to deliver ecosystem services greater than those provided by turfgrass. Using replicated experimental plots and large-scale landscape installations in Chicago's urban parks, we are assessing ecosystem service provisioning of turfgrass lawns relative to short-statured native graminoids, short-statured prairies, and tallgrass prairies. Specifically, we assess how these plantings compare in terms of stormwater infiltration, soil carbon and nitrogen, pollinator support, plant diversity and temperature mitigation across five parks. In this talk, we will present preliminary results from the first year of data collection. This work advances our understanding of how urban greening can be best leveraged to meet city's sustainability and conservation goals, including supporting biodiversity and ecological interactions as well as flooding and urban heat island mitigation.

Topic: Education and Outreach

A-343

Hands-On Activities Reduce Plant Awareness Disparity but do not Increase Interest in Plants Over Animals

Author: Lisa Wallace, Taylor Sloey, Erik Yando
Affiliation: Old Dominion University

Plant awareness disparity (PAD) occurs because people notice plants in an environment less frequently than they do animals, resulting in a lower appreciation for the value of plants and understanding less about them. Pedagogical strategies to increase plant awareness often focus on increasing knowledge, assuming that knowledge directly leads to greater interest and appreciation of a topic. However, PAD is also driven by a lack of attention to and low relative interest in plants, among other factors, which are not typically addressed in general biology classes. There is a critical need to understand the student population to effectively implement pedagogical practices aimed at reducing PAD. At Old Dominion University, we have updated the plant biology curriculum to improve outcomes for students wanting to focus on the study of plants in their degree program and to produce biology majors with greater plant awareness. Here, we report results from an assessment of PAD among students in our Botany course and test the impact of experiential learning activities on PAD. Although introductory in its focus, Botany is an intermediate-level, elective course in our curriculum that is typically taken by juniors or seniors who have completed pre-requisites in general biology, ecology, evolution, genetics, and cell biology, and advanced courses in a variety of topics. We introduced a 6-week internship experience in the lab in 2023 and a semester-long CURE in 2024 and used the Plant Awareness Disparity Index (PAD-I) to assess students' knowledge, attention, attitude, and relative interest in plants at the beginning and end of each semester. Consistent with our predictions, students exhibited less PAD by the end of the semester, but mean scores on the individual components of PAD varied. We did not find that type of experiential activity had a significant effect on reducing PAD. Students started the course with a strong awareness of the importance of plants to humans and the biosphere, perhaps because of exposure to these concepts in other classes in our curriculum. Nevertheless, students frequently lacked personal experiences with plants at the start of the class. Activities that involved observing and interacting with plants were emphasized in internships and the CURE and resulted in significant gains in students' attention and attitude toward plants by the end of the course. Still, these experiences did little to improve interest in plants over animals. These results have provided us with a baseline to improve upon while confirming the value that hands-on interactions with plants have in reducing PAD among students at ODU. We encourage adoption of the PAD-I for evaluation of diverse student populations and pedagogical practices, as results may facilitate meta-analyses that can identify strategies that are most helpful in engaging students in greater awareness of plants. Targeted strategies may be especially important to attracting students to study plants within general biology programs and to advancing the next generation of plant professionals.

Topic: Biogeography

A-344

Geographically Divergent Habitats and Climate Underlie Intraspecific Phenotypic Diversification at the Northern Range of a Widespread Orchid, Platanthera dilatata

Author: Marlin Bowles, Lisa Wallace
Affiliation: The Morton Arboretum, Old Dominion University

The integrated phenotype of an organism is determined by responses of individual traits to abiotic and biotic forces and may be correlated or uncorrelated. For example, floral phenotypes are thought to respond to pollinator-mediated selection, but variation in vegetative traits may reflect stronger responses to abiotic factors, which may explain why ecotypes can be associated with different habitats. Understanding what factors influence the integrated phenotype is of great interest in ecological and evolutionary biology. Here, we compared variation across floral organs and with leaf and inflorescence traits in the orchid *Platanthera dilatata* to evaluate the degree to which trait variation is integrated. N ectar spur length is thought to be driven by pollinator tongue length, as demonstrated in other species of *Platanthera*, but much variation exists in other traits of *P. dilatata* which are not obviously associated with how pollinators interact with flowers. We analyzed floral, inflorescence and leaf measures from 146 digital herbarium specimens of *P. dilatata* from Alaska, USA and bordering Russia and Yukon, Canada to quantify intraspecific phenotypic variation at its northern range, to determine if phenotypic variation is structured in association with regions and habitats, and to evaluate the influence of abiotic factors on these phenotypic patterns. Our results suggest that at its northern range, *P. dilatata* displays continuous phenotypic variation and that traits may be under varying degrees of climatic, habitat and pollinator-mediated selection. Plants with larger leaves, inflorescences, sepals and lips tended to predominate in coastal meadows with moderate climates, while those with smaller leaves, inflorescences, sepals and lips tended to predominate in continental wet or alpine meadows with extreme climates, as well as fens and muskeg bogs. By contrast, nectar spur length was poorly correlated with leaf, inflorescence and flower size but still exhibited ecological structure, with shorter spurred flowers occurring in the Aleutians and interior Alaska and longer spurred plants found most frequently in muskegs. We found significant association between flower, inflorescence, and leaf trait variation and elevation and climatic factors, but this was not the case for nectar spur length. These results suggest that ecological factors operating at varying spatial scales may underlie *P. dilatata* phenotypic variation and that differentiating phenotypes by spur-lip length relationships is problematic because of the continuous and uncoupled variation in phenotypes. Further work is needed to differentiate between genetically fixed and plastic responses to these processes, as well as the influence of historically isolated lineages originating from glacial refugia and post glacial migration.

Topic: Population Genetics/Genomics

A-345

Shedding Light on the Genetic Architecture of Adaptive Introgression in a Populus Hybrid Zone

Author: Sammy Mutegi, Michelle Zavala-Paez, Alayna Mead, Jill Hamilton
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Plant evolution in response to global change relies on standing genetic variation, the raw material upon which natural selection may act. However, hybridization and introgression may offer an additional source of recombinant variation to facilitate rapid evolution in response to changing selective pressures. Despite this understanding, the mechanisms through which introgression may influence adaptive potential in rapidly changing environments remain unclear. In temperate and boreal trees, climatic fluctuations during glacial and interglacial periods have promoted hybridization during secondary contact. *Populus trichocarpa*, a temperate forest tree species distributed

across the Pacific Northwest of the United States and Canada hybridizes freely with *P. balsamifera*, a boreal species where the distribution range of the two species overlaps. The resultant hybrid zones provide genetic variation upon which selection may act, and introgression may facilitate adaptation to novel environmental conditions beyond that of the parental species. Using whole genome resequencing data of parental and admixed genotypes of *P. trichocarpa* and *P. balsamifera* sampled from multiple replicated contact zones, we test for signatures of selection that might indicate adaptive introgression. We will use selective sweeps based on estimates of genetic differentiation (Fst, Dxy) with ABBA BABA tests and Bayesian genome cline analysis. To tease apart the impact of selection from neutral demographic processes we will also quantify nucleotide diversity (π_W) across the genome. To further identify the mechanisms contributing to adaptive introgression, we will test for the relationship between environment and genotype using latent factor mixed model. Given the repeated contact zones spanning environmental gradients between the two species, we expect to identify both genome-wide signatures of adaptive introgression alongside transect-specific signatures that may inform the evolutionary trajectory of parents and hybrids under changing environmental conditions. Ultimately, the study will shed light on the role of hybridization in adaptation to climate change.

Topic: Biodiversity Informatics & Herbarium Digitization

A-346

Evidence of Plasticity in Triodanis perfoliata: Differential Flowering Response to Interannual Spring Temperature and Variation Across North America

Author: Leidy Laura Arias Martinez, Jennifer Weber
Affiliation: Southern Illinois University

Examining long-term trends in flowering time shifts provides valuable insights, but can mask dynamic interannual variation that may reveal the capacity for short-term phenological responses. Digitised herbaria and citizen science initiatives are valuable resources for accessing large temporal and spatial phenological data for response at long temporal and spatial scales. This study examines the interannual and intraspecific dynamics of flowering time shifts in *Triodanis perfoliata* (Campanulaceae) using a comprehensive dataset of 1,493 herbarium and citizen science records spanning 1895-2022 across the contiguous United States. Building on previous work demonstrating a long-term advance in flowering time (Berg et al. 2019), we examine the influence of interannual temperature variation on flowering time and explore how these responses vary across a wide geographic range. We find a significant correlation between interannual spring temperature variation and flowering time, with cooler springs associated with delayed flowering and warmer springs associated with earlier flowering. Critically, we found that the magnitude of this relationship varied among *T. perfoliata* populations, with individuals in cooler, higher latitude regions being less sensitive to interannual temperature variation than those in warmer, lower latitude regions. This differential sensitivity suggests potential adaptive or plastic responses to local climatic conditions and may have implications for gene flow and the long-term ecological and evolutionary trajectory of *T. perfoliata* populations. This study highlights the importance of considering both long-term trends and interannual variation in phenological research, and emphasises the need for further investigation into the drivers and consequences of intraspecific variation in phenological sensitivity.

Topic: Symbioses: Plant, Animal, and Microbe Interactions

A-347

Interplay of Fungi and Pine: Exploring Tri-trophic Interactions

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Pinyon-juniper woodlands are a diverse and expansive semiarid ecosystem in the southwestern United States, characterized by dominant tree species from the Pinus and Juniperus genera. Pinus edulis is one of the primary pine species in these woodlands, and supports a habitat for a large diversity of wildlife. However, over the past decade, its populations have declined significantly due to prolonged droughts associated with climate change, triggering negative cascading effects throughout the ecosystem.

In the root systems of pinyon pines, there is a symbiotic mutualistic interaction between the pine tree and fungi. This interaction, known as a mycorrhizal association, enhances the uptake of water and nutrients, acts as a barrier against soil-borne pathogens, and helps the tree withstand drought conditions—all of them key adaptations for coping with climate change. In return, the fungi receive carbohydrates from the host tree. One of the primary fungal partners, Geopora pinyonensis (Ascomycota), plays a crucial role in this symbiosis, with prior research highlighting its contribution to Pinus edulis survival during drought.

Recently, an unprecedented fungal growth was observed on the surface of the reproductive structure of Geopora pinyonensis. This interaction is classified as fungicolous fungi, wherein one fungus interacts with another. Depending on the ecological context, fungicolous fungi could be mutualistic or parasitic, with mycoparasitism being the most commonly observed form. Such interactions can negatively impact the host fungus by reducing reproductive success and resilience. However, there is currently no documentation in the literature of this novel fungicolous fungi association involving Geopora pinyonensis, presenting a unique opportunity to investigate whether this interaction exerts beneficial or harmful effects on the Pinus edulis.

We hypothesize that the fungicolous fungi within Geopora is a parasitic organism capable of disrupting its host's physiological processes, potentially compromising the mycorrhizal association essential for the survival of Pinus edulis. Our primary objective is to characterize and identify the nature of the interaction between Geopora and the other unidentified fungus. Our secondary objective is to assess the potential impact of this interaction on P. edulis.

To achieve our objectives, we employed both morphological and microscopic analyses, in addition to genetic analyses based on genomic DNA and PCR amplification of the conserved Internal Transcribed Spacer (ITS) region. Morphological evidence confirms the presence of a distinct Ascomycete fungus exhibiting hyphal and primordia development, leading to fruiting body formation within the reproductive body of Geopora, which this behavior is associated with parasitic interactions. Genetic analyses are underway to identify this organism and better understand its role within this tri-trophic system.

This study represents a foundational step in characterizing a novel fungal-fungal interaction and its potential implications for mycorrhizal function and P. edulis survival under climate stress.

Topic: Mycology

A-348

High truffle fungi diversity in southern Oregon uncovered by conservation dog

Author: Hilary Rose Dawson, Heather Dawson, Jonathan Frank, Carolyn Delevich, Bitty Roy
Affiliation: Australian National University, University of Oregon, Southern Oregon University

Hypogeous aromatic fungi ('truffles') contribute significantly to overall fungal diversity but are difficult to find using traditional survey methods because they fruit underground, leading to under-documentation and a lack of data on species distribution and ecology. Truffles evolved to emit strong aromatic compounds to attract wildlife mycophagists for spore dispersal, a trait that culinary truffle harvesters exploit using trained truffle dogs. We trained a conservation dog to recognize a broad range of truffle aromas across diverse fungal lineages to increase efficiency in finding these cryptic fungi. We present a case-study demonstrating the value of using a 'truffle diversity dog' through a survey of the floristically diverse Cascade-Siskiyou National Monument (CSNM), located on the southwestern Oregon and northwestern California border, U.S.A. The dog uncovered high biodiversity in this region, locating 103 truffle species in 34 genera across 23 families. The trained dog was particularly valuable for locating truffles that are visually difficult to distinguish from the substrate (e.g. the truffle genus *Genea*) and species that produce few fruiting bodies. Fewer than half of the unique taxa matched public sequence records, and many are likely new to science. We found high species turnover between oak and conifer habitats, suggesting high host specificity in truffles. The wide range of fungal taxonomic diversity found in this study by a conservation dog demonstrates the value of training dogs to generalize to all types of truffle aroma, providing a promising method to efficiently describe understudied fungal biodiversity.

Topic: Ecophysiology

A-349

Native Eucalyptus dieback alters sub-alpine carbon cycling across scales

Author: Hilary Rose Dawson, Zachary Brown, Leo Lovesy, Sabina Aitken, Mark Hovenden, Adrienne Nicotra
Affiliation: Australian National University, University of Tasmania

Large-scale tree dieback events are a global concern that will alter carbon cycles in tree-dominated ecosystems, with potentially dramatic loss of ecosystem services. These changes are particularly impactful in systems where the forest canopy is monospecific, like in our example of the current snow gum (*Eucalyptus pauciflora* spp. *niphophila*) dieback event in the Australian sub-alpine region. Loss of canopy can alter microclimate water and light availability in ways that exacerbate ongoing effects of climate change, such as increased heat. This altered microclimate may lead to changes in the composition of dominant understory plant functional types to favour woody shrubs. These microclimate and community shifts can have corresponding changes in landscape scale processes, affecting water availability and carbon storage. We present a case-study where we integrated data across scales from leaf and wood traits to understory fluxes to landscape eddy covariance fluxes to understand how snow gum canopy loss impacts carbon dioxide fluxes in the Australian Alps. Healthy snow gum woodland had a negative net ecosystem exchange in 2024, drawing down 206.8 $gC/m^2/yr$. Dieback affected snow gum trees had smaller leaves and a higher Huber value (ratio of wood to leaf area) than unaffected trees, reflecting leaf water stress from wood-borer girdling of trunks. Under canopy cover, understory communities dominated by grasses had higher soil and ecosystem respiration than shrub understories. However, there was no difference in soil and ecosystem respiration between grass and shrub-dominated communities in the open. Our results emphasize the importance of sub-alpine woodlands for regional carbon balances. Healthy tree canopy provides significant atmospheric carbon drawdown, and dieback reduces the leaf area available for this service.

Topic: Lichen and Bryophyte Diversity, Conservation, and Evolution in the Americas

A-350

Results from a diversity inventory of lichenized fungi along the south coast of Sonora and Baja California Peninsula.

Author: Eduardo Gutierrez
Affiliation: Arizona State University

Mexico is considered a megadiverse country in terms of its species and ecosystem diversity. The Sonoran Desert and the California Floristic Province are located in the western part of the country, where desert, tropical, and Mediterranean vegetation occur. Among many other factors, the temperature, aridity, and occurrence of fog in different magnitudes provide multiple and different types of habitats in the surrounding Gulf of California and the Pacific Ocean. The Mexican states covering these phytogeographic regions are Sonora, Baja California, and Baja California Sur. Lichens are a highly diverse group of organisms, very well adapted to most habitats. In terms of lichenology, the northwestern region of Mexico is also the best-studied in the country, but because of the disparity in surveying the different states, species richness in Mexico overall is still unknown. The three states that I surveyed are recognized as the ones with the highest number of species: Baja California (710), Sonora (516), and Baja California Sur (511). If the number of species and the amount of lichen records in western Mexico are compared, the Baja California peninsula surpasses Sonora by far. Nevertheless, in all three states, many areas remain to be explored. The objectives of this study were: 1) an inventory of lichen diversity from the coast of Sonora and the Baja California peninsula along latitudinal and longitudinal gradients, and 2) comparing lichen diversity of the localities sampled according to their biogeographic regions. Multiple localities were surveyed along the coast of the Baja California peninsula and the state of Sonora. The inventory resulted in a total of 114 species, with fourty-seven new species records: twenty-seven not previously reported from these states, fourteen reported for the first time from a new habitat, and three species new to Mexico. We also discovered five species possibly new to science, four in Sonora, and one in Baja California Sur. The state of Sonora accounted for the highest number of species (sixty-seven), compared to both states of the Baja California peninsula (thirty-three in the northern state of Baja California and thirty-seven in the Baja California Sur). Comparing the different habitats overall, the type of vegetation with the highest number of species was found in coastal shrub (fifty-three) along the coast of Sonora. The Mediterranean region of Baja California (twenty-three) and the Vizcaino Region (twenty-nine) were also biogeographic regions with high species richness. Sonora and Baja California Sur were the states that shared the most species. The lichen genera represented by the highest species number were: *Buellia* (7), *Dirinaria* (5), *Lecanora* (7), *Parmotrema* (5), *Peltula* (5), *Polycauliona* (6), *Ramalina* (6). Species possibly new belong to *Buellia* s.l., *Lecanora*, and *Ramalina*.

Key words: Lichens, lichenology, Mexican biogeography, Gulf of California, Sinaloan coastal shrubland

Topic: Phytochemical

A-351

Genetic and volatile chemical signatures in the Polemonium viscosum complex: a combined approach to species delimitation

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The *Polemonium viscosum* complex, a group of alpine flowering plants, exhibits distinct floral fragrances. Two closely related species, despite their morphological and geographic parallels, demonstrate very different fragrances: *P. viscosum* smells "skunky" while *P. confertum* smells "sweet". Taxonomic confusion between the two has persisted, and it is unclear if *P. confertum* really is a distinct species from *P. viscosum*. By integrating floral scent analysis with high throughput phylogenetics, this work will resolve species boundaries and assess whether floral scent divergence corresponds to genetic differentiation. The integration of chemical and phylogenetic approaches represents an underutilized method for investigating species boundaries in taxonomically challenging alpine plant groups. The *Polemonium viscosum* complex presents a unique opportunity to explore floral scent variation and its role in speciation, with implications for conserving endemic and rare alpine plants. Is speciation occurring in sympatry driven by divergence in floral scent profiles, or is there a single species exhibiting two distinct floral scent profiles to optimize ecological opportunities in an alpine environment with limited pollination potential?

Topic: Reproductive Processes

A-352

A Decade of Global Change: Do We See a Change in Pollination?

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Pollination is essential for the reproduction of most flowering plants and is often facilitated by pollinators such as bees, flies, and butterflies. However, in the last decade, increased occurrences of fires, droughts, and temperature fluctuations due to global change have raised concerns for both plant and pollinator populations. Numerous studies have documented how these novel environmental challenges impact both plant and pollinator distribution, phenology, morphology, and behavior. Yet, little is known about how global change is affecting the pollination process itself, particularly across periods longer than just a few field seasons. Our study examines floral samples from serpentine seeps in California – known biodiversity hotspots that have experienced varying degrees of environmental change. Plant species, both endemic and widespread with different pollinator relationships were selected. Samples were collected back in 2010, and again in 2021 through 2025 to explore how changes over time may influence pollination dynamics. Pollen on stigmas of spent flowers was characterized to address three major questions regarding pollination quality and quantity from these time points. First: How much conspecific (same species) pollen is being delivered by pollinators? Second: Are pollinators transferring pollen from other species? Third: How many of these pollen grains were able to form pollen tubes to continue toward fertilization? Comparative analyses of these three key points reveal that pollen quality as well as the number of heterospecific (different species) pollen grains deposited have declined across species over the past decade. Overall, our long-term study is providing valuable insights into how pollination dynamics are shifting in the context of global change.

Topic: Ecology

A-353

Post-Hurricane Forest Dynamics: Drivers of Delayed Mortality and Implications for Forest Recovery

Author: Alyssa Brown
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A mechanistic understanding of the processes that drive post-disturbance forest response is essential for assessing resilience in a changing climate. Delayed mortality following hurricanes is well-documented but poorly understood and remains unrepresented in the "building and thinning" model of post-hurricane forest recovery. Using a causal inference framework, we identify individual and neighborhood damage as key drivers of delayed mortality following Hurricane Maria in El Yunque, Puerto Rico. We compare delayed mortality dynamics following Hurricane Hugo and Maria to explore how these mechanisms change with storm severity. In addition, we assess the effect of delayed mortality on understory recruitment dynamics. Our work improves the attribution of biomass loss to disturbance events while forming a more complete model of post-hurricane tropical forest recovery. Finally, these findings suggest unexpected physiological tradeoffs and carry implications for predicting patterns of community response under novel disturbance regimes.

Topic: Ecology

A-354

Revealing the Ecological Role of Canary Island Date Palms as Hosts for Epiphytic Diversity in the Greater Los Angeles Area

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Although only one species is native to California, palms have become emblematic of the California landscape. Of the many introduced palms to California, the Canary Island date palm (Phoenix canariensis) is one of the most commonly encountered species found in urban regions of the state. Throughout these geographic areas, individuals are managed in that the old leaves at the base of the leaf crown are often periodically trimmed in a manner that resembles the fruit body of pineapples or 'piñas'. This practice creates a unique microhabitat for a community of insects, birds, small mammals, and vascular plants. Over the course of two years we visited over two thousand Canary Island date palms in the Greater Los Angeles area and compiled a list of all epiphytic vascular plant taxa we observed, their relative abundance, and their primary mode of dispersal. We found a total of 64 taxa with endozoochorous dispersal being the most common. Interestingly, a number of our observed taxa represent individuals that are not well documented as escaping cultivation in California, underscoring the role of human-modified environments in shaping urban biodiversity. The observed epiphytic diversity not only reflects the ecological complexity inherent in urban green spaces but also underscores the Canary Island date palm's unintended function as a biodiversity reservoir in metropolitan areas. This study contributes to our understanding of urban ecosystems. We discuss ecological attributes of the date palm microhabitat and the dynamics of epiphytism in their subcrown canopies, highlighting an opportunity for enhanced integration of ecological considerations in urban planning and management.

Topic: Ecology

A-355

A Case for Causal Inference: Beyond n=1 for a More Rigorous Disturbance Ecology

Author: Alyssa Brown
Affiliation: Columbia University

Anthropogenic climate change is creating novelty in disturbance regimes with unknown ramifications for community recovery. Community resilience hinges on ecological memory, which arises from exposure to disturbance through time. This raises a critical question: will communities remain resilient to disturbance under these changing conditions? Complicating this issue, compound, interacting disturbances make it difficult to isolate the effects of a single event. Yet assessing ecosystem resilience is essential to make meaningful, generalizable predictions to anticipate ecosystem responses at local and global scales.

Causal inference is a promising, underutilized tool with the potential to address these difficulties. This approach enables researchers to use observational data to answer mechanistic questions, even when multiple disturbance events may influence questions of interest. Given its complex disturbance history in recent decades, we apply this conceptual approach to El Yunque, Puerto Rico, to demonstrate how causal inference can address otherwise unsolvable research questions. We propose practices for leveraging this framework, even outside of formal statistical analysis, to improve the rigor and generalizability of work in our field. Collectively applying these principles, we can promote synthesis and move toward bridging the gap between theoretical and applied science— essential tasks given recent funding constraints.

Topic: Bryology and Lichenology

A-356

Why does Polytrichum commune exhibit green coloration in shade and yellow-green in sun?

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Polytrichum commune, a common haircap moss, exhibits distinct coloration depending on its exposure to sunlight: shaded individuals appear green, whereas those in direct sunlight exhibit a yellow-green hue. This study investigates the physiological mechanisms responsible for this color variation, focusing primarily on pigment composition and photoprotection strategies. Samples were collected from shaded and sunny environments, and additional shaded samples were experimentally transitioned into sunlight to examine adaptive changes. These samples were analyzed for pigment concentrations (chlorophyll and carotenoids), carotenoid-to-chlorophyll ratios (CAR/CHL), electron transport rates (ETR), and non-photochemical quenching (NPQ).

Results revealed chlorophyll and carotenoid concentrations in sun-exposed samples were 56% and 65% of those in shaded samples, respectively. However, sun-exposed moss consistently displayed CAR/CHL ratios 1.2 times higher than shaded samples. The higher CAR/CHL ratio directly contributes to the yellow-green coloration observed under high light conditions. Experimental sunlight exposure of shaded moss supported these findings, showing a decrease in chlorophyll and carotenoid concentrations (57% and 71%) and an increase in CAR/CHL (1.2 times) and NPQ (2.2 times) values, indicating enhanced photoprotection. Notably, NPQ levels in sun-exposed moss were approximately twice those found in shaded samples, emphasizing the critical role of carotenoids in dissipating excess light energy and safeguarding the photosynthetic apparatus from photodamage. The ETR measured at 820 μmol m^{-2} s^{-1} PAR in sun-exposed moss were double (33 μmol m^{-2} s^{-1}) those observed in shaded moss (16 μmol m^{-2} s^{-1}), indicating significantly enhanced photosynthetic efficiency under intense illumination. Environmental parameters, including temperature and humidity, measured concurrently, showed negligible differences (temperature ratio 1.0, humidity ratio 0.87), confirming increased light intensity (10 times) as the primary driver of these physiological adaptations.

In addition to physiological adaptations, structural analyses highlighted the specialized lamellae on *Polytrichum commune* leaves, which facilitate efficient gas exchange and optimize photosynthesis under varying light conditions. This structural adaptation enables the moss to rapidly adjust pigment ratios and enhance photoprotective mechanisms, allowing it to thrive even under rapidly changing environmental conditions.

The implications of this research extend beyond understanding bryophyte ecology, offering broader insights into plant biology. The observed efficiency of NPQ mechanisms in *P. commune* provides valuable information for agricultural biotechnology, potentially informing the development of crops capable of better tolerating fluctuating or extreme lighting conditions. Furthermore, due to their sensitive pigment-based responses, bryophytes such as *P. commune* have potential utility as bioindicators of environmental stress, particularly for monitoring UV-B radiation linked to climate change.

In conclusion, *Polytrichum commune* effectively adjusts its pigment composition and photoprotective mechanisms in response to sunlight exposure, demonstrating a robust adaptability and ecological success. This study provides key insights into moss adaptive strategies, suggesting their potential relevance in ecological monitoring and possible applications in agricultural innovation.

Topic: Pteridology

A-357

A backbone for filmy ferns: Resolving deep relationships in Hymenophyllaceae with next-generation DNA sequencing

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Hymenophyllaceae is a distinctive family of ferns characterized by their one-cell-thick leaves, and its monophyly is widely accepted. Traditionally, the family was divided into two broadly defined genera, *Hymenophyllum* and *Trichomanes sensu lato* (= subfamily Trichomanoideae). However, the currently widely accepted view based on molecular phylogenetic data as well as morphological and ecological characteristics splits *Trichomanes sensu lato* into eight genera (Ebihara et al. 2006). While each of these genera has been shown to be monophyletic, relationships among them have remained unresolved due to the limited information content of traditional Sanger sequencing data.

The aim of this study was to clarify phylogenetic relationships among the major lineages of Hymenophyllaceae. We sampled representatives covering all genera, subgenera, and sections proposed by Ebihara et al. (2006) and applied a target enrichment method using next-generation sequencing to recover over 300 nuclear gene regions for phylogenetic analysis, which were supplemented with over 70 plastid regions obtained from bioinformatic skimming of off-target reads. As a result, previously unclear intergeneric relationships were resolved. In particular, we found strong evidence suggesting that Trichomanoideae comprises two major clades, a topology which had only been weakly supported by previous studies using plastid markers. Additionally, *Trichomanes siamense* Christ was shown to represent a novel lineage not belonging to any of the previously recognized subgenera of *Trichomanes sensu stricto*, and therefore warrants recognition as a new subgenus. Furthermore, we reassessed the evolution of epiphytism within Trichomanoideae based on the newly inferred phylogenetic relationships.

Topic: Defining forces in fern evolution: Celebrating the contributions of Kathleen Pryer and Michael Windham

A-359

PPG II and beyond: Building an open, community-driven taxonomic system for ferns and lycophytes

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Since the advent of molecular phylogenetic analysis starting in the late 20 th century, evolutionary relationships within pteridophytes (ferns and lycophytes) have rapidly come into focus. During this time, foundational studies led by the Pryer Lab revolutionized our understanding of pteridophyte evolution. This prompted the first major re-evaluation of fern classification informed by molecular phylogenetics (Smith et al. 2006), which was further updated and expanded by the Pteridophyte Phylogeny Group I (2016) classification. PPG I was remarkable for its community-driven approach, synthesizing the expert opinion of over 90 pteridologists. Since then, nomenclatural novelties in pteridophytes have accumulated, along with an ever more refined fern tree of life. Here, we present the first major update to PPG, PPG II. This classification expands the community-based approach of PPG I by including a greater number of contributors (nearly 200, representing 42 countries) and making all taxonomic discussions completely open and transparent (pteridogroup.github.io). Furthermore, PPG II is partnering with World Flora Online (www.worldfloraonline.org) to serve its taxonomic classification system through an online portal with continuous, collaborative updates from PPG community members.

Topic: Ecophysiology

A-361

Range-wide phenotypic differences affect drought response

Author: Haley Branch, Henry Arenas-Castro, Pauline Raimondeau, Vanessa Tonet, Craig Brodersen, Erika Edwards, Jennifer Coughlan
Affiliation: Yale University, Yale

Populations across the range of *Mimulus guttatus* experience vastly different climates. Therefore, phenotypic differences that arise due to geography and climate impact how populations respond to severe climatic events, such as drought. Using a range-wide sampling of over 800 accessions, we assessed baseline phenotypic differences in vegetative and floral traits prior to stress and then conducted a dry-down experiment. Since natural growing season ends with a terminal drought for this species, we asked whether populations would differ in their capacity to withstand such drought and whether this correlated to latitudinal gradients in climate. We found that floral traits (flowering time, size, and outcrossing rate) directly correlated with latitudinal differences. Although we did not find any geographical correlation with vegetative and physiological traits (specific leaf area, stomatal conductance, stomatal size, trichomes), we did find that rates of wilting differed across individuals, resulting in distinct wilting "syndromes". These syndromes caused some individual plants to withstand drought for much longer periods before dying. This study demonstrates the vulnerability of such riparian species as climate changes, precipitation becomes more unpredictable, and drought intensity increases earlier in the growing season.

Topic: Disabled in Botany: Breaking Barriers in Plant Science Research

A-362

Ableism as foundation for ecology and evolutionary biology

Author: Haley Branch
Affiliation: Yale University

Academia was built on the idea that certain bodies and minds should be excluded from gaining higher education. This ideology has perpetuated throughout all fields of the academy, especially in ecology and evolutionary biology. Our field has been detrimentally hurt by the idea of 'the survival of the fittest', which although is rarely used now, remains in the discourse. The founders of evolutionary biology and theory predominately shared similar lived experiences, resulting in a narrow and eugenics framework for the way that evolutionary biologists generally ask questions, conduct research, and analyze data. With increasing diversity of lived experiences, the field of evolutionary biology has expanded the breadth of research questions that are being asked. A consequence of this is the isolation and exclusion of many students who then do not pursue ecology and evolutionary biology. This includes disabled people, who make up a significantly smaller proportion of ecologists and evolutionary biologists at every level of the Academy, compared to the demographics of the surrounding population. The exclusion of these voices and perspectives limits the questions that we ask and the way we interpret the results we see. For instance, there remains a large gap in understanding how "disability" presents itself in nature and this could be a direct cause from a small number of disabled persons within our fields. The role and importance of these types of differences within populations is generally lacking and mostly studied through an anthropological lens on apes and mammals. Including more disabled perspectives will enhance our understanding of the natural world and increase our appreciation of biodiversity. One avenue to increasing disabled perspectives in ecology and evolution is by increasing access to field research. By increasing transparency of fieldwork and the corresponding research stations, more individuals will likely pursue this type of work.

Topic: Pteridology

A-364

The Fern Gametophytes of Alma Grace Stokey, a Pioneering Female Botanist and her Life's Work

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Alma Grace Stokey was educated at Oberlin College (A.B.) and the University of Chicago (PhD) in the early 1900s. She spent most of her career at Mount Holyoke, where she became a full professor and the chair of the botany department. In 1953, Dr. Stokey became the tenth and first female honorary member and of the American Fern Society.

Throughout her career, she published overly 30 articles, many of them on the biology of ferns and fern gametophytes. After her death, her personal papers and field notes were preserved and passed down through three generations of fern biologists.

This collection contains more than 10,000 gametophyte illustrations from over 200 species that Dr. Stokey cultured in her lab and illustrated from direct observation. Very little of this work has been shared publicly - approximately 90% of the collection remains unpublished. Dr. Stokey's drawings are meticulous and represent an enormous contribution to science and an opportunity to understand the evolution of fern gametophyte biology. In parallel to the morphological drawings, the collection contains dozens of correspondence from some of the most important plant biologists of the time, including Panchanan Maheshwari and Warren H. Wagner, which offer a unique insight into both the development of the discipline and the history of women in botany in the early twentieth century. Through cross-institutional collaboration between Eddie Watkins, Professor at Colgate University, Joshua Finnell, Associate University Librarian at Colgate University, Ken Rossi, University Archivist at Oberlin College, Deborah Richards, Head of Archives and Special Collections at Mt. Holyoke, and Tracey Kry, Digital Collections Archivist at Mount Holyoke College, a complete collection of all Dr. Stokey's personal papers, unpublished field notes, correspondence, and renderings have been assembled and professionally digitized to create a complete archive of her works. The collection is currently undergoing manual curation to create a detailed metadata schema and online digital repository for the works, with the ultimate goal of making this archive accessible to interdisciplinary scholars and students from around the globe.

Ferns are the only land plants that have both free-living gametophytes and sporophytes. However, far less is known about gametophytes due to their small, ephemeral nature and the historical perspective that they were the less important part of the fern life cycle. Recently, interest in the gametophyte phase of ferns and land plants more generally has increased due to their potential to help us understand early land plant evolution and more work is being done to understand their ecology, physiology, evolution, and life history. However, there is still little understanding of many aspects of fern gametophyte biology, especially how they have evolved within ferns, and even descriptions of morphological traits and variation are lacking. Fern gametophytes can be challenging to grow and exhibit highly plastic morphology, which can make them difficult to describe. The work of Dr. Stokey offers an exciting opportunity to utilize detailed, thorough descriptions made by an expert in fern gametophytes to generate a deeper understanding of early plant evolution.

Topic: *Comparative Genomics/Transcriptomics*

A-365

Gene Sharing Between Sporophyte and Gametophyte Phases Constrains Adaptive Evolution in Ferns

Author: Elissa Sorojsrisom, Barbara Ambrose, Deren Eaton
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Plants alternate between multicellular haploid gametophyte and diploid sporophyte life phases. Ferns are the only land plants in which both phases are free-living and photosynthetic. We collected a transcriptomic time series of the model fern, Ceratopteris richardii throughout gametophyte development to characterize changes in gene expression throughout the fern life cycle and compare gametophyte vs. sporophyte gene expression profiles. Additionally, we characterized changes in transcription factor expression throughout development and identified genes involved in gametangia (sex organ) patterning.

We then extended the bioinformatics pipeline from our Ceratopteris time series to a comparative approach utilizing 10 fern species from across the order Polypodiales (includes ~80% of fern species). We sequenced transcriptomes of field-collected sporophyte samples from at least five distinct populations and gametophyte samples that were lab-cultured from field-collected spores. Using differential gene expression analysis, we compared sporophyte vs. gametophyte gene expression profiles within each species to identify consistent patterns across ferns.

The patterns we observed from our Ceratopteris time series were largely repeated in our comparative dataset. One of the most striking patterns is that most genes (~90%) are shared between both phases in ferns (i.e. they are expressed in both the gametophyte and the sporophyte). This raises interesting implications for how selection acts on new mutations in ferns compared to plants with a dominant phase (i.e. bryophytes and seed plants). To investigate selection in ferns, we utilized the MK-test on our dataset and find that phase-specific genes tend to exhibit stronger signatures of positive selection than shared genes. This may indicate that the high degree of gene-sharing between phases constrains adaptive evolution in ferns, representing an exciting avenue for further investigation.

Topic: *Development and Structure*

A-366

Across the Bryophyte-Angiosperm Divide: an 8-stage homologous framework for the evolution and patterning of the land plant gametangia

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The fundamental sexual reproductive structures of the gametophyte are the archegonium and antheridium (together called gametangia), which produce egg and sperm respectively. The gametangia show remarkable morphological conservation across nonvascular and free-sporing vascular plants, but are structurally reduced in seed plants. Many studies have investigated the patterning and molecular genetics of gametophyte development in flowering plants as well as in Bryophytes, such as *Marchantia polymorpha* and *Physcomitrium patens*, but comparative studies incorporating representatives from lycophytes, ferns, and gymnosperms are lacking. Furthermore, whether and how the gametes and gametangia are homologous across green algae and land plants is not known.

We review the last 150 years of botanical literature on the subject of gametangia morphology and development to generate an eight-stage ontogenic framework that unites the development of the female and male sex organs of land plants and proposes homologies across all land plant lineages. This framework is paired with a review of the limited molecular genetics studies currently available that investigate the underlying genetic mechanisms responsible for patterning land plant gametangia. This study synthesizes data from diverse fields and sometimes elusive sources to identify clear future research directions to generate testable hypotheses about this aspect of the evolution and development of land plants and larger trends in land plant evolution.

Our review spans over a century of research, synthesizing key ideas about the origin, development, and evolution of gametangia across land plant lineages. We trace the evolution of these crucial reproductive structures, drawing on historical studies as well as the latest molecular and developmental insights. By placing these developments into a shared framework, we seek to lay a foundation by identifying testable hypotheses and experimental approaches that will elucidate the evolution and development of gametangia in the broader context of plant life cycles.

Although analyses of patterning provide strong working hypotheses, contributions from molecular genetics and functional studies will be necessary to determine the complete story of how these structures and the gametes they produce have changed throughout the evolution of land plants. We hope that this review will not only contribute to the growing body of literature highlighting gametophyte biology but will also serve as a valuable resource for educators and students, offering a solid foundation for understanding gametangia development and plant life cycles, and guiding future research that will provide new perspectives on this fascinating area of plant biology.

Topic: *Conservation Biology*

A-367

Reproductive biology and ecology of the Zapata Bladderpod (Physaria thamnophila; Brassicaceae): an endemic to the Tamaulipan thornscrub in southwestern Texas.

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The Zapata Bladderpod (*Physaria thamnophila*; Brassicaceae) is a federally and state endangered species endemic to the Tamaulipan thornscrub of South Texas with documented occurrences in Northern Mexico. In this study we focus on documenting the breeding system, flower visitors, reproductive success, and seed germination of this species. From 2022-2024, data were gathered at eleven sites ranging from federal, private, and NGO lands. Methodology included organza bags to exclude pollinators, hand pollinations to determine pollen compatibility, cameras to capture flower visitors,

fruit and seed counts to access reproductive output, and seed germination using gibberellic acid. Overall, we have determined that: 1) *Physaria thamnophila* is an outcrosser; 2) the species requires pollinators for production of fruits and seeds ; 3) *Physaria thamnophila* supports a diverse guild of flower visitors within the Tamaulipan thornscrub; 4) fruit and seed sets across populations vary; and 5) seed germination is not contributing to its rare status. All the data gathered during this study has expanded our knowledge of the biology and ecology of *Physaria thamnophila* and can contribute to future reintroduction efforts for the species. The latter is extremely important due to the anthropogenic pressures associated with habitat loss and degradation facing *Physaria thamnophila* and the Tamaulipan thornscrub in southwestern Texas.

Topic: Systematics & Taxonomy

A-368

Evolution and diversification of subtribe Flaveriinae (Asteraceae) on gypsum soils

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Island Biogeography, the pattern of distribution in which organisms are separated into distinct island-like populations by changes in the terrain and/or soil type has long been a subject of intense interest for biologists and is of great importance for understanding evolution and biodiversity. Gypsum is a mineral that frequently occurs in these "island" like deposits where it is home to a unique flora.

This study focuses on one evolutionary lineage of flowering plants as a lens through which to understand broader patterns relating to how speciation is affected by the unique ecology and specialized adaptations of gypsum species. The particular group of flowering plants, named Flaveriinae, are herbs and shrubs primarily found in the Chihuahuan Desert. To date there has not been a comprehensive molecular study of the relationships among the genera and species of Flaveriinae. By sequencing several hundred genes across many populations we hope to gain insight on the evolutionary relationships of Flaveriinae and revise our understanding of the species boundaries within Flaveriinae. Findings may shed light on fundamental questions relating to the origins of plant diversity and the processes that govern it.

Topic: Biodiversity Informatics & Herbarium Digitization

A-369

Using digitized herbarium specimens to examine leaf morphology in Quercus macrocarpa over the past century: a course-based undergraduate research experience

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As herbaria across the world work tirelessly to digitize their specimens, it creates new opportunities for research, including cost-effective and flexible course-based undergraduate research experiences (CUREs). In Fall 2024, my Plant Systematics class designed and implemented a study examining variation in leaf morphology of *Quercus macrocarpa* Michx., to see if leaf size, relative width, lobe depth, and petiole length varied with yearly average temperature, annual precipitation, and year of collection. Using the website iDigBio.org (Integrated Digitized Biocollections), the NOAA database of climate records for each US county, and the free image analysis software ImageJ, we collected data on 390 digitized herbarium specimens from 1888 through 2021. We found that either average temperature or annual precipitation, or a combination of both, significantly predicted all of the leaf morphological traits that we measured. However, the year the sample was collected did not significantly predict any morphological traits in our multiple linear regressions. *Quercus macrocarpa* has a large range, spanning across most of the eastern half of the United States, from Minnesota down to Texas. It appears that *Q. macrocarpa* has not experienced any large shifts in morphology across its range throughout the past century, but that its leaf morphology does respond to climatic variations. Our study also demonstrates the usefulness of digitized herbarium specimens in course-based undergraduate research experiences.

Topic: Population Genetics/Genomics

A-370

Restoring the American Elm (Ulmus americana): Insight into the Historic and Current Genetic Structure to Inform Future Reintroductions.

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This study investigates the current and historic genetic structure of *Ulmus americana* (American elm), a North American tree severely impacted by the introduction of Dutch elm disease (DED). The causal agents, *Ophiostoma ulmi* and *Ophiostoma novo-ulmi*, are fungal pathogens introduced to North America in the late 1920s. Historically, *U. americana* was a prevalent urban and riparian species. Its widespread decline led to a decrease in canopy coverage in cities and interruptions to ecosystem processes in riparian areas. There is an increasing interest in trying to restore these iconic trees to ecosystems and urban areas; however, there is limited information to guide the selection of appropriate source material. Given the significant losses of this species, we sampled approximately 900 remnant tree and herbarium specimens to look at the historic genetic structure of this species. We hope to identify regions with high genetic diversity, correlate genetic differentiation with landscape features, and detect genetic bottlenecks caused by DED. Due to the historic riparian habitat of *U. americana*, we hypothesize that genetic differentiation will be closely linked to HU-2 watersheds and that DED negatively affected genetic diversity. To test these hypotheses, we developed a custom amplicon panel targeting nuclear and chloroplast gene regions in addition to barcode regions of common diseases. To elucidate any genetic patterns, we will use programs like STRUCTURE, TESS, and BOTTLENECK. The findings will provide crucial insights for the U.S. Forest Service to develop regionally appropriate reintroduction strategies, enhancing the restoration of riparian ecosystems. This research not only supports the recovery of *U. americana* but also offers a restoration framework for restoring other tree species devastated by diseases.

Topic: Development and Structure

A-371

A stomate by any other name? The open question of hornwort gametophytic pores, their homology, and implications for the evolution of stomates

Author: William Friedman, James Fortin
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Advances in bryophyte genomics and the phylogenetic recovery of hornworts, mosses, and liverworts as a clade have spurred considerable recent interest in character evolution among early embryophytes. Discussion of stomatal evolution, however, has been incomplete; the result of the neglect of certain potential stomate homologues, namely the two-celled epidermal gametophytic pores of hornworts (typically referred to as 'mucilage clefts'). Confusion over the potential homology of these structures is the consequence of a relatively recent consensus that hornwort gametophytic pores ('HGPs' – our term) are not homologous to stomates. We explore the occurrence and diverse functions of stomates throughout the evolutionary history and diversity of extinct and extant embryophytes. We then address arguments for and against homology between known sporophyte- and gametophyte-borne stomates and HGPs and conclude that there is little to no evidence that contradicts the hypothesis of homology. We propose that an intergenerational transference of a basic stomatal developmental program might well account for the novel expression of stomates in gametophytes of hornworts, if stomates first evolved in the sporophyte generation of embryophytes. Finally, we will explore phylogenetically based hypotheses for the evolution of stomates in both the gametophyte and sporophyte generations of early lineages of embryophytes.

Topic: Phylogenomics

A-372

The "Trees" of Texas Flora: Investigating Phylogenetic Diversity and Where to Branch Out Next (It's All Coming Together)

Author: Bowen Forman, Madison Bullock, Matt Johnson
Affiliation: Texas Tech University

Phylogenetic trees can show evolutionary history and relationships between groups of living things, but they may have gaps that could lead to inaccurate species relationships. Texas flora are one such case, with an estimated 5000-6000 native plant species, or around 25% of all native North American flora, and approximately 400 endemic species. We aim to sequence all recorded flowering plant taxa in Texas and create a phylogenetic tree of their relationships. Using the resources of the Kew Tree of Life Explorer and specimens housed at the E.L. Reed Herbarium at Texas Tech University, we will target sequence via the Angiosperms353 probe set and analyze relationships among Texas flowering plants. We have two goals in this study: 1) to identify any gaps in our data that may indicate under sampled groups, and 2) to compare phylogenetic diversity of Texas ecoregions, which have large variations in climates. This information could inform conservation management decisions by focusing on protecting areas with the highest phylogenetic diversity instead of number of species.

Topic: Phylogenomics

A-373

Evolution and conservation implications of Japanese Calanthe (Orchidaceae) species based on mRNA-captured genomic information

Author: Mayu Katafuchi, Yumeko Tarusawa, Ryosuke Ito, Junichi Nagasawa, Tomohisa Hashimoto, Edgardo Ortiz, Yuji Isagi
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All 19 taxa in the Japanese orchid genus *Calanthe* are listed as endangered in Japan. However, species-level phylogenetic relationships, which are critical for effective conservation, remain unclear. While chloroplast genome sequencing, RAD-seq, and RNA-seq are commonly used for phylogenetic analysis, their application to *Calanthe* has been hindered by several challenges: chloroplast capture by hybridization causing phylogenetic uncertainty, large nuclear genome sizes (ca. 10 Gb), and limited availability of RNA sampling from rare species in the wild. To overcome these issues, we applied a modified exome capture method (Puritz & Lotterhos, 2018) targeting mRNA sequences for 41 samples representing 18 taxa of Japanese *Calanthe*. This approach yielded ca. 5 million base pairs from 6,584 loci for phylogenetic reconstruction. The resulting nuclear phylogeny was broadly consistent with previous studies based on ~4,000 bp from nuclear and chloroplast regions but suggested reevaluation in three clades: 1) The Ogasawara endemic *C. hoshii*, previously treated as a subspecies of *C. triplicata*, was found to be more closely related to *C. hattorii*. 2) The Izu Islands endemic *C. izuinsularis*, traditionally allied with *C. aristulifera*, was closely related to both *C. aristulifera* and *C. mannii*. 3) The phylogenetic uniqueness of *C. discolor* and its subspecies (*C. discolor* var. *amamiana,* var. *tokunoshimensis, and* var. *kanashiroii*) were clarified, revealing their close relationship, except for var. *amamiana*. By successfully applying a nuclear-targeted approach to this genus of orchids with large genomes, we have constructed a robust phylogeny and established a genetic foundation for future conservation strategies. Ongoing analyses include elucidating the patterns of reticulated evolutionary processes such as introgression and calculating *Ks* (*dN/dS*) values to assess genetic vulnerability across species, which will inform new conservation strategies for these endangered species.

Topic: Biodiversity Informatics & Herbarium Digitization

A-374

Collection Biases Across the Northern Appalachian Region: How Can We Complete the Record?

Author: Olivia Leek, Mason Heberling, Theresa Culley, Eric Tepe
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The Appalachian Mountains are a diverse area ecologically and culturally, yet much about the region is often overlooked. Rich in natural resources, Appalachia has been historically disturbed from the mining of oil, gas, coal, and lumber—exploitation which continues to the present day. The Appalachian Regional Commission (ARC) has divided this broad cultural and geographical zone into several smaller, more manageable sections which can be useful for focused studies based on the cultural, economic, and ecological differences. Although more of the Appalachians are currently protected than ever before, the northern range has notably fewer federally protected lands compared to the southern portion. Here we investigate the herbarium collections, ca. 1 million records, from the Northern Appalachian region (as defined by the ARC). This study examines the completeness of our knowledge of the flora by how thoroughly the area has been collected and whether there are any biases in the herbarium record. Data for these analyses are drawn from regional institutions and compiled with other herbaria from around the world on aggregate websites such GBIF and SEINet. Of the 26 active herbaria in the region, only half have data published on these platforms. Questions driving the analysis include the following: do parts of the region appear underrepresented in the herbarium record? Or, are there any major gaps that should be a target for future collecting? Is there a collection bias in local areas which are nearby herbaria, or possibly in locations deemed more botanically interesting, such as state parks? Here, we review the number of collections and species per county within the northern region of Appalachia as a preliminary assessment of the completeness of our knowledge of the northern Appalachian flora. In general, numbers of collections are markedly biased toward counties with national forests vs. counties without protected lands. This information can be used by collectors for future surveys to better represent the flora of Northern Appalachia.

Topic: Biodiversity Informatics & Herbarium Digitization

A-376

BIOFAIR Data Network: Building an Integrated, Open, Findable, Accessible, Interoperable, and Reusable Data Network

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Biodiversity data integration is the process of combining diverse datasets from multiple sources to provide a unified framework for both users and computer applications, thus allowing for the combination, manipulation, and subsequent analysis of data. Over the last two decades, there has been a wealth of data on the occurrence of organisms, their phenotypes and genotypes, and the environments in which they live that have been mobilized into a digital form. The volume, quality, depth, and breadth of this data provide a powerful information resource that if curated and integrated with intention can be used to address complex global biological, environmental, and public health challenges.

The Biodiversity Collections Network (BCoN), with funding from the National Science Foundation, has spent the last year facilitating conversations around Building an Integrated, Open, Finable, Accessible, Interoperable, and Reusable (BIOFAIR) data network (bcon.aibs.org/biofair). With the conclusion of six domain-specific listening sessions (Federal Agencies, Genetic and Genomic Data, One Health, Ecological Data,

Climate and Environmental Data, and Biodiversity Informatics) and an interdisciplinary workshop, this talk outlines community priorities, needs, and aspirations for developing a BIOFAIR data network.

Building a BIOFAIR Data Network will require a two-pronged approach: advancing technological capacity while addressing the social and cultural requirements of data integration. This includes sustained digitization of our natural history collections; investment in human capital for the development of collection, storage, maintenance, and analytical capabilities for diverse types of data, including acoustic and observational data; and the development of training and curricula to enable FAIR data practices. Such an effort requires a culture of collaboration, incentives for participation in the creation of FAIR data, and coalescence across data domains to develop standards for the creation of integration tools that provide appropriate citation, attribution, and annotation mechanisms.

Topic: Ecology

A-377

Progress and persisting gaps in dryland field ecology, a systematic review

Author: Grace Magavern, Rose Marks
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Ecological research has focused primarily on temperate and tropical systems, but arid systems remain understudied, despite comprising over ⅓ global landmass. Increasing severity, frequency, and spread of droughts has sparked growing interest in dryland ecology, but it is unclear how this recent attention has changed the field. Here we review ~4,900 papers on dryland field ecology published over the past nine decades, and identify broad changes in key terminology, researcher demography, and focal taxa. We also outline how the physical demands and risks of ecological field research disproportionately affect researchers and are further compounded by the extreme conditions of drylands.

Our analyses show a dramatic shift in terminology, suggesting important changes in how researchers describe arid systems. Many diverse taxa have been studied in drylands, with the plant kingdom being well-represented and the proportion of plant to animal studies varying widely by nation. Author demographics also show considerable variation. For example, the gender ratios of publishing authors, while more equal in some locations, remain significantly imbalanced. Finally, affluent nations dominate the publication landscape in dryland field ecology, despite having a low proportion of arid land area. Field sites and study locations also skew towards wealthy nations with large hyper-arid regions like sub-Saharan Africa virtually absent in the literature. These analyses reveal promising recognition of drylands as critical study systems; however, persistent gender imbalance and underrepresentation of some important arid regions calls for more equitable representation of study regions and researchers.

Topic: Functional Genetics/Genomics

A-379

A Dobzhansky-Muller incompatibility may contribute to reproductive isolation between Penstemon kunthii and P. amphorellae

Author: Gracie Friedrichs, Lena Hileman
Affiliation: University of Kansas

Reproductive isolation between diverging populations restricts gene flow either before or after fertilization. These are known as pre- and postzygotic reproductive barriers, which contribute to speciation. Following reproductive isolation, independent lineages can acquire mutational differences that, when combined back into a single genome, reduce the fitness of hybrids. This phenomenon is called hybrid breakdown, first modeled by Bateson, Dobzhansky, and Muller (e.g., Dobzhansky-Muller incompatibilities). *Penstemon kunthii* and *P. amphorellae* are closely related species that have some level of pre-zygotic reproductive isolation due to differences in pollination syndrome and geographic distribution. I propose that in addition to pre-zygotic isolation, these two species exhibit a postzygotic genetic mechanism contributing to isolation. Among individuals in an F2 population derived from a cross between *P. kunthii x P. amphorellae,* I find the occurrence of pollen inviability consistent with a two-locus Dobzhansky-Muller incompatibility model.

Topic: Systematics & Taxonomy

A-380

Systematics of Polygonaceae: a plastome data analysis including all genera in Polygonoideae

Author: Tanja Schuster, Philipp Resl
Affiliation: Natural History Museum Vienna, University of Graz

The knotweed family Polygonaceae Juss. (ca 1,200 species) is mostly known for some highly invasive weeds and a few species have commercial value as ornamentals, food crops, or timber. It is a wide-spread group occupying a diversity of habitat types, includes a variety of growth forms (trees, lianas, mat-forming shrubs, and forbs), and is morphologically diverse.

In this study, we analysed plastome data of representatives of all genera of Polygonoideae Eaton including the last previously unsampled genus *Eskemukerjea* Malick & Sangupta. Using a genome skimming approach, we generated substantially more data than available before to better resolve phylogenetic relationships that previously received moderate to little support and to include those genera not yet analysed with high throughput sequencing data. In an effort to include more accessions for particular target groups (e.g., *Reynoutria* Houtt.), our Maximum Likelihood analysis (IQ-Tree 2.3.6) also utilized plastomes generated for previous studies available via GenBank in addition to the newly sequenced data.

As in most analyses involving such relatively large amounts of data, the relationships among clades were for the most part well-supported with 100% bootstrap support. Outside of Polygonoideae, chloroplast data continue to support *Afrobrunnichia* Hutch. & Dalziel as sister to all other Eriogonoideae Arn. sampled. Regarding Polygonoideae, our results again indicate that *Oxygonum* Burch. ex Campd., endemic to Africa and Madagascar, likely is sister to all other members of this clade. Based on these chloroplast data, *Eskemukerjea* may be included in Persicarieae Dum., which is contrary to previous results that tentatively placed it with Rumiceae Dum., or as belonging to *Fagopyrum* Mill. based on morphology. With this larger dataset, *Harpagocarpus* Hutch. & Dandy is again indicated as belonging to *Fagopyrum*. Most other relationships and circumscriptions of genera in this plastome data analysis are similar to previous results. These include: *Antenoron* Raf. is nested in *Persicaria* Mill., *Aconogonon* (Meisn.) Rchb. and *Rubrivena* M.Kr á l are included in *Koenigia* L., *Fallopia denticulata* (C.C. Huang) Holub belongs to *Pteroxygonum* Dammer & Diels, *Emex* Neck. ex Campd. is included in *Rumex* L., *Polygonella* Michx. is sunken into *Polygonum* s.s., *Fallopia multiflora* (Thunb.) Haraldson is included in *Reynoutria*, and *Homalocladium* (F.Muell.) L.H.Bailey is nested in *Muehlenbeckia* Meisn.

Different information in the form of nuclear data, additional accessions, and a thorough investigation of salient morphological characters of *Eskemukerjea* should be explored before sinking it into *Persicaria*. In general, as a next step, the comparison of a substantial set of nuclear data would be useful to complement the phylogenetic signal from this chloroplast data, as analyses including a small number of markers (mainly nrITS) have previously indicated conflict in some areas of the tree.

Topic: Macroevolution

A-381

Linking Functional Traits and Niches to Lineage Diversification in Asclepias

Author: David Kunkel, Mark Fishbein
Affiliation: Oklahoma State University

The interaction among functional traits, the abiotic environment, and lineage diversification are poorly understood and rarely tested explicitly. Previous efforts to link functional traits to the abiotic environment, specifically in relation to leaf traits, have resulted in the development of the Leaf Economics Spectrum, which identifies correlations among leaf traits and their association with particular environments and places them on a spectrum from conservative to acquisitive strategies. Of interest here is the role that these leaf traits play in facilitating ecological divergence within and among plant groups.

The milkweed genus *Asclepias* represents an excellent study system to identify associations between leaf functional traits, ecological niches, and lineage diversification, as it represents a group that underwent rapid radiation beginning in the Miocene and extant taxa exhibit a great degree of variation in their ecological niches. In addition, work previously focusing on leaf surface traits and chemical defenses has suggested a link between these traits and diversification. Here, I investigate the relationship between ecological niches and lineage diversification in *Asclepias* utilizing leaf functional traits (e.g., leaf length:width ratio, trichome density, and leaf mass per unit area (LMA)) as a

possible mechanism coupling the two. I hypothesized that 1) species utilizing a conservative strategy are associated with lower trichome density, larger and denser leaves and occur in more mesic environments with clay or silt soils, as opposed to those using an acquisitive strategy which are associated with greater trichome density, smaller and lighter leaves and occur in more xeric environments with sandy soils. I also hypothesize that 2) functional traits associated with acquisitive strategies are also associated with increases in diversification rate. I measured leaf functional traits on 118 American species of *Asclepias* using herbarium specimens.

To characterize the climatic and edaphic niches of American *Asclepias*, I utilized a combination of publicly available occurrence and environmental data. Correlations among traits and niche variables were determined using a phylogenetic generalized least squares regression. To analyze relationships between niche and/or trait evolution and diversification rate, I utilized Quantitative-State Speciation and Extinction (QuaSSE) with a plastome phylogeny with nearly complete taxon sampling. In addition, I utilized the Missing State Speciation and Extinction (MiSSE) modeling framework to act as a null model and compared this model to the results of QuaSSE to verify whether functional trait evolution and ecological niche correlate with diversification rate.

Preliminary results suggest support for the hypothesis connecting traits with particular environment as species within the Sonoran Desert Clade tended to have higher leaf length:width ratios (longer, narrow leaves) and being more associated with drier climates than species found within the Temperate North American clade which is generally more associated with mesic environments and had lower leaf length:width ratios (more balanced leaf shapes).

Topic: Crops and Wild Relatives

A-382

Uncovering Climate-Resilient Traits Through Ecological Niche Modeling of Cocoyam and Taro Wild Relatives Across Africa

Author: Sebastian Fernandez, Makenzie Mabry, Pamela Soltis, Douglas Soltis
Affiliation: University of Florida

Taro (*Colocasia esculenta*) and cocoyam (*Xanthosoma sagittifolium*) are increasingly popular as edible backyard tubers. They enrich diets globally, especially within rural African communities where nutritional diversity is often limited. Rising air temperatures and drier conditions within the region threaten to disrupt the growth of these staple food crops. Therefore, uncovering novel ways to fortify or supplement the production of these species is imperative to prevent widespread nutritional deficiencies across Africa. We addressed these challenges by examining the crop wild relatives (CWRs) of taro and cocoyam, which hold the potential to be sources of climate-adaptive traits or dietary replacements in areas where C. esculenta and X. sagittifolium may not grow or thrive. Comparable research on the resilience of yam, potato, and cassava CWRs identified numerous species that were likely to withstand and possibly flourish under future climate conditions in west Benin. These findings highlight the importance of further analyzing additional root tubers for climate-ready traits across the continent. Using Ecological Niche Models (ENMs), we identified the factors that influence the habitat suitability of taro and cocoyam CWRs. We sourced and georeferenced herbarium records from natural history collections of four *Colocasia* and 33 *Xanthosoma* CWRs. Leveraging CWR occurrence records and environmental variables (e.g., soil pH, carbon) and 19 layers of the current (1970-2000) bioclimatic variables from the WorldClim v2.0 database, ENMs for each species were generated. High-performing models based on Area Under the Curve (AUC) and Omission Rate tests (OM) were then projected across Africa to analyze shifts in species' current and future habitat suitability. CWRs projected to expand in habitat suitability under future climate conditions indicate species to be further investigated for climate-ready traits that can be harnessed to fortify food security strategies and breeding programs across the continent.

Topic: Tropical Biology

A-383

Evolution of Fruit Color in Palicourea, a Genus of Neotropical Flowering Plants

Author: Aislinn Mumford, Ana Maria Bedoya, Shelby Oliveaux, Charlotte Taylor, Laura Lagomarsino
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Palicourea Aubl., the hyper-diverse genus of Neotropical flowering plants, will serve as a model to better understand how fruit and flower traits have dynamically evolved across space and time. *Palicourea* is a bird-dispersed genus within the coffee family Rubiaceae containing approximately 650 species, many of which were formerly placed in the genus *Psychotria* L. Typically shrubs and small trees, *Palicourea* species are notable for their striking inflorescence morphology, charismatic color diversity, and co-occurrence within ecological communities. The genus *Palicourea* is notable for having brightly colored flowers, variously colored fruits, and a high frequency of co-occurrence between species within ecological communities. With the help of a newly inferred, expanded phylogeny, I will present ancestral state reconstructions of gross inflorescence and fruit color in *Palicourea*, test for phylogenetic signal, and determine if there is geographic clustering. The multifunctional roles of plant pigments will be discussed along with the possible drivers of fruit color, including selection by mutualists, climatic and geographic variation, and phylogenetic constraints.

Using *Palicourea* as a model, this talk will explore broad biogeographical trends and the macroevolution of fruit traits, filling in the gap of field studies characterizing the role reproductive traits play in facilitating niche overlap.

Topic: Systematics & Taxonomy

A-384

The Origins of Living with Fire: Evolution of Adaptation to Savanna Habitats in Neotropical Woody Bamboos

Author: Elizabeth McMurchie, Lynn Clark
Affiliation: Iowa State University

Bamboos are unusual among the grasses in that the majority of bamboo species are primarily found in forest habitats. Most species of the ecologically and economically important Neotropical woody bamboo (NWB) genus *Guadua* follow this trend, being limited to forests or gallery forest habitats along rivers. However, several species of the *G. paniculata* species complex, which includes *G. paniculata*, *G. refracta, G. venezuelae*, and possibly the enigmatic *G. maculosa*, are found primarily in open savanna habitats where they typically experience frequent fires. These species share several macromorphological similarities, including relatively small size, narrow foliage leaves, subequal culm leaf sheaths and blades, and short flowering structures. Micromorphologically, these species also have several features unusual in other *Guadua* species, including abundant papillae on the abaxial and often adaxial leaf surfaces and broad, saddle-shaped silica bodies. Adaptation for savanna habitats in the NWB is not unique to the *G. paniculata* species complex, however, with several species of Arthrostylidiinae having independently adapted to open, fire-prone conditions. We investigated whether the habitat preference and macro- and micromorphological features of the *G. paniculata* species complex evolved multiple times or a single time within the genus *Guadua*. We also examined the evolutionary relationships between the Arthrostylidiinae species primarily found in savannas and campo rupestre habitats and the remainder of Arthrostylidiinae that are more typical of forests. Using a targeted capture approach with the Angiosperms353 bait set, we used both nuclear and chloroplast genes to infer the phylogenetic relationships of *Guadua* and the Guaduinae as a whole, as well as a smaller set of Arthrostylidiinae, using the Chusqueinae as an outgroup. We used HybPiper to assemble gene trees that were reconstructed using maximum likelihood, IQ-Tree2 to estimate individual gene trees, and Astral to estimate the nuclear and chloroplast species trees. Our preliminary data indicate that adaptation to savanna habitats occurred only once in *Guadua*, with independent adaptation to savanna and campo rupestre habitats occurring in the Arthrostylidiinae.

Topic: Evolutionary history of the Gnetales

A-385

Cone morphology, development, and sporadic structural gynodioecy in Gnetales with an emphasis on Ephedra species from Israel

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For over a century, gymnosperms of the order Gnetales (*Ephedra*, *Gnetum*, and *Welwitschia*) have been the focus of attention because of their similarities with angiosperms in structure, development, and reproductive biology. These have been variously interpreted as potentially synapomorphic or homoplastic. The molecular phylogenetic framework supports the latter option, but even so, the combination of several and not always functionally linked angiosperm-like traits in one group is impressive. Gnetales is the only extant gymnosperm lineage with a tendency to bisexuality of reproductive structures, whereas these are strictly unisexual (except for teratology) in all other extant and most of the extinct gymnosperm lineages. The bisexual condition found in *Welwitschia* and some species of *Gnetum* and *Ephedra* resembles the bisexuality of most angiosperm flowers. The bisexuality is likely ancestral in angiosperms and thus was one of their key evolutionary innovations. However, well-investigated species of the Gnetales possessing bisexual reproductive structures can be characterized as structurally gynodioecious and functionally dioecious, because pollen-producing plants never develop seeds, whereas seed-producing plants have no traces of even reduced male organs. It is difficult to find exact analogues of this mating system among angiosperms. Is there any developmental constraint against the evolution of monomorphic bisexuality through structural gynodioecy in gymnosperms? We use *Ephedra foeminea* as a model to study structurally bisexual and female cones. Ovule initiation coincides with cone determinacy: the main cone apex produces no more primordia above the ovules. This resembles the developmental link between floral determinacy and gynoecium development. The uppermost male organs are developmentally delayed relative to more distal sterile ovules in male plants of *E. foeminea*. The complete absence of branching in homologous positions of female cones may be seen as a stronger manifestation of the same inhibition pattern. Angiosperm flowers are at least at first glance uniaxial structures whereas bisexual cones of *E. foeminea* are clearly not, but the pseudanthial theory considered them potentially homologous. It is interesting in this context that the exact number of branching orders is difficult to determine (or maybe it is unstable) in *Ephedra*. Mundry & Stüztel (2004) convincingly interpreted lateral male structures (antherophores) of *E. distachya* as pairs of fused strobili (thus, the entire male cone must be 3-axial). Male cone development in *E. ciliata* and *E. aphylla* suggests, in contrast, its 2-axial nature, and *E. foeminea* provides a continuum between the patterns supporting 2- and 3-axial interpretations. We documented occasional completely male (though determinant) strobili in *E. foeminea* and rare instances of the uppermost lateral organs where one half of the antherophore was homeotically replaced by sterile ovule. This suggests independent regulation of cone determinacy and femaleness. The phylogenetic position of *E. foeminea* does not contradict the idea of its intermediate position as a structurally gynodioecious species derived from a hypothetical monomorphic bisexual ancestor to the more pervasive dimorphic sexual system of dioecious species. That the opposite evolutionary trend is possible can be concluded from the discovery of structurally bisexual cones in a new species from the derived North American clade of *Ephedra*.

Topic: Education and Outreach

A-387

Integrating Fieldwork and GIS to Teach Forest Structure and Carbon Estimation in the Northeastern U.S.

Author: Mariana Vazquez-Alonso
Affiliation: Connecticut College

This poster presents an undergraduate-level course designed to teach students the fundamentals of forest structure, biomass, and carbon estimation through a hands-on integration of fieldwork and Geographic Information Systems (GIS) using QGIS. Targeted at students with no prior technical experience, the course builds skills in vegetation classification, remote sensing, and ecological data analysis with a focus on forests in the Northeastern United States.

The course is structured around four thematic modules, and centered on a key forest topic. Students participate in both lecture-based discussions and lab sessions that involve field surveys, tree identification, and measurement techniques, all linked to GIS-based spatial analysis. Emphasis is placed on real-world applications, such as estimating forest carbon stocks through Light Detection and Ranging (LiDAR) case studies. Students read and discuss selected scientific literature, encouraging them to engage critically with current research.

Labs are a core component of the course, allowing students to apply theoretical knowledge to practice. Working in pairs, students collect and analyze data, conduct spatial analysis, and develop a final project proposal that synthesizes their learning. Evaluation includes quizzes, reading-based assignments, lab work, and a final project presentation. Participation and collaborative engagement are also essential components of the course assessment.

This educational approach equips students with both ecological and geospatial competencies while fostering scientific inquiry, collaboration, and field-based problem-solving. By merging botanical fieldwork with spatial technology, this course aims to prepare students for interdisciplinary research and careers in plant science, conservation, and environmental data analysis.

Topic: Molecular Ecology

A-388

Heritable somatic mutation as a mechanism for adaptation in Mimulus guttatus

Author: Ariana Walczyk, Mitch Cruzan
Affiliation: Portland State University

Mutation is the source of genetic variation that allows evolution to occur. Plants are unique in that the somatic mutations occurring during mitosis can be passed to offspring, as germ cells at the tip of the plant's stem produce both vegetative and reproductive tissue. During stem growth, this population of germ cells has the potential to undergo a type of clonal evolution called cell lineage selection. Cell lineage selection filters out expressed deleterious mutations that cause slow cell division, leaving behind neutral and unexpressed deleterious mutations (passengers) and expressed beneficial mutations (drivers). Driver mutations confer beneficial fitness effects promoting increased growth and cell division rates, outcompeting and displacing germ cells without the driver mutation. Previous work from our group has shown that one generation of autogamy (within flower self-fertilization) can result in increased salt tolerance in yellow monkeyflower and increased drought tolerance in bush monkeyflower, potentially due to the subset of selfed progeny that are homozygous for new beneficial somatic mutations. To test the fitness effects of individual somatic mutations, I grew Mimulus guttatus plants under salt stress and identified candidate driver mutations that appeared and underwent cell lineage selection within the stem. I used within-flower autogamous crosses to produce offspring that were homozygous non-mutant (aa), heterozygous (Aa), and homozygous mutant (AA) for each candidate driver. Offspring were grown under the same salt stress conditions as the parent plant and genotyped at candidate driver loci. The fitness of each offspring plant was compared to its genotype at candidate driver loci to determine the fitness effects of individual somatic mutations. I also used the offspring fitness data to determine the dominance (h) and strength of selection (s) of each mutation to determine which candidates are drivers and which are passengers. This research will lead to a greater understanding of the potential for cell lineage selection to contribute to plants' ability to adapt to novel environments through somatic mutation accumulation. By improving existing models of plant evolution, this work has the potential to inform conservation efforts and impact agricultural research in a time of global warming.

Topic: Systematics & Taxonomy

A-389

How to be a big genus? Ficus L. as a emergening model

Author: Nicole Mitidieri-Rivera, Elliot Gardner, Julianne Phipps, Nyree Zerega, Leandro Pederneiras, Alexander Damián-Parizaca, Kenneth Sytsma
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If we replayed the tape of life, would large lineages evolve into the same dazzling diversity observed today? While the macroevolutionary drivers underlying plant diversification have been investigated for some large genera, many clades remain understudied. *Ficus* L., with 876 species, one of the largest and most ecologically important genera in Moraceae, is renowned for its iconic inflorescence, intricate pollination mutualism, and broad ecological adaptability. As the sole member of the monotypic tribe Ficeae,

Ficus occupies a unique evolutionary position within a family that also includes major crop plants such as common fig, breadfruit, breadnut, cempedak, jackfruit, che, and mulberries. We used a well-sampled, dated phylogenomic backbone of Moraceae to investigate diversification patterns and their associated drivers in *Ficus* and allied genera using Maximum-Likelihood and Bayesian process-based methods. We also assembled a morphological matrix of 508 species in Moraceae to investigate patterns of trait evolution based on stochastic mapping.

Our results indicate that diversification within Moraceae is closely associated with shifts in global paleoclimate. Evolutionary transitions in floral traits within Moraceae are linked to changes in pollinator guilds; however, HiSSE (Hidden State Speciation and Extinction) models suggest that these shifts alone may not fully account for the diversification dynamics of the genus. This study advances our understanding of the drivers of diversification in big pantropical genera, emphasizing the need to integrate multiple lines of evidence to holistically reconstruct the evolutionary history of ecologically and morphologically diverse plant taxa.

Topic: Conservation Biology

A-390

Diversity and conservation of loulu, Hawaii's endemic palms

Author: Susan Fawcett, Kenneth Wood, Isaac Lichter-Marck, Warren Wagner
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The single native genus of palm in the Hawaiian Islands (*Pritchardia*) has diversified across the archipelago, resulting in an estimated 23 species, which play an important role in Hawaiian culture and traditions. Threatened by rats, ungulates, other invasive species, and human development, 11 are now federally listed as endangered species. With the recent range expansion in the Hawaiian Islands of the biocontrol-resistant invasive Coconut Rhinoceros Beetle, these iconic palms now face an existential threat. Of fundamental importance to conservation of this unique lineage is an improved understanding of evolutionary relationships between these taxa, and a taxonomic classification system that accurately represents diversity of the group. Using molecular phylogenetic evidence from *Angiosperms 353* target enrichment nuclear data in combination with detailed morphometric analyses of living plants, we revisit conflicting taxonomic hypotheses, and explore undescribed diversity. We highlight current efforts and encouraging advances in *ex situ* conservation strategies, centered on the National Tropical Botanical Garden's living collection of more than 1000 trees, working in partnership with state and federal agencies, botanical gardens, and non-profits.

Topic: Phylogenomics

A-391

New phylogenomic insights on adaptive radiation of the allotetraploid Hawaiian silversword alliance (Madiinae, Compositae)

Author: Bruce Baldwin, Susan Fawcett, Andrew Kostic, Bridget Wessa, William Freyman
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Prior evolutionary studies of the endemic Hawaiian silversword alliance (*Argyroxiphium*, *Dubautia*, *Wilkesia*; Madiinae, Compositae) have been highly informative about insular adaptive radiation of these extraordinary plants. A phylogenomic perspective has been needed, however, to resolve key evolutionary and biogeographic events during the silversword alliance radiation that have remained obscure from lack of comprehensive phylogenetic resolution, extensive cytonuclear discordance, and some incongruence between molecular and cytogenetic (structural genomic) evidence of relationships. DNAs from representatives of all 46 recognized minimum-rank taxa of the silversword alliance (except one we described last year, *D. haupuensis*) from all islands and nearly all volcanos of occurrence were target enriched for 461 nuclear loci using a custom bait kit for Hawaiian Madiinae. Illumina sequencing reads of the 461 target loci were assigned to each of the two subgenomes of these Hawaiian allotetraploids using diploid perennial California tarweeds of the "Madia" lineage as clade references. Pseudo-coalescent (ASTRAL) trees for the two silversword alliance subgenomes were congruent for notable clades that corroborate previous cytogenetic or morphology-based hypotheses of relationship and that were unresolved or equivocal based on earlier molecular phylogenetic analyses. In the subgenome tree with highest resolution and clade support, most relationships are robustly resolved, including those among the deepest clades and among the true silverswords and greenswords (*Argyroxiphium*). These results provide a richer understanding of life-form and finer-scale morphological evolution, inter-island dispersal (including biogeographic ties of younger-island endemic lineages to the oldest high island of Kauai), and necessary taxonomic refinements of conservation significance.

Topic: Ecology

A-392

Methods in Demographic Monitoring and Modeling for New Mexican Rare Plant Species

Author: Daniel Hughes
Affiliation: Institute for Applied Ecology

A major aspect of conserving biodiversity focuses on the preservation of rare plant species. Often, rare plant conservation focuses on monitoring as many individuals or populations of a species as possible, mainly using pure-count censuses and basic indicators of presence/absence. This is a reasonable approach considering the limited resources available to conservationists and ecologists. However, this methodology misses much of the complexity that directly effects the population dynamics of rare plants, including factors likely crucial to species survival.

The BLM Rare Plants project funded by the New Mexico Bureau of Land Management is pursuing a more in-depth, long-term, method of studying threatened and endangered New Mexican plant species, especially those with highly limited ranges. This approach focuses less on constant monitoring of all populations of the species, and more on intense demographic monitoring of individuals at long term sites. By using a standardized protocol (that has for some species been implemented since 2017 - seven field seasons) the BLM Rare Plants project can quickly but efficiently gather large amounts of demographic and life-history data. It has been collecting this data for 11 rare species in New Mexico and adds more each year. For species that have been monitored more than five years. the project is able to combine its wealth of detailed life-history data with knowledge about these plant's life history to assign stage classes to each individual over the years, and create highly specific transition matrices that describe survival, mortality, and life-stage transitions for each species.

With enough years of data collection for each plant, we are able to make preliminary projections for the species by multiplying the current populations by transition matrices, which can lead to interesting and sometimes unexpected results. Importantly, these transition matrices have been determined by true-life data, rather than theoretical predictions. The more years of data collection we do, the more accurate these transition matrices are expected to become. Moreover, by analyzing sensitivity values, we are able to determine which stage classes, and transition between those classes, have the greatest effect on the species population dynamics.

Basics about life-history and demography are severely understudied for many rare plant species. This program's methodology not only answers these questions, it directly applies them to potentially actionable conservation. This poster will examine the benefits and obstacles of the NM BLM Rare Plants project's exciting approach, compare them to more traditional methods of conserving rare plants, and finally examinine the future directions our stage-based demographic monitoring may take in the future.

Topic: Population Genetics/Genomics

A-393

Investigating Genetic Spillage in a Erythranthe cardinalis Common Garden Experiment

Author: Lydia Duran, Niveditha Ramadoss, Seema Sheth, Lluvia Flores-Rentería
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Common gardens are critical to studying the trait variations in plant species and how environmental or genetic factors influence them. During common garden experiments, non-native species and non-local populations must be monitored closely to reduce their chances of escaping from the experimental site, as it can lead to genetic spillage, which is the introduction of foreign genetic material with potential unwanted phenotypes/genotypes into the native ecosystems. This could decrease the fitness of native populations and threaten natural habitats. This study will investigate a possible spillage of genetic material from an existing common garden experiment of the Scarlet Monkeyflower (*Erythranthe cardinalis*). This garden consists of six populations that originated in three regions across its distribution along a latitudinal gradient (North, Central, and South), and were propagated at Santa Margarita Ecological Reserve in Southern California to

evaluate how native plants respond to climate change. A population of E. cardinalis was spotted a kilometer away from the common garden, leading to the question of whether it is a wild population or an escapee from the greenhouse experiment. Leaf samples were collected from individuals of each provenance established at the common garden, as well as the "wild" population. DNA was extracted from all samplesand further processed for DArT sequencing to generate genome-wide SNPs. Genetic clustering analyses, such as DAPC, PCoA, and ADMIXTURE, were used to determine the genetic proximity of the putative "wild" population against the six provenances from the common garden. Clustering analyses of all individuals revealed that the "wild" population is genetically related to southern populations, suggesting that it is a local group. A focused analysis of only the southern and wild populations showed that the wild individuals formed a distinct cluster, suggesting they are not escapees but represent a natural populationin that region. Although a spillage was not detected, these findings serve as a reminder for researchers to monitor their garden experiments to control escapees and reduce the possibility of a spillage from occurring.

Topic: Phylogenomics

A-394

Complete plastid genome of Iris orchioides and comparative analysis with 19 Iris plastomes

Author: Tae-Young Choi, Hyeonsoo Jang, Hwang Keum Ja, Soo-Rang Lee
Affiliation: Chosun University

Iris is a cosmopolitan genus comprising approximately 280 species distributed throughout the Northern Hemisphere. Although Iris is the most diverse group in the Iridaceae, the number of taxa is debatable owing to various taxonomic issues. Plastid genomes have been widely used for phylogenetic research in plants; however, only limited number of plastid DNA markers are available for phylogenetic study of the Iris. To understand the genomic features of plastids within the genus, including its structural and genetic variation, we newly sequenced and analyzed the complete plastid genome of I. orchioides and compared it with those of 19 other Iris taxa. Potential plastid markers for phylogenetic research were identified by computing the sequence divergence and phylogenetic informativeness. We then tested the utility of the markers with the phylogenies inferred from the markers and whole plastome data. The average size of the plastid genome was 152,926 bp, and the overall genomic content and organization were nearly identical among the 20 Iris taxa, except for minor variations in the inverted repeats. We identified 10 highly informative regions (matK, ndhF, rpoC2, ycf1, ycf2, rps15-ycf, rpoB-trnC, petA-psbJ, ndhG-ndhI and psbK trnQ) and inferred a phylogeny from each region individually, as well as from their concatenated data. Remarkably, the phylogeny reconstructed from the concatenated data comprising three selected regions (rpoC2, ycf1 and ycf2) exhibited the highest congruence with the phylogeny derived from the entire plastome dataset. The result suggests that this subset of data

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Topic: Phylogenomics

A-395

Species delimitation in the Polygonatum odoratum complex (Asparagaceae) based on phylogenomic and morphometric data

Author: Tae-Young Choi, Hyo-Sik Won, Hwang Keum Ja, Hyeonsoo Jang, Soo-Rang Lee
Affiliation: Chosun University, Daegu University

Defining species and delineating boundaries among closely related species is challenging particularly for species complexes with a recent history of diversification. The Polygonatum odoratum complex, consisting of seven taxa, presents a compelling example showing unresolved taxonomic boundaries. Here, we aim to delimit taxonomic boundaries in the complex using genomic and morphometric data. Target enrichment was employed to analyze 40 accessions representing the seven taxa in the complex. We inferred the species tree using coalescent and maximum likelihood approaches with nuclear and plastid data. Additionally, we examined 14 morphological characters from 851 herbarium specimens and conducted morphometric analysis using factor analysis of mixed data. The phylogenomic analysis, based on 297 genes, strongly supports the presence of three monophyletic clades with a recent diversification history (<4 million years). Coupled with our morphological examinations, our findings demonstrate the existence of three distinct species, revising the previous classification of seven taxa. By applying an integrated species concept, our study resolves the species boundaries and updates the taxonomy of the P. odoratum complex.

Topic: Population Genetics/Genomics

A-396

Molecular dynamics of saltcedar invasion: deciphering origins and patterns of hybrid swarm

Author: Soo-Rang Lee, Tae-Young Choi
Affiliation: Chosun University

Biological invasions provide an ideal context for hybridization, as previously isolated species or lineages come into sympatry. Hybridization can drive invasiveness by generating novel phenotypes with fitness advantages and mitigating losses of genetic and phenotypic diversity. In this study, we investigated saltcedar, a highly invasive plant in the United States, by genotyping 319 individuals including the parental species Tamarix chinensis and T. ramosissima. Using high-density genome-wide data, ecological niche modeling, and demographic analyses, we traced the origins of invasive saltcedar and characterized hybrid swarms across four major river basins in the western US. Our results revealed a widespread hybrid swarm dominating invasive saltcedar populations. Phylogenetic network and niche modeling analyses confirmed that the morphologically similar parental lineages are distinct species and the progenitors of the hybrid swarm. These findings indicate that hybridization has played a critical role in the invasion success of saltcedar, enabling it to colonize and persist in diverse and challenging environments. The invasion of saltcedar in the US highlights the complex ecological and evolutionary dynamics of hybridization in anthropogenically influenced systems, offering valuable insights into the impacts of hybrids with multiple origins.

Topic: Conservation Biology

A-397

A Conservation Plan for Eriogonum kennedyi var. pinicola (Kern buckwheat; Polygonaceae)

Author: Nina House, Ava Joseph, J. Travis Columbus
Affiliation: University & Jepson Herbaria, California Botanic Garden

Eriogonum kennedyi Porter ex S. Watson var. *pinicola* Reveal (Kern buckwheat) is a perennial, matted herb in the Polygonaceae family (buckwheat family). It is endemic to California, with only four known occurrences in the Tehachapi mountains. All occurrences are threatened by wind farm development, in addition to off-road vehicle activity, invasive plants, road and trail construction and maintenance, and recreational use. It is currently ranked as a 1B.1 by the California Native Plant Society. Despite several threats, its narrow distribution and its rarity, *Eriogonum kennedyi* var. *pinicola* is not currently listed under the federal Endangered Species Act or the California Endangered Species Act. Several gaps in our understanding of this plant exist, especially related to life history, longevity, response to disturbance, pollination bilogy, and seed dispersal mechanisms. A conservation plan was undertaken to fill in these knowledge gaps and inform future conservation efforts. With field work now finished, this presentation will cover what was known, what was learned, and conservation recommendations.

Topic: Symbioses: Plant, Animal, and Microbe Interactions

A-398

Pollinator-Driven Diversification: Understanding Inflorescence Architecture Evolution

Author: Chiara Smythies, Mandilee Hill, Jesus Martinez-Gomez, Jose Miguel Rojas Villa, Alejandro Rico-Guevara, Carrie Tribble
Affiliation: University of Washington, University of California Santa Barbra, Universidad de Antioquia

Inflorescence architecture—the structural arrangement of flowers—plays a critical role in mediating plant-pollinator interactions, influencing both reproductive success and macroevolutionary patterns. However, research has largely focused on inflorescence development, while how architectural traits influence pollinator interactions and evolutionary implications remain underexplored. This study investigates how variation in inflorescence functional traits influences the behavior of specialized pollinators and plant diversification in Bomarea (Alstroemeriaceae), a morphologically diverse genus of tropical Andean plants. We hypothesize that interactions with specialized pollinators, particularly hummingbirds, drive trait evolution and diversification in Bomarea. Using morphological and environmental data from digitized herbarium records, we applied phylogenetic comparative methods, Markov models, and the HiSSE model to assess trait-diversification associations. To link trait evolution with ecological function, we also quantified pollinator behavior–visitation rates, pollinator composition, floral approach,

and handling time–across four representative Bomarea species using video analysis. Our findings contribute to a deeper understanding how inflorescence traits mediate plant-pollinator interactions and shape diversification in one of the world's largest biodiversity hotspots.

Topic: Hybrids and Hybridization

A-399

Natural recently formed polyploids provide novel research opportunities

Author: Douglas Soltis, Patrick Edger, Shunsuke Yoshioka, Mario Vallejo-Marin, Pamela Soltis, Rie Shimizu-Inatsugi, Kentaro K. Shimizu5 Shimizu, Armel Salmon, Simon Hiscock, Malika Ainouche
Affiliation: University of Florida, Michigan State University, University of Zurich, Uppsala University, Rennes University, University of Oxford

Recently formed allopolyploid species offer unprecedented insights into the early stages of polyploid evolution. We examine seven well-studied neopolyploids (formed in the last 300 years), representing different angiosperm families, and explore commonalities and differences in their evolutionary trajectories. Although each neopolyploid is a unique case study, we observed shared patterns, such as rapid genomic and phenotypic changes, coupled with unique responses to genome doubling. While investigation of these neopolyploids has greatly improved our understanding of polyploidy, major knowledge gaps remain. Our review highlights the need for further research into the diverse impacts of whole-genome duplication on gene expression, epigenetic modifications, and ecological interactions. It is noteworthy that all of these recently formed polyploids arose due to human activity in natural environments, underscoring the profound consequences of polyploidization in a rapidly changing world. Understanding the immediate effects of polyploidy is crucial not only for evolutionary biology but also for applied research; polyploidy can lead to novel traits, as well as improved stress tolerance and increased crop yields. Future research directions include investigating the genetic and epigenetic mechanisms underlying polyploid evolution, as well as exploring the potential of newly formed polyploids for crop improvement and environmental adaptation.

Topic: Ecology

A-400

Climate change impacts community level flowering differently across geographic regions of the west coast of the United States

Author: Anna Mele, Mitch Cruzan
Affiliation: Portland State University

Over the last 50 years studies have been conducted using herbarium data to measure plant flowering phenology in relation to climates. These studies have largely found that flowering time has advanced across a number of species and environments in response to climate change. Previous studies using herbarium records as a proxy for flowering time have been conducted over limited geographic regions and have not estimated flowering time shifts in response to climate change. In this study we use herbarium records to examine changes in flowering time over a broad geographic region, including three states of the west coast of the United States: Washington, Oregon, and California. We established a database of more than 90,000 herbarium collection records representing 72 springtime flowering, native, herbaceous species across a variety of ecoregions. To estimate flowering-time interpolated surfaces, we used Empirical Bayesian Kriging in ArcGIS for pre- and post-1970 collection dates based on Z-scores calculated from collection Day of Year (DOY) for each species, creating a map that represents the nuanced impacts of multiple variables on shifting phenologies. We considered the effects of latitude, longitude, elevation, distance from the coast, and 19 bioclimatic variables to determine which combination of factors had the greatest impact on flowering time, and which ecoregions were being effected the most. Models with geographic or bioclimatic predictor variables explained more than 50% of variation in flowering time across all species. We found significant differences among plant life forms and ecoregions for both DOY and phenological responses to climate change. These results suggest that the impacts of climate change may vary depending on plant growth form and geographic location.

Topic: Conservation Biology

A-403

Garryanalyzer: An Open-Source ImageJ Plugin for Quantitative Morphological Analysis of Quercus Leaves

Author: Tan Bahar, Ziqi Xie, Keith Karoly
Affiliation: Reed College, Portland State University

This poster introduces Garryanalyzer, an open-source ImageJ plugin for morphological analysis of *Quercus* leaves, with a specific focus on differentiating between *Quercus garryana* and *Quercus robur*, two species found in the PNW. This plugin automates the quantification of key morphological traits, namely Petiole to Blade Length Ratio and Ellipsoid Score in the applied case of our two *Quercus* species. Most existing morphometric softwares such as TomatoAnalyzer and MorphoLeaf are not open-source, and therefore cannot be as easily customized or readily applied to species identifications in the field. By combining user input with automated shape-fitting algorithms, Garryanalyzer provides a robust and reproducible method for leaf morphometric analysis for *Quercus*, as well as serving as a modular resource for other applied morphometric tools.

This work directly addresses the need for applied ecological methods for non-model organisms. Accurate species identification is crucial for ecological monitoring, restoration, and conservation efforts. *Q. garryana* is the only native white oak species in the PNW, and is important for the formation of a unique oak savanna ecosystem. *Q. robur* is an imported ornamental species from Europe and has been found to be mistakenly planted as *Q. garryana* in natural areas in habitat restoration projects. Garryanalyzer contributes by advancing morphometric analysis techniques, specifically by developing a user-friendly and accessible tool for rapid and accurate species identification in the field.

Garryanalyzer, built upon the widely used ImageJ platform and released under an open-source license, serves as a flexible template for developing similar tools for other non-model plant species. In contrast to other morphometric softwares, we focused on releasing our work as a modular design with accessible code, so that field and lab researchers can use the plugin as a template to be adapted to analyzing diverse morphological features in various plants.

Topic: Ecology

A-404

Urban expansion boosts nonnative phylogenetic diversity but filters native taxonomic and evolutionary lineages in roadside plant communities

Author: Luis Santiago-Rosario, Dylan Craven, Snell-Rood Emilie, Sarah Hobbie, Marek-Spartz Mary
Affiliation: University of Minnesota, Universidad Mayor

Urbanization drives ecological change, reshaping landscapes, fragmenting habitats, and altering biodiversity patterns worldwide. Roadside plant communities—often overlooked in urban ecology—offer a valuable lens to understand the ecological consequences of urban expansion, as they are directly exposed to both environmental stressors and pathways for species dispersal. Here, we investigated how urbanization influences taxonomic and phylogenetic diversity in native and nonnative roadside plant communities across 175 sites spanning seven cities—four in the United States (including one in Puerto Rico), and three in Chile. We quantified urbanization using two metrics: building area (m^2) and total road length (m), both standardized per square kilometer.

Across all cities, we found that total species richness significantly declined with increasing building area, as did Shannon diversity, while Simpson diversity remained unchanged. When decomposed by geographic origin, taxonomic diversity in nonnative species showed no significant response to urbanization. In contrast, native species exhibited a significant, positive interaction between road length and building area for richness, Shannon diversity, and Simpson diversity, suggesting that road networks in urban contexts may facilitate dispersal or create microhabitats that facilitate the persistence of native species in more urbanized sites.

Phylogenetic diversity (PD) declined significantly with increasing building area for all and native species, but not for nonnative species. Standardized PD (ses.PD) also decreased for native species, indicating increased phylogenetic clustering in urban settings. For all and nonnative species, ses.PD did not vary significantly across urbanization gradients.

In contrast, mean phylogenetic distance (MPD) increased significantly for nonnative species with building area, as did standardized MPD (ses.MPD). We did not observe statistically significant changes in either MPD or ses.MPD for native or all species. When weighting evolutionary lineages by their abundances, neither the weighted MPD nor its standardized version varied significantly in response to urbanization for all, native, or nonnative species.

We found that results for mean nearest taxon distance (MNTD), which emphasizes more recent speciation events, were generally consistent with those of MPD. Our results show that abundance unweighted, weighted, and standardized MNTD increased significantly with building area for nonnative species, indicating greater phylogenetic overdispersion in nonnative assemblages in more urbanized areas. This pattern of overdispersion is mainly driven by the abundance of certain nonnative species and not by species presence. Additionally, we found that all versions of MNTD did not vary significantly in response to urbanization for all or native species.

Together, our findings reveal that native and nonnative roadside plant communities respond differently to urbanization in some North and South American cities. Urbanization reduces native species diversity, leading to phylogenetically clustered communities, while increasing lineage diversity of nonnative species in roadside habitats. The greater-than-expected lineage diversity of nonnative species supports the idea that urban contexts may act as "melting pots" for distantly related nonnative species with a similar capacity to deal with abiotic stressors in cities, such as pollution and roadside management. These contrasting patterns underscore the need for urban biodiversity assessments to consider species' geographical origin and evolutionary history, especially when informing management strategies in increasingly built environments.

Topic: Ecophysiology

A-405

Exploring Foliar Water Uptake in Neotropical Epiphytes

Author: Malinda Barberio, Katherine McCulloh, Duncan Smith
Affiliation: University of Wisconsin, University of Wisconsin - Madison

Vascular epiphytes account for 9% of total plant diversity and are commonly found in tropical rainforest canopies. Rainforests receive between 2,000 and 10,000 mm of rain annually, however, tropical epiphytes' lack of connection to the soil results in a dry microclimate. In response to these microclimates, epiphytes have evolved numerous water acquisition and drought resistance strategies. One key adaptation is foliar water uptake, the capture of water directly through leaf tissue, which is one of the primary mechanisms of epiphytic water uptake and has been documented in over 85% of plant species worldwide. Various functional traits such as an increase in trichome density, stomatal pore length, stomatal density, and a decrease in leaf thickness can improve the efficiency of foliar water uptake. Conversely, an increase in trichome density and leaf thickness and a decrease in stomatal size and density can slow desiccation. However, the relationship between functional traits and their effect on the rate of foliar water uptake and drought tolerance in epiphytes is poorly understood. Furthermore, few studies consider the various approaches different epiphytic groups employ for water uptake and conservation strategies. This study investigates traits associated with water uptake and storage and their effects on drought tolerance and foliar water uptake in nine neotropical epiphytes from Bromeliaceae, Orchidaceae, and Polypodiaceae. We designed a novel mist experiment to replicate in situ leaf-wetting events. In doing so, we evaluated the potential mechanisms of foliar water uptake and considered alternative strategies these species may employ to survive in the canopy microclimate. As global climate patterns change, leaf-wetting events in the tropics will shift. Information on species' capabilities to withstand drought and rapidly uptake water provides key insights into how tropical rainforest composition will change with climate shifts.

Topic: Conservation Biology

A-407

How partnership on multiple levels, from local, state and federal initiatives, have helped to preserve imperiled species in the southeastern U.S.

Author: Jennifer Cruse-Sanders, Jordan Argrett, Will Rogers, Jennifer Ceska, Heather Alley
Affiliation: University of Georgia

Globally, plant species diversity is fundamental for supporting ecosystem function, landscape resilience, and food security. And yet, plant species diversity is threatened with some of the highest rates of extinction in our world. It is imperative that conservation horticulture methods for propagation and restoration of species are not only developed widely, but are also shared to meet the pressing grand challenges we face. As one example, the southeastern U.S. is a global biodiversity hotspot, recognized as such for high rates of endemism and perceived threats to natural ecosystems. The state of Georgia, in the southeastern U.S., with some of the highest numbers of plant species diversity in the U.S., has more than 700 plant species that are imperiled and facing significant conservation challenges. Even more significant are diverse plants considered common species that are not tracked through conservation programs but are nearly disappearing before our eyes. This program will share highlights from our efforts to conserve rare species through horticultural interventions and our efforts to make common plants even more commonly available for essential conservation needs that anticipate a growing need in our communities.

Topic: Biogeography

A-408

Uncovering Frasera's Past: Phylogenomics and historical biogeography of a North American taxon

Author: Yuxin Wei, Ingrid Jordon-Thaden, Bing Li, Kenneth Sytsma
Affiliation: University of Wisconsin-Madison, Murray State University

Understanding how species evolve and adapt to their environment is key to evolutionary biology. Frasera, a North American plant genus in Gentianaceae with 16 species, is a valuable system for exploring how climate and geography shape biodiversity. Despite its ecological and morphological diversity, the evolutionary history of Frasera remains poorly understood. In this study, we performed whole-genome sequencing at approximately 10× coverage for 9 Frasera species and 1 outgroup. We used GetOrganelle to assemble complete chloroplast genomes and constructed a time-calibrated phylogeny using a Bayesian MCMC framework. To investigate the geographic origin and historical biogeography of Frasera, we applied the probabilistic modeling framework BioGeoBEARS. Together, these methods provide new insights into the evolutionary history of Frasera and the ecological and geographic drivers of its diversification.

Topic: Systematics & Taxonomy

A-409

Evolutionary Tends in Neptunia (Fabaceae) and How They Relate to the Broader Legume Clade

Author: Ellie Becklund, John Schenk
Affiliation: University of Connecticut, Ohio University

Ecological release is an evolutionary pattern by which selective niche pressures are reduced and a species' population expands into new niche space. This process is important because it can generate ecological and morphological variation, potentially leading to speciation. The post-speciation effects of ecological release are challenging to identify due to the difficulty in inferring the ancestral niche. In *Neptunia* Lour. (Fabaceae), we can study the macroevolutionary effects of ecological release on niche breadth and morphological evolution due to the presence of species that occupy different ecosystems; the two aquatic species have pantropical distributions, whereas the terrestrial species occupy distributions within continental bounds. Our objectives were to understand the evolutionary patterns and processes that led to the differences in ecological niches and distributions, and how *Neptunia* and other aquatic legumes evolved convergent traits to survive aquatic environments. We reconstructed the evolutionary relationships among *Neptunia* species through phylogenomic methods with Angiosperms353 and determined if ecological release in the two aquatic species led to a shifted or broadened climatic niche compared to their terrestrial sister species from bioclimate data and occurrence records. We hypothesized that aquatic species evolved from a marginal intermediary step from a terrestrial ancestor, and used phylogenetic comparative methods to infer the evolutionary transitions in *Neptunia*, *Sesbania* Adans., and the Dalbergioid clade (*Aeschynomene* L. and *Discolobium* Benth.). The anatomical strategies of aerenchyma were compared from stem and root histology of representative aquatic, marginal, and terrestrial legume species. *Neptunia* was comprised of 20 terrestrial and two aquatic species that were closely related. The aquatic species and terrestrial sister groups overlapped in multidimensional niche space but were significantly different, and the aquatics occupied a broader precipitation and temperature niche than their terrestrial relatives, highlighting the effects of ecological release after speciation. In the three clades with aquatic species, the aquatic state evolved at least six times and through a marginal intermediary step and evolved different strategies in

different tissues to survive in water. The evolution back into aquatic ecosystems had a profound effect on the species' anatomy, and aquatic legumes provided an excellent study system to understand macroevolutionary effects of evolutionary processes.

Topic: Pteridology

A-410

Defining the microclimate that enables fern gametophyte survival in the Santa Monica Mountains

Author: Naomi Kruse, Helen Holmlund, Stephen Davis, Tami Kruse
Affiliation: Pepperdine University

Ferns are plants that boast independent sporophyte (S) and gametophyte (G) generations. When conditions are right, a germinated spore develops into a small gametophyte (typically <1 cm). Understanding the ecological and physiological factors that impact gametophytes under field conditions is important, as sporophyte existence depends upon the successful fertilization that occurs upon them. We hypothesized that the dual lifestyle of ferns would result in different pressures acting upon each generation, leading to microclimates unique to the generation. We defined microclimates as abiotic and biotic factors impacting both generations, measuring slope, aspect, air and leaf surface temperatures, relative humidity (RH), light levels necessary to photosynthesis, and dark-adapted fluorescence (Fv/Fm) as a measure of chloroplast function. RH was used to calculate dew point and vapor pressure deficit (VPD). We discovered 22 gametophytes within small caverns on northern-facing slopes nearing 80º, within a half meter of sporophytes with slopes of 68º. We determined leaf surface temperature to be G<S (8.9ºC vs 13.9ºC) along with differences in surrounding air temperatures, yet similar relative humidity. Gametophyte VPD (0.155 kPa) was close to the condensation level, whereas the sporophyte VPD was 0.719 kPa, similar to angiosperms. There was 47% less light absorbed with G<S. Fv/Fm was significantly different by 6.0% (G 0.75 vs S 0.86). There are uniquely different microclimates, distinct to the fern gametophyte and sporophyte generations. The gametophyte microclimate suits the physiologic need for conserving water, necessary for its reproductive niche.

Topic: Biology of mycoheterotrophic and parasitic plants

A-411

CUCP Platform: Accurate Identification of Cuscuta Species Through Chloroplast Genome Analysis

Author: Yang Jae Kang, Joo-Seok Park, Claude dePamphilis, Juan Cerda, So-Yon Park, Suyeon Ha, Jin Hwa Park, Halim Park
Affiliation: Gyeongsang National University, Penn State University, University of Missouri

Dodder plants (Cuscuta species) threaten global agriculture by parasitizing crops and reducing yields. Accurate identification of these species is challenging due to morphological similarities, reduced character sets for traditional taxonomy, limited reference specimens, and their adaptability to different hosts. Even experts struggle with identification, as hybridization and unclear species boundaries, polyploidy, and host-parasite molecular exchanges can alter their characteristics. As a result, Cuscuta species are frequently left unidentified or misidentified in herbaria and the published literature. While next-generation sequencing enables chloroplast genome analysis from short reads, using these data for species identification remains complex due to the need for preparing reliable reference sequences, making sequence alignments, and constructing genotype matrices. Traditional approaches using genetic markers or phylogenetic analyses require expertise and significant manual effort. To help prepare for rapidly growing genomic datasets throughout the genus, we developed CUCP, a web platform leveraging 36 Cuscuta chloroplast genomes through a genotype matrix that matches unknown samples against reference sequences, creates large matrices of variable characters, and rapidly places them in phylogenetic trees with the reference genomes. By utilizing whole chloroplast genome alignments and variations rather than single primer-based approaches, CUCP provides higher resolution for species discrimination. The platform accepts raw chloroplast genome assemblies without requiring gene annotation, making it more accessible for rapid species identification. This platform delivers accurate results within 60 seconds, significantly faster than conventional methods while maintaining comparable accuracy. CUCP's interface and regular database updates make it suitable for routine screening and large-scale projects. The platform transforms species identification from a laborious, error-prone process to a rapid, reliable solution, with a growing database of reliable reference chloroplast genomes. Future improvements will require a major expansion of the reference database beyond the current 36 species, which represents only a small fraction of Cuscuta diversity. This will help to address agricultural challenges posed by these parasitic plants, and to facilitate a better understanding of the diversity and complex roles of Cuscuta in nature.

Topic: Phylogenomics

A-412

Phylotranscriptomic Investigation of the Apocynaceae Family: Repurposing old data for new evolutionary insights

Author: Shawn Arreguin, Nathanael Walker-Hale, Joseph Walker
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Large transcriptomic datasets have not been used to interrogate evolutionary relationships within the flowering plant family Apocynaceae. However, similar to many flowering plant clades, an abundance of publicly available transcriptomic data exists. These transcriptomes, initially generated for other uses (e.g., differential gene expression or genome annotation), can cost-effectively be repurposed for phylotranscriptomics. We reuse 55 transcriptomes (47 ingroup and 8 outgroup taxa) and complement this with a newly sequenced transcriptome of Asclepias viridiflora. We analyze the group for evidence of whole genome duplication, gene duplication, and gene tree conflict to better understand the processes that underlie these relationships. We hope this study can provide both a framework for the relationships of Apocynaceae and a new, cost-effective approach to obtaining and repurposing data for phylotranscriptomics.

Topic: Graeme P. Berlyn Tribute: Light and Life of Forests from Terrestrial to Subtidal and their Regeneration

A-416

Comparative morphology of leaves of con-generic tree assemblages of moist temperate and tropical realms

Author: Mark Ashton
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Abstract: Seedling leaves are perhaps the ultimate plant ecosystem organ adapted to the various biological and physical processes that define the future composition and structure of a forest. As such investigations of seedling leaves provide a window into the mechanisms by which plants can adapt to different availability of environmental resources (light, water, nutrients) or that can endure a variety of interacting biological stressors (pathogens, herbivory). One such axis of investigation into this window is to gauge how changes in seedling leaf form and morphology compare within and among genera that co-exist within the same forests. I here demonstrate how leaf structure changes within and among multiple close assemblages of species that have evolved within forest climates that have differing degrees of seasonality in tropical and temperate forests of the Asian (*Shorea, Mesua, Syzygium*) and American realms (*Acer, Quercus*). These genera represent the core structure and diversity of tree species that represent their late-successional forest types – namely in this study the Oak-Maple forests of New England, US and the Mixed Dipterocarp Forest of Sri Lanka. I present comparisons in leaf structure (thickness, stomatal size and frequency, leaf shape and size) for species within and among these genera in relation to differing amounts of light and relate this to their site affinities and successional positions with their respective forests.

Topic: Bryology and Lichenology

A-417

Structure-from-Motion Photogrammetry for Modeling Lichen Morphology and Growth in 3D

Author: Aidan Yu, Guillermo Ortiz, Spence Gustav, Frank Bungartz
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Lichens serve as vital bioindicators, reflecting environmental changes in air quality, climate, and ecosystem health. Traditional methods of monitoring lichen growth, however, can be limited in precision and scalability. Although 3d photogrammetry has been previously tested on larger subjects, precise applications on a lichen scale are much fewer. Our research introduces a refined photogrammetric workflow using macro lenses, high-resolution DSLR cameras, and advanced modeling software (Metashape, Meshlab) to create detailed 3D models of lichens. Models range from entire lichen communities to individual thalli. Models were created on saxicolous lichen communities

in the southwestern US. Using comparative software, we analyzed sequential models to detect and map changes in lichen morphology over time—ranging from individual specimens to entire lichen communities. Models were accurate enough to detect marginal thallus extension and broader changes in lichen communities through color thresholds. For the first time, we analyzed and mapped both volume and surface area differences. This method enables the precise visualization of growth, loss, and structural variation, enhancing our ability to understand lichen growth patterns, lichen-substrate interactions, and macro-scale ecological monitoring.

Topic: *Systematics & Taxonomy*

A-419

Hyb-Seq characterizes densely reticulate relationships within a widespread oak complex

Author: Henry Landis, Eric Roalson, Jeremiah Busch
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Hybridization is increasingly recognized as a widespread driver of diversification across plants. The development of network methods enables systematics researchers to identify and model reticulate relationships within phylogenetic histories, including the discernment of hybridization from other sources of phylogenetic discordance such as incomplete lineage sorting (ILS). Network methods represent a critical advancement in understanding how hybridization has contributed to extant species relationships and may shape future evolutionary trajectories. The genus *Quercus* (oaks) is highly mosaic, meaning that its phylogenetic history features substantial discordance among interdependent gene tree histories, requiring an integrative approach such as network methods to resolve with clarity. The *Q. x undulata* complex, first described over six decades ago, comprises seven interconnected species native to the southwestern United States. Molecular investigations of the complex to date have been limited, leaving open questions as to the extent of genetic interconnectivity, including the timing and directionality of historical reticulation, as well as the relative contributions of hybridization and ILS to observed patterns. In this study, we aim to address these open questions by collecting novel samples from across the full geographic and environmental extent of the *Q. x undulata* complex for high-throughput sequencing. We use a Hyb-Seq approach with a custom probe set tailored to *Quercus* sequencing, yielding 400 nuclear single-copy genes. We leverage the Species Networks applying Quartets (SNaQ) function of the PhyloNetworks package as a model-based approach to infer historical reticulation from a set of gene trees and species tree. Additionally, we conduct sequence-based estimations of triplet-based ancestry via HyDe and gene tree discordance via phyparts to identify specific individuals or genetic lineages bearing signals of hybrid ancestry.

Topic: *Dryland Floras*

A-420

Adaptive Strategies and Evolution of Leaf Succulence in Zygophyllaceae: Insights into Dryland Flora Photosynthesis

Author: Bharti Parihar, Douglas Soltis, Pamela Soltis
Affiliation: University of Florida

Zygophyllaceae, a cosmopolitan family with approximately 285 species, exhibit diverse adaptations to arid environments and provide an exemplary model for studying the evolution of leaf succulence and photosynthetic diversity. This diversity is crucial for understanding the ecological and physiological resilience of dryland floras, as these ecosystems face increasing threats from climate change. The family showcases a range of photosynthetic strategies including C_3, weak to modest CAM, and C_4 pathways, decoupling the typical association of leaf succulent plants with CAM. This study investigates these diverse photosynthetic pathways to deepen our understanding of how leaf succulence evolves in response to arid conditions, independent of the specific photosynthetic mechanism employed. Inferences of photosynthetic pathways in Zygophyllaceae have largely relied on the carbon-isotope ratio approach. Although powerful, this method has limitations, particularly in detecting weak or facultative CAM and in distinguishing between C_3-CAM intermediates and full CAM pathways due to overlapping $\delta^{13}C$ values. Environmental factors such as light, humidity, CO_2 concentration, and stomatal behavior can influence $\delta^{13}C$ values, potentially leading to the misclassification of photosynthetic pathways under stress conditions. This study utilized direct physiological measurements, including gas exchange data collected with the LiCor 6400XT, to overcome these limitations and provide a more accurate classification of photosynthetic types within the family. In addition, acid-titration tests performed on three species studied—*Tetraena stapfii*, *Fagonia minutistipula*, and *Tetraena simplex*—indicated no evidence of obligate CAM. However, the results remain consistent with the possibility of facultative or weak CAM, and this result should be investigated further. This finding is particularly significant for dryland conservation, as it may reflect broader adaptive strategies among desert plants. By integrating genomic data with physiological insights, future research aims to elucidate the adaptive strategies of Zygophyllaceae species, enhancing our understanding of the role of photosynthetic diversity in the evolution of arid-zone flora. This comprehensive approach will not only reveal the evolutionary trajectories of leaf succulence but also underscores the importance of these adaptations for the survival and thriving of plants in dryland ecosystems. This study contributes new insights into plant resilience in arid and semi-arid ecosystems that may serve to inform conservation strategies and sustainable agricultural practices, highlighting the critical need to understand and protect dryland biodiversity in the face of environmental challenges.

Topic: *Phytochemical*

A-421

Untargeted metabolomics and molecular networks of anthocyanin and betalain-producing species across Caryophyllales

Author: Alex Crum, Katrina Freund Saxhaug, Aaron Lee, Jin Oong, Adrian Hegeman, Ya Yang
Affiliation: University of Wisconsin-Superior, University of Minnesota, University of Minnesota, Twin Cities

The plant order Caryophyllales is a compelling system to better understand specialized metabolism. The group is notable for the betalain pigments, which are hypothesized to be part of a wider diversification of tyrosine-derived metabolites enabled at least in part by the duplication and neofunctionalization of the gene arogenate dehydrogenase (ADH). This diversification has also been suggested to be at the expense of the diversity of phenylalanine-derived metabolites. Because phenylalanine-derived specialized metabolism plays key roles in plant defense, abiotic stress management, etc, we hypothesized that tyrosine metabolites may functionally replace them in stress responses in species with the neofunctionalized ADH. Previous work has suggested that tyrosine metabolites are responsive to herbivory in these species. We also expected that tyrosine metabolite diversity would be higher in species with the neofunctionalized ADH, and lower in species with just the ancestral copy, with the reverse being true for phenylalanine metabolites. To explore specializedmetabolism diversity in the order, we exposed 13 species across Caryophyllales to simulated herbivory via methyl jasmonate and high light conditions. Species represented both anthocyanin and betalain lineages, as well as a wide range of habitats and growth forms. Untargeted LC-MS, as well as LC-MS/MS followed by feature-based molecular networking was performed to identify putative tyrosine- and phenylalanine-derived metabolites and differential responses to treatments across lineages.

Topic: *Phytochemical*

A-422

In-vitro screening of native plant crude extracts against major plant pathogens affecting Cannabis and specialty food crops of Louisiana.

Author: Jennifer Blanchard
Affiliation: Louisiana State University

Louisiana's hot and humid climate provides the perfect environmental conditions for the growth of fungal and bacterial plant pathogens. These fungal infections are an obstacle to the success of commercial production of *Cannabis sativa* in the state. Two of the most recent and significant fungal diseases are southern blight caused by *Sclerotium rolfsii* and stem canker caused by *Botrytis cinerea*. However, there is a lack of formal and professional knowledge regarding fungi that infect medicinal hemp plants, and practical and effective methods for managing the casual agents of these diseases. The objective of this study was to identify the natural plant products from two native plants of Louisiana, that have been reported in the Native American ethnobotanical literature to have antifungal/antibacterial properties. An in-vitro bioassay experiment was conducted using the agar plug diffusion method testing the antifungal inhibition of crude ethanol extracts from the two species against each of the two pathogens *Sclerotium rolfsii* and *Botrytis cinerea*, on four plates each of Extract 1 *Diospyros virginiana* L. and Extract 2 *Equisetum hymale* L. of 1/4PDA spiked at a dose of 250ppm, 500ppm, 750ppm, and 1000ppm against a control plate of 1/4PDA for six days. Based on this initial crude extract bioassay there is a highly significant difference in the two crude extracts (p=0.000105)

when tested against *Botrytis cinerea*. There is also a significant difference in concentration. The test against *Sclerotium rolfsii* did not find any significant inhibition from either of the plant extracts tested. A second experiment was conducted to test the antifungal bioactivity of the fractionated crude extract. The fractions were obtained using hexane, chloroform, ethyl acetate soluble fractions of Extract 1 *Diospyros virginiana.* From this experiment it was observed that t he F2 fraction (Chloroform) significantly inhibited the growth of mycelium vs a negative control (p=0.0001). From our findings we will continue the research study to test the antifungal potential of the crude ethanol extract as well as the fractionated extracts against known standards and commercial fungicides against *Botrytis cinerea*. The goal of the study is to integrate the antifungal compounds and their application for the development of best practices in *Cannabis* production. This study is currently planned to be expanded to other specialty food crops impacted by *Botrytis cinerea* including strawberry (*Fragaria* × *ananassa*) and grape (*Vitis sp*.).

Topic: *Systematics & Taxonomy*

A-423

Phylogenomics of Aristolochia subg. Siphisia (Aristolochiaceae) reveals widespread incomplete lineage sorting and supports a novel pollinator-filtering hypothesis

Author: Yifan Wang, Joyce Onyenedum, Shuai Liao
Affiliation: New York University, South China Botanical Garden, Chinese Academy of Sciences

Aristolochia subgenus *Siphisia* constitutes a monophyletic lineage of predominantly lianescent species, with occasional shrubs or herbs, and is characterized by remarkable diversity in perianth morphology. Members of Siphisia serve as larval hosts for endangered Lepidoptera and are widely used in traditional medicine. Despite its ecological and ethnobotanical significance, Siphisia systematics remains unresolved due to limited genomic resources and insufficient phylogenetic signal across previously sampled loci. Here, we present a phylogenomically informed framework for Siphisia, integrating 46 newly collected accessions and seven public datasets across 44 taxa. Using genome skimming (~30× coverage) and HybPiper, we recovered Angiosperms353 nuclear loci, including supercontigs, for phylogenetic reconstruction via concatenation and coalescent approaches. The resulting species trees resolve seven strongly supported monophyletic clades, each defined by distinct biogeographic patterns and morphological synapomorphies. Comparative plastome analyses from de novo assemblies explored quadripartite structure, plastid phylogeny, GC content, and gene synteny. Cytonuclear discordance was concentrated in species-rich Asian clades, while hybridization signals were rare and limited to deep backbone nodes in North American lineages. These results indicate that incomplete lineage sorting, rather than introgression, accounts for most gene–species tree conflicts and likely reflects strong reproductive isolation following speciation. We also revise a previously taxonomically ambiguous complex—the now well-supported A. versicolor species group—based on integrated phylogenomic and morphological evidence. Within this group, we describe five previously unrecognized cryptic species and identify a novel pollination syndrome involving floral adaptations for pollinator filtering. This syndrome may contribute to prezygotic isolation and recent diversification, and it challenges the prevailing assumption that Aristolochia pollination is universally governed by a trapping–release mechanism—suggesting this model may not apply to subg. Siphisia.

Topic: *Development and Structure*

A-424

Twist and transcribe: unraveling the molecular basis of circumnutation-driven twining in Phaseolus vulgaris

Author: Yifan Wang, Joyce Onyenedum
Affiliation: New York University

Twining in vines represents a remarkable form of dynamic plant movement, first described in detail by Charles Darwin. Unlike the slow circumnutation observed in most plants, twining vines display rapid, directional movements resembling active foraging behaviors—aggressively searching for structural support. Despite its ecological and evolutionary significance, the molecular basis underlying this rapid yet highly organized movement remains poorly understood. Using the common bean vine (*Phaseolus vulgaris*), a cosmopolitan legume crop, we investigate the molecular mechanisms that modulate twining. This behavior is powered by a specialized motor region in the shoot, which drives circumnutation either through: (1) a developmentally programmed process triggered at specific growth stages; or (2) a responsive, environmentally induced mechanism activated when contact with a support is lost—prompting the motor to relocate precisely to the affected region. We conducted the first comparative transcriptomic analysis targeting these motor zones to characterize gene expression profiles associated with both developmental initiation and environmental reactivation of twining. Key questions addressed include: What are the primary signals that trigger the onset of circumnutation? Is it shoot length, plastochron stage, hormone gradients, or a combination of these factors? What molecular cues inform the plant that support has been lost and a new searching behavior should begin? Finally, how do gene expression profiles compare between developmentally programmed and environmentally triggered motor activation? Our findings will shed light on how plants coordinate complex movement behaviors at the molecular level, bridging plant biomechanics, development, and environmental sensing.

Topic: *Paleobotany*

A-425

Impact of new taxa and morphological interpretations on seed plant phylogeny and the origin of angiosperms

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Over the past two decades, discoveries of new fossil taxa, improved data on poorly known fossils, major reinterpretations of the morphology of several key taxa, and increasingly robust molecular evidence on the topology of extant clades have challenged previous hypotheses on seed plant phylogeny and the origin of angiosperms. To test the impact of these developments, we have amassed a new data set including *Doylea* (Early Cretaceous, Canada and Mongolia, putatively related to the mainly Triassic seed fern order Umkomasiales, = corystosperms), *Petriellaea* (Triassic, Antarctica and South Africa), *Ktalenia* (Early Cretaceous, Argentina, with *Ruflorinia* leaves), the ginkgophyte *Karkenia* (Early Cretaceous, Argentina and Siberia), and *Protoephedrites* (Early Cretaceous, Canada), and substantially redefined many previously used characters. We have rescored characters of glossopterids in light of evidence that the ovule-bearing structures are axillary cladodes with ovules on the surface facing the subtending leaf, treated ovules of Bennettitales as lacking a cupule, and interpreted *Doylea* as having compound strobili with axillary fertile short shoots bearing ovules enveloped by sterile appendages of the short shoot. In some cases, we have experimented with current alternative interpretations on the organization of the ovuliferous structures (e.g., as a simple strobilus or a megasporophyll in *Pentoxylon*, as a simple or compound strobilus in Bennettitales). Our analyses associate glossopterids with coniferophytes rather than angiosperms; *Doylea* with conifers rather than corystosperms; *Protoephedrites* with Gnetales; and *Ktalenia*, *Petriellaea*, and *Caytonia* with angiosperms. The positions of Bennettitales and *Pentoxylon* are particularly unstable, largely due to the uncertain morphological homologies of their reproductive structures; in some analyses *Pentoxylon* is associated with glossopterids and Bennettitales are associated with Gnetales. Many of these results are consistent across different methods (parsimony, maximum likelihood, Bayesian inference), models for character evolution, and use of topological constraints (backbone trees) based on molecular data. As found previously, analyses of morphological data with Bayesian inference associate Gnetales with coniferophytes, as indicated by molecular data, whereas parsimony analysis associates them with angiosperms and related extinct groups. These results may favor origin of the angiosperm leaf by webbing of a pinnately compound or lobed leaf, rather than differentiation of vein orders in a simple taeniopterid- or glossopterid-type leaf; and derivation of the carpel from a megasporophyll with pinnately borne cupules (bitegmic ovule homologs), rather than a leaf plus an axillary cupule-bearing branch. Use of methods to evaluate uncertainty helps focus attention on areas where future investigation has the highest potential for resolving persistent problems.

Topic: Phycology

A-426

Algae diversity in ephemeral pools along the upper section of Leon Creek Greenway, San Antonio, Texas

Author: Jeffrey Hutchinson
Affiliation: University of Texas at San Antonio

Pools within ephemeral streams are isolated throughout the year except during high precipitation events when flow occurs and the pools become connected. Ephemeral streams and isolated pools that contain water for various periods have received minimal attention in Central Texas. Algae are major primary producers in freshwater systems. Algae, including cyanobacteria, were sampled over a 1.5 km stretch in 12 pools within the ephemeral stream in Leon Creek over 12 months at an approximate interval of every 2 weeks for a total of 31 sampling events. Samples were collected in the littoral zone at an average water depth of 20 cm. The pools were isolated and some pools were dry during sampling. At each sampling event, 50 ml water samples were collected at each pool from biofilm, floating filamentous algae, leaf litter, sediment, and the water column with a pipette. Basic water quality variables (temperature, pH, and conductivity) and present/absence of water were recorded at the time of sampling. Algae samples were analyzed within 48 hours of collection under a compound microscope at 10 or 40 x magnification. Algae were classified to the lowest taxa using a gridded slide. Algae species richness, evenness, and diversity were evaluated seasonally and compared to water level fluctuations. The results of the study will be presented at the conference.

Topic: Phycology

A-427

Algae response to rehydration following six months desiccation from filamentous algae mats and sediment in ephemeral pools in Leon Creek Greenway, San Antonio, Texas

Author: Jeffrey Hutchinson
Affiliation: University of Texas at San Antonio

Aquatic and riparian plants are rare or not present in ephemeral streams in Central Texas due to variable precipitation and infrequent flash flooding. Ephemeral streams are common in Central Texas and only flow following precipitation events. Within these ephemeral streams, isolated pools of varying sizes are common and contain water for less than 2 weeks to greater than 12 months before drying out. Following rehydration, algae form the basis of the food web emerging from spores and cysts. During the summer of 2024, greater than 90% of the pools went dry during an extended drought. Filamentous algae and sediment samples were collected in the dry pools during July 2024 and maintained in the lab under ambient conditions for six months. In January 2025, twenty-five replicates of filamentous algae (10 g) and sediment (10 g) samples were rehydrated with tap water. Algae were identified to the lowest taxa level in five random samples at 1, 2, 4, and 8 weeks post-rehydration using a compound microscope. The study has been completed and the results are currently being written up. The final results will be presented at the conference.

Topic: Paleobotany

A-428

Ultrastructure of in situ pollen and phylogenetic position of Saportanthus (Lower Cretaceous, Portugal)

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The genus *Saportanthus*, described from lower Albian sedimentary deposits in the Lusitanian Basin of Portugal, includes three species with bisexual flowers, 6–8 tepals, 5–15 stamens, and a half-inferior syncarpous ovary of 1–3 carpels. The genus was first illustrated by Friis, Crane, and Pedersen as a putative monocot, but their subsequent phylogenetic analyses placed it within the magnoliid order Laurales, a very old lineage of angiosperms, along with *Lovellea* (upper Albian, Australia) and *Jamesrosea* (lower Cenomanian, Myanmar). The unusual pollen, with microstriate sculpture on the proximal face and a wide distal zone of psilate to rugulate exine surrounding one or two weakly sculptured apertures, was originally studied only with SEM. The aim of the present study was (1) to elucidate the exine ultrastructure of *in situ* pollen from flowers of *Saportanthus dolichostemon* and *Saportanthus parvus* with TEM and (2) to evaluate the phylogenetic positions of *Saportanthus*, *Lovellea*, and *Jamesrosea* using a morphological data set that includes both extant angiosperms and the fossils, with the arrangement of extant taxa fixed to backbone constraint trees based primarily on molecular analyses. The exine ultrastructure is best preserved in *S. dolichostemon*. The proximal non-apertural exine has a thick tectum, an infratectum of more or less fused granules, and a thin nexine consisting of an ectexinous foot layer and a discontinuous endexine. Endexine makes up more of the nexine in the distal psilate/rugulate zone and all of it at the aperture. The aperture in *S. parvus* appears to be a simple sulcus, in contrast to the trichotomosulcus of *S. dolichostemon* and two sulculi of *S. brachystemon*. Our analyses show that the most parsimonious position of *Saportanthus* is attached to the stem lineage leading to monocots; synapomorphies of the two taxa are two perianth whorls (or series), all sepaloid tepals, and syncarpous gynoecium. The presence of both foot layer and endexine favors this result over a position in Laurales or Magnoliales, which are united by foliated nexine structure. The link with monocots is found whether floral phyllotaxis is scored as unknown, spiral, or whorled; it is most weakly supported if floral phyllotaxis is spiral and most strongly if it is whorled. By contrast, our analyses confirm that *Lovellea* and *Jamesrosea* are securely nested in Laurales, with *Lovellea* sister to all Laurales except Calycanthaceae and *Jamesrosea* sister to *Gomortega*, implying considerable diversification of the order by the end of the Early Cretaceous. These results imply that *Saportanthus* is one of several major extinct lineages of Early Cretaceous angiosperms. If it is sister to monocots, it implies that ancestral monocot features such as two whorls of sepaloid tepals and syncarpy evolved before boat-shaped pollen and several ovules per carpel.

Topic: Ecology

A-429

Assortative mating and triploid fertility may contribute to weakening frequency dependent selection against allopolyploids

Author: Aidan Harrington
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The chief barrier to polyploid establishment is minority cytotype exclusion, which occurs when mating is frequency-dependent and post-zygotic reproductive isolation is high. However, both requirements are rarely examined in natural populations or with allopolyploids. Allopolyploids may be particularly likely to become established because newly-formed allopolyploids are often phenotypically divergent from diploid progenitors, leading to opportunities for assortative mating. Additionally, triploids formed between allopolyploids and diploids frequently produce euploid gametes, which may contribute to polyploid persistence. In this study, I used a combination of field and crossing experiments to test for evidence of minority cytotype exclusion between the allopolyploid *Clarkia rhomboidea* and its diploid progenitors. In contrast to frequency-dependent mating, polyploids disproportionately received intraspecific pollinator visits and avoided interspecific visits relative to expected frequencies. In terms of postzygotic isolation, crossing success was low, as expected, but triploids were partly fertile. Together, these results suggest that minority cytotype exclusion may be minimal for allopolyploids, particularly if an allopolyploid is phenotypically divergent from progenitors. We do not preclude the possibility that reproductive isolation has evolved after the formation of *C. rhomboidea,* and we are working to determine whether similar results are obtained with synthetic neopolyploid lines of *C. rhomboidea*.

Topic: Ecology

A-430

Determining the presence of a potential novel pathogen in coast live oak (Quercus agrifolia)

Author: Vince Rivas, Lluvia Flores-Rentería, David Lipson
Affiliation: San Diego State University

Coast live oak (*Quercus agrifolia*) serves as a keystone species in California, supporting lifecycles and biotic interactions for thousands of other species and providing crucial environmental services, such as carbon sequestration, erosion control, and the promotion of groundwater infiltration. Recently, nonviable, black acorns have been observed in coast live oak populations in parts of San Diego County; however, these abnormal acorns have not been described in literature, indicating the potential presence of a new disease. The goals of this study are as follows: 1) determine the spatial distribution of symptomatic, black acorns throughout San Diego County, 2) describe and compare the microbial community assemblage between acorns in symptomatic and asymptomatic trees, and

3) determine if pathogens from acorns can be transmitted to seedlings through soil. In order to achieve objective 1, I sampled twelve sites throughout the County to assess coast live oak trees for the presence of symptomatic, black acorns. For objective 2, I have collected infested acorns from various sites and will perform DNA extraction and PCR using specific primers to target conserved regions: internal transcribed spacer (ITS) for fungi and 16S rRNA for bacteria. This region will be sequenced and matched against a library for pathogen identification at the genetic level. For objective 3, I will germinate acorns with inoculum from symptomatic and asymptomatic acorn samples. After conducting morphological assessments on 12 survey sites throughout the County, we found that 75% of the sites contained at least one symptomatic tree. The majority of the sites were inland, particularly in North County, but we will continue to explore the microbial community assemblage between these populations to better understand what is the cause of these symptomatic acorns. As novel disease outbreaks are predicted to increase with climate change, this research hopes to reveal if a new disease has infected the coast live oak.

Topic: Plant phenology in an era of rapid global change: new perspectives and frontiers

A-431

A Two-Decade Flowering Record from a Botanical Garden Reveals Phenological Shifts in Japanese Plants

Author: Ai Nagahama, Hitomi Uemura, Taro Nikaido
Affiliation: National Museum of Nature and Science

Recent phenological studies have shown that the onset of flowering is significantly affected by global warming, leading to shifts in plant phenology. It has been reported that spring-flowering species bloom earlier, whereas autumn-flowering species bloom later as temperatures increase, but it remained unclear whether both trends were prevalent in Japan. In this study, we examined responses to temperature increase and trends in phenological shifts using flowering records of 350 Japanese native species collected at the Tsukuba Botanical Garden over the past 20 years. We observed that 64 species exhibited a significant negative correlation with temperature and advanced flowering trends, whereas 17 species exhibited a significant positive correlation and delayed flowering. The former bloomed mainly in spring (March–June), whereas the latter bloomed mainly in autumn (September–November). The distributions of 57 species that were significantly correlated with temperature increases but did not show clear advancement or delay were biased toward spring, suggesting that spring-flowering phenology should be carefully monitored.

Topic: Population Genetics/Genomics

A-432

The value of a specimen: Herbarium genomics provides emergent insights in invasion history

Author: Fernando Hernández, Courtney Patterson, Cameron Corbett, Lauren Kosslow, Brandon Hendrickson, Craig Barrett, Nic Kooyers
Affiliation: University of Louisiana, Lafayette, West Virginia University

Reconstructing invasion histories is critical to understanding the factors underlying the success or failure of biological invasions. Founder effects, multiple introductions, and admixture between different introduced populations are common during invasions, but are often difficult to discern from contemporary population genetic data. Inclusion of historical samples has the potential to better dissect invasion timelines, but the extent of improvement in estimating the magnitude and timing of key events is unknown. Here, we reconstruct the invasion history of two important invasive species in the eastern United States : white clover (*Trifolium repens*) and Japanese stiltgrass (*Microstegium vimineum*). For each species, we leverage hundreds of low-coverage whole genome sequences of contemporary and herbarium specimens from the native and introduced ranges. The inclusion of herbarium specimens provides more nuanced evidence of origins of introduced populations and the timing of admixture. White clover invasion history is characterized by multiple, independent introductions from France, the UK, and Spain, with a geographic pattern consistent with the colonization history of North America by Europeans. However, the time-series analysis reveals a substantial turnover of lineages in the southern part of the United States, indicating that both colonization history and natural selection shaped the genetic makeup of introduced populations. For Japanese stiltgrass, the two major genetic clusters present in the native range were independently introduced in the northeastern and southeastern United States. Though admixed individuals are common in the introduced range, the time-series analysis of genetic ancestry shows that range expansion largely preceded admixture, suggesting that admixture is a result rather than a consequence of rapid range expansion. Our results highlight the importance of incorporating historical samples into biological invasion research to elucidate the causes and consequences of rapid range expansion and invasion success.

Topic: Physiology

A-433

Early ontogenetic trait variation in a heteroblastic island endemic

Author: Ana Flores, Kasey Barton
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Plants face shifting environmental conditions as they develop through ontogeny, and ontogenetic trait variation is thought to have evolved in response to these changing selection regimes. While considerable evidence has accumulated for ontogenetic trait variation, most of this has characterized trait trajectories across the juvenile – adult vegetative phase change. In contrast, relatively little is known about ontogenetic trait variation during the earliest stages following germination during seedling establishment. Here, we characterize ontogenetic trajectories of physiological and morphological traits during early ontogeny in the heteroblastic species, Acacia koa, testing whether ontogenetic trajectories demonstrate phenotypic plasticity in response to drought stress. Ontogenetic trait variation was characterized within 10 maternal sibships of A. koa representing multiple populations in the Hawaiian Islands. Morphological and physiological traits directly involved in water balance and growth were characterized in 3 early ontogenetic stages, germinants (cotyledons), seedlings (cotyledon-true leaves), and juveniles (over 4 true leaves). To determine whether ontogenetic trait trajectories demonstrate phenotypic plasticity to water availability, plants from each sibship were grown under well-watered control and simulated drought conditions. Significant interactions between ontogeny and drought would indicate plasticity in ontogenetic trajectories, and a significant three-way interaction between ontogeny, drought, and sibship would suggest genetic variation in plasticity of ontogenetic trajectories. We detected considerable variability in the functional traits measured. In general, physiological traits were more plastic than morphological traits. Moreover, we detected plasticity in the ontogenetic trajectories of photosynthesis and stomatal conductance rates. In contrast, we detected no evidence that sibships varied in their ontogenetic trajectories, potentially indicating a limitation of these from evolving in response to natural selection pressure. Tremendous functional trait variability can occur during the earliest ontogenetic stages, although these are rarely considered in trait-based ecology. Considering the important role of increasing drought under climate change, phenotypic plasticity and lack thereof for early ontogenetic trait trajectories should be a future research priority.

Topic: Ecophysiology

A-434

Cuticular conductance and its temperature response in Themeda triandra: implications for grassland resilience to climate stress.

Author: Anu Middha
Affiliation: Western Sydney University

Grasslands serve as important ecosystems that offer critical services including biodiversity preservation and climate regulation while performing carbon sequestration. These systems face growing threats from both increasing global temperatures and changing patterns of rainfall. Researching physiological traits that lead to plant drought and heat resistance is essential to predict plant behaviours and develop future restoration strategies. Our research examines how minimum cuticular conductance (g_{min}) and phase transition temperature (T_p) affect *Themeda triandra*'s ability to withstand drought and heat stress across Australia.

Our study looked at six *T. triandra* accessions that come from regions with different climate conditions spanning cool-wet to hot-arid environments. The plants were cultivated within controlled glasshouse environments while g_{min} measurements were carried out for well-watered as well as drought conditions. Temperature-dependent cuticular water loss measurements enabled us to find the phase-transition temperature (T_p) which represents the threshold where g_{min} starts to increase rapidly. We also measured leaf mass per area (LMA) to study how structural traits might align with physiological characteristics.

At the species level, drought did not lead to a significant change in g_{min}, though individual accessions exhibited highly variable responses, ranging from a 48% reduction to a 31% increase. These divergent patterns suggest strong accession-specific plasticity in cuticular conductance. Under control conditions, g_{min} was not associated with climate-of-origin; however, under drought, g_{min} was significantly correlated with seasonal climatic variables- negatively with summer rainfall and positively with summer temperature- while annual means (mean annual precipitation and mean annual temperature) showed weaker or no relationships. This indicates that growing-season conditions may be stronger drivers of functional trait variation than long-term climate averages. Notably, accessions from hotter and drier environments exhibited higher g_{min}, contrary to classical expectations that predict reduced cuticle permeability as a drought adaptation. Moreover, g_{min} was positively associated with LMA, challenging the assumption that thicker, denser leaves are inherently less permeable.

T_p values varied substantially across accessions (35-55 °C) but showed no significant relationship with any climatic variable, suggesting that cuticular thermal stability may be governed by other factors, such as wax chemistry or leaf surface microstructure. Percent change in g_{min} from control to drought (%Δgmin) was also unrelated to climate, further highlighting the complexity of drought response strategies.

Overall, our findings reveal considerable intraspecific variation in cuticular traits and challenge traditional assumptions about how plants adapt to drought and heat. By identifying the environmental correlates- and limits- of g_{min} and T_p, this research provides insight into the physiological mechanisms underlying stress tolerance in grasses and offers a foundation for selecting climate-resilient genotypes for future grassland conservation and restoration efforts.

Topic: *Biogeography*

A-435

Biogeographic patterns and taxonomic reassessment of Viburnum carlesii (Adoxaceae) based on genome-wide SNP data

Author: Yun Gyeong Choi, Sang Hun Oh, Watanabe Yoichi
Affiliation: Daejeon University

Viburnum carlesii Hemsl. (Adoxaceae), commonly cultivated as an ornamental shrub, is deciduous and native to the low hills of Korea and western Japan. Due to a wide range of morphological variations, the taxonomic identity of this species has remained unclear. Traditionally, *V. carlesii* var. *carlesii* is characterized by round leaves, short and wide corollas, and densely clustered inflorescences, while *V. carlesii* var. *bitchiuense* features elliptic leaves, long and narrow corollas, and loosely arranged inflorescences. Plants classified as var. *carlesii* are found in maritime vegetation along the western coast of the Korean peninsula, Ulleungdo Island, and Tsushima Island, whereas those corresponding to var. *bitchiuense* are located in inland forests in Korea and western Japan. Morphological intermediates are also present in the eastern part of the Korean peninsula. To understand the patterns of morphological variation and genetic differentiation associated with the morphotypes, genome-wide SNP data were generated from 25 populations (164 individuals). Results of phylogenetic analyses of 67,139 SNP loci indicate that var. *bitchiuense* is independently derived from var. *carlesii*, suggesting that the inland forest morphotype may represent local adaptation. Biogeographic analyses imply that the ancestors of *V. carlesii* likely existed in the southern region of the land bridge connecting China, Korea, and Japan during the Last Glacial Maximum. Early divergence and migration of ancestors led to the Tsushima Island population as well as the populations of Oki Islands and Ulleungdo Island. The population on the Korean peninsula is monophyletic and sister to the Honshu population, exhibiting two separate migration lineages: a coastal route along the western coast of Korea and an inland forest route. Our genomic data support the classification of *V. carlesii* as a single species without varieties.

Topic: *Biogeography*

A-436

Genetic structure and the potential for cryptic divergence in the Ulleungdo Island population of Viburnum furcatum (Adoxaceae)

Author: Yun Gyeong Choi, Sang Hun Oh, Watanabe Yoichi
Affiliation: Daejeon University

Island biodiversity often displays complex and unpredictable evolutionary patterns. Ulleungdo Island, a volcanic oceanic island located in the East Sea (Sea of Japan), is well known for its high level of endemic plant diversity. However, to fully understand the origins of biodiversity on Ulleungdo, it is essential to investigate non-endemic taxa that are distributed both on the island and on the mainland. *Viburnum furcatum* Blume ex Maxim. (Adoxaceae) is a representative non-endemic deciduous shrub found in temperate mountainous regions across Ulleungdo Island, Jeju Island, and Japan. In this study, we conducted Genotyping-by-Sequencing (GBS) on 95 individuals from 15 populations across Ulleungdo Island, Jeju Island, and Japan, generating a total of 102,656 SNP loci. Genetic diversity analysis revealed that the Ulleungdo population had the highest observed heterozygosity (0.215) and the lowest inbreeding coefficient (–0.087), indicating a genetically stable and independently structured population. STRUCTURE, PCA, and maximum likelihood (ML) phylogenetic analyses also demonstrated that the Ulleungdo population formed a distinct genetic cluster, clearly separated from populations in Jeju and Japan. Pairwise F_{ST} values revealed strong genetic differentiation, with a maximum value of 0.781 between Ulleungdo and other regions. These results suggest that, despite being a non-endemic species, the Ulleungdo population of *V. furcatum* has diverged genetically due to geographic isolation. Although morphologically similar to conspecific populations, the Ulleungdo population exhibits distinct genetic divergence, indicating that cryptic divergence may be occurring within this island population.

Topic: *Development and Structure*

A-437

Stage-Specific Transcriptome Dynamics Reveal Identity Maintenance of EC-Derived Protoplasts in Angelica gigas Nakai

Author: Han-Sol Lee, Donghwan Shim, Bae Young Choi, Hyunwoo Cho, So-Young Park
Affiliation: Chungbuk National University, Chungnam National University

Plant protoplasts have long served as a model system for studying cell fate transitions at the single-cell level. However, the physiological responses of freshly isolated protoplasts and the molecular mechanisms underlying the recovery of cell division capacity remain poorly understood. In medicinal crops such as *Angelica gigas* Nakai, studies on gene expression dynamics and regulatory mechanisms during protoplast regeneration are still limited. This study aims to elucidate key molecular events associated with early tissue reorganization by comparing gene expression profiles across distinct developmental stages of protoplast culture. We extracted genomic DNA from *A. gigas* leaves and performed HiFi long-read sequencing to obtain genomic resources. For transcriptomic analysis, we isolated total RNA from three developmental stages: (1) EC, (2) freshly isolated protoplasts (Pt), and (3) micro callus (MC) stage, which represents early cell division. Additionally, we isolated protoplasts from both EC and non-embryogenic callus (NEC), and conducted RT-qPCR at the same three stages and subsequent timepoints to assess the retention of EC identity. Differentially expressed gene (DEG) analysis revealed five distinct gene expression clusters. In particular, Cluster 4 displayed a recovery of EC-specific expression patterns at the MC stage, with notable upregulation of genes related to the cell cycle, cell wall biosynthesis, and hormone signaling (auxin and cytokinin). At the Pt stage, stress-responsive genes such as *AgWIND1* were specifically upregulated, while *AgWUS* showed stochastic expression exclusively during the MC stage. *AgBBM* was differentially expressed in a cluster that exhibited similar expression trends to EC during the MC stage, suggesting its involvement in early reprogramming and division. RT-qPCR validation showed significantly higher expression of embryogenesis-related genes in EC-derived protoplasts compared to NEC-derived protoplasts, indicating partial maintenance of EC identity immediately after isolation. Our findings provide insight into the transcriptomic dynamics of protoplast regeneration and highlight the regenerative capacity retained by EC-derived protoplasts. This study offers a foundation for genome editing and regeneration studies in *A. gigas* and could facilitate the development of non-GMO molecular breeding strategies for medicinal plants.

Topic: *Hybrids and Hybridization*

A-438

Invasion within: Ogre LTR retrotransposons dominate the genome of invasive Carpobrotus

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The study of invasive alien species has gained momentum due to their profound impacts on native biodiversity and ecosystem function. In the Mediterranean region, the incidence of biological invasions is rising, likely driven by the temperate climate, globalisation, and intensified human activity. Invasive plant behaviour is frequently associated with hybridisation events that can enhance ecological adaptability and facilitate long-term establishment in new habitats.

Carpobrotus species—succulent plants native to South Africa, Chile, and Australia—have been widely introduced along mild-climate regions, in particular in the Mediterranean basin and the California coasts, where they often outcompete native flora and reduce biodiversity. Within this genus, homoploid hybridisation is well documented, particularly in the *Carpobrotus edulis* × *C. acinaciformis* complex. These taxa exhibit intermediate morphological traits, complicating taxonomic resolution and ecological monitoring.

To untangle the evolutionary and invasion dynamics of this complex, we generated phylogenomic data from both native and introduced populations. We constructed an evolutionary framework for the species using whole plastome de novo assemblies, 5S rDNA sequences, genome size measurements, karyological analyses, and repeatome profiling with RepeatExplorer2 and TAREAN.

Strikingly, our analysis revealed that more than —one of the largest known transposable elements. While functional implications remain speculative, this finding raises intriguing questions about the role of large repetitive elements and their abundance, in shaping the adaptability and competitiveness of invasive plant hybrids.

Topic: *Molecular Ecology*

A-439

A higher load of deleterious mutations has a detrimental effect on tree growth

Author: Rosalía Piñeiro Portela, Lowana Cahn, Katharina Budde, Agathe Hurel, Adélaïde Theraroz, Giovanni Vendramin, Sara Pinosio, Isabelle Lesur, Marina de Miguel, Christophe Plomion, Myriam Heuertz, Santiago González-Martínez
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A high proportion of deleterious mutations in the genome is predicted to cause a reduction in fitness known as genetic load. In plants, most studies focus on how detrimental mutations increase as a consequence of population bottlenecks, for instance in cultivated species as a negative outcome of domestication or at the margin of species ranges. However, the actual adverse effect of genetic load on individual phenotypes remains little characterised, especially in wild plant species with large populations and long lifespans.

We estimated genetic load based on genomic data in populations of the conifer maritime pine (*Pinus pinaster*, Ait.) on the island of Corsica (two different datasets including 133,656 SNPs in 393 individuals

and 10,185 SNPs in 334 individuals) and examined its association with phenotypic traits related to growth, phenology, and water-use efficiency measured under common garden conditions.

Our results revealed a strong negative correlation between genetic load and tree height on the Mediterranean island of Corsica, thus suggesting a negative cumulative effect of deleterious mutations on tree growth at the regional scale. This association was further confirmed by a wide-range analysis including 464 individuals from 34 populations across the entire range of maritime pine in the western Mediterranean, Atlantic Europe, and North Africa. Our study is one of the first to experimentally demonstrate adverse phenotypic effects (reduced tree growth) of genetic load in a long-lived plant.

Topic: *Reproductive ecology and evolution of plants in stress-prone environments*

A-440

Lobed oak leaves: when and where did they evolve?

Author: Kristel van Zuijlen, Kieran Althaus, Andrew Hipp, Thomas Denk
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Leaf shape is an important axis of plant adaptation to abiotic environment. Leaf lobing in particular has been hypothesized to play a variety of functions, including leaf temperature regulation, controlling support and supply of leaves, regulation of water use and photo synthesis, increasing the efficiency of leaf packing in buds, and herbivore defense (e.g., Royer et al., 2005; Givnish and Kriebel, 2017; Zohner et al. 2019). Most studies have looked at leaf variation across space in contemporary samples. Yet environment has changed dramatically over time as well, allowing for parallel investigations of the evolution of lobedness across continents. In this study, we investigate the evolution of leaf lobedness in oaks (*Quercus* L., Fagaceae), a clade of ca. 425 species distributed broadly across the northern hemisphere. Oaks originated near the Paleocene-Eocene (56 Ma) and thus evolved through a period of time during which Earth transitioned from a globally equable climate, mostly tropical, with temperate climates largely confined to the poles, to one in which plants have had to adapt to a wider range of climatic stresses. Oaks have colonized a wide range of these novel climates, ranging from dry, near-desert conditions to temperate rainforest, and from boreal to tropical climates. We analyze (1) a new dataset of more than 400 fossil leaf collections and more than 50 fossil collections of pollen, acorn, or other reproductive structure with (2) an existing restriction site associated DNA sequencing (RAD-seq) dataset for ca. 320 oak species and (3) climatic data for both extant and fossil species to investigate when, where, and in association with what climatic conditions of leaf lobedness evolved in oaks. We demonstrate that while the crown phylogenetic diversity of the genus arose early in the Eocene, lobedness did not evolve until near the Eocene-Oligocene boundary, when climate cooled dramatically worldwide, and it evolved in parallel in clades spanning North America and Eurasia, and on both sides of the Rocky Mountains. Thus the tremendous ecological variation among contemporary oak species echoes their long history of adapting to novel, stressful environments.

Topic: *Dryland Floras*

A-441

Edaphic and geological history shape the floristic and phylogenetic compositions of Caatinga seasonally dry forests at local scale

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Large-scale studies of floristic composition have revealed phytogeographic patterns across and inside tropical dry forests of the Americas showing high degree of floristic turnover between the isolated forest nuclei, indicating that these forests have evolved in isolation over millions of years with in situ speciation within some of the nuclei leading to high levels of endemism. Here, we used a forest plot dataset to study how geological formations affect floristic composition and phylogenetic community structure in the Brazilian Caatinga. We hypothesize that the three distinct geological formations found in the Caatinga (crystalline, limestone, and sandy) show distinct floristic composition and phylogenetic patterns despite their close geographical proximity. Our results show clear differences in floristic composition and phylogenetic patterns across the crystalline, limestone and sandy Caatinga where dry forests growing on similar substrate and geological formations are most similar to each other, even when highly disjunct. Vegetation growing on crystalline basement do not form a distinct cluster based on floristic composition due to large taxonomic and phylogenetic turnover. Overall, soils and geological formations drive community composition inside the Caatinga dry forest nucleus more than geographic distance or climatic variation. Our results highlight the great environmental heterogeneity found within Caatinga that includes three main geological formations each with their unique ecological processes and in situ speciation.

Topic: *Ecology*

A-442

Conservation and Taxonomic Assessment of a Rare Appalachian Endemic

Author: Rebecca Beneroff, Scott Schuette, Chris Martine
Affiliation: Bucknell, Western Pennsylvania Conservancy, Bucknell University

Penstemon canescens (Britton) Britton (Plantaginaceae), known colloquially as Appalachian Beardtongue, is a shale-barrens endemic species distributed through much of the Appalachian Mountain range. Recently, observations of P. canescens at the upper extent of its range have raised the question whether it may be a lumped taxon warranting examination of its functional systematic traits. Questions regarding the taxonomic identity of the species date back to Francis Pernell's 1935 field description, where he noted the species "varied greatly in the width and hairiness of the leaves, and especially in the size of the flowers". The combination of taxonomic uncertainty and unclear distribution in Pennsylvania has led the Pennsylvania Natural Heritage Program to prioritize P. canescens as a species in need of assessment, in part because of its frequent occurrence in globally rare shale-barrens communities. This study seeks to clarify both the taxonomy and the range of P. canescens in Pennsylvania by employing field observations, records on community science platforms, and the combined study of living plants and historical herbarium collections.

Topic: *Systematics & Taxonomy*

A-443

Phylogeny and biogeography of the Daphne group (Thymelaeaceae)

Author: Su-Chang Yoo, Sang Hun Oh
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The Thymelaeaceae are evergreen or deciduous trees, shrubs, or herbs with approximately 50 genera and 800 species. This family is cosmopolitan, and most species are distributed in tropical and temperate regions of Africa, India, and Australia. The Daphne group in the subfamily Thymelaeoideae includes about 14 taxonomically difficult genera distributed in Europe, East Asia, the Pacific islands, and South America. All species of Thymelaeaceae in Korea belong to the Daphne group. Phylogenetic relationships of the Daphne group are reconstructed to clarify the classification of the group and to understand biogeographic history. Nucleotide sequences of the ITS, matK and rbcL regions were determined from 43 species belonging to nine genera. The phylogenetic analyses suggest that traditional classification of *Daphne* and *Wikstroemia* are not monophyletic. As some species of *Daphne* are nested within *Wikstroemia*, *Daphne* should be defined narrowly, and *Wikstroemia* should expand to include *Daphne genkwa*. The disc shape traditionally used to differentiate *Daphne* and *Wikstroemia* show a reverse evolution in *D. genkwa*, indicating that it can't be considered a distinguishing trait for the two genera. *Wikstroemia* is sister to *Stellera*, and *Daphne* is sister to *Thymelaea* and *Diarthron*, suggesting that *Daphne* and *Wikstroemia* are distantly related. A clade of *Edgeworthia* and *Rhamnoneuron* is sister to a clade of *Daphne*, *Diarthron*, *Stellera*, *Thymelaea* and *Wikstroemia*. It is weakly supported that *Daphnopsis* and *Dirca* are sister to all other genera of the Daphne group. Biogeographic analysis shows that the Daphne group should have originated in East Asia. Multiple dispersal events should have occurred from East Asia to Europe in *Daphne*. *Wikstroemia* species in Hawaii and central Asia should have been derived independently from East Asia. The South American *Daphnopsis* is biogeographically unusual in that a long-distance dispersal should have been assumed from East Asia to South America.

Topic: *Paleobotany*

A-444

Palynoflora of a new Quereuxia record in western Alabama, U.S.A.: Floristics and evidence for a mid Coniacian age

Author: Nina Baghai-Riding, Carol Hotton, Olivia Pharr, James Starnes, Elizabeth Hermsen, Chase Egli, Adiel Klompmaker
Affiliation: Delta State University, National Museum of Natural History, Mississippi Department of Environmental Quality, Milwaukee Public Museum, University of Alabama

The enigmatic rhizomatous aquatic angiosperm *Quereuxia* Krysht. ex Baikovskaja, 1963, an element in many Late Cretaceous-Paleogene western North American and northeastern Asian floras, has recently been recognized in a locality in Pickens County, Alabama, extending the geographic range of this taxon. Leaves of *Quereuxia* were collected from two outcrops 16 meters apart in the McShan Formation. The McShan Formation unconformably overlies continental deposits of the Tuscaloosa Group and represents fluvial-deltaic beds intermediate in the marine transgression to the overlying Eutaw Formation. The light gray to buff, laminated leaf-bearing unit, plus two darker gray mudstones about 50 cm below the megafloral level, were sampled for floristic analysis and dating. More than 70 morphotaxa have been identified. All three samples were dominated by spores (between 50-60% of the total of a 300-point count), including bryophytes, lycophytes, and ferns (Anemiaceae, Schizaeaceae, Gleicheniaceae, Dipteridaceae, Polypodiales and ferns of uncertain affinity). Gymnosperms comprised 25-30% of the total and included mainly Pinaceae as well as rare Araucariacee, Cupressaceae, and Cheirolepidiaceae, a family of extinct xerophytic conifers. Angiosperms comprised 15-22% of the total and included monocots, eudicots of uncertain affinity, and members of the Normapolles group (= Fagales). All samples contained many freshwater algal cysts (not included in counts). The abundance of land plant spores and algal cysts and the absence of dinoflagellates indicate that these sediments were deposited in a freshwater pond or shallow lake. Biostratigraphically significant taxa were compared to the three palynological assemblage zones devised by Christopher (1979) for the middle and upper Magothy Formation of the mid-Atlantic region, which were later revised by Christopher & Prowell (2010) and Sugarman et al. (2021). The presence of *Praecursipollis plebius* (= *Praecursipollis* sp. A of Christopher (1979)), *Plicapollis* cf. *P. incisa*, and *Complexiopollis* sp. V of Christopher (1979) suggests that the McShan palynoflora belongs to the middle *Pseudoplicapollis longiannulata-Plicapollis incisa* Assemblage Zone, because the First Appearance Datum of *Plicapollis incisa* is at the base of this zone, and the Last Appearance Datum of *Complexiopollis* sp. V is just above the top of this zone. *Santalacites minor*, also present in our McShan palynoflora, is one of the nominate species in the underlying *Complexiopollis exigua-Santalacites minor* Assemblage Zone. However, given the presence of the other taxa mentioned above, our palynoflora is unlikely to belong to this lower Assemblage Zone. Following the updated correlations of Sugarman et al. (2021), our samples are therefore likely middle Coniacian in age.

Topic: *Ecology*

A-445

Techniques to enhance germination for the propagation and restoration of longleaf pine (Pinus palustris) understory plant communities.

Author: Kylie Gieser, Nicholas Flanders
Affiliation: Old Dominion University

The historical range of the longleaf pine (*Pinus palustris)* ecosystem ranged from eastern Texas through the southern edge of Virginia, but its acreage has been drastically reduced over the past century. *Pinus palustris* is a keystone species, but the understory plant communities are equally important as they frequently include many rare and endangered species endemic to this ecosystem. Native understory vegetation also promotes the frequent fire critical to the maintenance of this ecosystem. Understory plant communities differ throughout the ecosystem's expansive range and can be locally heterogeneous dependong on influences from biotic and abiotic factors. Restoration of longleaf pine communities at the northern edge of their range in southeastern Virginia and northeastern North Carolina is limited by the availability of locally sourced understory plant seeds and seedlings. Some organizations in this portion of the range have started collecting seed from native understory species with the intent to germinate them on a large scale. However, many of the target species have unknown germination requirements, and those requirements may vary throughout the species' range. To

increase understanding of longleaf pine understory species ecology and determine the best practices for propagating collected seeds, we conducted a cold stratification on understory herbaceous plant species present at an intact longleaf pine forest at the northernmost range of the ecosystem (Blackwater Ecological Preserve near Zuni, Virginia). In fall 2024, we collected seed from seven species at the Preserve: *Solidago odora, Eupatorium rotundafolium, Eupatorium pilosum, Lespedeza capitata, Lespedeza hirta, Andropogon ternarius, and Schizachyrium scoparium.* Seeds were subjected to each of four cold stratification duration treatments as well as a control: 15 days, 30 days, 45 days, and 60 days. After cold stratification, seeds were plated on moistened filter paper in a clear Petri dish (10 seeds per replicate with 8 replicates of each species and cold stratification treatment combination). Seeds were observed for germination in a temperature and light-controlled growth chamber over a 30-day period. The effect of species and treatment on overall germination percentage and germination rate (time to germinate) was tested using an ANOVA and time to event analysis. Through this study, we aim to provide important information about germination requirements for under-documented longleaf pine associate species to foster more holistic ecosystem restoration approaches in the future.

Topic: Systematics & Taxonomy

A-446

A preliminary targeted sequence capture phylogeny of Engelmanniinae (Asteraceae: Heliantheae).

Author: Abby Moore, Tilottama "Tilo" Roy, Jennifer Clevinger
Affiliation: University of Oklahoma, Missouri Western State University, Walsh University

The Engelmanniinae is a subtribe of the Heliantheae that is most diverse in North America with a couple of species extending south into Central America. Its most diverse groups are *Silphium*, centered around the Great Plains, and the *Balsamorhiza-Wyethia* clade, centered in western North America (*Balsamorhiza*) and the California Floristic Province (*Wyethia*). We used targeted sequence capture data to reconstruct the relationships of the majority of the species in this group. Although the *Balsamorhiza/Wyethia* clade itself was well-supported, relationships within the clade were often poorly supported, potentially due to hybridization. The remaining genera of which there were multiple samples (*Berlandiera*, *Lindheimera*, *Silphium*) were all fully supported.

Topic: Hybrids and Hybridization

A-447

Examining Triad Hybridization in the Oak Syngameon

Author: Izzy Hudson, Antonio Castilla
Affiliation: Oklahoma State University

Hybridization and introgression can serve as a powerful mechanism for the diversification of plant species. While existing research has offered val uable insights, further studies are needed to deepen our understanding of the geographic patterns of hybridization (i.e., hybrid swamps) regarding how they impact phenotypic differentiation and indivi dual fitness. The genus *Quercus* (oaks: Fagaceae) serves as a strong study system for exploring this relationship due to weak reproductive barriers between species within th e g roup.

Quercus havardii (shinnery oak) is an endangered low-growing shrub that plays a critical foundational role in the s and-shinnery ecosystem in the so uthern U. S. Previous work has suggested hybridization between *Q. havardii* and its close relatives, *Q. stellata* (post oak) and *Q. mohriana* (M ohr oak) wh ere their ranges either overlap or have overlapped in the past. However, the existence of genetic admixture in *Q. havardii* popula tions has not yet been explored and thus its geographic variation is largely unknown. We will be exploring potential hybridization between *Q. havardii* and two other oak species that overlap with its eastern range: *Quercus stellata* and *Quercus mohriana*.

Utilizing both field-collected and herbarium specimens, this project aim s to identify hybrid swamps in the shinnery oak range through both genomic and p henotypic analyses. We will sample allopatric populations of each study species, as well as sympatric populations where *Q. havardii* co-occurs with each hybridizing species. To further broaden the geographic scope of the study, we will also incorporate herbarium specimens. We hypothesize higher levels of genetic admixture and phenotypic differentiation in sympatric populations of *Q. havardii* with the hybridizing species, and lower admixture and increased phenotypic distinctiveness in allopatric populations. The se findings will contribute to a better understanding of the overall genetic variation of this e ndangered species, helping to better inform conservation strategies.

Topic: Biogeography

A-448

Mapping Ecological Zones Using Terrain-Derived Environmental Models Across the Cumberland Plateau and Cumberland Mountains

Author: Mkayla Motley
Affiliation: Geological Survey of Alabama

Remote sensing has long played a key role in mapping forest and wetland communities, though traditional classification methods using moderate spatial resolution imagery often yield inconsistent results. Mapping these communities using high-resolution remote sensing and terrain-based modeling has the potential to enhance resource management, conservation, and ecological restoration. Ecological Zones provide a spatially explicit framework for understanding potential vegetation distributions based on environmental variables such as moisture, temperature, soil fertility, solar radiation, and disturbance. Developed originally in the Southern Appalachian Mountains, Ecological Zones are defined using intensive field derived description of plant communities that are modeled with digital terrain derivatives. While conceptually similar to Biophysical Settings (BpS), Ecological Zones offer finer spatial resolution and more detailed vegetation specificity.

This study evaluates and refines Ecological Zone models across the Cumberland Plateau and Mountain regions, along with adjacent low-relief ecoregions. The goal is to improve predictive accuracy, clarify the role of key environmental drivers, and demonstrate the scalability of this method for ecological planning and management. A multi-stage modeling approach was employed, beginning with the collection of field data from 1,916 plots. High-resolution digital terrain models (DTMs) derived from LiDAR were used to extract 23 environmental variables, which were input in MAXENT statistical models to predict suitable habitat for each Ecological Zone. These models were merged and refined through expert review, post-processing filters, and ecotone analysis.

Environmental variables with the highest predictive value included distance to cliffs, sandstone-conglomerate and shale geology, and elevation-dependent precipitation patterns. Slope, solar radiation, and the Terrain Shape Index were especially effective for distinguishing moist, concave coves from dry, convex ridges. Limestone geology reliably identified calcareous woodlands and mesophytic forest types, while curvature metrics, though minor contributors in model fitting, helped refine boundaries in ecotonal zones. Interactions among variables—such as elevation, slope position, and solar exposure—formed complex but interpretable patterns that reflect local physiographic variation. Models showed highest reliability in zones with distinct topographic or geological signatures.

Ecological Zones offer a robust framework for characterizing landscape heterogeneity, particularly in fire-adapted systems where disturbance history and terrain features shape vegetation patterns. Post-modeling improvements, including ecotone adjustment and high-resolution terrain data, significantly increased spatial realism and model accuracy. Accuracy assessments using field reference plots validated the model outputs and supported their use in operational ecological mapping.

This modeling approach has been successfully applied across multiple Appalachian ecoregions and extended into the Atlantic Coastal Plain and Piedmont, reinforcing its applicability across a range of environmental gradients. Ultimately, this work provides a detailed, spatially explicit understanding of ecological diversity on the Cumberland Plateau and beyond. It supports conservation, land management, and restoration planning by identifying key environmental drivers of vegetation patterns and offering a scalable framework for ecosystem analysis across complex terrain.

Topic: Dryland Floras

A-449

Unravelling evolutionary patterns of abiotic stress resistance in hot and cold desert plants

Author: Marc Fradera-Soler, Natasha Barbolini, Aelys Humphreys
Affiliation: Stockholm University

Plants in hot and cold deserts face multiple abiotic stressors, including drought, frost, and salinity, yet many desert plant lineages are older than the desert environments they currently inhabit, which expanded over the last 34 Ma. Thus, these lineages represent compelling systems for studying the evolution of abiotic stress polyresistance (i.e. resistance to multiple abiotic stressors). It is particularly urgent to enhance our

understanding of how plants evolve abiotic polyresistance in the context of the current climate emergency, as plants encounter increasingly intense and novel combinations of abiotic stressors.

Focusing on drought and frost, we employ various phylogenetic comparative methods to reconstruct the evolutionary trajectories of distinct hot and cold desert plant lineages. This approach allows us to reveal both similarities and differences in terms of evolution of stress resistance among these groups. We then compare the reconstructed evolutionary pathways with our previous hypotheses and assumptions. In this presentation, I will share preliminary results of our analyses and outline the next steps for this research.

Topic: *Botanical History*

A-450

Botany of the 1860 Chadbourne Expedition to West Greenland

Author: Arthur Gilman
Affiliation: University of Vermont

The history of botanical exploration and the investigation of Greenland's flora is well known. However, although Greenland is geologically part of North America and its flora is richly related to that of North America, it has been somewhat ignored by North American botanists, at least as to vascular plants. Instead, nearly all botanical investigation has been conducted by Danish botanists, with the resulting literature published in Copenhagen. Recently, inspection of Greenland plant specimens at the University of Vermont's Pringle Herbarium uncovered a significant scientific expedition to its west coast in 1860 that has hitherto not entered the botanical literature. In an era when student-involved exploring trips were just beginning in America, Paul A. Chadbourne, Professor at both Williams College (Massachusetts) and Bowdoin College (Maine), arranged a pedagogical expedition in the summer of 1860 to Labrador and Greenland, with a stated goal of collecting specimens for the "cabinet" of the Natural History Society of Williams College. Traveling by schooner from Maine, the party consisted of 19 members. Seven students were left at Caribou Island (now Île de la Demoiselle) in the Straits of Belle Isle, Labrador. The remaining 12 members, mostly students, arrived near Sukkertoppen (Maniitsoq) on the west coast of Greenland on 19 July; they engaged in nature study and collection of specimens there and at Godthaab (Nuuk) for nearly a month before returning. Two sets of plants specimens resulted, one originally at Bowdoin and now at the Pringle Herbarium, and the other originally at Williams and now at Muskingum University. Together they total more than 200 specimens and over ninety taxa—the largest and most systematically collected set of vascular plants collected in Greenland before 1900. This presentation will detail this remarkable trip and its surprisingly detailed documentation which, due to a variety of factors, has been overlooked as a source of early knowledge of the Greenland flora.

Topic: *Symbioses: Plant, Animal, and Microbe Interactions*

A-451

Infection Relationships of Rose Rosette Disease in a Cultivated Rose Garden Collection

Author: Ray Volkin, Lisa Wallace
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Rose Rosette Disease is a lethal viral disease caused by Rose Rosette Virus (RRV), which is spread by the Eriophyid mite, Phyllocoptes fructiphilus. RRV infects many species of roses, including several kinds of ornamental roses, causing aesthetic damage before lethality, and it negatively impacts both the floral and landscaping industry. Since plants do not have an adaptive immune system and there are no commercially available treatments for most viral diseases, plant viruses require preventative measures to reduce disease spread. Additionally, the mite vector for RRV poses many challenges; the mites are microscopic and miticide applications are less effective, they can spread via wind and animal, and their reproductive cycle leads to difficulties in complete eradication. In this project, spatial relationships of symptomatic roses and virus presence were studied to illustrate potential causes for disease outbreak in the cultivated collection at the Norfolk Botanical Garden. This collection includes over 1,700 roses, representing over 400 species and cultivars. Disease outbreaks could be caused by an endemic population of the virus, or they may be associated with repeated introductions of RRV from infected plants, visitors, or other means. Samples from 359 asymptomatic roses and 30 symptomatic roses were tested for RRV. Latency in cultivated varieties has not been studied, and in all tests, no asymptomatic roses showed presence of viral material. Mapped samples were subjected to hotspot analysis to evaluate spatial clustering of infected roses. Hotspot analysis was conducted at various band distances to determine if different mechanisms of vector spread might influence spatial patterns of the virus. Hotspots associated with smaller band distance would represent localized vector spread, occurring either from ambulation or short-distance wind or phoresy events, whereas those occurring across larger distances suggest phoresy or wind dispersal of mites, which can be further supported using genetic sequencing of the isolated virus. Short distance hotspots (i.e., with bands of 1-10 meters) were found to occur near specific cultivated varieties, posing a threat to other plantings of the same or different varieties nearby, while other instances of RRV did not occur within a hotspot. In analyses with the band distance exceeding 20 meters, no hotspots were found. Isolated occurrences outside of hotspots demonstrate either strong maintenance practices to reduce and remove disease instances, success in miticide treatment, lack of vigor in the viral strain or the vector capable of transmitting to neighboring plants, or potential resistance or susceptibility in certain cultivars. Sequencing of isolated viral material will further explain RRV spatial patterns in and outside of disease hotspots and potential reasons for the observed patterns.

Topic: *Trees, Traits, and Time*

A-453

Physiological plasticity across time and space in Joshua trees

Author: Karolina Heyduk, Sara Sciulla, Jeremy Yoder, Christopher Smith, Michael McKain, Todd Esque, Lesley DeFalco
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Joshua trees are iconic species of the Mojave Desert, yet are threatened by land use change and a warming planet. The extent to which they are locally adapted or exhibit phenotypic plasticity in response to environmental perturbation is unknown. Here we explore the ecophysiology of Joshua tree seedlings across space and time to better understand the extent of adaptation and plasticity in shaping the species' current and future range. We combine common garden experiments across the Mojave with lab-based studies that examine the role of high nighttime temperature. Together our results suggest the species use an alternative form of photosynthesis, respond plastically to year-to-year environmental variation, and have metabolic adaptations to high light and high temperature environments. Our results in total suggest levels of resistance in these species to unfavorable environmental conditions, at least at the seedling stage, and provide hope for the species' resilience. These results also reshape our understanding of CAM evolution more broadly in the Agavoideae, the subfamily that includes Joshua tree.

Topic: *Systematics & Taxonomy*

A-454

Genomic insights into a desert specialist: Sequencing the enigmatic Tiganophyton karasense to illuminate evolution across the Brassicales

Author: Makenzie Mabry, Alex Harkess, J Chris Pires, Mark Olson, Pamela Soltis, Douglas Soltis, Quinten Bafort, Yves Van de Peer, Kenneth Oberlander, Eugene Marais, Gillian Maggs-Kölling
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Tiganophyton karasense is a recently described species endemic to the hyper-arid ||Karas region of southern Namibia and the sole representative of the family Tiganophytaceae. Its phylogenetic and morphological distinctiveness and ecological specialization make it a valuable model for understanding lineage diversification and drought adaptation within Brassicales, an order comprising over 4,700 species across 18 families. Brassicales are economically important, encompassing numerous crops such as cabbage, broccoli, canola, papaya, and moringa, as well as species with ecological or medicinal significance. As part of the Brassicales Genome Initiative, we are generating a chromosome-scale reference genome for T. karasense using PacBio HiFi and Hi-C sequencing, complemented by transcriptome and small RNA data for genome annotation. In parallel, we are resequencing ten individuals collected from three wild populations to assess intraspecific genetic variation and potential signatures of local adaptation. Field collections were conducted in collaboration with researchers at the Gobabeb - Namib Research Institute. These genomic resources will establish the first reference for Tiganophytaceae and enable comparative analyses across Brassicales. In

particular, they provide an opportunity to investigate the evolutionary history of drought tolerance, woody growth form, and specialized metabolism in a lineage that diverged early within the order. This work will contribute to phylogenomic reconstructions of trait evolution and inform efforts to identify genetic pathways relevant to climate resilience and sustainable bioenergy applications.

Topic: *Systematics & Taxonomy*

A-455

Lions and tigers and bears, oh my! An updated phylogeny of the Arthrostylidioid bamboos (Poaceae: Bambusoideae: Bambuseae: Arthrostylidiinae) exposes three new genera

Author: Christopher Tyrrell, Cristielle Jesus-Costa, Pedro Viana, Edgar Afonso, Luiz Oliveira, Lynn Clark, Ana Paula Santos-Gonçalves
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The Neotropical woody bamboo subtribe Arthrostylidiinae (Poaceae: Bambusoideae) comprises 200 morphologically diverse species classified in 16 genera. Studies repeatedly support monophyly of the subtribe and recover four major internal clades. The largest genus in the subtribe, *Aulonemia* (~50 spp.), has been relatively undersampled in prior work with only 5 (~10%) of the taxa included in molecular phylogenetic study. The morphology of *Aulonemia* is heterogeneous, with several species having characteristics that resemble or overlap with other genera including the as-yet phylogenetically unsampled genus *Myriocladus*. Our aims were to 1) place a representative of *Myriocladus* within the Arthrostylidiinae phylogenetic hypothesis, 2) test the monophyly of *Aulonemia* in the context of the broader subtribe, and 3) revise the taxonomy, as appropriate, towards a natural classification for the Arthrostylidiinae. We sequenced *Myriocladus virgatus* and increased taxon sampling for *Aulonemia*, then inferred a multi-locus plastid phylogeny of the subtribe. The phylogenetic position of *Myriocladus* within Arthrostylidiinae was resolved--for the first time--and was sister to the earliest diverging clade. We tested several evolutionary hypotheses by constraining topologies and confirmed a polyphyletic *Aulonemia*. Four species of *Aulonemia* (*A. radiata, A. effusa, A. setosa*, and *A. setigera*) were resolved as distantly related to the other members of *Aulonemia* and appear in the earliest diverging clade: one species showing a close relationship with *Cambajuva* and the other three related to the newly sequenced *Myriocladus*. These phylogenetic results, combined with morphological evidence, supported the establishment of three new genera: *Quixiume, Stelanemia*, and *Vianaea*, to accommodate the four remarkable *Aulonemia* species, thereby increasing the generic richness of the subtribe to 19.

Topic: *Physiology*

A-456

Changes in phloem physiology do not correlate with anthocyanin accumulation in young and senescing leaves

Author: Jessica Savage, Rebecca Rooney
Affiliation: University of Minnesota - Duluth

Anthocyanin synthesis can be triggered by a buildup of soluble sugars in leaves. Because phloem physiology can impact the carbon balance in a leaf, it has been hypothesized that changes in phloem physiology might alter sugar concentrations, leading to leaf reddening during early development and autumnal senescence. Often in young leaves, anthocyanin concentrations are the highest when leaves are carbon sinks and not exporting carbon. Once they begin exporting carbon, they show a decline in anthocyanins. Similarly, in senescing leaves, higher anthocyanin concentrations are associated with later stages of senescence that are often assumed to be tied to declines in carbon export. In this study, we tested the hypothesis that anthocyanin accumulation in young and senescing leaves corresponds to lower rates of carbon export. We estimated carbon export with a mass balanced approach by examining changes in leaf mass and net carbon assimilation during the day. To understand changes in carbon export and pigments during leaf expansion, we sampled red bud leaves at three different stages of early leaf development. For our work on leaf senescence, we sampled red oak leaves weekly in the autumn. In neither study system did we see a direct relationship between carbon export in the phloem and anthocyanin pigments in the leaves. In red buds, anthocyanins are higher in young/sink leaves, but not all sink leaves are red. A similar pattern was found in oaks where anthocyanin accumulation increased during leaf senescence. However, carbon export is sustained through the early stages of color change. These data suggest that although changes in carbon export can impact the carbon balance in the leaf and could indirectly impact anthocyanins, color change in young leaves and senescing leaves is not directly tied to changes in phloem physiology.

Topic: *Hybrids and Hybridization*

A-457

Hybridization Patterns and Morhpological Variation in Quercus welshii

Author: Lainey Kirshberger, Lana Daniels, Antonio Castilla
Affiliation: Oklahoma State University

Hybridization can be an important source of genetic and phenotypic variation in plant species with weak reproductive barriers and overlapping geographic ranges. This additional variability may be especially important for endemic species with restricted distributions and limited gene flow. Our study investigates the endemic oak species Quercus welshii and its hybridization with other species in the Quercus x undulata complex, examining the geographic patterns and their implications for phenotypic variation. Specifically, we assessed genetic admixture in our focal species, Quercus welshii, with four sympatric species (Q. gambelii, Q. turbinella, Q. grisea, and Q. arizonica) using Bayesian clustering analysis. We then examined the correlation between admixture proportion in Q. welshii populations and the geographic distance to the nearest population of a potential hybridizing species. Additionally, redundancy analysis was used to investigate the relationship between proportion of admixture and leaf trait variation.

We found substantial genetic admixture between Q. welshii populations and other congeneric species. Our analysis also supported the hypothesis that our populations would be more likely to hybridize as the geographic distance to other known hybridizing species decreased. Finally, our results support that admixture proportion in Q. welshii populations influences leaf trait variation. This study is the first step in better understanding how hybridization affects the genetic and morphological variation within populations of Q. welshii, which is of special concern when creating conservation programs for the species. However, whether these morphological changes confer an adaptive advantage is unclear and should be investigated further.

Topic: *Comparative Genomics/Transcriptomics*

A-458

How do different tissue preservation methods impact transcript quality and recovery in Arabidopsis thaliana?

Author: Alexa Tyszka, Joseph Walker, Edwige Moyroud
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Transcriptomic studies enhance our knowledge of the tree of life and are a cost-effective means of obtaining large amounts of genetic information. The most restrictive step of obtaining transcriptomes is preserving RNA using cold temperatures. Ultracold preservation is thought to be necessary due to the fragility of the molecule. However, RNA persists for decades in herbarium specimens and mammal skins preserved in museums. The influence a lack of ultracold storage has on RNA preservation in plant tissues on a short time scale is unknown. With this study, we aim to characterize the persistence and degradation of RNA for transcriptomic purposes across short time scales (from 1 day to 6 months) by preserving leaves from Arabidopsis thaliana in different conditions. The preliminary results from this study include measures of RNA quality and quantity. As a part of the ongoing study, we will sequence transcriptomes and quantify gene expression levels across six different preservation conditions and time points with the ultimate goal of comparing transcriptome completeness and quality. The results from this study will provide information about the fragility of RNA for transcriptomic purposes and provide insights on whether RNA degradation is uniform or whether transcripts with certain characteristics or corresponding to specific gene groups are more likely to be lost first. This will allow researchers to make informed choices about the advantages and disadvantages of each treatment condition.

Topic: Defining forces in fern evolution: Celebrating the contributions of Kathleen Pryer and Michael Windham

A-459

Cutting the Gordian Knot: Can HybSeq help resolve reticulate relationships in Isoetes?

Author: David Wickell, Jacob Suissa, Peter Schafran
Affiliation: University of Connecticut, The University of Tennessee, Boyce Thompson Insititute

Quillworts (*Isoetes*) comprise an ecologically diverse, globally distributed lineage of vascular plants. However, their phylogenetic relationships remain poorly understood due to limited sampling, reduced morphology, and frequent hybridization. While low-copy genes and chloroplast sequences have been useful for resolving relationships in other plant lineages, they often fail to capture the complex evolutionary histories of Isoetes, particularly in clades that have undergone rapid radiations and/or frequent hybridization. To address these challenges, we conducted hybridization-based sequencing (HybSeq) using the GoFlag probe set to target hundreds of nuclear loci across 114 individuals comprising at least 92 species. This approach provided phylogenetic signal at multiple evolutionary scales while allowing us to identify taxa of likely hybrid origin and phase alleles to resolve reticulate relationships within Isoetes. Our results reveal new insights into the diversification of quillworts and highlight strengths and challenges of using HybSeq for clarifying patterns of hybridization and speciation in this phylogenetically complex lineage.

Topic: Biogeography

A-460

Genetic analysis at varying scales along a seepage slope gradient: a case study in the monocot genus Xyris using nuclear and plastid markers.

Author: Elizabeth White, Edgardo Ortiz, Pamela Soltis, Douglas Soltis
Affiliation: University of Florida

Xyris (Xyridaceae) is a cosmopolitan group of monocots that have high levels of species diversity and endemism in the North American Coastal Plain (31 species, 27 range-restricted endemics). The North American Coastal Plain (NACP) itself is an understudied biodiversity hotspot, and this study aims to parse the biogeographic history of characteristic seepage slope plant communities within the NACP using a phylogeographic

Topic: Symbioses: Plant, Animal, and Microbe Interactions

A-461

Microbial Associations of White Clover (Trifolium repens)

Author: Brandon Hendrickson, Courtney Patterson, Nevada King, Nic Kooyers
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Microbial associations may play a critical role in shaping plant invasions. Predator escape from co-evolved pathogens can facilitate spread in novel environments while the absence of horizontally transmitted mutualists or the acquisition of novel pathogens may constrain invasion success. Although suites of morphological and physiological traits associated with plant invasiveness are well documented, the functional role of plant-associated microbiota remains less understood. In this study, we investigate the microbial associations of white clover (*Trifolium repens*) using bycatch from short read illumina sequencing. First, we performed reciprocal transplant experiments between the native and introduced ranges to determine which microbial taxa are range-specific and their effect on fitness. Second, we identify climatic drivers of microbiome composition across biogeographic regions. Third, we conduct genome-wide association mapping and identify several plant genomic loci linked to two ecologically important endophytes—one associated with nitrogen fixation and the other with drought tolerance. Finally, using herbarium specimens collected over the last century across North America, we demonstrate a temporal shift in microbial functional diversity, with decreasing association with nitrogen-fixing taxa and increasing association with drought-tolerant microbes. Together, these findings reveal dynamic shifts in microbial composition across time and space and suggest that changes in microbial partnerships may play a pivotal role in the success and ecological expansion of introduced species. This work underscores the importance of incorporating microbial ecology into invasion biology and highlights how extended phenotypes can mediate plant adaptation in novel environments.

Topic: Phytochemical

A-462

A Breath of Fresh Control: Dissecting the Resistance Pathways of Botrytis cinerea to Linalool

Author: Melanie Madrigal, Jordan Dowell
Affiliation: Louisiana State University

The generalist pathogen Botrytis cinerea constantly threatens agricultural production, as it infects over 500 species of crops(e.g., corn, soybeans). This broad host range results in billions of dollars in yield loss. Given its wide host range, pesticide applications are a more feasible option for pathogen control than genetic engineering of resistant crops. However, many commercial pesticides are long-lived, increasing risks of evolved resistance and hindering ecosystem processes. Recent studies have focused on using volatile plant-specialized metabolites (SMs) as alternative control strategies due to their ability to readily break down in their environment and incorporation as common food additives for flavor. Specifically, linalool and other SMs have demonstrated inhibitive effects on single isolates of B. cinerea. Yet, few studies have examined the impact of SMs across genetically diverse populations of B. cinerea. Further, B. cinerea's wide genetic variation enables it to resist many commercial pesticides through variation in ABC and MFS transporters. In our work, we exposed a population of genetically distinct isolates of B. cinerea to the specialized metabolite linalool to explore variation in inhibitory responses, leading towards the identification of the genetic architecture of SM resistance. We characterize isolate-specific responses using in vitro culture and growth assays across varying SMs, improving our understanding of SM efficacy against B. cinerea and leading towards novel avenues of more sustainable biocide development.To explore the applications of linalool and its efficacy, we applied linalool through several routes of exposure, fumigation to explore fumigant activity, in-agar exposure to assess direct surface-level inhibition, and liquid culture assays to evaluate growth in a fully submerged environment. This multi-pronged approach provides greater insight into isolating specific responses under distinct exposure conditions, improving our understanding of how B. Cinerea responds to linalool across different application routes. Our work advances the development of targeted, plant-derived pesticide blends for use across eudicots to control a widespread pathogen.

Topic: Plant phenology in an era of rapid global change: new perspectives and frontiers

A-463

Phenological response to climatic change depends on spring warming velocity

Author: Robert Guralnick, Theresa Crimmins, Erin Grady, Lindsay Campbell
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Continuing global change is altering the timing of life cycle events such as flowering and leaf emergence. Understanding these phenological changes is crucial for predicting ecological responses and informing conservation strategies. Despite burgeoning evidence of phenology shifts, a unifying model characterizing generalities and underlying processes determining the tempo of phenological change across space, time and species has remained elusive. In this study, we introduce a framework that integrates spring temperature, the velocity of spring warming, and species-specific thermal requirements in order to predict phenological shifts in response to climatic changes. Our framework posits that the rate of temperature change during spring (spring warming velocity) interacts with species' thermal requirements to determine phenological timing. We hypothesize that species active earlier in the growing season and located in regions experiencing slower spring warming will exhibit heightened sensitivity to temperature changes, leading to more pronounced advancements in phenological events. This prediction stems from the interplay between species' inherent thermal requirements and the temporal dynamics of temperature increases in their habitats. To test our hypothesis, we utilized a unique dataset from the 1850s along with data from the National Phenology Network and iNaturalist, focusing on the Eastern United States. In particular, we generated flowering and leaf onset timing in the past and present, and examined both latitudinal trends in phenological response as well as spring velocity and climate context. Modeling results strikingly confirm predictions from our framework, showing that while temperature sensitivity is higher in regions with low temperature velocity, the greatest realized change in phenological onset is northern areas where warming rates have been fastest. Our framework captures essential processes governing phenological response but is simple enough to allow broad application without extensive calibration common in mechanistic models, making it a valuable tool for predicting phenology responsiveness in face of accelerating change.

Topic: Crops and Wild Relatives

A-464

Uncovering the demographic history and selection signatures in Brassica oleracea

Author: Sarah Turner-Hissong, Makenzie Mabry, Paul Blischak, Katherine Guill, Melvin Oliver, Ella Katz, Daniel Kliebenstein, Graham King, J Chris Pires, Timothy Beissinger, Jeffrey Ross-Ibarra
Affiliation: Bayer Crop Science, University of Florida, University of Missouri, UC Davis, University of California, Davis, Southern Cross University, Colorado State University, University of Goettingen

Understanding the demographic history of domesticated plant species provides critical insights into crop origins, patterns of adaptation, and opportunities for crop improvement. Brassica oleracea is a particularly striking example, with selection on distinct plant organs leading to morphologically diverse crops such as kale, cabbage, broccoli, cauliflower, Brussels sprouts, and kohlrabi. To investigate the evolutionary processes underlying this diversity, we conducted whole-genome resequencing on 172 accessions spanning 13 domesticated morphotypes and four closely related wild species. These data were integrated with publicly available resequencing data from an additional 123 accessions, resulting in a dataset of 295 individuals and over 3.2 million high-quality SNPs. We performed a comprehensive set of analyses, including phylogenetic reconstruction, population structure inference, demographic modeling, genome-wide scans for selective sweeps, and polygenic selection tests. Our results reveal clear population structure among morphotypes, support a domestication timeline of approximately 4,000–5,000 years ago, and identify both shared and morphotype-specific genomic regions under selection. Traits associated with selection include leaf morphology and glucosinolate content—features central to yield, palatability, and defense. These findings provide new insight into the evolutionary history and genetic architecture of domestication in B. oleracea, offering valuable targets for future crop improvement.

Topic: Comparative Genomics/Transcriptomics

A-465

Fruiting traits and genetic variation in Viburnum (Adoxaceae)

Author: Sang Hun Oh, Yun Gyeong Choi, Hyun-Jun Kang
Affiliation: Daejeon University

The relationship between Seed Dispersal Syndrome (SDH) and genetic variation within a species remains largely unknown. For plant species that interact with avian seed dispersers, the specific characteristics of fruit maturation may have led to different patterns of genetic variation among species. Species of *Viburnum* L. (Adoxaceae) are well-known examples dispersed by birds. To investigate the correlation between fruit traits and genetic variation, we generated genome-wide SNP data from five *Viburnum* species, which exhibit one of two types of fruit maturation: (1) fruits that mature synchronously in red and are persistent, and (2) fruits that initially develop in red as an intermediate stage before ripening to black and becoming deciduous. Results from phylogenetic and ordination analyses demonstrate strong geographical signals for species with sequentially maturing fruits, but not for those with synchronous maturing fruits. The latter species exhibit higher genetic diversity within populations than the former. There is no evidence of a specific disperser for any *Viburnum* species. Our comparative analysis suggests that the fruit maturation types associated with the longevity of ripened fruits should influence the frequency of diaspora migration, resulting in contrasting patterns of intraspecific genetic variation.

Topic: Comparative Genomics/Transcriptomics

A-466

Mating systems shape transposable element dynamics in Mimulus (monkeyflowers)

Author: Eleanore Ritter, Andrea Sweigart
Affiliation: University of Georgia

The shift to self-fertilization (selfing) is one of the most common evolutionary transitions in flowering plants and results in dramatic genomic consequences. Owing to reduced effective population size, selfing species often have increased homozygosity, reduced genetic diversity, and more deleterious mutations. Despite how common selfing is in flowering plants, empirical evidence of the impact of selfing on transposable element (TE) evolution in flowering plants is somewhat mixed, and evolutionary theory is somewhat conflicted as well. Here, we investigated how transitions to self-fertilization impact TE dynamics in the genus *Mimulus* (monkeyflowers) using two pairs of closely related outcrossing and selfing species from two independent transitions to selfing. Preliminary work has shown that the selfing species differ from their outcrossing relative in both the distribution of TEs across chromosomes and in the relative dates of TE insertions within the genome. Future work looking at intra- and interspecific TE presence/absence variation will provide more insights into the processes driving TE dynamics in selfing plants. Ultimately, this work will provide powerful insights into the fate of TEs in selfing lineages and a glimpse into the evolutionary processes that have shaped the TE landscapes of *Mimulus* genomes.

Topic: Population Genetics/Genomics

A-467

Temporal patterns of gene flow between populations of Pedicularis cranolopha in the Hengduan Mountains

Author: Jared Meek, Deren Eaton, Richard Ree, Jason Leung
Affiliation: Columbia University, Field Museum

Plant dispersal and gene flow are powerful processes that influence the genetic diversity and population structure of species. This is especially true in heterogeneous mountain environments where diverging populations can more easily become isolated by geographical and elevational barriers. The Hengduan Mountains Region (HMR) is a biodiversity hotspot that contains hundreds of endemic plant species thought to be produced in this manner, but the extent to which gene flow can continue across such barriers in this region is unclear. Here, we use whole-genome sequencing to identify the population structure of a widespread species complex (*Pedicularis cranolopha*) and identify historical patterns of gene flow between populations despite their separation by geographic barriers. With this historical context of gene flow, we also develop a temporal genomics framework using historical and contemporary samples to test whether gene flow among these populations has increased in recent decades due to anthropogenic activity dispersing seeds across landscape barriers.

Topic: Macroevolution

A-468

Macroevolutionary patterns of growth-defense trade-offs across 16 genera of temperate woody plants

Author: Justin Gambill, Jordan Dowell, Chase Mason, Eric Goolsby, Michael LaScaleia
Affiliation: Louisiana State University, University of British Columbia Okanagan, Okanagan College, Harvard University

The leaf economic spectrum (LES) describes plants based on their resource aquisition strategy. Many studies have used this framework to assess the macroevolutionary correlations of plant traits and changes in the environment over evolutionary time.In addition to resource acquisition, the relationship between chemical defenses and the broader LES in plants largely remains unresolved.This study aims to analyze LES and chemical defense trade-offs across 16 genera of temperate woody plants in an attempt to understand general patterns.Quantitative leaf ecophysiological traits, nutrient, and metabolomic profiles were compared to assess macroevolutionary correlations of trait integration and chemical diversification. Using ancestral state reconstruction, we find several common syndromes associated with life history strategy and the degree of chemical diversity exhibited at the species and genera-specific levels.Expanding our understanding of common traits associated with successful establishment in new environments across diverse taxa will not only provide general ‘rules of thumb’ for adaptation but may specifically indicate how specific species of importance may adapt to environmental stressors based on evolutionary trends.

Topic: Biology of mycoheterotrophic and parasitic plants

A-469

Exploring hemiparasitism in Cuscuta subgenus Monogynella (Convolvulaceae) using phylogenomics

Author: Asawari Albal, Saša Stefanović
Affiliation: University of Toronto Mississauga

Cuscuta (dodders) represents one of the 12 independent origins of haustorial parasitism in angiosperms. It consists of ~200 species circumscribed into four subgenera (*Monogynella*, *Cuscuta*, *Pachystigma*, and *Grammica*) and is the only parasitic genus in Convolvulaceae (the morning-glory family). This group shows a significant diversity in plastid functionality and represents a rare mixotrophic system within parasitic plants, where different trophic modes can be found at a lower (species) phylogenetic level. *Cuscuta* species range from chlorophyllous hemiparasitic members of *Monogynella*, to "cryptically" photosynthetic members of the other subgenera, to the two completely holoparasitic clades within *Grammica*. Apart from a few placeholders in broad scale phylogenies, Subgenus *Monogynella*, had not been extensively sampled and studied.

Previously, we conducted molecular systematics analyses using plastid and nuclear markers with an exhaustive sampling representing 12 out of the 15 presently recognised species and provided the first in-depth *Monogynella* molecular phylogeny. To obtain greater resolution for the backbone, and study the different organellar genomes, we selected 31 samples, carefully chosen to represent the phylogenetic diversity of each clade from our molecular phylogenies and sequenced them using high-throughput sequencing. We assembled complete and partial organellar genomes from these specimens and conducted phylogenetic analyses.

Trees obtained from our plastid dataset match our molecular phulogenies with increased backbone support. Phylogenetic trees obtained from the entire nuclear ribosomal arrays were congruent with mitochondrial trees. However, our results showed previously unreported discordance between the plastid and the nuclear/mitochondrial phylogenies.

Monogynella plastomes showed similar features to other *Cuscuta* plastid genomes, including losses of genes, introns, as well as variable inverted repeat regions, a reflection of their parasitic lifestyle. The fine-scale nature of the plastomes has allowed us to phylogenetically traingulate locations of gene loss events and enchances out current understanding of the step-by-step model of plastome evolution in Cuscuta. Unlike plastid genomes, we did not find extensive gene loss in their mitochondrial counterparts. We have not found any instances of horizontal gene transfer as has been previously reported in other *Cuscuta* species. Using this research, we aim to further ascertain the position of *Cuscuta* in the Convolvulaceae phylogeny.

Topic: Conservation Biology

A-470

Investigating the Impact of Vitrification on Shoot Tip Survival in Threatened Oak Species

Author: Max Winkeljohn, Valerie Pence, Theresa Culley, Megan Philpott
Affiliation: University of Cincinnati, Cincinnati Zoo & Botanical Garden

Of the nearly 500 species of oaks (*Quercus* spp.) that exist worldwide, over one-third are of some conservation concern. Within that group, at least 112 species have been assessed as Vulnerable, Endangered, or Critically Endangered, and thus are in urgent need of safeguarding efforts. However, as exceptional species, oaks are unable to be conventionally seedbanked and instead require alternative methods such as cryopreservation to be effectively preserved *ex situ*. Despite this need, oak cryopreservation has been relatively under studied compared to cryopreservation of other agricultural or economically important crop species. One of the primary challenges to implementing this technique for a wide range of species is the relatively low survival of the shoot tips after being frozen in liquid nitrogen (LN), often resulting from the intracellular formation of damaging ice crystals. Although this may be prevented through the use of vitrifying agents, several of the most popular cryoprotectants are also inherently cytotoxic and may actually decrease shoot tip survival at longer exposure intervals. However, this interaction has not been well studied in oaks thus far, which may hinder attempts to cryopreserve threatened species. To address this gap, shoot tips of two endangered oak species, Engelmann Oak (*Q. engelmannii*; Qe) and Hinckley's Oak (*Q. hinckleyi*; Qh), were treated with Plant Vitrification Solution 2 (PVS2) for intervals ranging from 0-90min, in order to identify the tolerance of each species to PVS2 and determine whether increased exposure would result in greater survival after freezing in LN. After testing, Qe demonstrated some sensitivity to the cryoprotectant solution, with survival through the PVS2 step decreasing notably at exposure intervals greater than 40 min. Furthermore, survival through LN remained low at all exposure intervals, which suggests that other factors may need to be investigated in order to improve survival of this species. However, Qh demonstrated greater tolerance to the vitrifying agents, with survival through PVS2 decreasing much more gradually at longer exposure intervals. Additionally, survival of this species through LN showed an obvious peak at 20-30 min of PVS2 exposure, offering a promising lead towards the development of an optimized oak cryopreservation protocol. These findings will help guide and inform future research and shall contribute to ensuring the successful long-term preservation of these threatened tree species.

Topic: Paleobotany

A-471

Flower of Monimiaceae from the Late Cretaceous of Antarctica

Author: Keana Tang, Selena Smith, Ari Iglesias, Kelly Matsunaga, Brian Atkinson
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Monimiaceae comprises 200 species within 28 genera that are distributed across tropical forests of the Southern Hemisphere. The sparse fossil record of the family extends back to the Late Cretaceous and is based on wood from Africa and Antarctica. Monimiaceae leaves have been reported from the Eocene of Patagonia (South America). Reproductive structures such as fruits or flowers remain unknown in the fossil record of this family. Here, we report a new fossil flower assignable to Monimiaceae from early to middle Campanian (Late Cretaceous; 82-80 Ma) deposits of the Sitio Feliz locality in James Ross Island, Antarctica. The permineralized fossil flower was serial sectioned using the cellulose acetate peel technique and studied using light microscopy. To assess potential relationships to Monimiaceae, the Antarctic flower was initially analyzed using the phyloscan method. A Bayesian phylogenetic analysis was then conducted using a recently developed morphological dataset of 56 floral and pollen characters to test the phylogenetic position of the Antarctic flower within Laurales. RoguePlots were constructed from the posterior sample of trees produced by the Bayesian analysis to visualize additional positions and assess phylogenetic uncertainty of the fossil flower. The Antarctic flower is characterized by the presence of an urceolate receptacle bearing fertile stamens and carpels. The apex of the flower is abraded and the perianth is not preserved. We estimate up to 14 stamens and 20 carpels are present in the flower. Stamens are arranged near the apex of the receptacle. Paired staminal appendages are present at the base of each filament. Anthers are bilocular and dehisce by longitudinal slits. Spheroidal pollen grains covered in spinules were found among the anthers and filaments. Carpels are present at the base of the receptacle. Each carpel has a long style and contains a single apically attached ovule. Based on these characters, the Antarctic flower is assignable to Monimiaceae as a new genus. Our phylogenetic analyses recovered the Antarctic flower within crown-group Monimiaceae as sister to *Hortonia*, the only genus in the family to have perfect flowers. However, an urceolate receptacle is absent in flowers of *Hortonia*. Within the posterior sample of trees, multiple phylogenetic positions within Monimiaceae were recovered for the Antarctic flower. These included placement as stem-group Monimiaceae, as well as sister to the two major clades in Monimiaceae. No additional positions were recovered outside of the family. The presence of fertile stamens and carpels inside an urceolate receptacle represents a unique combination of characters in Monimiaceae that is not found in living members of the family, and phylogenetic analyses suggest it may be an early crown member of the family. The Antarctic fossil flower provides unequivocal evidence of an extinct lineage of Monimiaceae in the Late Cretaceous and sheds new light on the floral diversity and early evolution of the family. Furthermore, the Gondwanan distribution of the family and the occurrence of this fossil flower in Antarctica provides additional evidence for the Cretaceous dispersal of Monimiaceae across South America, Antarctica, and Australia.

Topic: *Macroevolution*

A-472

Well-resolved phylogeny supports repeated evolution of keel flowers as a synergistic contributor to papilionoid legume diversification

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The butterfly-shaped keel flower is a highly successful floral form in angiosperms. These flowers steer the mechanical interaction with bees and thus are hypothesized to accelerate pollinator-driven diversification. The exceptionally labile evolution of keel flowers in Papilionoideae (Fabaceae) provides a suitable system to test this hypothesis.

Using 1456 low-copy nuclear loci, we confidently resolve the early divergence history of Papilionoideae. Constrained by this backbone phylogeny, we generated a time tree for 3326 Fabales to evaluate the tempo and mode of diversification within a state-dependent evolutionary framework.

The first keel flowers emerged *c.* 59.0 million years ago in Papilionoideae, predating the earliest fossil by 3–4 million years. The Miocene diversification of Papilionoideae coincided with the rapid evolution of keel flowers. At least six independent origins and 32 losses of keel flowers were identified in Papilionoideae, Cercidoideae, and Polygalaceae. However, the state-dependent diversification model was not favored.

Lack of radiation associated with keel flowers suggests that diversification within Papilionoideae was not solely driven by pollinator-mediated selection, but instead an outcome of the synergistic effects of multiple innovations, including nitrogen fixation and chemical defense, as well as dispersal into subtropical and temperate regions.

Topic: *Paleobotany*

A-473

Cretaceous calcareous concretion containing callitroid Cupressaceae cone cluster

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The Callitroideae subfamily of Cupressaceae is comprised of eight genera of coniferous trees and shrubs that occupy a wide range of ecological habitats across the Southern Hemisphere. The subfamily is morphologically diverse and contains woody seed cones with few decussate or whorled ovuliferous complexes. Divergence time estimates place the origin of Callitroideae during the Late Cretaceous and it is believed that they had a widespread distribution across Gondwana throughout this interval. However, we have only a limited understanding of the early evolution of these conifers. While Callitroideae have a rich Cenozoic record, the only unequivocal Cretaceous fossils are a seed cone from Australia and wood fragments from Argentina. Here, we introduce a new callitroid fossil from Late Cretaceous deposits of Antarctica, which help to fill this gap in our knowledge of their early fossil record. The specimen is represented by seven seed cones permineralized within a calcium carbonate concretion from the Sitio Feliz locality of the Santa Marta Formation, Beta Member (Campanian; 82–80 Ma) of James Ross Island, Antarctica. The seed cones are mature, fully dehisced and terminal on a branching shoot system. Each cone is ca. 11 mm long, 5 mm wide, and consists of four valvate ovuliferous complexes arranged in two opposite decussate pairs. The most basal pair of ovuliferous complexes are slightly shorter than the apical pair. At the center of the cone is a small columella, which extends 1 mm beyond the cone axis and contains a large resinous cavity. The ovuliferous complexes are bifacially flattened, 1 mm thick, 5 mm wide, and have well-developed vasculature. At least three resin canals supply the base of the ovuliferous complex. A small umbo is located distally on the ovuliferous complex but does not extend beyond it. The subtending shoots are weakly flattened with dimorphic decussate leaves. The new seed cones are strikingly similar in morphology, anatomy and size to the cones of the *Libocedrus*-group of Callitroideae (*Austrocedrus*, *Libocedrus, Pilgerodendron*, *Papuacedrus*), all of which have seed cones with four flattened, decussate ovuliferous complexes and a central columella. It is most like *Austrocedrus*, which has a minute umbo located at the distal end of the ovuliferous complex. Preliminary phylogenetic analyses place this new fossil sister to *Austrocedrus* chilensis and likely represents a new species of the genus. This new taxon is among a growing list of anatomically preserved fossils described from the Cretaceous of Antarctica that provides insight into the evolution, ecology, and diversity of Gondwanan plants. These new seed cones are, to date, the oldest known of the *Libocedrus*-group and will have impacts for reconstructing divergence times, phylogenetic relationships, and biogeographical interpretations of Cupressaceae.

Topic: *Paleobotany*

A-474

Fossil leaves of Sindora (Fabaceae, Detarioideae, Detarieae) from the Plio-Pleistocene of central Vietnam

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Fabaceae fossil leaf records are abundant, but their identification below the family level is usually challenging due to the lack of distinctive leaf architecture in most genera. Our recent discovery of the Pliocene-early Pleistocene Kon Tum flora from the Central Highlands Region of Vietnam revealed a tropical lowland forest characterized by predominantly small, entire-margined leaves. From over 80 morphotypes across eight sites, we identified numerous taxa including *Ficus* (Moraceae), *Syzygium* (Myrtaceae), *Dipterocarpus* (Dipterocarpaceae), *Barringtonia* (Lecythidaceae), *Bridelia* (Phyllanthaceae), *Cinnamomum* (Lauraceae), *Bauhinia* (Fabaceae), *Calophyllum* (Calophyllaceae), and others. We focus here on a distinctive fabaceous leaf type. The leaflets are short-pulvinulate and microphyll to notophyll in size, with an entire margin, oblong to slightly obovate shape, convex to cuneate base, and emarginate apex. The secondary venation is craspedodromous, with over 10 pairs of nearly straight veins terminating in thick marginal veins, frequent intersecondary veins, and reticulate higher-order venation. The diagnostic feature is a swollen mark (terminal gland) on the midvein near the apex. Our survey of over 2400 Fabaceae cleared leaves and additional herbarium specimens revealed that similar craspedodromous secondary venation occurs primarily in the tribe Detarieae (subfamily Detarioideae), and only *Sindora* shows the terminal gland, enabling confident identification of our fossils. The Detarioideae (81 genera, ca. 760 species) have a pantropical distribution, with highest diversity in Africa (ca. 47 genera, ca. 330 species), followed by the Neotropics (ca. 16 genera, ca. 247 species) and tropical Asia (ca. nine genera, ca. 124 species). Prior to our discovery, reliable fossil leaves for this subfamily were documented only from the late Oligocene to Miocene of Ethiopia. *Sindora* is a tropical deciduous tree genus comprising 20 species across South China, Indochina, and Malesia (centered in Borneo), with one species in Africa (Gabon). The trees typically occur scattered in lowland primary forests or as remnants in mature secondary forests, functioning as canopy or emergent trees. Their ecological role is poorly documented, but they are bee- or fly-pollinated. Various species are used for timber, medicine, and oleo-resin, and their seed arils are locally used for betel chews. Species-level comparisons are difficult due to overlapping leaf morphology among several extant species similar to the fossils, including *S. siamensis*, *S. supa*, *S. leiocarpa*, and *S. wallichii*. Only *S. siamensis* currently occurs in Indochina, as a common component of deciduous dipterocarp forests. Despite its characteristic leaf architecture, *Sindora* previously lacked reliable fossil records beyond dubious leaves and ambiguous woods (reported as *Hopeoxylon* associated with multiple generic affinities, from the Eocene to Pliocene of the Indian subcontinent plus northern Africa and Saudi Arabia). Our discovery represents the first definitive *Sindora* leaf fossils, which constitute one of the most abundant elements at one Kon Tum flora site, comprising 8% of all categorized specimens, and representing the only probable deciduous taxon identified so far. This fossil evidence establishes that *Sindora* has been a significant constituent of Indochinese tropical monsoonal forests since at least the Plio-Pleistocene.

Topic: *Functional Genetics/Genomics*

A-475

The genetic basis of a novel self-pollen recognition system in Phlox drummondii (Polemoniaceae)

Author: Grace Burgin
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Genetic mechanisms to recognize and reject self-pollen (termed “self-incompatibility”) have evolved independently many times throughout flowering plant evolution. Of the few known mechanisms, each achieves self-incompatibility through distinct molecular pathways with a unique genetic basis, and most self-recognition systems remain uncharacterized.

We combine classical genetic crosses with genomic tools to identify the genetic basis of a novel self-recognition mechanism in the wildflower, *Phlox drummondii*. We find no expression of known self-recognition genes (so called "S-loci") in pistil transcriptomes, consistent with a currently uncharacterized self-recognition mechanism having evolved in the lineage containing *Phlox*.

We use a bulk segregant analysis to map self-recognition to a single genomic region in two independent populations. Analyses of expression and polymorphism for genes within this region narrow our search to a single gene candidate which we name "*PdPIRK*". Allelic variation at *PdPIRK* predicts cross-compatibility in a full diallel cross, providing further confirmation of its role in self-recognition. We functionally validate *PdPIRK*'s role in self-pollen recognition by silencing its expression which causes increased self-compatibility and cross-compatibility in an allele-specific patten. Our work identifies the genetic basis of a novel self-recognition system in flowering plants, adding to our understanding of the diverse mechanisms through which flowering plants achieve this evolutionarily significant phenotype

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Topic: Systematics & Taxonomy

A-476

Unravelling the evolutionary success of big plant genera

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Big angiosperm genera comprise over 500 species and are key players in global biodiversity, representing 25% of all plant species, and provide unique insights into the evolutionary assembly of species radiations. Yet, the factors driving their exceptional diversity remain poorly understood. My PhD explores the evolutionary and ecological mechanisms behind the success of the 87 big angiosperm genera with >500 species each, shedding light on their taxonomic stability, biological traits, distribution and evolution. Key objectives include understanding how taxonomic reclassifications impact genus size, identifying climatic and geographic hotspots of species diversity, and understanding morphological trait diversity in big genera. I will use a generalized mixed-Yule coalescent (GMYC) approach to test whether big genera represent real evolutionary units or artifacts of human classification. By leveraging extensive biodiversity datasets and collaborating with taxonomic specialists, this study will bridge classical taxonomy with modern analytical tools. The research outputs are expected to contribute to unravelling broader patterns and processes that shape global plant biodiversity, and to answer if genera are real.

Topic: Ecophysiology

A-477

Photosynthesis evolution at extremes: Assaying physiological diversity within Montiaceae

Author: Ellie Jose, Anri Chomentowska, Lan Wei, Erika Edwards
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Crassulacean acid metabolism (CAM) photosynthesis is a critical plant adaptation to hot and arid environments. Across many independent origins, some species have evolved to utilize CAM photosynthesis facultatively during periods of stress, such as drought (a phenotype characterized as C_3+CAM). While "normal" C_3 photosynthesis involves carbonaccumulation during the day, CAM photosynthesis dictates CO_2 fixation at night to minimize daytime transpiration water loss. In this study, we surveyed species in Cistantheae, a subclade of Montiaceae, to interrogate the distribution of CAM photosynthesis across a diverse lineage adapted to different environments. We tested ten species across four clades within Cistantheae: *Calyptridium*, *Philipiamra*, *Montiopsis*, and *Cistanthe*. Expression of CAM in these species was measured through titratable acidity assays in fully watered and drought states and carbon isotope analysis. Our assays show significant upregulation of CAM in eight species within *Cistanthe* and *Philipiamra*, confirming the characterization of those species as C_3+CAM. The *Calyptridium* and *Montiopsis* clades tell a different story, with results denoting two independent evolutionary reversals back to C_3. These two instances show both a physiological and anatomical shift away from C_3+CAM: a loss of diurnal acid accumulation during drought and a loss of succulence. Environmental data in tandem with these findings show the reversal from the energy-costly CAM pathway back to C_3 under higher elevation, alpine growing conditions. Understanding the environmental and organismal context in which CAM function is lost provides another means for assessing the adaptive significance of CAM metabolism.

Topic: Hybrids and Hybridization

A-478

Quantifying the effects of polyploidy on reproductive isolation in Texas Phlox

Author: Christina Steinecke
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Reproductive isolation (RI), which reduces gene flow among populations, typically results from multiple isolating barriers rather than a single, symmetrical mechanism. Empirical estimates of the importance of barriers to gene flow between recently diverged species are crucial for understanding speciation. To fully understand speciation, RI must be studied across various mechanisms. Polyploidy, or whole-genome duplication (WGD), occurs in nearly all flowering plant families and is often considered an instantaneous route to postzygotic RI and speciation. Polyploid genomes are generally incompatible with progenitor diploids, as backcrossed hybrids (e.g., triploids) are often sterile or inviable. While many hypotheses address polyploid formation and associated RI barriers, few studies systematically examine the roles that these barriers play in the evolutionary origins and establishment of polyploid s. *Phlox villosissima* (A. Gray) is a perennial tetraploid wildflower native to central Texas. It is s uspected to be an allopolyploid that likely arose from hybridization between *P. pilosa* subsp. *pilosa* (a perennial with variable ploidy) and *P. drummondii* (a diploid annual). Here we estimate RI across prezygotic and postzygotic mechanisms to investigate whether *P. villosissima* is reproductively isolated from other *Phlox* species, whether postzygotic RI is stronger than prezygotic, and how cytotype and life history influence RI. We hypothesize that *P. villosissima* experiences RI with both parental species via multiple mechanisms, that ecological and phenological differences strengthen within-ploidy prezygotic RI, that life history strategies enhance prezygotic RI, and that postzygotic RI is strongest between diploid and tetraploid species. This work empirically tests assumptions about RI in closely related, sympatric species differing in ploidy and life history allowing us to tease apart how various genomic and organismal factors can contribute to the way in which RI evolves.

Topic: Paleobotany

A-479

Organically preserved leaves from the Eocene Anglesea flora reveal first early Paleogene records of four angiosperm families in Australia

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The late middle Eocene Anglesea flora, from the Alcoa coal mine in Anglesea (Victoria, Australia; paleolatitude 58°S), is renowned for its organically preserved plant fossils representing terminal-Gondwanan Australian ecosystems. Extensive collections made at Anglesea during the 1980s and early 1990s by the late D. C. Christophel recovered thousands of leaves and dozens of flowers and fruits from clay lenses of coastal-plain fluvial origin (Salt Creek Formation, Demons Bluff Group). Although the mine permanently closed in 2015, making further fieldwork no longer possible, a significant portion of the leaf material is currently housed at the Melbourne Museum of Victoria, much of which remains to be systematically studied and described. Here, we report several organically preserved leaves and associated cuticle preparations from Anglesea that exhibit diagnostic features of angiosperm families previously unrecognized in the early Paleogene of Australia, including Dilleniaceae, Euphorbiaceae, and the lauralean families Atherospermataceae and Monimiaceae. These findings mark the first new family-level identifications for the Anglesea vascular-plant flora in over three decades.

Leaves attributed to Dilleniaceae are characterized by craspedodromous secondary venation terminating in prominent glandular teeth, reticulate tertiary venation, and tiny (<20 µm) paracytic stomata. A single leaf specimen with peltate petiole insertion, small teeth, disc-shaped glandular scales, and large sunken stomata (<50 µm) with ornate subsidiary cells is consistent with the genus *Macaranga* (Euphorbiaceae). Leaves assigned to Atherospermataceae have a multistranded midvein, festooned semicraspedodromous secondary veins, and serrate teeth with glandular tips, as well as anomocytic stomata (<40 µm) with striated subsidiary cells. Finally, Monimiaceae leaves exhibit festooned semicraspedodromous secondary veins, irregularly spaced glandular teeth, as well as distinctive paracytic stomata (<40 µm). The addition of four new angiosperm families to the early Paleogene fossil record of Australia highlights the

ongoing potential for discovery at historical paleobotanical sites, and reinforces the importance of the Anglesea flora as a window into terminal-Gondwanan ecosystems and the early evolution of Australian rainforests.

Topic: *Phytochemical*

A-480

Elemental stoichiometry in Australian showy mistletoes: The influences of hosts and spatial effects on nutrient assimilation

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Organisms often experience stoichiometric mismatches when the elemental composition of their resources differs from their own biochemical needs. In parasitic mistletoes, which extract nutrients from host plants, such mismatches can be caused by physiological adaptations and can have consequences for ecological interactions, with important implications for nutrient cycling, community dynamics, and evolutionary trajectories. Mistletoes typically exhibit distinct elemental profiles compared to their host plants, but the patterns of misaligned elemental concentrations between mistletoes and their hosts across different environmental conditions and taxonomic groups remain unclear.

In this study, we quantified the concentrations of 13 elements (Al, B, C, Ca, Cu, Fe, K, Mg, Mn, N, Na, P, S, Zn) in leaf tissue from 165 mistletoe–host pairs for showy mistletoes (Loranthaceae), representing 89 species combinations across three regions of Australia. Using bioconcentration ratios, host-mistletoe elemental relationships, and spatial mixed-effects models, we tested whether mistletoes accumulate particular elements and assessed the degree to which their elemental concentrations mirror those of their hosts. We considered taxonomic identity, species pairings, and spatial autocorrelation to identify key drivers of elemental relationships.

Our results revealed that mistletoes accumulated higher concentrations of B, Cu, P, K, and Na, while having lower concentrations of Fe and N compared to their hosts. Elemental differences were highly variable across host-mistletoe pairs, influenced by host family, mistletoe genus, and spatial autocorrelation. These findings highlight the complex ecological and spatial factors that govern plant host-parasite elemental dynamics.

This study underscores the complex and context-dependent nature of nutrient uptake and assimilation in parasitic plants and how their life histories may differ from autotrophic plants (i.e., plants interacting with the soil). By selectively bioaccumulating certain elements like B, Cu, P, K, and Na, mistletoes appear to employ a nutrient strategy that likely supports their unique physiological needs, including high transpiration rates, extended reproductive phenology, and osmoregulatory capabilities, among others. The ability of mistletoes to selectively assimilate nutrients based on ecological and physiological requirements highlights their role as dynamic components in nutrient cycling and community interactions across diverse Australian ecosystems.

Topic: *Development and Structure*

A-481

Comparative anatomy of above and below ground leaf morphologies in bulbous plants

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Bulbous plants are those with buds located on a vertically compressed stem surrounded by overlapping layers of leaf tissue that acts as the site of resource storage, typically below the soil surface. In the monocot order Asparagales, the bulbous habit has repeatedly evolved. Across these evolutions remarkable above ground leaf diversity exists, ranging from broad, dorsiventral ("dicot-like") to narrow, ensiform (sword-shaped) leaf forms. How this diversity in leaf form translates to below the soil surface is not well understood. Here, to study how characteristics change along the length of a bulbous plant leaf and how these changes may influence leaf morphology, we take a comparative anatomical investigation of three bulbous species from Amaryllidaceae (*Brunsvigia* sp. and *Boophone* sp. with ensiform leaves) and Asparagaceae (*Massonia* sp. with broad, prostrate leaves). We compare anatomy of both the above ground (photosynthetic) and below ground (storage tissue) leaf parts using light microscopy. For the above ground leaf parts, we specifically examine leaf anatomical characters including stomatal distribution, epidermal, and mesophyll characteristics. Belowground, we examine cellular structures such as hydrenchyma, parenchyma and other storage tissues. For both the above ground and below ground traits, we quantify their size, shape, and number using ImageJ. Across species, our study focuses on identifying structural adaptations correlated with the distinct leaf morphologies and their potential functional implications. By examining these traits in phylogenetically related but morphologically divergent taxa, we aim to better understand the potential adaptive significance of leaf morphologies found across bulbous plants. Our comparative approach will provide insights into how the ecological niche of these species contributes to the morphological diversification of bulbous plant leaf forms. More broadly, our findings will better our understanding of monocot leaf evolution overall.

Topic: *Functional Genetics/Genomics*

A-482

Is Evolution Predictable? Parallel Trait Evolution and Genetic Architecture in Mimulus Species

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The repeatability of evolution is a central question in evolutionary biology, offering insight into how natural selection drives the diversity of life. In particular, determining whether parallel phenotypic evolution arises from shared or distinct genetic mechanisms helps illuminate the pathways through which species adapt to similar environments. To address this, I am investigating the genetic basis of parallel trait evolution in serpentine-adapted *Mimulus guttatus* and rocky-outcrop-adapted *Mimulus lacinatus*. These species exhibit convergent evolution in early flowering time, leaf lobing, and red floral spotting—traits likely associated with adaptation to harsh environments. Using a comparative QTL mapping approach, I analyzed phenotypic and genotypic data from four F2 hybrid mapping populations generated by intercrossing a typical wet seep *M. guttatus*, serpentine *M. guttatus*, and *M. lacinatus*. My results suggest that floral spotting is likely controlled by one or two loci of large effect in both species, while flowering time and leaf lobing are more polygenic, influenced by many loci of small effect. These findings provide insight into the extent to which evolutionary outcomes—and their underlying genetic architecture—are predictable across independently adapting lineages. Ongoing genomic analyses will further clarify the degree of genetic parallelism underlying these repeated trait shifts.

Topic: *Population Genetics/Genomics*

A-483

Genomics of common stinging nettle (Urtica): disentangling evolution and sex determination in a North American species complex

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The stinging nettle complex includes both the Eurasian *Urtica dioica* s.s., which exists as both diploids and tetraploids and is introduced in North America and the North American subspecies *U. dioica* ssp. *gracilis*, which is native to North America and generally diploid. It is a highly variable and actively evolving group notorious for its taxonomic complexity. The European material is dioecious, while the North American plants are monoecious. It is a group of great interest for both evolutionary biology and the study of sex determination. We have produced high-quality haplotype-resolve genomes of both male and female European diploids using PacBio HiFi as well as Hi-C long-range interaction data. We assembled haplotypes of ~550Mb, which showed a number of interesting features, including two copies of a gene putatively encoding the pain-inducing neurotoxic peptide urthionin. The genome also displays a high degree of structural variation. To assist in distinguishing male and female (XY) haplotypes, the sequenced male was chosen as the progeny of the sequenced female, allowing identification of the male (Y) haplotype, and a putative sex-determining region (SDR) contains sequences unique to the Y-haplotype. In future we plan to assemble a monoecious native North American nettle in order to compare the SDR region of the genome between monoecious and dioecious types. Further comparative genomics holds the promise of untangling the biosystematics of this complex. We hope that these genomic resources will stimulate work on this interesting genus across North America.

Topic: *Macroevolution*

A-484

Analyzing reproductive disparity across seed plants using a flexible character scoring system

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Seed plants have evolved extremely diverse reproductive structures in response to functional demands relating to pollination, seed protection, and seed dispersal. Some groups exhibit greater disparity and more morphological variation through time than others, but quantifying differences among major clades is difficult because they often show highly divergent structures and may lack homologous organs. Understanding patterns in the evolution of plant reproductive disparity at the broadest phylogenetic scales is therefore challenging. Here we develop a discrete character scoring framework in which a set of 50 morphological characters can be applied separately to any organ that composes a plant reproductive structure. We calculated morphological distances between representative extant gymnosperm and angiosperm genera based on scoring all organs in the reproductive structure individually ('structural analysis'), which allows them to be compared based on potential homologies, or by combining character scorings into a homology-free aggregate set of morphological features ('combined analysis'). We used these approaches to ask how major seed plant clades occupy a single reproductive morphospace. In general, high-level gymnosperm clades (e.g. orders) occupy localized regions of morphospace but show high variation among clades, whereas major angiosperm clades (e.g., magnoliids, eudicots) occupy similar but broad regions of character space. Among all seed plants, pairwise morphological distances among taxa increases with pairwise divergence ages, but maximum morphological distance increases faster among angiosperm clades, especially in the structural analysis. This pattern is consistent with the wide diversity of organs that compose angiosperm flowers, such as staminodes and perianth elements. Gymnosperms therefore appear to show lower rates of reproductive evolution than angiosperms; clades occupy more restricted areas of morphospace and fill space slowly through time. A direct comparison of such distantly related and structurally divergent groups is possible through the analytical framework that we use here, which allows placement of disparate reproductive structures into a single morphospace.

Topic: *Functional Genetics/Genomics*

A-485

A deeper dive into the genetics of Bouteloua curtipendula in Southwest New Mexico

Author: Mickie Barraza, Sara Fuentes-Soriano
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There is currently a lack of standardized guidelines for seed sourcing, making it difficult to trace bulk seeds back to individuals with desirable traits—particularly restoration projects using native species like Bouteloua curtipendula. Without reliable sourcing methods, it is challenging to ensure that seeds have the genetic characteristics necessary for long-term restoration success. To address this, our project focuses on characterizing the genetic diversity of B. curtipendula, a grass species widely used in restoration efforts. By examining the potential link between genetic variation and ecological performance, we aim to enhance seed productivity and provide data to support breeding programs. Our study focuses on six wild populations from southwestern New Mexico, where we are estimating genome size and chromosome counts to assess ploidy variation.. Preliminary results reveal two distinct phenotypes (i.e. plant size) groups and genome sizes clustering at low and high extremes within a single population with may suggest mix cytotypes or polyploid variants. Although polyploidy has been previously documented in central and northern New Mexico populations, our findings suggest it may also be widespread in the southwest. Future research will aim to determine the extent and distribution of polyploidy and cytotypes within and among populations of Bouteloua curtipendula and to estimate the potential correlation with functional trait diversity such as germination, establishment, or seed production rates.

Topic: *Education and Outreach*

A-486

How well do CURE labs train students to assess the spread of invasive and weedy species in Minnesota?

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Course-Based Undergraduate Research Experiences (CURE) in Plant Biology at St. Cloud State University allow undergraduate students to complete research projects using data from digitized natural history collections. Students enrolled in Fall 2023 and Spring 2025 semesters implemented independent research studies via a CURE module adapted from the Biological Collections in Ecology and Evolution Network (BCEENET) to assess how invasive species and weedy nonnative species distributions have changed in Minnesota over time. First we generated a list of Minnesota plant taxa that are either weedy and nonnative or invasive with 300 or more occurrence records in GBIF. Then, each student selected a taxon, did some literature searches and review, and developed a hypothesis about their species. Most hypotheses concerned either the effectiveness of Minnesota's invasive species statutes or population distribution changes due to various ecological or geographic factors. Raw occurrence data were downloaded from GBIF and then filtered and georeferenced to ensure high-quality maps could be made and analyzed in QGIS to generate maps representing species distributions at various time points. Students were then encouraged to draw conclusions that either support or refute their hypotheses, implement double-blind peer review, and then present their work in both written and graphical abstracts. We present an overview of the results of these studies and provide assessment results alongside commentary on how well these labs train students on the scientific method, invasive species biology, and technical skills.

Topic: *Bryology and Lichenology*

A-487

The disjunct distribution of bryophytes in the Neotropics and Africa: a Collections-based synthesis

Author: Lova Marline
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A feature of the biogeography of many groups is disjunction, where related taxa are found in separate, often widely separated geographic areas with no populations in between (despite seemingly suitable habitat). Studying disjunctions offers an opportunity to better understand historical connections between taxa in distant regions and how species dispersal mechanisms contribute to distribution patterns across scales. Among plants, disjunctions between the Neotropical region and the African region (including its associated islands) have received attention but the drivers of observed patterns remain poorly understood. Disjunct distribution patterns are hypothesized to result from various processes such as historical land connections, the fragmentation of a once more continuous distribution, and long-distance dispersal. Previous analyses, however, have suffered from inadequate representation of specimens from important geographic areas and taxonomic uncertainty, leading to limited confidence in the validity of many supposedly disjunct taxa. Bryophytes provide an opportunity to better characterize the relationships between taxa shared between the Neotropics and-Africa. Notably for the bryophytes, disjunct distributions are common and often observed at the infra-specific level, with subpopulations of a single species observed in both the Neotropics and Africa. A screening of the literature revealed 41 species and 8 genera or infrageneric liverwort taxa with Neotropical-African ranges. Delgadillo (1993) reported 334 shared moss species between the Americas and Africa, of which 45 are exclusively from South America and Africa.

This research aims to synthesize data on the geographic connections between the bryophyte floras of the Neotropical and African regions. A comprehensive synthesis and literature update are needed to clarify the current state of knowledge regarding Neotropical–African disjunct bryophytes. Based on published literature, herbarium collection and open-access resources (e.g., GBIF, Tropicos), this study (1) provides a detailed overview of the distribution of Neotropical–African bryophytes at both the genus and species levels and (2) explores the connectivity between the Neotropical and African regions, assessing the geographic connections among bryophyte floras and pinpointing regions of overlap.

Topic: *Lichen and Bryophyte Diversity, Conservation, and Evolution in the Americas*

A-488

Understanding secondary succession of lichen communities: a tool for conservation

Author: Natalia Mossmann Koch, Mariana Cardenas Henao, Daniel Stanton
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Understanding how ecosystems recover after disturbance is of extreme importance for conservation. The community patterns of environmentally sensitive taxa, such as lichens, can offer valuable insights into ecosystem recovery during secondary succession. Here we compare secondary succession in the lichen communities of two contrasting ecosystems: neotropical evergreen forests and temperate grasslands. Considering the high conservation value of both forests and prairies, this work aims to demonstrate 1) how the understanding of taxonomic, functional and phylogenetic patterns of lichen communities along natural forest succession can be used as tool for conservation, and 2) what are the lichen community patterns observed after agriculture abandonment in prairies in Northern US. We used the replacement of time by space approach for both studies. For the forest succession data, we sampled epiphytic lichens along a 60-year natural succession gradient of Atlantic rainforest in southern Brazil. Functional analyses were based on a qualitative functional approach assessing nuanced traits, such as a greater resolution over photobiont identity, type of cortex, and chemical compounds. For the US prairie data, terricolous lichens were sampled from previously agriculture fields in Minnesota along a gradient of almost 100 years at Cedar Creek Ecosystem Science Reserve. In the forest succession chronosequence, we found changes in taxonomic, functional, and phylogenetic composition, structure, and diversity. Functional traits such as photobiont genera, type of cortex, reproductive structures, and propagule size showed strong responses to forest succession. In the prairie succession, there was an increase in lichen cover and richness with time until the mid-successional stages, but a steep decrease afterward, when plant biomass outcompeted lichen communities. Mature forests with a closed canopy impose strong environmental filtering that is reflected in lichen species turnover, limiting diversity, but also holding different functional and phylogenetic composition. Intermediate to old prairie fields showed higher lichen diversity than younger ones. So, understanding community taxonomic, functional (including often-overlooked lichen functional traits) and phylogenetic patterns has the potential to be used as important tools for assessing changes along secondary succession in forests and prairies across the Americas and can thus contribute to a better knowledge of lichen conservation.

Topic: *Pteridology*

A-489

Beyond Species and Tropics: Rethinking Niche Conservatism in the Fern Order Cyatheales

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Niche conservatism, the tendency of lineages to retain ancestral ecological traits, offers key insights into species distributions and biodiversity patterns. Traditionally studied at the species level within tropical contexts, niche conservatism can also be explored across broader taxonomic and geographic scales. We expand the scope by examining phylogenetic and tropical niche conservatism (PNC and TNC) within Cyatheales, an ecologically diverse order of ferns comprising eight families distributed across tropical, subtropical, and temperate zones.

Species-level analyses often equate geographic ranges with realized niches, emphasizing abiotic environmental needs. However, this approach may overlook evolutionary history, dispersal constraints, and biotic interactions. Assessing niche patterns at the genus and family levels allows for the detection of broader ecological trends and deeper evolutionary signals. Genera and families, as evolutionary units, offer more robust frameworks for exploring niche retention and divergence across clades.

We evaluate niche overlap across family-level and genus-level comparisons in Cyatheales to test whether ecological similarity aligns with phylogenetic relatedness. While many Cyatheales species exhibit traits consistent with TNC, thriving in warm, stable tropical forests, others persist in more variable climates, indicating ecological flexibility within the clade.

This study goes beyond species-level analysis to explore how ecological niches change or remain stable over time and across different groups. The results provide important insights for evolutionary biology, biogeography, and conservation, especially in identifying lineages with strong niche conservatism that may be more at risk from climate change.

Topic: *Plant phenology in an era of rapid global change: new perspectives and frontiers*

A-490

Indiana Jones and the Temple of Bloom: Herbaria as the New Archaeological Sites for Plant Phenology

Author: Rocio Perez-Barrales, José Grande Allende
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Herbaria harbour a vast collections of preserved plant specimens, serving as invaluable "time capsules" that offer insights into historical plant phenology. Using herbaria collections, botanists can become the new Indiana Jones, just as archaeologists unearth clues from ancient ruins, by carefully annotating the phenological status of plants as it remained when pressed in herbaria. Hence, these plant collections offer a unique opportunity to study long-term phenological patterns of species, and therefore investigate the association between climatic shifts on flowering and fruiting dates. In this context, *Linum bienne* Mill. (Linaceae), a species native to the Mediterranean and Atlantic Europe, serves as a fascinating case study. The species exhibits latitudinal variation in the timing of flowering, influenced by local climatic conditions. We used digitalised specimens available in GBIF, and retrieved phenological data including floral buds, mature flowers and fruits from sheets with detailed information on dates of collection and localities (either with coordinates or detailed information of the location of the sampling site). Then, we explored associations between dates of collection as day of the year, latitude and longitude with different phenological proxies (i.e. % floral buds, % open flowers, % fruits). By retrieving data from herbarium sheets within the native range and using distribution models, this study explores the geographic and temporal shifts in Linum bienne's flowering phenology. Our findings not only elucidate changes in phenological trends over the past 200 years, but also establish a foundation for predicting how *Linum bienne* and similar species may adapt to future environmental changes. In this way, herbaria act as the new "archaeological sites" for studying plant responses to climate change, unlocking valuable insights into the evolution and resilience of plant species in the face of global change.

Topic: *Biogeography*

A-491

Digging into the general dynamic model: How island ontogeny leads to shifts in the evolutionary drivers of lineage divergence

Author: Brock Mashburn, Alexander Linan, Timothée Le Péchon, Sevathian Jean-Claude, Ken Olsen, Christy Edwards
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The general dynamic model (GDM) of oceanic island biogeography proposes that evolutionary processes shift predictably with island ontogeny, yet direct tests of its micro-evolutionary predictions remain rare. In this study, we refine and extend the GDM by outlining explicit expectations linking ecological speciation, genetic drift, and extinction to distinct stages of island geomorphology. Focusing on the radiation of *Hibiscus* sect. *Lilibiscus* in the Mascarene archipelago, we combine phylogenomic, population genomic, and demographic approaches to test these predictions across three islands at discrete ontogenetic stages: young (Réunion), middle-aged (Mauritius), and old (Rodrigues). We find evidence that ecological speciation and high intra-specific gene flow characterize lineage divergence on the young island, vicariance and drift dominate population divergence on the middle-aged island, and extinction has left a strong signature of lineage divergence on the oldest island. These results provide rare empirical support for the GDM's process-based predictions and offer a general framework for linking geomorphological change to evolutionary dynamics in island systems. Our approach sets the stage for a new generation of population genetic studies capable of directly testing evolutionary processes underlying insular biodiversity.

Topic: Graeme P. Berlyn Tribute: Light and Life of Forests from Terrestrial to Subtidal and their Regeneration

A-492

Multi-scale resilience of plant communities to drought in a semi-arid ecosystem in central Chile

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Impacts of global change on terrestrial biodiversity are increasing, and have been largely attributed to land-use change. However, climate change may also affect biodiversity, as extreme events such as droughts are becoming increasingly frequent and severe, by shifting plant distributions based on species' capacity to tolerate or avoid drought stress. Functional traits that integrate plant responses to climate change can therefore provide insights into the mechanisms, such as ecological trade-offs of traits along environmental gradients, that underlie shifts in species distributions, which can lead eventually to changes in biodiversity via community structure and trait distributions. However, how and to what extent these emerging plant communities will be able to resist or recover from global change drivers remains relatively unexplored.

We therefore evaluated the potential resilience at multiple ecological scales to future global change drivers in semi-arid ecosystems that have been subjected to an long-term, extreme drought. More specifically, we i) examined the effects of trade-offs between plant ecological strategies, i.e., coordinated patterns of functional traits associated with plant's ability to tolerate drought stress or acquire resources for growth, and environmental gradients on species' distributions; and ii) determined the impacts of environmental gradients associated with water availability on the diversity of plant ecological strategies that underpin resilience to global change drivers.

Across the Aconcagua River basin, we established 59 50 m^2 rectangular plots distributed from the Andes Mountains to the Pacific Ocean and measured 11 leaf and xylem functional traits to determine plant ecological strategies and their diversity. We used hierarchical Bayesian models to examine the interactive effects of plant ecological strategies and gradients in recent (2010-2021) and historic (1961-2010) drought severity, soil hydraulic capacity, and topography on the probability of species occurrence. We identified the principal abiotic and biotic drivers of trait diversity using Random Forest models.

Our results show that positive trade-offs between hydraulic safety-efficiency and current drought severity, soil hydraulic capacity, and the topographic wetness index determine where species occur. More specifically, we found that species with greater hydraulic efficiency occur in areas with higher soil hydraulic conductivity and that accumulate water, while species with greater hydraulic safety occur in areas with greater drought severity during the current drought.

In parallel, our models revealed that recent drought severity, plant diversity, and the topographic wetness index explain spatial patterns of diversity in the hydraulic safety-efficiency trade-off and the fast-slow continuum. While the plant communities most vulnerable to drought stress, i.e., those dominated by species associated with hydraulic efficiency, faced the highest drought severity since 2010, the most taxonomically diverse communities exhibited the highest safety-efficiency diversity. We also observed that plant communities with high species evenness exhibited low trait kurtosis.

Overall, our results highlight how an extreme drought has begun to reshape species distributions, favouring species with greater hydraulic safety, resulting in a lagged response to current climatic conditions at the community level. However, the underlying biotic properties of plant communities, such as species richness and evenness, may promote ecological processes such as facilitation that could enhance resilience.

Topic: Crops and Wild Relatives

A-494

Temporal and taxonomic patterns of nutrient acquisition in perennial herbaceous species: Implications for ecology and crop development

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Understanding how perennial plants acquire essential nutrients over time and across different lineages is important for both ecological theory and agricultural innovation. In this study, I investigate temporal and taxonomic variation in resource acquisition across eight undomesticated perennial herbaceous species representing three plant families (Asteraceae, Fabaceae, and Poaceae). These species were established in a common garden experiment in 2019 and 2020 at Shaw Nature Reserve (Gray Summit, MO, USA), with plants grown under uniform field conditions in a replicated block design. Over two growing seasons (2022 and 2023), leaf samples were collected from individual plants at three timepoints per year, enabling the analysis of temporal shifts in elemental composition. In 2022, paired soil samples were also collected to assess environmental heterogeneity across the site. Elemental concentrations were quantified using inductively coupled plasma mass spectrometry (ICP-MS), allowing for a detailed examination of ionomic profiles within and across species, families, and seasons. By integrating multiyear, multispecies ionomics data with information on planting history and developmental timing, this study evaluates how resource acquisition varies among taxonomic levels and how it shifts within a growing season and across years. This work provides insight into the consistency, plasticity, and phylogenetic structure of nutrient uptake strategies in long-lived herbaceous species. Findings from this study may be used to inform efforts to improve nutrient-use efficiency and adaptation in emerging perennial crops and support broader ecological understanding of plant-environment interactions.

Topic: Ecophysiology

A-495

Callose is critical in overwintering and wounding: how does it change under stress?

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When a plant is damaged, under stress, or diseased, its cells produce the polysaccharide callose to defend against pathogens and react to stress. After wounding, callose is deposited in pores between cells including in intracellular connections between sugar-conductive phloem cells (sieve tubes) in the plant vascular system. A similar response is observed in the wintertime when callose builds up in the sieve pores of many tree species in response to changing seasons. However, what explains differences among species in their rate of callose accumulation and their overwintering strategies is incomplete. Callose accumulation is crucial for defense against pathogens and mechanical damage and helps plants survive through harsh, cold winters. Understanding how these mechanisms work can help us understand how plants react to different stresses and respond to changing seasons.

To understand whether callose accumulation and retention during winter correlate with overwintering strategy, we sampled sixteen temperate tree species in the late winter. We took microcores and stem samples to estimate callose in the tissue using a fluorometric assay and histological techniques. We assigned an overwintering strategy based on prior literature. We found that Acer negundo overwinters one to two layers of open sieve elements and found it to contain the most callose per area in the phloem tissue. The majority of other species retain less callose and broadly overwinter partially differentiated cells, but do not retain open sieve elements. We also measured callose in a variety of different plants after wounding. Our goal was to find what environmental stressors affect the callose wounding response. We examined wounding under drought, low light, and salt stress. Understanding stress-related wounding response will help us determine what action to take after a plant community has been exposed to certain conditions.

Topic: Plant phenology in an era of rapid global change: new perspectives and frontiers

A-496

Leveraging iNaturalist Data to Classify Superblooms in North American Deserts

Author: (JT) Jared Miller, Pamela Soltis, Douglas Soltis, Robert Guralnick
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Seasonal wildflower blooms are dynamic ecological events driven by both biotic potential and favorable abiotic conditions. In the arid landscapes of the American Southwest, these factors contribute to a phenomenon known as superblooms. Long recognized and appreciated by the desert communities and their visitors, superblooms are atypical events of mass annual plant flowering. Although lacking a precise definition, their broad spatial extent and short temporal duration imply wide-scale optimal conditions for the underlying seedbank's germination and flowering. The conditions necessary for these widespread events are thought to consist of well-timed above-average rainfall and cooling, such as those witnessed in 2017, 2019, and 2023 in California's deserts.

While it is agreed that several iconic annuals, such as California poppies (Eschscholzia californica) and desert bluebells (Phacelia campanularia), contribute to the major superblooms, less is known about whether and how much species composition varies across regions. Recent efforts have incorporated satellite imagery to track and model these events; however, such approaches rely on color indices and lack taxonomic resolution, limiting insights into community composition. One approach to addressing these gaps in the spatial and temporal characterization of superblooms, while accounting for contributing species, is to leverage the extensive biodiversity data generated by citizen science platforms such as iNaturalist. Superblooms are iconic events that bring a wealth of visitors documenting the event unfolding across the region. We leverage recent large-scale phenology annotations from a machine learning pipeline to fit models that can detect weeks with significantly elevated observation intensity within 50×50 km hexagonal grid cells across a large portion of the desert Southwest. Our results indicate pronounced peaks in observation activity during 2019 and 2023, supporting the hypothesis that superblooms are detectable through citizen science data. These candidate superbloom events allow us to examine the spatial and temporal extents of these events and how much species composition varies across years and regions. Leveraging these insights, we aim to better understand how superblooms unfold and provide a means to begin predicting the broadscale conditions that best predict the intensity and extent of these events.

Topic: Symbioses: Plant, Animal, and Microbe Interactions

A-497

Microbial Interactions for Stress Mitigation: Role of Methylotrophic Bacteria in Alleviating Heat and UVB Radiation

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Climate change exacerbates environmental stressors, such as heat and ultraviolet (UV) radiation, which significantly impact crop growth and productivity. This study explores the role of UVB-resistant methylotrophic bacteria in alleviating the adverse effects of heat and UV radiation on mung bean (*Vigna radiata* L.), a critical legume crop, under both controlled and field conditions. A total of 55 methylotrophic isolates were obtained from desert plants, with 15 strains demonstrating resistance to UVB radiation for up to 4 hours. These strains, identified as *Methylorubrum* and *Methylobacterium* species, exhibited consistent plant growth-promoting (PGP) traits, including the production of IAA-like substances, siderophores, and ACC deaminase activity, even under UVB stress.

Seed priming with these methylotrophs significantly improved seed germination, root and shoot elongation, and chlorophyll content, while enhancing antioxidant properties such as superoxide dismutase, peroxidase, and phenylalanine ammonia lyase activities. Notably, the methylotrophic treatment mitigated UVB-induced oxidative stress, reducing cellular damage and enhancing the physiological performance of mung bean plants. The community-level physiological profile (CLPP) analysis of treated plants confirmed increased microbial activity, further supporting the beneficial effects of the bacterial inoculation.

In field trials, methylotrophs showed a remarkable improvement in mung bean growth, pod formation, and yield attributes, with increases in pod numbers (25.44–32.78) and yield (10.81–23.63 q/ha) compared to untreated controls under both UVB shielded and non-shielded conditions. The biochemical analysis of the methylotrophs revealed the presence of carotenoids, flavonoids, and other antioxidants, which are likely responsible for their UVB protection mechanisms. The adaptive morphological changes, such as biofilm formation and altered cell shape, were also observed in response to UVB exposure, highlighting the robustness of these bacteria under stress.

This study underscores the potential of methylotrophic bacteria as sustainable biotechnological solutions to enhance crop resilience against UVB radiation and heat stress, promoting agricultural sustainability and food security in the face of climate change.

Topic: Bryology and Lichenology

A-498

Big Data = Big Mess? Suggestions to standardize collection and data management routines for lichenized fungi

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Biodiversity data repositories maintained by the *Global Biodiversity Information Facilities* (GBIF) or by Symbiota portals such as the *Consortium of Lichen Herbaria* have increasingly become “big data” sources for biogeographic and even ecological research. The data managed by these portals must be considered “raw”. Specimen identification accuracy cannot necessarily be trusted. Occurrence records are typically skewed by sampling bias towards sites easily accessible, or individual preference for surveying more diverse habitats. Historic specimen records are nevertheless often the only baseline data available. Unlike other data sets, these physical specimens can be re-examined, identification records updated, and georeferences added. Unfortunately, beyond basic species distribution, historic records are often limited; specimens were typically collected with sparse additional information. Even today, universal standards, which information routinely should be recorded when collecting specimens do not exist. The extended specimen concept has become a popular catchphrase, suggesting that linking specimens to external data sets can leverage information far beyond otherwise limited occurrence records. But what about more efficient collection procedures? Here we discuss how establishing standardized collection routines already in the field can significantly improve primary data quality. Following a simple, yet efficient protocol must not necessarily distract from the taxonomic objective to collect large numbers of specimens. On the contrary, implementing better collection routines integrates a primarily taxonomic approach with a more powerful perspective to biodiversity science, generating richer and more useful primary data. Instead of relying on secondary evidence, data harvested as integral part of collections are immediately available, for example, to generate ecological species profiles as part of taxonomic revisions and ecological assessments.

Topic: Biodiversity Informatics & Herbarium Digitization

A-499

Diverse modes of lifestyle and niche specialization sculpt the foliar ground plan in parasitic broomrapes

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Plants’ lives are a constant battle for water and light. Yet over 4,000 parasitic plants have escaped this fundamental selective regime and instead, evolved unique mechanisms to exploit their hosts. This major transition in lifestyle has manifested itself vividly in the light-collecting, water-redistribution organ — leaves. In angiosperms, leaves vary dramatically in shape, size, surface texture, and venation, all contributing to optimal resource capture and adaptive versatility under diverse environmental conditions. Parasitic plants, as a rule, are thought to possess leaves of a minimalistic design. Greatly reduced scales or bracts are often found in non-photosynthetic holoparasites and simple leaves with entire margins are common in photosynthetic hemiparasites. The broomrapes (Orobanchaceae), however, represent an exception. The family comprises species across the entire spectrum of parasitism and spans a wide range of complexity in foliar architecture in adaptation to the living environments. To assess the variation in parasitic plant leaf morphology and comprehensively evaluate how lifestyle and niche specialization have contributed to such variation, we analyzed 4,239 leaves across 345 species (13.5% species diversity) and 79 genera (76.0% genus diversity) in Orobanchaceae using a combination of quantitative morphology, computer-vision, and macroeovlutional comparative approaches. Our preliminary results demonstrate up to five-orders-of-magnitude of variation in leaf size with larger leaves commonly found in free-living and hemiparasitic species from warm and humid climates. On the other hand, holoparasites exhibit convergence to small scaly leaves and bifurcating venation from broad leaves with network-like venation. Our study highlights the importance of leaf architecture in the adaptation of plants across the spectrum parasitic habits and heterogeneous environmental conditions, and showcases the uses and benefits of harnessing digital information derived from herbarium specimens.

Topic: Biodiversity Informatics & Herbarium Digitization

A-500

Global distribution and invasiveness of Solanum elaeagnifolium based on herbarium and citizen scientist data

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Solanum elaeagnifolium (silverleaf nightshade) is a perennial herb in the Solanaceae, and is a highly successful invasive weed that has caused significant economic and agricultural losses both in its native range and in many regions globally. Native to southwestern United States, northern Mexico, and northern Argentina, *S elaeagnifolium* has invaded all continents except Antarctica over the past century, spreading to more than 40 countries, including widespread regions in the Mediterranean Basin, Australia, and southern Africa. Its ecological tolerance, adaptability to arid and semi-arid conditions, and successful reproductive system have contributed to its spread. The aim of this study is to analyze the historical and geographical patterns of the range expansion *S. elaeagnifolium* across both its native and non-native ranges, focusing on the native range and three areas where the species is especially abundant, to better understand the dynamics of its global expansion. We used occurrence records from the Global Biodiversity Information Facility (GBIF) and iNaturalist, incorporating both herbarium specimens and recent human observations from the mid-19th century to 2025. Results indicate that invasion in the Mediterranean basin intensified after 2000, especially in Greece and Spain, while records from Southern Africa shows two major expansion peaks. In Australia, preserved specimens peaked in the 1970s, while human observations surged in the 2000s, reflecting a shift from herbarium collections to digital reporting and possibly the species' widespread establishment. Israel, a key entry point in Asia, showed a recent rapid spread post-2015. Within its native range, the species exhibits long-term establishment, especially in Texas (North America) and Argentina (South America), and in recent decades, has been expanding into adjacent areas. This study demonstrates that *S. elaeagnifolium* thrives in both natural and disturbed environments, suggesting that its density and distribution are influenced by disturbance, warming and aridification associated with changes in climate and land use. The alignment of its global spread with climate change trends and anthropogenic disturbance highlights the importance of integrating historical occurrence data in invasive species monitoring. Our findings demonstrate that combined natural history collections and iNaturalist datasets complement each other and are valuable tools for understanding invasion biology and informing conservation efforts.

Topic: Ecology

A-501

Assessing Distribution and Richness of Genus Impatiens in Sri Lanka: An Approach for Conservation

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The genus *Impatiens* L., belonging to the family Balsaminaceae, comprises more than 1,000 species widely distributed across tropical and temperate regions globally. In Sri Lanka, a tropical island, 24 native species of this genus were documented, including 18 endemic species and 3 introduced species. The primary objective of this study was to model the current distribution and predict environmentally suitable habitats for the genus *Impatiens*, with a particular focus on assessing species richness and identifying conservation priorities. A Stack Species Distribution Modeling (SSDM) approach was employed, utilizing 617 sampling points obtained from the National Herbarium of Sri Lanka and the Global Biodiversity Information Facility. The Maximum Entropy algorithm was applied to develop the SSDM under current and projected future climate scenarios for 2021-2100. The niche analysis used the most important climatic variables for each scenario. The findings indicate no significant alteration in the areas with the highest species richness between the current distribution and the predictions for 2050. However, a notable increase is anticipated by 2070, followed by a drastic decline projected for 2090. For niche hypervolume analysis, the fundamental niche of the current distribution is determined by Precipitation Seasonality and the realized niche is determined by the Precipitation of the Driest Month. For 2050, Precipitation of the Driest Month is identified as the facilitator to maintain its fundamental niche areas, while Annual Precipitation will determine the niche expansion. In both 2050 and 2070, the fundamental niche will be operated by Precipitation Seasonality, and the realized niche will be governed by Precipitation of the Wettest Month. Furthermore, the gap analysis reveals that the highest-rich areas are expected to shift from Sri Lanka's southern slope of central highlands to its eastern slope over time, while no observable changes are detected in areas classified as moderately rich, low-rich, or lowest rich. Therefore, conservation measures should be taken to ensure the existence of the genus *Impatiens* because the eastern slope of the central highlands of Sri Lanka is more prone to anthropogenic pressure.

Topic: Bryology and Lichenology

A-502

Morphological variation in liverwort traits influences community assemblage along an elevational gradient in northern Madagascar

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Epiphytic bryophytes play a crucial role in forest ecosystems by contributing to water retention, nutrient cycling, and microhabitat creation. However, despite their ecological importance, epiphytic bryophytes remain poorly studied, especially in terms of their functional traits and responses to environmental change. This study addresses this gap by investigating epiphytic liverwort communities along an elevational gradient in northern Madagascar. We aim to assess the relationship between functional diversity among liverwort species and community assembly using a trait-based approach, focusing on how habitat filtering and niche differentiation shape community structure.

Epiphytic bryophytes were collected at 10 elevations along an elevational transect from 250 to 2050 m. We measured 12 morphological traits related to resource use, life history, defense, desiccation resistance, and photosynthetic activity. Functional evenness (FEve) and functional dispersion (FDis) were calculated for each community. To investigate functional responses underlying community assembly, we measured community-weighted means (CWM) and variances (CWV) for each trait along the transect. We analyzed trait-environment relationships using multiple general linear models and evaluated community assembly processes (convergence or divergence) across the gradient.

Community assembly is influenced by environmental conditions and vegetation structure. At lower elevations, higher temperatures and taller vegetation lead to trait convergence, particularly in size-related traits. In contrast, at higher elevations, increased species richness is associated with trait divergence. Habitat filtering drives trait convergence at lower elevations, while niche differentiation becomes more important at species-rich higher elevations.

Morphological traits reveal how habitat filtering and niche differentiation jointly influence species distribution. Including physiological traits like water-holding capacity and carbon fixation in future studies will provide deeper insights into ecosystem processes. These findings contribute to understanding tropical forest ecosystems.

Topic: Hybrids and Hybridization

A-503

Phylogenomic analysis reveals complex taxonomic issues related to hybridization in Arctostaphylos (Ericaceae)

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Arctostaphylos (Ericaceae), better known as manzanitas, is among the most diverse woody genera in Western North America. The majority of manzanitas are narrow endemics from the California Floristic Province and many are considered threatened or endangered. A stable and molecularly supported taxonomy would be essential for informing researchers' understanding of diversification in the genus and would help direct our allocation of limited conservation resources. However, manzanita taxonomy has been the subject of long historical debate and most molecular studies have yielded uninformative or ambiguous results. Our team has been working on a genus-wide phylogenomic study of manzanitas using the ddRADseq method, and our preliminary results indicate support for the significant majority of the current *Arctostaphylos* taxonomy. Here we present evidence of notable taxonomically complicated exceptions of unsupported taxa. These situations appear to be related to widespread hybridization. Clustering analyses reveal similar hybrid origin of *A. rudis* (Santa Barbara County, California), and the *A. pungens* populations in San Benito and Monterey Counties,

California. Although morphologically and ecologically very different, individuals from both groups have a similar genomic architecture composed of a mixture of two distant lineages of *Arctostaphylos*. Individuals are both genotypically and phenotypically variable, and the parentage of these hybrid complexes is unclear, making these individuals challenging to categorize taxonomically. A similarly taxonomic challenge is revealed in our phylogenetic analysis of *A. glandulosa*, which demonstrates that individuals currently classified as *A. glandulosa* are paraphyletic: many individuals have independent origins (in some areas this is even true of neighbouring populations), and individuals are often very distantly related to each other. Studying and discussing these types of taxonomic complexities is a very important exercise for the current phylogenomic era and the high frequency of reticulate evolution it reveals. Are our current taxonomic systems and species concepts able to adequately account for these scenarios?

Topic: Systematics & Taxonomy

A-504

Evolution and diversity of Chusquea (Poaceae: Bambusoideae: Bambuseae)

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Although bamboos (Bambusoideae) are typically associated with the Eastern Hemisphere, especially China, India and Japan, >600 bamboo species (of over 1700) are native to the Americas. Of these, 204 (one-third) belong to Chusquea, the most diverse genus of bamboo, and the description of new species in this genus continues unabated. Chusquea is the most widespread Neotropical woody bamboo genus, extending from 25° 40'N in Mexico to 47° S in Chile and Argentina. Species of Chusquea grow primarily in montane forests and high elevation grasslands in Mesoamerica, the Greater Antilles, the Andes and eastern Brazil, and are often dominant elements in these habitats. Chusquea has the broadest elevational range of any bamboo genus, from sea level to over 4300 m, although few of its species occur below 1000 m. Morphologically, Chusquea has a uniform spikelet structure of four glumes and one fertile floret with no rachilla extension, but exhibits extreme vegetative diversity, from aerially unbranched culms bearing leaves to 4 m long and 30 cm wide to highly branched culms with 2-200 subsidiary branches per node, bearing leaves 1-40 cm long and 0.06-8.5 cm wide. Understanding of the complex evolutionary history of the woody bamboos, which involves ancient hybridization and polyploidy, has been enhanced by recent phylogenomic analyses, but until recently only plastid genomic resources (and limited ITS data) for Chusquea were available. Elucidation of species-level diversification has been hampered by lack of resolution in the plastid sequence data but also likely rapid and recent radiation in the Euchusquea clade (subg. Chusquea and subg. Swallenochloa) and homoploid hybridization. We explored the utility of targeted sequencing using the Angiosperms353 universal probe set in resolving relationships within Chusquea. We recovered an average of 327 nuclear genes from leaf material stored in silica gel for as long as 30 years. From those, 289 genes were employed to estimate the species tree. Our tree topology is very similar to previous plastid trees, showing strong support for four major lineages. Subg. Platonia is sister to subg. Rettbergia + the Euchusquea clade, with subg. Magnifoliae sister to that whole clade. Within the well supported Euchusquea clade, Chusquea sect. Tenellae (subg. Chusquea) is strongly supported as sister to a clade of the remaining sampled species, which comprise species from both subg. Chusquea and subg. Swallenochloa. Although some relationships within the Euchusquea clade are well supported, many are not, and neither subgenus is recovered as monophyletic.

Topic: Paleobotany

A-505

Analysis of Archaeobotanical Remains and Dating of the Site 45-JE-14, Quilcene, Washington

Author: Lucy Katzman-Tranah
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Archaeobotanical analysis continues to be a growing field interest in archaeological excavations and post-excavation analysis. This research aims to demonstrate the importance of archaeobotanical sampling as a complement to traditional excavation, even in years post excavation. During analysis we revisited previously excavated archaeological soil samples from Quilcene, Washington and extracted the remains of short-lived plants such as twigs and parenchyma, which were C14 dated to 3,000-1,500 years BP. Because these dates were 3,000 years disjointed from thermoluminescence dates previously calibrated from stone tools at Quilcene (Kiers et al., 2010), we concluded that the site was occupied at a number of different times and used as a burn pit for edible plants. After concluding that lithics found at Quilcene were likely unrelated to botanical remains, we analyzed fragmented samples of parenchyma and nutshell, which were identified to be a number of culturally significant species on the Olympic Peninsula of Washington. Archaeobotanical remains at Quilcene serve to lend a second dimension to existing archaeological conclusions about the site.

Topic: Systematics & Taxonomy

A-506

Phylogenetic novelties: Two new genera of herbaceous bamboos (Poaceae, Olyreae) from the Brazilian Atlantic forest

Author: Iasmin Laiane De Castro Oliveira, João Vieira, Alessandra Schnadelbach, Lynn Clark, Reyjane Patricia Oliveira
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The Atlantic Forest is one of six phytogeographic domains in Brazil and is characterized by its complex topography with extreme variations in elevation, from *restinga* areas and mangroves at sea level to higher elevation forests at over 2,000 meters. Along with the Amazon, the Atlantic forest houses the highest diversity of herbaceous bamboos (Poaceae: Bambusoideae: Olyreae) in the Americas, with the southern region of Bahia state exhibiting the greatest degree of endemism. Over the past three decades, many taxonomic issues have been resolved for this group using molecular systematics, including circumscriptions of genera and species and revealing relationships that were previously unknown. T he new circumscriptions of Buergersiochloinae and Olyrinae, in addition to recovery of the non-monophyly of *Olyra*, are examples of these findings. A revision of this genus, in conjunction with molecular phylogenetic analyses using plastid data, led us to identify five lineages that are being segregated from *Olyra* as new genera, based on vegetative morphology, synflorescence structure, and female anthecium characters. Two of these new genera are presented here and compared with their sister lineages. The first differs from other Olyrinae genera by having the culm nodes thickened, purplish, and pilose with whitish retrorse hairs to glabrous, the leaf blades ovate-lanceolate, the female anthecia fusiform and ornamented with very deep-rounded excavations; this may also be an annual plant. The second is the only one with the female anthecium completely ornamented with conspicuous prickle hairs covering its entire surface, the leaf blades very asymmetric at the base, with the largest leaf blade of the culm being the lowest one, becoming progressively smaller toward the apex of the culm. Both new genera are endemic to southern Bahia, from Indigenous territory, and have been named in their honor.

Topic: Phylogenomics

A-507

Pondweeds350: a phylogenomic toolkit to transform hybrid detection and phylogenetic inference for Potamogetonaceae, Alismatales

Author: Laura Frost, Zacc Ramm, Kaitlyn Sampson
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Pondweeds (Potamogetonaceae; Alismatales), a dominant submersed freshwater plant family in the Northern Hemisphere, have remained taxonomically challenging due to high levels of phenotypic plasticity and hybridization. While advancements in molecular technology have improved hybrid detection and characterization, low genetic variation in universal loci has precluded robust taxonomic and phylogenetic resolution. To date, hybrid identification and phylogenetic inference in pondweeds has relied heavily on two nuclear ribosomal spacers (ITS and 5S-NTS) and a few chloroplast loci (*e.g.*, *trn*T-*trn*L, *mat*K, *rbc*L) via Sanger sequencing. We present pondweeds350, a custom probe set for hybrid-enriched target sequence capture designed to capture 350 variable nuclear genes in Potamogetonaceae with utility in the broader Alismatales. Using a dataset generated from 288 field-collected and herbarium samples of North American (NA) pondweeds, we outline the design of the probe set with Sondovač, including selection of 205 genes that overlap with Angiosperms353, 132 targets specific for Potamogetonaceae, and 11 functional genes; explore the success of pondweeds350 for the advancement of systematic and evolutionary investigation in Potamogetonaceae, resulting in the first robust phylogeny of NA pondweeds; and address implications for the use and utility of nuclear ribosomal spacers for hybrid species assessment in the family and in plants more broadly. See Zacc Ramm's talk for further discussion of macroevolutionary patterns and processes revealed through use of the probe set.

Topic: Bryology and Lichenology

A-508

Building a Functional Trait Framework for Antarctic Mosses

Author: Zoie Yetley, Scott Kiel, Becky Ball, Angelica Casanova-Katny, Hannah Prather, Todd Rosenstiel, Sarah Eppley
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Maritime Antarctica is undergoing rapid climate-driven transformation, with glacier retreat unveiling new ice-free area for plant colonization. Mosses—dominant components of Antarctic terrestrial ecosystems—are among the first colonizers of these newly exposed landscapes, yet their ecological functions remain underexplored. This study applies a trait-based framework to understand how Antarctic mosses shape ecosystem development across successional gradients formed by glacier retreat. Fieldwork conducted across three sites in the South Shetland Islands involved sampling four dominant moss species across three successional zones (periglacial, intermediate, developed). We assessed 20+ functional traits encompassing thermal conductivity, water holding capacity, albedo, tissue nutrient content and a suite of morphological features from canopy to cell scale. Preliminary results reveal patterns of inter- and intra-specific variation in functional traits in dominant moss species across successional stages. These results begin to provide a conceptual framework for understanding plant functional roles across glacial succession in Antarctica and lend a better understanding to the effects of Antarctic greening.

Topic: Comparative Genomics/Transcriptomics

A-509

Postmating prezygotic affairs: evolution of the reproductive transcriptome among 8 tomato species with diverse mating systems

Author: Timothy Biewer-Heisler, Leonie Moyle, Jacob Jiles, Matthew Gibson
Affiliation: Indiana University

We assessed differences in postmating prezygotic tissue-specific gene expression (in pollen, style, ovule, and leaf) between eight closely related plant species with different mating systems—Solanum lycopersicum (domesticated tomato) and seven wild relatives. Our analyses investigated constitutive differences between reproductive and non-reproductive tissues, mating systems, and male and female-related tissues. In addition, we investigated differential resource contributions of the pistil to growing pollen tubes and the rates of gene expression evolution for important reproductive gene families, including pollen tube growth factors and ovule signals. From our dataset, we found higher rates of gene expression evolution in reproductive tissues, rapid gene expression evolution of ovule signal peptides, and mating system-related differences in rates of gene expression evolution. Our study contributes to our understanding of reproductive trait evolution at multiple postmating prezygotic stages, highlighting the influence of selfing versus outcrossing mating systems on pollen-style and pollen-ovule interactions.

Topic: Floristics

A-510

The rate of novel taxon description over time in California, Canada, and the Southeastern United States and implications for botanical conservation worldwide

Author: Wesley Knapp, Alan Weakley, Bruce Baldwin, Luc Brouillet, Jason Alexander, Jordan Teisher, Kay Havens, Reed Noss, Derick Poindexter, Johnny Randall, Michael Lee
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Many scientists have hypothesized that we are now in the 6th mass extinction in Earth's history, with extinction rates rising as we progress through the Anthropocene. We must address areas with insufficient scientific knowledge to prevent biodiversity loss. The most fundamental and urgent question of biodiversity conservation is, "What species exist?" Without fundamental knowledge of what species exist, all other downstream conservation questions (i.e., what conservation actions do they need to persist?) are impossible to answer.

Undescribed species pose a significant conservation challenge. Most conservation action happens at the species level in the United States and Canada. Globally, the IUCN completes conservation status assessments and assigns extinction risk categories (i.e., Critically Endangered or G1) for plant and animal taxa and natural communities (ecosystems), while NatureServe performs this function in the United States and Canada. Classification and assessments for ecosystems lag far behind that of species.

The need to describe plant life is pressing, and the rate of new species discovery needs to be better known. Many previous analyses on new vascular plant species discovery rates are limited in that they fail to consider nomenclature complexities or accept all newly published names as scientifically distinct. These earlier studies have provided a quantitative output of newly published names, which has limited utility as a new name is not necessarily a newly discovered species. A newly described taxon is just a hypothesis, and only some of these hypotheses will be accepted over time. New combinations of previously published names are commonplace and are required when the understanding of the flora improves. Such combinations are frequently needed when new genera are established, and these combinations may constitute most new names published but are not newly discovered taxa.

We develop careful nomenclatural qualifiers to determine the rate of novel species description over time for California, Canada, and the southeastern United States since the establishment of the Linnaean binomial system (1753). We compiled all accepted taxa found in the Jepson eFlora Project for California, Brouillet et al. VasCan database and Weakley's Flora of the Southeastern U.S. We then populated nomenclatural data for each taxon using the Tropicos Database to determine the date of the first description. We also used the NatureServe database to determine the conservation status of each taxon.

In this talk, we will discuss conservation implications across time. Our results indicated that we are still in the age of discovery, even in this well-studied area. We present data showing botanical luminaries' impact in each region across time and data on the conservation status of newly described species. Though these results vary by geographic area, it is apparent that discovering the rarest plants in a flora takes careful study and ample time. Many of the newly described taxa since 2000 are already at risk of extinction (G1-G3).

Topic: Ecophysiology

A-511

Trees just go "nuts": prioritizing C allocation to yield in almond trees

Author: Shreya Veeravelli, Mina Momayyezi, Ian Wright, Sebastian Castro Bustamante, Andrew Gal, Hung Nguyen, Andrew McElrone, Morgan Furze
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Perennial tree crops store nonstructural carbohydrates (NSCs) as energy reserves that can be used to support plant processes during photosynthetically inactive periods associated with environmental stress or dormancy. In d eciduous tree crops, which lose their leaves in the autumn, the NSC reserves accrued by the end of the growing season /beginning of the dormant season are critically imp ortant for downstream processes. Not only do these NSC reserves support wintertime respiration, but they may also influence physiological processes in the next year's growing season. However, few studies have focused on how variation in NSC reserves at the beginning of the dormant season and at the end of the dormant season may influence subsequent processes like growth, flowering, and yield. To quantify the seasonal NSC fluctuation surrounding the dormant season and how these storage patterns influence subsequent growing season processes, we conducted a comparative study of four almond varieties (*Prunus dulcis* (Mill.) D.A. Webb cv. Butte, Carmel, Monterey, and Nonpareil) in an orchard setting (California, USA). Branch, stem, and coarse root tissues were assessed for soluble sugar and starch concentrations in November 2021 and March 2022. We then assessed the correlation between these NSC data and metrics of subsequent growing season processes including stem growth and yield, and we further explored long-term trade-offs between stem growth and yield using historical data from 2017-2022. Overall, total NSC concentrations in aboveground organs were generally lower in Nonpareil compared to the other varieties. However, root total NSC concentrations did not differ between varieties, likely reflecting their shared rootstock. Between the two timepoints surrounding the dormant season, there was a significant decrease in total NSC concentrations in all organs, indicating their use for wintertime respiration as well as leaf out and flowering

early in the growing season. When assessing relationships between NSCs and stem growth and yield, we observed a significant positive correlation between branch total NSC concentrations in November 2021 and yield in 2022, following the expectation that branches are the closest source of C to support flowering/yield. Interestingly, when assessing trade-offs between stem growth and yield from 2017-2022, we found that as basal area increment of the stem increased, yield tended to decrease. Over time from 2017 to 2022, yield has been prioritized over stem growth in these varieties, even during a 3-year period (2020-2022) when trees were water-stressed due to an inadvertent irrigation system malfunction. Overall, these findings advance our understanding of crop tree C physiology and can be used to identify climate resilient tree crop varieties and improve orchard management strategies.

Topic: *Reproductive Processes*

A-512

Ants, plants, fur, wind, and fire

Author: Chris Martine, Abigail Motter, Kaitlin Henry, Rebecca Beneroff, Diamanda Zizis, Melody Sain
Affiliation: Bucknell University, Bucknell

Despite being a well-studied and economically important group, *Solanum* is still rife with mysteries and surprises. The Australian bush tomatoes of *S*. subgenus *Leptostemonum*, particularly the ca. 45 species in the "*S. dioicum* + *S. echinatum* Group," continue to be a model of adaptive radiation linked to reproductive biology characters. Already established as an ideal clade for studying sexual system evolution given the presence of andromonoecy, cosexuality, and functional dioecy, our recent undergraduate-driven work in the group has generated new inferences in reproductive biology including seed dispersal strategies (censer and trample bur dispersal), plant-insect interactions (extra-floral nectaries), and clonal spread (specialized storage roots).

Topic: *Biodiversity Informatics & Herbarium Digitization*

A-513

Climate, topography, and tropical heritage: phylogenetic diversity and endemism of North American Apocynaceae

Author: Sierra Hubbard, Mark Fishbein
Affiliation: Oklahoma State University

The integration of phylogenetic data and species occurrence records provides a way to investigate how spatial biodiversity patterns are driven by evolutionary and biogeographic history. Although Apocynaceae is one of the largest angiosperm families, its spatial patterns of phylogenetic diversity and endemism have not yet been formally assessed. We use recently digitized herbarium records and community science observations to examine patterns of species richness, phylogenetic diversity, and phylogenetic endemism of Apocynaceae native to North America (~400 spp.). We use spatial autoregressive and generalized linear modeling approaches to predict diversity and endemism from environmental variables. Based on regional-scale analyses that highlight the strong influence of terrain ruggedness on phylogenetic diversity and related metrics, we examine the effects of several terrain variables in addition to bioclimatic data. We used a categorical analysis of neo- and paleo-endemism to identify endemism hotspots at the continental and regional scales. Given the tropical origin of Apocynaceae, we hypothesized that spatial phylogenetic patterns and climate-diversity relationships would reflect tropical conservatism in this family. Specifically, we expected to observe a latitudinal gradient in PD at the continental scale that is strongly associated with seasonality in precipitation and temperature. The Chihuahuan Desert emerged as a center of low Relative Phylogenetic Diversity (RPD), indicating clustering of relatively young Apocynaceae lineages. This pattern, which was evident at the continental scale but not at the regional scale, suggests a link between the relative ages of biomes and assemblages of taxa within. South Texas represents the only common area of Apocynaceae endemism between the two spatial scales.

Topic: *Phylogenomics*

A-514

Phylogenetic Reconstruction of Honeysuckles (Lonicera) using Plastid Genomes to Identify Cytonuclear Discordance

Author: Kendall Villalobos, Mansa Srivastav, Aaron Lee, Dianella Howarth, Michael Donoghue, Wendy Clement
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Lonicera, or honeysuckles, include nearly 150 species distributed largely in the northern hemisphere. Honeysuckles are an excellent group to study the evolution of organ fusion, as many species exhibit fusion of leaves and reproductive structures such as petals and ovaries. To facilitate evolutionary studies, a well-supported and well-resolved phylogeny is required. Phylogenetic reconstructions in plants are frequently based on plastid DNA, which, in contrast to bi-parentally inherited nuclear DNA, is maternally inherited. As a result, plastid-based phylogenies provide an important point of comparison to nuclear data that allows for identification of past evolutionary events such as hybridization. Here, we reconstruct the most comprehensive species tree of Lonicera using whole plastid genomes that now enables comparison with published phylogenetic studies based on nuclear sequence data. We sampled 88 species of Lonicera in addition to eight outgroup species in closely related genera and had libraries prepared for genome skimming and sequencing using 2x150 paired-end Illumina HiSeq. Additionally, we included 35 Lonicera genomes published in GenBank. We explored different approaches to phylogenetic reconstruction and here present our best estimate of the evolutionary history of this clade based on plastome data. Our analysis identified at least three instances of cytonuclear discordance between our plastid-based phylogeny and previously published nuclear phylogenies. Our investigation of these incongruences will also include key morphological traits and tests of hybridization to better understand the species relationships and evolutionary history of honeysuckles.

Topic: *Ecophysiology*

A-515

Comparing Autumn Phenology Between Urban Tree Species in Different Microclimates

Author: Mary-Margaret Benware, Grace Collins, Emmeline Seest, Xuan Li, Zhongzhong Niu, Jian Jin, Scott McAdam, Brady Hardiman, Morgan Furze
Affiliation: Purdue University

Urban areas typically experience higher temperatures than their rural counterparts due to increased impervious surfaces and decreased vegetation, described as the urban heat island effect. This causes a mosaic of microclimates across cities which may have varying effects on the physiology and phenology of trees. Previous work has shown that warmer temperatures due to urbanization can contribute to longer growing seasons; however, less is known about species-specific responses at the end of the growing season. To address this knowledge gap, we compared leaf senescence in 10 deciduous species growing in both "hot spots" and "cold spots," which differed by 2° C based on 10-year average Landsat surface temperature data. Leaf senescence was quantified by measuring chlorophyll *a*, chlorophyll *b*, and total carotenoid content weekly in the leaves of 72 trees for 12 weeks. We hypothesized that trees growing in "hot spots" would have delayed senescence and/or a slower rate of pigment degradation than trees growing in "cold spots." Our initial findings show species-specific phenological responses to different microclimates; *Acer rubrum* and *Ginkgo biloba* exhibited a slower rate of pigment degradation in "hot spots" compared to those in "cold spots." Pigment degradation did not significantly differ between microclimates for the other species, suggesting that the phenology of these species might be under more strict photoperiod control. Additionally, we collected leaves from a subset of these trees and measured leaf-level multispectral indices and leaf nonstructural carbohydrate (NSC) content. Our next steps include: (1) exploring the relationship between NSCs and spectral indices to develop noninvasive methods to estimate the progression of leaf senescence, and (2) to continue to explore species' differences in the timing of leaf senescence (i.e., Does the rate of senescence differ between species? Do trees in "hot spots" retain their leaves longer?). Understanding how temperature drives species-specific responses in urban areas can help better predict the end of the growing season and enhance carbon cycling models in response to ongoing climate shifts.

Topic: *Macroevolution*

A-516

The evolution of drought tolerance in Caryophyllales, the role of betalains

Author: Tom Carruthers, Stephen Smith
Affiliation: University of Michigan

Caryophyllales are diverse in drought prone environments. Species within the clade possesses several distinctive traits - some with well-known associations with water limitation such as succulence, and others with hypothesised links to water limitation but with a less precise functional characterisation i.e. betalain pigmentation (unique to Caryophyllales) or medullary bundles. We investigate the evolution of these traits, and their relationship with the evolution of drought tolerance. To do this, we estimated a dated phylogenetic tree for Caryophyllales using transcriptomic data and a morphological matrix that enabled a novel "tip-dating" approach. Age estimates from this transcriptomic tree were used to date a species level phylogenetic tree incorporating over 4,400 species. We showed that the evolution of betalain pigmentation enabled Caryophyllales to evolve in drought prone conditions and that most of the succulent (and drought tolerant) lineages within Caryophyllales evolved within betalain pigmented lineages. By contrast medullary bundles have little clear relationship with drought-prone environments. The metabolic pathway underpinning betalain pigmentation is well characterised. We therefore also characterise how different components of this complex metabolic pathway evolved in the context of our dated phylogenetic tree.

Topic: *Conservation Biology*

A-517

The Science of Saving Plants: Advancing Conservation Through Research and Collaboration

Author: Wesley Knapp, Tina Stanley, Fowler Shannon, Matora Fiorey
Affiliation: Center for Plant Conservation

For over 40 years, the Center for Plant Conservation (CPC) has served as a leading authority on science-based best practices to conserve rare and endangered native plants—with particular expertise in the collection, storage, and utilization of wild rare plant seeds for conservation purposes. CPC is the hub of an 81-partner network found on three continents. The CPC National Collection safeguards the 4,400 most imperiled native plants found in North America north of Mexico. This living conservation resource ensures the long-term survival of rare species through strategic ex situ stewardship.

CPC's work is grounded in its *Best Plant Conservation Practices to Support Species Survival in the Wild*, an evolving set of science-based guidelines that inform ex situ and in situ conservation strategies. Continually refined through research and fieldwork, these guidelines are integrated into CPC's Rare Plant Academy (RPA), a digital hub providing conservationists with educational training materials, a video library, and a knowledge-sharing forum. Through key initiatives such as regional seed collection in biodiversity hotspots across the U.S., pioneering scientific research studies, and cutting-edge database tools, CPC is expanding practitioners' collective knowledge while building capacity and streamlining conservation efforts.

Looking ahead, CPC will continue to lead initiatives and best practices to prevent plant extinction while providing leadership and assistance to plant conservation practitioners in new but essential ways, such as plant taxonomy, data synchronization, and prioritization efforts.

By integrating best practices with cutting-edge research and training, CPC and its partners are shaping the future of rare plant conservation and ensuring a legacy of stewardship for generations to come.

Topic: *Population Genetics/Genomics*

A-518

Circumscription of the Heterotheca subaxillaris Complex

Author: Alicia Marmolejo, Sara Fuentes-Soriano
Affiliation: New Mexico State University

Goldenasters group (camphor weeds) are common wildflowers and weeds found in the summer and fall floras of most mid and subtropical regions of North America. The genera that are members of this group are *Braduria, Chrysospis, Heterotheca, Noticastrum, Osbertia, Pityopsis,* and *Tomentaurum*. *Heterotheca* is the largest genus within this group, consisting of 28 species divided into three sections. These species are found throughout southern Mexico to southwestern Canada, spanning almost the entire United States, except for Alaska. The circumscription of species and infraspecific taxa within *Heterotheca subaxillaris* varies, with one interpretation recognizing three species and three varieties—*Heterotheca subaxillaris*, *Heterotheca latifolia* (*H. latifolia* var. *latifolia*, var. *macgregoris*, and var. *arkansana*), and *H. psammophila*—while another interpretation includes two subspecies with three varieties: *H. subaxillaris* subsp. *subaxillaris* (var. *subaxillaris*) and *H. subaxillaris* subsp. *latifolia* (var. *chrysopsidis* and var. *psammophila*). Plant height, stem width, length of trichromes, petiole length, size, shape, head size, toothing of leaf margins, and pigmentation of phyllaries have been used to delineate taxa within the *Heteroteca subaxillaris* complex. However, these features are highly variable and often overlap. The main goal of this study is to investigate species and infraspecific units within the *Heterotheca subaxillaris* complex. Using phylogenetic data, a preliminary exploration of Compositae-Paraloss-1272 bait sets is discussed, based on a sample of 193 individuals representing taxa from the coastal, southwestern, and western parts of the U.S., as well as coastal populations from Israel. This study aims to support or refine current taxonomic intraspecific circumscriptions of the *Heterotheca subaxillaris* complex. Additionally, the phylogenetic framework generated in this study will help address ongoing research related to the invasion history of this species in Israel and further our understanding of its genetic diversity.

Topic: *Dryland Floras*

A-519

Life history in grasses is evolutionarily labile and independent of photosynthetic pathway

Author: Laura Schat, Marc Fradera-Soler, Maria Vorontsova, Siri Fjellheim, Aelys Humphreys
Affiliation: Stockholm University, Royal Botanic Gardens, Kew, Norwegian University of Life Sciences

Hot and dry environments are characterized by low, unpredictable precipitation and high temperatures, creating challenging conditions for plant survival and growth. Plants in these environments have evolved adaptive strategies to enhance water use efficiency and ensure reproductive success, such as an annual life history and C4 photosynthesis. These adaptations are thought to have played key roles in the evolutionary success of grasses. A combined occurrence of annualism and C4 photosynthesis may represent a joint strategy to maximize fitness in hot and dry environments. However, the extent to which these traits co-evolve or are selected for together in remains unexplored. To address this, we first modelled the evolutionary history of life history, using a range of methods that take trait lability into account. Having determined that life history is a labile trait in grasses, and that this lability varies among clades, we next used Pagel's models of independent and correlated evolution to test whether life history evolution differs between C3 and C4 lineages for over 4000 species of grasses. To account for trait lability and potential type 1 statistical errors, we used models that allow transition rates to vary in different parts of the tree. Life history has shifted repeatedly from the ancestral perennial state to annual across the tree, and the rate of transitions are highest in clades with C4 photosynthesis. However, we did not find a correlation between the evolutionary histories of life history and photosynthetic pathway. These two traits evolve as independent strategies and are not functionally or evolutionarily linked. Our results indicate that annualism and C4 photosynthesis may have been shaped by similar selective pressures but have evolved through separate evolutionary trajectories in grasses.

Topic: *Systematics & Taxonomy*

A-520

Estimating a molecular phylogeny of Eriogonum kennedyi varieties

Author: Ava Joseph, J. Travis Columbus
Affiliation: California Botanic Garden

Eriogonum kennedyi (Polygonaceae) comprises five varieties endemic to the Transverse Ranges and Sierra Nevada Mountains of California. One variety, *E. kennedyi* var. *austromontanum*, has a federally threatened status due to the high development risk on the rare pebble plain habitats of the San Bernardino Mountains. However, uncertainty has arisen in how far its range extends, as observations of *E. kennedyi* in the western Transverse Ranges have been identified to be either var. *austromontanum* or the more common var. *kennedyi*. To add further complexity, the widespread *E. wrightii* var. *subscaposum* grows sympatrically with *E. kennedyi*, and potentially intergrades with *E. kennedyi* var. *austromontanum*, as individuals with intermediate inflorescence forms have been observed growing where the two species co-occur. Using ddRADseq,

this project aims to estimate the molecular phylogeny of all five *Eriogonum kennedyi* varieties in order to better understand the units of diversity in this group, and identify the level of gene exchange with *E. wrightii* var. *subscaposum*. Our preliminary findings show a clear geographic signal in the phylogeny, with *E. kennedyi* resolving in multiple clades nested within *E. wrightii* var. *subscaposum*.

Topic: Floristics

A-521

Garden loosestrife (Lysimachia vulgaris, Primulaceae), an emerging invasive plant species of riparian corridors in the Mid-Atlantic region of the US

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Lysimachia vulgaris (garden loosestrife, Primulaceae) is an herbaceous perennial native to Europe that has been identified as an aggressive invasive species in parts of North America. The status of the species in the Mid-Atlantic region of the US, however, is so far poorly determined. Using recent field observations (from iNaturalist, iMapInvasives, and EDDMapS records) we here report localized incursions of *L. vulgaris* in the Susquehanna River Valley of central Pennsylvania, along with notes on its ecology, threats to native plant communities, broader distribution in the state, and preliminary data on possible methods of eradication.

Topic: Phylogenomics

A-522

Phylogenomic analyses reveal ten major clades of Araliaceae and support geography-climate mediated radiations associated with mountains and islands

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Understanding the biogeographic patterns and processes at a global scale is fundamentally key to the study of global climate change and conservation. The Asian – Australasian regions harbor rich biodiversity and represent an ideal natural laboratory to explore biogeographic exchanges and pathways, tropical – temperate biome transitions, and plant diversification in response to tectonic movements and climate changes. The comparative biogeographic analyses of Asian – Australasian plant lineages with their close allies in the New World and Africa will provide significant insights into global patterns of biodiversity assembly. In this study, we reconstruct the phylogenetic relationships and analyze the global biogeographic exchanges in Araliaceae, a family with a dominant pantropical distribution, using an extensive taxon sampling of 603 accessions representing 94% of Araliaceae genera and 168 nuclear loci. Our phylogenomic analyses support ten major clades in the family: the *Astrotricha* clade, the *Harmsiopanax* clade, the *Hydrocotyle – Trachymene* clade, the *Pseudopanax – Plerandra* clade, the *Polyscias* clade, the *Aralia – Panax* clade, the *Raukaua – Cheirodendron* clade, the *Cussonia – Astropanax* clade, the *Osmoxylon* clade, and the large Asian – New World Palmate clade. The biogeographic inference supports an Australasian origin of the family and suggests extensive biogeographic exchanges among major Gondwanan landmasses in the Paleogene. An early Eocene long distance dispersal from Australasia to continental Asia led to a major deep radiation in continental Asia with subsequent boreotropical expansions (at least four times) into the New World from Asia. Subtropical East Asia and the adjacent tropical southeast Asia developed a rich forest flora that was highly influenced by the East Asian monsoon, the Indian monsoon, the uplift of the Qinghai-Tibetan plateau, and the development of the Malesian Archipelago. During the Neogene, biogeographic exchange between the Sunda and Sahul regions became highly active after the collision of the Australian continental crust with southeast Asia, and Australasian – Pacific dispersals facilitated the radiations in several major clades. The geography – climate mediated radiations have been observed independently in Asia, the Neotropics and the Pacific, driving the diversification in both tropical and temperate biomes.

Topic: Ecophysiology

A-523

How bulbs get swole: resource allocation patterns across bulbous plants

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Geophytes are plants with belowground perennating buds and storage organs which aid survival during disturbances, such as frosts, droughts, or fires. Geophytism can be accomplished through different types of morphologies, such as tubers (i.e. potato), rhizomes (i.e. ginger), corms (i.e. crocus), and bulbs (i.e. onion). Of these, bulbs are unique in that leaf tissue predominately participates in resource storage rather than stem or root tissue. The bulb storage organ is made up of swollen leaf tissue called scales, typically arranged in concentric layers surrounding the apical meristem. These scales vary in size, shape, and number across species, even within members of the same genus, and these differences may reflect alternative resource allocation strategies. It is not well known how variation in bulb morphology influences biomass and resource allocation across the different components (i.e., leaf, stem, root) of bulbous plants. To further our understanding of biomass and resource allocation patterns across bulbous plants, we dissected and measured the wet and dry mass of the individual components of the bulb for 16 different taxa. We calculated the water content of each individual component including each individual bulb scale. We then ran a phylogenetic generalized linear model to investigate the relationship between the different components. Overall, we found positive correlations between basal plate diameter (i.e., stem base diameter) and root mass, root and shoot mass, and leaf and stem mass

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Topic: Population Genetics/Genomics

A-524

River phylogeography: microevolutionary history of Podostemaceae in river islands in Panama

Author: Ana Maria Bedoya
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Fast-flowing aquatic habitats (i.e., river rapids and waterfalls) are dynamic units whose reconfiguration is linked to mountain building. These habitats are "islands within rivers", with patchy distributions, a reduced area, rocky substrates, and extreme but homogeneous conditions. Therefore, fast-flowing aquatic habitats provide ready-made natural laboratories to study evolution. Only one group of angiosperms has evolved to live attached to rocks in fast-flowing aquatic ecosystems in the Americas: riverweeds (Podostemaceae), the largest family of strictly aquatic flowering plants. In this talk I will discuss how populations of riverweeds evolve in natural laboratories within and across selected rivers of Panama. Using whole-genome sequence data from plants collected in field expeditions, I aim to test predictions derived from island biogeography (e.g., if gene flow decreases with distance in 'islands within rivers'), and investigate the direction and extent of gene flow along the course of single rivers and its role in maintaining genetic diversity in populations.

Topic: Dryland Floras

A-525

Stem photosynthesis and hydraulics are independent in photosynthetic stems from a tropical dry forest

Author: Eleinis Avila-Lovera, Wilmer Tezara
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Stem photosynthesis is common in desert and Mediterranean ecosystems, and most of our knowledge of stem photosynthesis physiology comes from these ecosystems. However, plants with photosynthetic stems also occur in seasonally dry ecosystems in the tropics, such as dry forests. Tropical dry forests, which are among the most threatened terrestrial ecosystems, support a remarkable biodiversity, including numerous plant species. Research in warm deserts has shown that stem photosynthesis and water transport (hydraulics) are interconnected. In this study, we tested whether this hypothesis holds true in trees from a tropical dry forest in the Macanao Peninsula, Margarita

Island, Venezuela, an area impacted by open-cast sand mining. Exploring the potential coordination between photosynthetic and hydraulic traits within and among organs can give us insights into the functional strategies plants use to cope with seasonal drought and disturbance. We measured gas exchange [photosynthetic rate (*A*), transpiration rate (*E*), and stomatal conductance (g_s)], and carbon and nitrogen isotope ratios ($\delta^{13}C$ and $\delta^{15}N$) in leaves and photosynthetic stems, and stem hydraulic traits in 12 tree species with photosynthetic stems. We found no relationship between sapwood-specific hydraulic conductivity (K_S) or other stem hydraulic traits and stem *A*. However, we did find that leaf-specific hydraulic conductivity positively correlated with leaf *A*, *E* and g_s. Additionally, tree species with high K_S also had high leaf $\delta^{13}C$, indicating that efficient stem water transport is associated with leaves having greater long-term integrated water-use efficiency. Interestingly, species with higher stem *A* also exhibited higher stem water-use efficiency. Taken together, our results suggest a coordination of hydraulics and photosynthetic traits between leaves and stems. However, this coordination is not present within photosynthetic stems.

Topic: Disabled in Botany: Breaking Barriers in Plant Science Research

A-526

Beyond boundaries: Investigating species boundaries in complex groups and accessibility in fieldwork

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One of the most important questions in evolutionary biology is what the patterns and processes are that underlie the creation and maintenance of species diversity. Delimiting species boundaries in taxonomically challenging groups where morphological differentiation is unclear and there is high potential for hybridization is essential for quantifying species diversity across changing landscapes. In plants, hybridization and polyploidy are key processes involved in generating these diversity patterns. Recent efforts to understand the combined effects of polyploidy and hybridization have found that neopolyploids acquire new alleles via their diploid parents as well as more distantly related lineages, both of diploid and polyploid origins. In this way, some polyploid species may obtain alleles that give them adaptive advantages to their environment. This "introgression with adaptive consequences" can occur when species boundaries are already blurry and allow for gene flow both within and between species. The ability to absorb new alleles through introgression with closely related species may allow for adaptive advantages in these polyploids, especially when shifting distributions results in secondary contact between previously isolated, closely related species. An excellent system to study the phylogeographic effects of glacial cycling, adaptive introgression, and polyploidy is in *Salix*. *Salix* has approximately 450 described species, roughly 35 of which are distributed in North American Arctic and alpine tundra zones. *Salix* is known for frequent hybridization and arduous identification due to extreme morphological similarity, highly reduced flowers, dioecy, and high concentrations of polyploidy (more than 40% of *Salix* species are polyploid or have polyploid populations). By examining polyploidy, hybridization, and disjunct species distributions in a widespread, complex group like *Salix,* this research spans population genomic to macroevolutionary studies and provides additional clarity on the creation and maintenance of species boundaries. Additionally, species boundaries are not the only barrier found in evolutionary biology, and as a disabled scientist, who is also passionate about increasing visibility and accessibility in botany, I will discuss how this project is made accessible both in the field and at home. It is important to note that all bodies have different abilities and these accommodations are just what are found to be useful for one specific scientist and are in no way helpful for everyone.

Topic: Physiology

A-527

Morphological Differences of Wild Quinine Across North America

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Parthenium integrifolium L. is native to much of the United States and is generally distinguished through its compact radiate heads with short white ray florets as well as the scabrous ovate to lanceolate leaves. However, populations across the range vary in their morphology as illustrated by many previously named subspecies of Wild Quinine which are now all synonymized with *P. integrifolium*. The named subspecies were based on specimens from Kentucky, Missouri, New York, Oklahoma, Massachusetts, and West Virginia; among the ecotypes, height is a notable difference as well as the number of heads per inflorescence and various leaf traits. To complement ongoing population genomic work concerning upper Midwest taxa, this study assesses the morphology of P. integrifolium across its range using images of digitized specimens. We report on differences and similarities among populations in leaf length, leaf margins, and number heads per inflorescence from 10-15 individuals sampled from 7 regions. Morphometric work will aid in interpretation of population-level results and help to develop hypotheses about the factors that affect body form and shape across the range of the species.

Topic: Reproductive Processes

A-528

Who's the Daddy? Genetic Analysis of Seeds in Wild Wintercreeper (Euonymus fortunei), an Invasive Ornamental Groundcover

Author: Robert Elam, Caitlin Barilleaux, Becca Erikson, Theresa Culley
Affiliation: University of Cincinnati

Originally brought to the US for horticultural purposes, the evergreen wintercreeper vine *Euonymus fortunei* is now considered largely invasive across the Midwest. Wild wintercreeper consists of a single tetraploid genotype, the ornamental 'Coloratus' cultivar, but it is still unknown how wild plants produces their abundant fruit. One possibility is that wintercreeper reproduces via apomixis such that seeds are identical to the maternal parent. We examined the mating system of wintercreeper by collecting leaves from 15 wild plants from Cincinnati, Ohio and analyzed embryonic tissue from their multiple fruits. We used microsatellites to identify any non-maternal parent(s), including possibilities such as other *Euonymus* species. During embryo extraction, we discovered that polyembryony was relatively common in this species, with 2-4 embryos found within 45% of all seeds. We determined that many of the 490 tested embryos were produced through apomixis (50%), followed by outcrossing (34.3%) and self-pollination (15.7%). Single embryos in a seed were most likely to be outcross-pollinated. The observed mix of sexually produced (outcrossed and selfed) and asexual (apomictic) offspring is also found in citrus and other species in Celastraceae. The observation that wild adult wintercreeper plants consist of a single genotype is consistent with the production of apomictic offspring. However, the lack of sexually-produced outcrossed wild plants, despite their appearance in the embryonic stage, is noteworthy and indicates that selective pressure in the field may negatively act against sexually-produced progeny and/or favor the apomictic genotype. Consequently, more research is needed into how different reproductive strategies may influence invasion in wintercreeper in order to advise land managers on appropriate control methods for this species.

Topic: Overcoming the barriers to on-going Castilleja research: From botanical enigma toward an emerging model system

A-529

Evaluating abiotic drivers of flower color polymorphism in the scarlet paintbrush, Castilleja coccinea

Author: Emma Fetterly, Jeremie Fant, Andrea Kramer
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Floral color polymorphisms are among the most prominent examples of intraspecific variation. The persistence of floral color variation is often attributed to pollinator-mediated selection, but it can also arise through adaptation to non-pollinator biotic and abiotic agents across heterogeneous environments, or neutral processes. Abiotic stress may drive indirect (pleiotropic) selection on flower color through anthocyanin accumulation, contributing to both pigmentation and stress tolerance. Intraspecific flower color variation is common in the genus *Castilleja* (Orobanchaceae) and may reflect complex ecological interactions. Here, we investigated drivers of flower color variation in *Castilleja coccinea*, an eastern North American taxon exhibiting striking scarlet and yellow morphotypes. We combined landscape-scale spatial analysis of community science observations with controlled greenhouse and common garden experiments. Spatial analysis revealed a strongly bimodal distribution of bract hue, with red morphs predominating range-wide and hotspots of yellow morphs concentrated in the Midwest. Significant spatial clustering suggested that morph distribution is nonrandom and associated with environmental factors such as habitat type and water availability. To test morph responses to abiotic stress, we experimentally manipulated water and light availability. We found strong associations between anthocyanin accumulation, vegetative traits, and bract color. Yellow morphs exhibited larger size, faster growth, and earlier reproduction, whereas red morphs displayed more resource-conservative traits and greater anthocyanin accumulation. Although overall evidence for strong differential

morph responses to abiotic stress was limited, significant morph-by-treatment interactions were supported for certain fitness-linked traits: red plants increased fruit-to-flower ratios under shaded conditions, while yellow plants, unexpectedly, exhibited greater aboveground biomass under drought. Collectively, these findings suggest that bract color is subject to selection and that morphs differ in vegetative trait syndromes, with limited evidence for differences in fitness-linked stress responses, which may facilitate the maintenance of floral color polymorphism across heterogeneous environments.

Topic: *Biodiversity Informatics & Herbarium Digitization*

A-530

Advancing 3D modeling of biodiversity: Overcoming photogrammetry's limitations with Gaussian Splatting

Author: Austin Mast, Alex Adkinson, Alex Leeds
Affiliation: Florida State University

Structure-from-motion photogrammetry (SfM) is a technique used to create digital 3D models from images or videos of physical subjects, with many applications for activities centered on biodiversity. While SfM (e.g., as implemented in Agisoft Metashape) excels at modeling some types of subjects using media from studio settings, it frequently fails with media taken in field conditions, where factors such as lighting, background, and camera movements are uncontrolled. Furthermore, SfM also frequently fails to model translucent, thin, reflective, or iridescent structures, which can be common in biodiversity subjects. Emerging 3D modeling techniques, such as 3D Gaussian Splatting (3DGS), have the potential to address the limitations of SfM in the biodiversity domain. Here, we introduce and evaluate 3DGS and three other recently introduced 3D modeling methods, using media from four biodiversity subjects captured in studio (controlled) settings and four subjects from field (uncontrolled) settings. We find that 3DGS outperforms SfM and the three other new methods for nearly all subjects and provide guidance on its use in the biodiversity domain.

Topic: *Ecology*

A-531

Origin of Invasive Miscanthus sinensis Populations in North America: Do Cultivars Play a Role?

Author: Theresa Culley, Olivia Leek
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Within the past decade, ornamental grasses have gained popularity due to their screening ability, rapid growth, and attractive traits such as leaf coloration and variegation. One commonly planted grass is *Miscanthus sinensis* - known as eulalia grass, Chinese silver grass, or Japanese silver grass. This non-native species has been sold in the US as more than 96 cultivated varieties over the last few decades. But as its popularity has increased, so too have wild populations in North America. The purpose of this study was to examine the possible role of commercial cultivars in the formation of invasive populations of *M. sinensis* in Ohio, Kentucky, North Carolina, Pennsylvania, and New Jersey. Using 15 microsatellite genetic markers, we tested whether invasive populations may result from cross-pollination among any of 36 locally available cultivars. If so, are there any cultivars more or less likely to contribute to these populations? We found that several different cultivars do contribute to invasive populations of *M. sinensis* in the Midwest, several of which have been advertised as having low seed set. Some populations also appear to consist of F1 hybrids or even an escaped cultivar. Consequently, spread of *M. sinensis* may be exacerbated by planting certain ornamental cultivars within the landscape, contributing to this species invasive behavior in the Midwest. This information can now be used by land managers, state regulators, gardeners, and the nursery industry to pivot to non-invasive alternatives to reduce impacts of this species in our natural areas.

Topic: *Ecology*

A-533

Pile burning in the chaparral awakens a fire follower, invites invasives, and encourages resprouting of native taxa at Jasper Ridge Biological Preserve ('Ootchamin 'Ooyakma)

Author: Adriana Hernandez, Tadashi Fukami
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Many California native plants have adapted to Mediterranean climate and to both periodical wildfires and Indigenous peoples' intentional fires. However, fires have been suppressed in many parts of California over the last few centuries, and it is unclear which of the fire adaptations that they have acquired, including resprouting, serotiny, heat induced germination, and smoke induced germination, are the major drivers of plant communities today as they respond to revival of intentional fires. Researchers are now grappling to understand how to approach burning as a vegetation management strategy in the long term, and findings will be useful and complementary to the effort to revitalize Indigenous science toward sustainable land stewardship. Prescribed pile burning took place in March 2024 in the chaparral and blue oak woodland at Jasper Ridge Biological Preserve ('Ootchamin 'Ooyakma), and burned piles were monitored to track vegetation regrowth. Plant presence, diversity, abundance, and resprouting were quantified at the center vs. edge of burned piles, and compared with unburned areas adjacent to piles. Within six months, plants were significantly more abundant in unburned vs. burned plots and more abundant in the edge vs. center of burned piles, as expected. The most common taxa in the chaparral were native resprouting plants including *Diplacus aurantiacus*, *Prunus ilicifolia*, *Toxicodendron diversilobum*, *Adenostoma fasciculatum*, and *Marah fabacea*. A rare fire follower *Malacothamnus arcuatus* var. *arcuatus* was awakened from the seed bank, with over 300 plants forming rings around the edges of piles where smoke and heat permeated the soil but was not so intense that it scorched the seeds. Invasive species were also observed in the burn pile areas, including hundreds of *Dittrichia graveolens*, where it had never been seen before. These invasive plants were immediately pulled by staff to prevent an infestation and possible transition to an undesirable ecosystem. The treated area will continue to be monitored for long-term research on the establishment of fire followers and occurrence of invasive species after pile burning.

Topic: *Ecology*

A-534

Public Gardens As Sentinels of Plant Invasion: New Plants of Rising Concern

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Established invasive plant species negatively impact natural areas and incur huge economic costs associated with control and management. A new approach to significantly reduce these effects is to identify and target plant species in their earliest stages of spread, using data being collected internally by many public gardens and arboreta across North America. These gardens have historically monitored and documented changes in their plant collections over time, including any spread of a plant from cultivation. These valuable data are being collected and shared in the form of a garden sentinel network. Launched in 2016 as Public Gardens as Sentinels against Invasive Plants (PGSIP), this initiative now includes 59 gardens across North America, each submitting reports of problematic species to a shared database, using standardized guidelines. We now examine this PGSIP dataset to answer: (1) Which plant species are most problematic across sentinel gardens? (2) Have these species already been reported outside of gardens (as state-listed or regulated)? (3) What up-and-coming species are of greatest concern within gardens? As of November 2024, PGSIP gardens in 28 US states and Canadian provinces had submitted 996 reports of problematic species, consisting of 597 unique taxa. The most commonly listed species was Amur corktree (*Phellodendron amurense*) in 12 gardens, followed by burning bush (*Euonymus alatus*) and wintercreeper (*E. fortunei*) in 8 gardens. Other frequently listed species in fewer gardens included golden rain tree (*Koelreuteria paniculata*), Norway maple (*Acer plantanoides*), and castor aralia (*Kalopanax septemlobus*), in addition to more well-known invasives such as common buckthorn (*Rhamnus cathartica*), Amur honeysuckle (*Lonicera maackii*) and Callery pear (*Pyrus calleryana*). Of the 597 species, 36% were

not listed by any state or province as invasive or noxious. Midwestern gardens also identified several newer species of concern on their watchlists, including Japanese tree lilac (*Syringa reticulata*) and Siberian squill (*Scilla siberica*). Although most of the top reported species were woody trees and shrubs, 63% of all problematic species were non-woody, including 49% herbaceous species. Taken together, this garden information can now inform the efforts of land managers in the field, invasion biologists, the horticultural industry, and agencies tasked with invasive plant monitoring and assessment.

Topic: Bryology and Lichenology

A-535

Distinct patterns of genome size and chromosome number evolution in bryophytes

Author: Nikisha Patel, Jessica Budke, Jillian Bainard
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Genome size varies by orders of magnitude across land plants, and the factors driving evolutionary increases and decreases in genome size vary across lineages. Bryophytes have the smallest genomes relative to other land plants and there is growing evidence for frequent whole genome duplication (WGD) across the lineage. However, the broad patterns of genome size, chromosome number, and WGD have yet to be characterized across bryophytes in a phylogenetic context. Using a phylogenetic approach and leveraging previously published data on genome size and chromosome number, we reconstructed the evolutionary history of these traits across the three major bryophyte lineages: hornworts, liverworts, and mosses. Each lineage of bryophytes exhibits a distinct pattern of genome size evolution and prevalence of WGD, with mosses having the most dynamic genome sizes and highest propensity for WGD. There is no correlation between genome size and WGD or genome size and chromosome number, potentially suggesting rapid genome downsizing following WGD. Genome size and chromosome number can have far reaching physiological and evolutionary implications that should be further explored. For instance, mosses can be poikilohydric (desiccation tolerant) plants, and having large genomes may be physiologically prohibitive given the cost to growth and metabolism associated with them. In addition, WGD may facilitate transitions from monoicy to dioicy. The findings in the present study emphasize the unique evolution of the bryophytes broadly and of the hornworts, liverworts, and mosses individually.

Topic: Population Genetics/Genomics

A-536

Plastid genomes and reduced representation sequencing of nuclear DNA reveal the invasion dynamics and history of Microstegium vimineum

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Invasive species cause negative impacts on biodiversity and economies globally. The ecological impacts of invasive species have been the focus of many studies in recent years; however, less is known about their evolutionary history, spread, and adaptation in new environments. One prolific invader native to eastern Asia, stiltgrass (*Microstegium vimineum*), was first collected in the United States approximately 100 years ago around Knoxville, Tennessee. Based on a previous study using digitized herbarium records, it was hypothesized that there were at least two introductions from phenotypically distinct source populations in Asia based on a pattern of awn presence or absence, with the awned form predominating in the northern regions of both the native and invasive ranges, and the awnless form in the southern regions. We took a two-fold approach, first using whole plastid genomes (plastomes) from approximately 200 individuals as a proxy to track seed dispersal between the native and invasive ranges and identify historical and contemporary invasion dynamics. Second, we used reduced representation sequencing of nuclear DNA via MIG-seq for approximately 400 individuals grown in a common garden across the invasive and native to quantify contemporary patterns of variation and the degree of admixture in the invasive range. All Southern US accessions appeared to initially comprise the same haplotype based on plastome data, indicating a single introduction, possibly from Japan. Northern US accessions revealed multiple haplotypes that are most closely related to accessions in China, Japan, and Taiwan. While the awn phenotype shows a strong north-south pattern that aligns with plastome introductions, there is clear evidence of long-distance seed dispersal as northern haplotypes are being found in the Southern US and *vice versa* in later time slices. Higher plastid nucleotide diversity was observed in the Northern US compared to that in the Southern US, with a spike in southern diversity in the last 30 years as northern haplotypes have dispersed into the southern range. Northern US nucleotide diversity was similar to that observed in the native range. Additionally, new haplotypes appeared over time, suggesting multiple introductions or a more diverse initial introduction than what would be expected under a severe genetic bottleneck resulting from a single introduction, which is corroborated by nuclear data. Furthermore, there is evidence for long-distance seed dispersal as new haplotypes are found in increasingly large areas over time. Similar clustering was observed in the MIG-seq data based on principal components analysis of 3428 nuclear variants, as most southern accessions clustered together with some accessions from Japan, and Northern US accessions had 3-4 distinct clusters containing various potential source populations from Asia. A STRUCTURE analysis identified strong evidence of admixture and some population substructure between awned and awnless populations. This aligns with plastome data that suggested there were multiple distinct populations that converged geographically over time in the invasive range. This indicates that the invasion of stiltgrass has a complex history, involving multiple introductions, long-distance seed dispersal, and admixture, adding to a growing body of studies that implicate multiple introductions in invasion success.

Topic: Macroevolution

A-537

A simple birth-death-reticulation model for studying the diversification of phylogenetic networks

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While methods for inferring phylogenetic networks and for modeling trait evolution on phylogenetic networks have advanced significantly in the last decade, we currently lack tools for studying the processes that produce phylogenetic networks: speciation, extinction, and reticulation. Reticulation events---such as horizontal gene transfer, hybridization, and allopolyploidization, among others---are central to many macroevolutionary hypotheses, for example, whether polyploid lineages are evolutionary dead ends. We derive the probability density function (pdf) of a phylogenetic network evolving under a simple birth-death-reticulation process. This pdf is suitable as a prior distribution for estimating phylogenetic networks from molecular data, and as a model for estimating rates of speciation, extinction, and reticulation. We show by simulation that the pdf is correct, and that rate parameters can be accurately estimated from phylogenetic networks. While quite simplistic, this model is a first step toward a better understanding of the macroevolutionary consequences of reticulate evolution.

Topic: Conservation Biology

A-538

Identification of Somatic Variation in Cryopreserved Oak Tissues

Author: Ryan Brooks, Megan Philpott, Valerie Pence, Theresa Culley
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Oaks (*Quercus spp.*) are an economically and ecologically important group of 400-500 species spread across the northern hemisphere. Despite their widespread distribution, the IUCN considers about a third of this group threatened by extinction. As habitat continues to be lost and degraded, ex situ conservation is necessary to prevent extinction of these species. Commonly, seed banking can be used in many plant species as an effective means of conserving genetic diversity long term, however exceptional plant species such as all oaks do not produce seeds suitable to conventional seed banking methods. Cryopreservation of totipotent cells in oaks is an alternative being utilized by the Center for Conservation and Research of Endangered Wildlife (CREW) at the Cincinnati Zoo and Botanical Garden. The dual process of cryopreservation and initiation into tissue culture (a necessary preparatory step) can be stressful on plant tissues and has already been shown to induce somatic mutations at varying degrees of severity. This project uses multiple methods to investigate the possible genomic and epigenomic changes that may be caused by different cryopreservation and tissue culture initiation procedures in a number of threatened oak species from across the southern United States, including *Q. hinckleyi*, *Q. engelmanii*, and *Q. georgiana*. Genomic changes were assessed using microsatellites, amplified fragment length polymorphisms, and RADseq, while epigenomic changes were assessed using methyl sensitive amplified polymorphisms and whole genome bisulfite sequencing. These results will be used to

ensure the fidelity of cryopreserved oak tissues in the CREW CryoBioBank and identify any particular steps where mutations might be induced more frequently. Better understanding the genetic changes in cryobanked tissues is critical in the future design and implementation of conservation efforts involving these rare oak species.

Topic: Ecophysiology

A-539

Phenotypic Variation in Resurrection Grass Microchloa afra

Author: August Lipari, Noor Sekhon, Cassandra Morley, Rose Marks
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Desiccation tolerance has evolved repeatedly across diverse plant lineages as an adaptation to extreme aridity. These plants have adapted to survive periods without water through a variety of genetic and cellular mechanisms, making them interesting candidates for studies on the nature and evolution of qualities that allow for survival in water limited conditions. Microchloa afra is a perennial resurrection grass native to Southern Africa, widely distributed across a variety of environments and capable of surviving multiple cycles of desiccation and rehydration. When cultivated in a common environments, plants native to mesic environments were found to suffer more tissue senescence during desiccation compared to plants native to xeric sites. Interestingly, this species harbors multiple cytotypes, and plants from xeric sites also tend to have larger genome sizes. Whole genome duplication increases vigor and stress tolerance in many plant species, and it is hypothesized that similar mechanisms could enhance desiccation tolerance and resilience in M. afra. Here, we catalog phenotypic diversity in 133 accessions of M. afra collected along a natural aridity gradient spanning over 1000 km and including 35 sites, characterizing differences in germination, pigmentation, leaf and panicle morphology, reproductive allocation, and ploidy. We define several distinct ecotypes in M. afra, distinguished by differences in size, shape, and reproductivity, and note how these patterns correlate with their native environmental conditions. We find that plants from warmer and more arid sites tend to be larger, and those from cooler, more mesic sites have a greater number of panicles and reach reproductive maturity more quickly, indicating drought-adaptation may trade-off with reproductive allocation.

Topic: Phylogenomics

A-540

Disentangling gene tree conflict induced by erroneous orthology inference associated with whole-genome duplications

Author: Keyi Feng, Stephen Smith
Affiliation: University of Michigan

Orthology is one of the most important preconditions for accurate phylogenomic inferences, but it is quite difficult to determine gene orthology in a flawless way for angiosperms. This is because ancient whole-genome duplications (WGDs) occur frequently and are widely distributed within flowering plants. After WGD events, angiosperms often experience diploidization and extensive gene copy loss. Different lineages often experience loss of different sets of genes, making orthology inference immensely complicated. Most popular orthology inference methods detect gene duplication via duplicated taxa in homolog clusters. However, with differential gene copy loss, certain homolog clusters may appear as duplication-free at the WGD-associated node and potentially leads to erroneous orthology inference and artificial gene tree conflict. Many well-known ancient WGD events coincide with high levels of gene tree conflict, e.g. the ones preceding core eudicots and the ones within Ericales and Caryophyllales. Interesting biological processes may be underlying these gene tree conflicts, but it is tremendously difficult to disentangle them with the presence of artificial gene tree conflicts. Here I present a new WGD-aware method that minimizes false orthology inference and artificial gene tree conflict in phylogenomic datasets. I will demonstrate the importance and the usage of this tool with several angiosperm phylogenomic datasets, such as Ericales, carnivorous Caryophyllales, and Caryophyllaceae.

Topic: Ecophysiology

A-541

Developing a modified Falcon tube method to assess desiccation tolerance in the leaves of fern sporophytes

Author: Meghan Oh, Helen Holmlund, Lailla Burka, Samuel Fitzgerald, Gabrielle Johnson, Charity McBay, Nataly Montoya, Christine Spears, Cole Robbins
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Desiccation-tolerant "resurrection" plants can survive losing nearly all their water (<-100 MPa) and subsequently recover after rehydration. Although desiccation tolerance is rare in vascular plants, new desiccation-tolerant species are still being discovered. The importance of observing and quantifying desiccation tolerance in plants is instrumental for advancing our knowledge of the survival mechanisms and strategies that plants use to withstand drying. Additionally, developing a field portable technique to quantify desiccation tolerance is essential for efficiently and accurately assessing desiccation tolerance across plant species. In order to address these objectives, we have modified the "Falcon tube method" from a previous study that prepared a field portable technique for quantifying desiccation tolerance in leaf tissue. In our study, we incorporated several novel adjustments to more accurately quantify desiccation tolerance in fern species with thicker leaves. 1) We lengthened the drying time from two to six days, allowing for our fern leaf samples to fully desiccate. 2) We lengthened the rehydration period from one to three days, allowing the ferns to fully recover pre-desiccation F□/F□. 3) We added a hydrated control treatment in order to demonstrate that the duration of the experiment was not so long as to allow natural senescence of excised leaves. (4) We add a mesh sleeve to the tube wall to allow us to collect F□/F□ data without opening the tube and changing the humidity. Ultimately, our modifications allowed us to accurately quantify desiccation tolerance in several fern species and identify an optimized protocol that we will apply to future studies on thick-leaved ferns.

Topic: Macroevolution

A-542

Get Low: Evolutionary Transitions to Non-flying Mammal Pollination in Protea L. (Proteaceae)

Author: Nora Mitchell
Affiliation: University of Wisconsin - Eau Claire

The Cape Floristic Region (CFR) of South Africa is one of Earth's greatest biodiversity hotspots. Nearly half of the extraordinary floristic diversity (9000 species) and high rates of endemism (70%) are associated with only 33 plant genera, including the iconic *Protea* (L.), Proteaceae. A majority of the 115 described *Protea* species are endemic to the CFR, where their diversification reflects abiotic factors such as climate, elevation, and edaphic heterogeneity, but the influence of species interactions on the evolution of this radiation is understudied. *Protea* have spectacular floral adaptations (shape, color, and scent) to different pollinator types, including birds, beetles, and non-flying mammals. Non-flying mammal pollination is relatively rare but has many documented cases in the family Proteaceae and is often related to changes in plant form, population genetics, demography, ecology, microbiome composition, floral chemistry, and overall evolutionary trajectories. Current evidence suggests multiple transitions to non-flying mammal pollination. Here, we use Anchored Phylogenomics to expand on a previous phylogeny of *Protea* to include >20 additional species and present preliminary evidence for evolutionary transitions between pollination syndromes, including multiple shifts to non-flying mammal pollination and associated morphological correlates across the genus. Deeper insights into the causes and consequences of these pollinator shifts build upon conceptual ideas about the nature of evolutionary radiations, advancing our knowledge within the context of species interactions more broadly.

Topic: Phylogenomics

A-543

Using Next Generation Sequencing to Address Taxonomic Uncertainties Surrounding Potentilla rupincola

Author: Natalie Hieber, Mitchell McGlaughlin
Affiliation: University of Northern Colorado

Next-generation sequencing (NGS) has become a powerful tool for resolving taxonomic uncertainties by uncovering genetic relationships between individuals that may otherwise be undetectable. This is particularly valuable for plant taxa historically classified using morphology alone. *Potentilla rupincola*, a rare Colorado taxon, presents such a

case. For over a century, botanists have debated whether *P. rupincola* is a distinct species or is merely a morphological variant of the more widespread *Potentilla effusa*. This study uses NGS to assess whether *P. rupincola* is a genetically distinct species. Although the genetic taxonomy has been studied for several species within the *Potentilla* genus, *P. rupincola* has not been examined in this context. Confirming its species status would clarify its conservation importance, as a distinct species would be endemic to Colorado and potentially threatened by wildfire mitigation activities within its range. This project involves three phases: (1) sample collection, (2) DNA extraction and sequencing, and (3) bioinformatic analysis. Field collections began in summer 2024, and initial genetic data have been obtained from several populations of both species, including individuals from the type specimen locality for *P. rupincola*. Preliminary results indicate little genetic differentiation between *P. rupincola* and *P. effusa*, but additional sampling is required to confirm these findings. Further analyses will incorporate herbarium specimens and outgroup taxa to strengthen phylogenetic resolution. If evidence supports species-level distinction, subsequent morphological analyses will seek to identify consistent diagnostic traits. Resolving the taxonomy of *P. rupincola* will support evidence-based conservation and resource management, enabling land managers to prioritize actions and allocate resources appropriately within their landscapes

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Topic: Overcoming the barriers to on-going Castilleja research: From botanical enigma toward an emerging model system

A-544

Hemiparasitic Castilleja are associated with consistent increases in plant diversity across alpine communities

Author: Jordan Argrett, Makena Lang, Anny Chung, Anders Hastings, Nina Wurzburger, C.F Williams
Affiliation: University of Georgia, Colorado State University, Rocky Mountain Biological Laboratory

As our understanding of community and ecosystem processes grows, so does the realization of key processes, such as the stabilizing effect of biodiversity and the importance of keystone species in regulating community and ecosystem function. Parasitic plants are a large and functionally diverse group of partial to fully heterotrophic plants that are incredibly understudied compared to their prevalence across natural systems. Parasites utilize haustoria to connect to host branches and stems aboveground (aerial parasites) or belowground roots (root parasites) to extract carbon, nutrients, and water for their growth and survival. The prevalence, distinct physiology, and potential as keystone species position parasitic plants as an essential puzzle piece in our understanding of ecological communities. *Castilleja* is a widespread genus in the Orobanchaceae, with around 200 species occurring across North America, South America, and Asia. The Genus is the most species-rich in Western North America. *Castilleja* are facultative root hemiparasites known to create haustoria across a wide range of species. The diversity of *Castilleja* and its prevalence across North America position the genus as an ideal group for comparison against our understanding of European Hemiparasites. We conducted a two-year observational study on hemiparasitic *Castilleja* species at the Rocky Mountain Biological Laboratory (RMBL) to address critical knowledge gaps for North American root-hemiparasitic plants. First, we established the relationships between three hemiparasitic *Castilleja* species and plant community diversity and composition. Secondly, we assessed host range and preference for each species in situ via direct and indirect sampling methods. To address our objectives, we posed three questions: (1) Is the presence of *Castilleja* species associated with more diverse plant communities? (2) Is the presence of *Castilleja* species associated with plant community compositional changes? (3) Do the *Castilleja* species of the Colorado Rockies exhibit host preference? The results of our research correlates *Castilleja* presence with a significant increase in species diversity, driven primarily by an increase in species richness. Castilleja's presence does not correlate with changes in large-scale plant community composition. However, our indicator species analysis suggests small correlations between co-occurring species cover and *Castilleja* presence at the site level. Lastly, plants within the genus appear to have a broad host range with limited but not negligible host preferences. Together, these results support the theory of the positive effects of hemiparasites on biodiversity. However, experimental work is required to target hemiparasitic Castilleja's direct and indirect effects on plant communities.

Topic: Ecology

A-545

Investigating the function of the awn and its role in invasion success of Microstegium vimineum (stiltgrass)

Author: Lauren Kosslow, Craig Barrett, Cynthia Huebner
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Invasive species can disrupt ecosystem processes and reduce biodiversity, but mechanisms underlying many invasions remain poorly understood. We focused on *Microstegium vimineum* (stiltgrass) and the role of in invasion success. This species is expanding both northward and westward in the US, and one possible explanation for northward expansion is the distribution of. Awns are bristle-like extensions from the floret that respond to changes in moisture and can aid in dispersal/burial in some grasses, but their function in *M. vimineum* remains unresolved. *Microstegium vimineum* has multiple awn forms (awned, awnless, short- or intermediate-awned) with a distinct awned-awnless distribution from north-south in the native and invasive ranges, suggesting awns may be favored by selection in certain conditions. that awns facilitate small-scale floret dispersal to safe sites and subsequent burial, which protects seeds from freezing at high latitudes and elevations, increasing survival and promoting northern expansion. Our goal is to elucidate awn function and its role in invasion success through reciprocal transplant and dispersal experiments examining the effects of awn type on germination, survival, and dispersal capabilities. were conducted over three years at four locations across the US, including sites at low/high latitude/elevation (Erie, PA, Morgantown, WV, Davis, WV, and Clemson, SC). Awn treatments included awned, awnless, and awn-removal to account for trait differences in the awned-type not due to the awn itself. In, the awned-type had the greatest germination frequency at high latitude and the awnless-type had the greatest mortality at high latitude/elevation, which supports our hypothesis of an advantage for the awned-type under conditions associated with high latitudes/elevations. However, there was no difference in germination between the awned-type and awn-removed treatment, suggesting the awn itself may not confer this advantage. In, we investigated awn function in seedbank survival over multiple winters. The awned-type had significantly greater germination in year 2 than the awnless and awn-removed treatments, suggesting the awn itself increases seedbank survival over multiple years. of this experiment showed no difference in germination between the awn treatments, likely due to a lack of remaining seeds in the seedbank. Ongoing investigating dispersal of awn treatments on various substrates further clarify awn function. Awn treatments include awned, awnless, short-awned, and awn-removed, while substrate treatments include hardboard (Masonite), soil, and soil with leaf litter. Preliminary results suggest the awned-type has the greatest dispersal ability overall, supporting the function of *M. vimineum* awns in small-scale dispersal to safe burial sites via hygroscopic movement. Our research uses the well-established *M. vimineum* as a study system to shed light on the dynamics of the invasion process. Elucidating *M. vimineum* awn function provides insights into traits conveying invasion success and mechanisms of northern range expansion, informing invasion risk assessment both into new regions and in response to climate change.

Topic: Comparative Genomics/Transcriptomics

A-546

Losing genes, gaining edits: relaxed selection and inverted repeat expansion fuel RNA editing accumulation in Schizaeales plastomes

Author: Blake Fauskee, Farley Kwok van der Giezen, Li-Yaung Kuo, Kathleen Pryer
Affiliation: Duke University, University of Western Australia, National Tsing Hua University

RNA editing is a post-transcriptional pyrimidine exchange process that occurs in the organellar genomes of nearly all land plants. Although confined to plastid and mitochondrial transcripts, it is carried out by nuclear-encoded PLS-type pentatricopeptide repeat (PPR) proteins that recognize and edit specific RNA targets in a one-protein-to-one-edit manner. While many editing sites are functionally neutral, RNA editing has been implicated in modulating organellar gene expression, particularly through edits at cryptic start and internal stop codons. Ferns—and some lycophyte lineages—are unique among vascular plants in exhibiting both C-to-U and U-to-C editing, making them valuable for studying the evolution of both forms. We focus on RNA editing in the plastid genome (plastome) of four Schizaeales species: *Schizaea dichotoma*, *Actinostachys digitata*, *Anemia phyllitidis*, and *Lygodium microphyllum*. The first two have non-photosynthetic gametophytes, while the latter two retain photosynthetic gametophytes. This contrast provides a unique opportunity to investigate how plastid

RNA editing evolves in lineages where photosynthesis is absent in one life stage. *Schizaea* and *Actinostachys* exhibit significantly more C-to-U edits than *Anemia* and *Lygodium*, despite substantial plastome reduction, including loss of the *ndh* suite and, in *Actinostachys*, all *chl* genes. Genes under relaxed purifying selection in *Schizaea* and *Actinostachys* accumulate more editing sites, and the number of edits per gene correlates with the degree of relaxation, suggesting relaxed constraint promotes editing proliferation. Both species also show expansion of the chloroplast inverted repeat (IR), and genes translocated into the IR exhibit reduced substitution rates and higher editing densities, suggesting IR expansion slows the loss of edits. RNA edits that restore cryptic start codons or correct internal stop codons are more conserved across species than other nonsynonymous edits. Finally, annotation of PPR proteins reveals few full-length editing factors, suggesting catalytic domains may assemble in trans—highlighting the modular nature of the fern editosome.

Topic: Defining forces in fern evolution: Celebrating the contributions of Kathleen Pryer and Michael Windham

A-547
Cystopteridaceae as a Model for Understanding Polyploid Evolution

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Affiliation: Utah State University, USU, University of Zurich

Polyploidy has long been recognized as a key evolutionary force in plants, yet its complex and reticulate nature has often made it one of the most challenging processes to study in a phylogenetic framework. Building on the foundational work of Kathleen Pryer (on *Gymnocarpium*) and Michael Windham (on *Cystopteris*), the fern family Cystopteridaceae is now emerging as a powerful model for understanding the evolutionary consequences of whole-genome duplication. With multiple, independently derived polyploid lineages, broad geographic distribution, and well-characterized diploid progenitors, Cystopteridaceae offers a unique opportunity to study genome duplication across evolutionary and ecological scales.

In this talk, I will highlight the distinctive biological and genomic characteristics that make the family especially tractable for polyploid research, including its reproductive biology, cytological behavior, and the availability of molecular and computational tools tailored for complex polyploid systems. I will also present recent findings from ongoing phylogenetic analyses, including the application of next-generation tools like PURC (for inferring true biological sequences) and *homologizer* (for probabilistic phasing of homeologs), as well as other models for polyploid networks. By integrating cytogenetics, next-generation sequencing, and phylogenetics, this work demonstrates how Cystopteridaceae can provide insights to major questions in polyploid evolution. This research not only honors the legacies of Pryer and Windham but also pushes forward the boundaries of what is possible in fern systematics and evolutionary biology.

Topic: Education and Outreach

A-549
Wing length in Pieris rapae compared to elevation

Author: Alexander MacQueen Pooler, Tyler Miller, Katie Weglarz
Affiliation: Westfield State University

Pieris rapae is one of the world's most common pest butterflies, causing severe damage to crops worldwide. Previous research on this species has found that the wingspan of *Pieris rapae* and temperature have a positive correlation. We were interested in the ability that allowed for wing size to adapt to environmental conditions that affect the butterfly. In this project, we explored if the wing size of *Pieris rapae* could also adapt to elevation changes in a similar way, as elevation change alters the work required to generate lift; larger wings would make it less difficult to fly at these higher elevations. Our hypothesis was that *Pieris rapae* collected at lower elevations would have smaller wing sizes compared to those collected at higher elevations. We used digital natural history data from iDigBio and Amazon Web Services (AWS) elevation tiles to compare wing length and elevation. We measured wing length using specimen photos from iDigBio in ImageJ. By combining our measurements with the specimen collection location we were able to use an R script to find the elevation for each butterfly. The script cleaned the specimen occurrence data, fetched the elevation data from AWS with the elevatr library, calculated a linear regression, and made visual representations of the data. We found that both the left and right wing lengths have a strong positive correlation to the elevation that butterfly specimens were collected. This supports our hypothesis, that wing size of *Pieris rapae* increases at higher elevations, displaying just how adaptable the wings of these butterflies are. This adaptability may partly explain why *Pieris rapae* is so successful and how it is able to live in different environments around the world. Further investigation into the adaptability of wing length in regard to elevation in other butterfly species could further explore this relationship is unique to *Pieris rapae* and potentially other invasive butterflies.

This research was conducted as a CURE developed by the Biological Collections in Ecology and Evolution Network (BCEENET). BCEENET CUREs use digitized natural history collections data and free open source tools to increase accessibility to undergraduate research opportunities while also participating in innovative research.

Topic: Reproductive Processes

A-551
Floral mimicry of decomposing substrates

Author: Katherine Goodrich
Affiliation: Widener University

Some flowers use scent and visual cues to advertise a reward they do not actually possess – a phenomenon called floral mimicry. Floral mimicry of decomposing substrates is particularly interesting, with flowers mimicking cues from a range of potential substrates (carrion, fermenting plant material, dung) and attracting diverse groups of saprophagous insects seeking to feed or oviposit on these substrates. Current studies documenting this type of floral mimicry show intriguing patterns of convergence in floral colors, scents, and texture, yet there is still much to for us to learn about key aspects of these decomposing models – and thus key aspects of the floral mimics – necessary for insect attraction and manipulation. I will present work documenting floral phenotypes in two species – *Asimina triloba* (Annonaceae) and *Symplocarpus foetidus* (Araceae) – that likely use this type of mimicry as a pollination strategy. I will also present work documenting naturally-occurring decomposing substrates, comparing the phenotypes of these substrates to the floral phenotypes. Finally, I will share our ongoing work to identify and compare insect taxa attracted to the flowers and to decomposing substrates, particularly focusing on insect taxa attracted to both deceptive flowers and ecologically-relevant substrates. This investigation helps elucidate boundaries and potential overlap between substrate properties and attracted insect communities within a close geographic area (southeastern PA). Ultimately, it provides insight into the ecology and evolution of a fascinating evolutionary trend in the diversification of Angiosperms.

Topic: Symbioses: Plant, Animal, and Microbe Interactions

A-552
Comparing fungal communities in Tsuga heterophylla seedling roots across nurse log decay and the forest floor

Author: Ellie Olpin, Carrie Woods
Affiliation: University of Puget Sound

Nurse logs are fallen, decaying trees that have been shown to facilitate the survival, establishment, and growth of tree seedlings, therefore making vital contributions to forest regeneration. Previous hypotheses posit that nurse logs promote seedling success by offering seedlings a refuge from competition with established forest floor plant communities. Alternatively, we hypothesized that changes in plant-fungi interactions across substrates may also influence seedling survival on nurse logs and the forest floor. We predicted that there would be a higher abundance of fungal pathogens on the forest floor and a higher abundance of ectomycorrhizal fungi on nurse logs, and that this pattern would shift across the stages of nurse log decay. We examined how fungal communities in seedling roots differed between nurse logs and the forest floor as well as across three nurse log decay stages. To study this, we collected western hemlock (*Tsuga heterophylla*) seedlings (5-10 cm) from nurse logs of each decay stage and the forest floor at three field sites on the Olympic Peninsula, WA. The fungal communities and functional guilds present in the root tips of these seedlings were characterized using Illumina sequencing and the FUNGuild database, respectively. Fungal community composition varied across substrates, such that the fungal communities in seedlings on the forest floor were most similar to the most decayed nurse logs and least similar to the least decayed nurse logs. The abundance of fungal pathogens was higher on the forest floor than on nurse logs, suggesting a role of pathogenic fungi in seedling success across substrates. However, the abundance of ectomycorrhizal fungi did not significantly differ across substrates. These results indicate that one mechanism by which nurse logs facilitate seedling survival is by providing seedlings an escape from soil-dwelling fungal pathogens on the forest floor, thus contributing to forest regeneration.

Topic: *Education and Outreach*

A-553

Human Impact on Pieris Rapae Wing Melanization

Author: Gabriella Garik, Katie Weglarz
Affiliation: Westfield State University

The cabbage white butterfly, *Pieris rapae*, exhibits sexual dimorphism influenced by factors such as pheromones, UV wing reflectance, flutter response, and wing melanization. Limited research on the human impact on wing melanization in *Pieris rapae* motivated this study. I hypothesized that human population density affects wing melanization, and to investigate this, I analyzed specimens sourced from IDigBio from 1821 to 2020, focusing on those collected in the United Kingdom and Japan. Using ImageJ, I measured wing spot melanization and cross-referenced this with human population data from NASA, focusing on the wing apex melanization. Initial analysis involved linear regression analysis of human population density and spot area for each wing and country and identified a significant correlation ($p < 0.05$). To refine the analysis, I concentrated on specimens from 1900 and 2020. This narrowed analysis showed no significant relationship between human population density and wing melanization, a result that was not consistent with the broader dataset (1821-2020). These mixed results indicate that further analysis of the complete dataset (1821–2020) is needed to better understand how human population density may influence wing melanization over time. This study highlights that the global event of industrialization may be a contributing factor to the homogenization of butterfly traits as the global population grows. It also raises additional questions about how the relationship varies across other countries not directly evaluated in this study. This research contributes to a better understanding of the global relationship between human population density and wing melanization in *Pieris rapae*. Understanding the morphological response of these butterflies as they relate to human population growth can provide valuable context for understanding differences between those individuals in densely populated urban areas and sparsely populated rural locations. This is particularly relevant as the global human population is has experienced exponential growth from 1821-2020.

This research was conducted as a CURE developed by the Biological Collections in Ecology and Evolution Network (BCEENET). BCEENET CUREs use digitized natural history collections data and free open source tools to increase accessibility to undergraduate research opportunities while also participating in innovative research.

Topic: *Physiology*

A-554

A Li-Cor walks into a muddy forest: photosynthetic physiology and genomics of Symplocarpus foetidus

Author: Claire Marino, Karolina Heyduk, Robert Bagchi
Affiliation: University of Connecticut

Symplocarpus foetidus (eastern skunk cabbage) is an early-blooming angiosperm native to the northeastern United States. Its cold weather emergence and domination of the forest floor in early spring is aided by its ability to perform thermogenesis via cellular respiration in the spadix, a floral structure central to its sexual reproduction. The thermogenic properties of *S. foetidus* are relatively well-studied, such as the influence of ambient temperature on thermoregulatory patterns. However, other important traits of *S. foetidus* such as primary reproductive strategy and seasonal physiology remain unclear. Here, I present preliminary data on whether *S. foetidus* reproduces primarily sexually or vegetatively, the extent of clonality within the species, and photosynthetic activity across the growing season until its senescence in mid-summer.

Topic: *Population Genetics/Genomics*

A-555

Museum genomics reveals temporal genetic stasis and global genetic diversity in Arabidopsis thaliana

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Maintenance of genetic diversity is a crucial element to the long-term persistence of species and the preservation of ecosystems' biodiversity. In this regard, global patterns of genetic diversity through time provide a unique opportunity to elucidate which evolutionary process are responsible for maintaining species' genetic diversity across their distribution range. However, continuous, long-term experiments tracking genetic changes over long time periods are very rare. Plant historical records archived in herbaria offer a perfect alternative since genetic data from samples stored in herbaria provide a direct window into past evolutionary events and their evolution until present time. Here, we used over 500 individuals collected from native populations of *Arabidopsis thaliana* during the last 250 years to obtain a broader view of genomic diversity across the species, and to test if population genomic composition is changing through time. In this regard, our study provides the most comprehensive picture of *Arabidopsis thaliana* genetic diversity on its native range, including geographic areas that were previously excluded from comprehensive population genetic analyses. We identified extensive and previously uncharacterized diversity in African populations that are under threat from anthropogenic climate change. Moreover, our results indicate that ancient and current samples from the same geographic region are more similar to one another than they are to samples from other geographic regions, regardless of their collection date suggesting no dramatic changes in population genomic composition of populations. Despite this similarity within regions across time, we did identify a pattern of genetic change every 100 years of the same magnitude as when comparing Eurasian populations that are 185 km apart. The latter is probably a consequence of a combination of drift and changing selection. However, we identified only mixed signals of polygenic adaptation at phenology and physiology QTL. Genes conserved across eudicots show different levels of directional allele frequency change, most likely due to variable purifying and background selection. Our study illustrates how herbaria specimens can uncover new dimensions of population diversity and help us understand how wild populations are evolving in recent history.

Topic: *Bryology and Lichenology*

A-557

Water holding capacity varies by species and organizational unit in four mosses

Author: Meg Lake, Jeff Diez, Bruce McCune, Jessica Allen, Sofia Green, Mark Schulze
Affiliation: University of Minnesota, University of Oregon, Oregon State University, NatureServe, University of California, Davis

A species' ecological role and distribution is driven by its functional traits. As non-vascular, poikilohydric plants, bryophytes present a nuanced response to changes in water availability and offer a unique opportunity to understand the relationship between traits and environmental properties on a microclimate level. Water holding capacity (WHC) is a key functional trait that influences ecosystem hydrology. In this study we investigated variation in WHC among species, at different elevations, and at different organizational levels (individual strands vs. intact moss mats). We expected to find that high elevation populations have higher WHC than low elevation populations of the same species and that mats would be better indicators of overall WHC of a given species. Our study focused on four species found across an elevational gradient at HJ Andrews experimental forest: Rhytidioposis robusta, Kindbergia oregana, Hylocomium splendens and Rhytidiadelphus triquetrus. Samples were gathered from three sites representing high and low elevation populations of each species where possible. Specimens were exposed to a rehydration and desiccation experiment. Oven dry weights and weights taken intermittently during the drying process were used to calculate WHC. Mean WHC capacity differed among species ($p<0.01$) and between shoots and mats ($p<0.01$), but not between elevations ($p=0.9$). We found a significant difference ($p<0.0$) in mean

WHC based on species by organizational level. The dry-down rates of shoots and mates wear much faster than for mats. We found significant variation in dry-down rates among species when looking at both mats and strands. Our research showed significant variation in WHC capacity and dry-down rates among species and organizational levels. Understanding the variation in water relations among these four species as they occur in situ, in mat form, potentially has explanatory power for distributional differences we see in this ecosystem while also contributing to our understanding of the hydrologic role of bryophytes in seasonally wet temperate forests.

Topic: *Education and Outreach*

A-558

Investigating leaf area as an invasive trait of common periwinkle

Author: Cody Kilpatrick, Claudia Stein
Affiliation: Auburn University at Montgomery

Non-native invasive plant species out-compete native organisms, reduce biodiversity, and can alter the abiotic environment as they spread. This can cause environmental and/or economic damage in their introduced ranges. Comparing morphological traits of invasive species in their native range to their invasive range can improve our understanding of the underlying mechanisms allowing species to become invasive in their introduced ranges. In this project, we used digitized herbarium data from the Integrated Digitized Biocollections (iDigBio) to compare the leaf area of *Vinca minor* in its native Eurasian range to its invasive North American range. *Vinca minor* was first introduced to North America as an ornamental in the 1700s. It is invasive in both open and shaded sites, forming dense ground cover mats. Here we focused on leaf area as it is an indicator of the plants' photosynthetic capacity, where an increased area allows the plant to capture more sunlight and thus increase its competitive ability.

Our results showed that mean leaf area of *Vinca minor* was significantly higher in its native range (mean leaf area 348.1 mm2) compared to its invasive range (mean leaf area 295.7 mm2). Having a smaller leaf area in the introduced ranges might indicate rapid adaptation to the new environment and/or climate conditions, or lower understory competition for light. It might also indicate a founder effect, where genetic variability of the initially introduced individuals was low and contained mainly individuals with smaller leaves. Understanding the mechanisms driving this decrease in leaf size in the invasive range, whether through evolutionary changes or phenotypic plasticity, will help inform effective management strategies for this species.

This research was conducted as a CURE developed by the Biological Collections in Ecology and Evolution Network (BCEENET). BCEENET CUREs use digitized natural history collections data and free open source tools to increase accessibility to undergraduate research opportunities while also participating in innovative research.

Topic: *Ecophysiology*

A-559

A comparative study of isohydric and anisohydric strategies in leaves and photosynthetic stems in two desert Utah sites

Author: Osedipo Adegbeyeni, Oranys Marin, Eleinis Ávila-Lovera
Affiliation: University of Utah

Water status in plants is an important indicator that reflects the strategies plants use to cope with and survive under limited water availability, especially in arid environments like deserts. During drought, plant stomata can either remain open to assimilate CO_2, at the expense of water loss and reduced leaf and stem water potential, or close to limit water loss, thereby maintaining a relatively stable water potential. These regulatory strategies are known as anisohydry and isohydry. Although photosynthetic stems are common in desert plant species, providing an additional source of carbon, the water status regulation mechanisms of these plants remain unclear. We investigated the water use strategies in 17 desert species that are either trees, shrubs or subshrubs, some with multiple woody green stems and others without green stems from two Utah desert sites: Rio Mesa (Colorado Plateau) and Beaver Dam (Mojave Desert), and compared the leaves with photosynthetic stems to study if their water potential regulation strategies differ. We measured predawn and midday water potential (Ψpd and Ψmd) and gas exchange traits, including stomatal conductance (g_s), transpiration rate (E), and photosynthetic rate (A), using a Li-COR 6800, and calculated intrinsic water-use efficiency (WUEint) and instantaneous water-use efficiency (WUEins) during the dry seasons of 2023 and 2024. Our results revealed no differences in stomatal regulation of water status between leaves and photosynthetic stems, based on the slope of Ψmd versus Ψpd (σ). At Rio Mesa, a higher-elevation site, most species exhibited anisohydric behavior ($\sigma > 1$). Conversely, at Beaver Dam, a warmer, lower-elevation site, many species exhibited partial to strict isohydric behavior ($0 \leq \sigma < 1$). We also found that stem WUEint was higher at Beaver Dam compared to Rio Mesa, due to the lower stomatal conductance of species at Beaver Dam. Because this work was performed during the dry season, the responses found here may not be representative of the whole year. We will be sampling in the wet season with greater water availability, which will allow us to compare leaves and stems of the same species (most species studied are drought deciduous, and many were leafless during the dry season when they were sampled).

Topic: *Population Genetics/Genomics*

A-560

Preliminary Results of a Genomic Study on the Narrowly Endemic Species Astragalus Ripleyi Barneby.

Author: Juan Jaramillo-Chico, Mitchell McGlaughlin
Affiliation: University of Northern Colorado

The conservation of species on our planet is an ever-growing concern and goal for a variety of groups, both public and private, across the world. To make effective conservation plans for any species, we must first know everything we can about it: the current status of the species, how large the populations are, and what factors pose the largest dangers to populations and the individuals that make them up. This project seeks to answer the first question for *Astragalus ripleyi* Barneby (Fabaceae). This narrowly endemic species is native to southern Colorado and northern New Mexico. Though it was originally described in 1952, hardly any information about this species has been introduced into the scientific literature. Apart from one mention by the original author of the species, the only published literature about *A. ripleyi* is a 2003 technical report detailing the extensive lack of information surrounding the species. As a part of this project, DNA has been extracted from individuals across 6 populations spanning the specie's north-to-south range in Colorado and next-generation sequencing techniques have been used to build a genomic library. Presented here are the preliminary results from these populations that demonstrate population level structure in the species, with three primary population clusters appearing along a north-south gradient. This type of data will be used to provide a report on the genetic structure of the species across its entire range, give a measure of genetic diversity, and list any concerns on the genetic health and conservation of the species.

Topic: *Biology of mycoheterotrophic and parasitic plants*

A-561

(Fungal) Friends in Low Places: Fungal Metabarcoding Reveals Saprotrophic Associations in a Rare North American Orchid

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Orchids are well known for their diverse symbiotic strategies, including mycoheterotrophy—the uptake of carbon (C) and nutrients from fungal hosts. While over 300 orchid species are fully mycoheterotrophic and achlorophyllous, a growing number of green, photosynthetic orchids are now known to exhibit partial mycoheterotrophy (PMH), combining photosynthesis with fungal-derived C uptake. These species are increasingly recognized as ecologically and evolutionarily significant. Although PMH orchids are often known to associate with mycorrhizal fungi, emerging evidence suggests that some instead rely on saprotrophic fungi, a lesser-known but potentially widespread strategy.

In earlier work identifiying PMHs in the orchid flora of Wisconsin, we found support for the status of Triphora trianthophoros, a rare diminuative terrestrial, as a putative PMH. Here, we combined stable isotope analyses with fungal metabarcoding to investigate fungal C use and symbiont identity across 16 populations spanning the species' North American range. Stable isotope data showed consistent enrichment in $\delta^{13}C$ and $\delta^{15}N$, further supporting a strong mycoheterotrophic strategy and confirming PMH function across diverse ecological contexts. Fungal ITS sequencing revealed that mature T. trianthophoros individuals associate not with typical orchid mycorrhizal fungi, but primarily with saprotrophic litter-decaying basidiomycetes in the genera Marasmius, Rhizomarasmius, and Cyclocybe. These findings suggest that T. trianthophoros represents a stable, saprotroph-associated PMH strategy and offer new insights into orchid–fungus symbioses, conservation planning, and the ecological diversification of mycoheterotrophy in temperate North America.

Topic: *Biodiversity Informatics & Herbarium Digitization*

A-562

Enriching and improving access to herbarium specimen data using new tools in online Symbiota data portals

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Millions of records of herbarium specimens are now digitally available for research, education, and resource management. Over 98 million specimen records and 44 million images can be found in portals built on the Symbiota software (symbiota.org), such as SEINet (swbiodiversity.org/seinet), the Bryophyte Portal (bryophyteportal.org), the Lichen Portal (lichenportal.org), and the Algae Herbarium Portal (macroalgae.org). These portals provide access and management for themed databases of specimen data, and they act as the primary collection management system for over 1,200 natural history collections worldwide. In the past year, the Symbiota Support Hub–a University of Kansas-based service team and infrastructure resource for Symbiota portals–has led the development of exciting new features, including new mechanisms to search, view, annotate, and download specimen data (symbiota.org/category/new). Here we demonstrate new tools available for use and how they can be used for research and collection management.

Topic: *Paleobotany*

A-563

The fossil record of plant defenses suggests rampant herbivory early in land plant history

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Permineralized plant fossils preserved in the Early Devonian (Emsian, ~400-395 myr) Battery Point Formation of Quebec (Canada) preserve unequivocal evidence of plant anti-herbivore defenses: secretory capitate glands and spinescent emergences (spines, hereafter) with sclerified cortex and specialized morphology. Secondary metabolites present throughout the epidermis and putative secretory cells in the cortex of other plants from the same rock unit provide additional, circumstantial evidence of anti-herbivore defenses. Additionally, anatomical structures interpreted as wounds induced by piercing-sucking herbivores in plants of the Battery Point Formation are accompanied by internal wound response periderm, and wound periderm covers surface wounds, some of which may have been produced by surface feeding herbivory. Coalified compression fossils preserved in broadly coeval rocks in Canada, Scotland, and Poland provide direct or indirect evidence of spines with glandular tips. Together, these data demonstrate that by ~400 million years ago, land plants had evolved diverse and sophisticated defenses against herbivory – using both mechanical and chemical means –, and mechanisms for healing wounds induced by herbivores. All these imply that by the end of the Early Devonian herbivory had reached significant levels of intensity and ubiquity. In turn, this suggests that plant-animal interactions involving herbivory had been evolving for a considerable time span prior to 400 myr ago. However, direct evidence of herbivory is sparse – the piercer-sucker wounds and putative surface feeding wounds of the Battery Point Formation plants. Coprolites containing vegetal material associated with Battery Point Formation plants cannot be pinned unequivocally on herbivores, as detritivores feeding on plant material cannot be ruled out as producers. The fossil record of Silurian - Early Devonian terrestrial animals is also sparse and the rare animal mouthparts documented to date cannot be attributed with certainty to herbivores, to the exclusion of detritivores. In this context, the evolution of plant-animal interactions involving herbivory can be traced back in time prior to the Emsian only based on indirect evidence provided by inferred plant defenses. We undertook an exhaustive survey of the Silurian - Early Devonian plant fossil record to quantify the frequency of occurrence of spines and other structures that could represent anti-herbivore defenses. While not all spines of early land plants necessarily had defense functions (some may have increased photosynthetic surface, minimized water loss or insolation, etc.), the occurrence of these structures provides the best approximation for the intensity of herbivory, in the absence of direct evidence. Our data show a steady rise of spine-bearing taxa after the Silurian (during which they were absent), throughout the Early Devonian, in both absolute numbers and percentages – from 4-8% of known taxa in the Lochkovian, to 20% in the Emsian. Among the plants bearing such (certain or putative) defenses, the Early Devonian witnessed a rise in numbers of both plants with chemical defenses and plants with stouter spines. These data suggest herbivory was present very early in the Devonian and that its incidence and intensity rose quickly starting at the beginning of the Devonian, much earlier than previously thought or implied by direct evidence.

Topic: *Education and Outreach*

A-564

Butterflies Under the Lens: Examining the Influence of Geography on Wing Melanization Patterns in Pieris rapae

Author: Noorah Khan, Saige Pompura
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Pieris rapae, or the cabbage white butterfly, is a species prevalent in Europe and North America. *P. rapae* have white wings with melanized spots and apexes on their dorsal forewings. Wing melanization serves many purposes, including thermoregulation. This study aims to determine if there is a relationship between latitude and region of origin and wing spot melanization that would support a thermoregulatory function of wing melanization. Given prior research and evidence supporting thermoregulatory functions, we predicted melanization spots would be larger in butterflies originating from higher latitudes and colder regions. Butterfly images and geographic data from Canada, USA, UK, and Ireland were collected from iDigBio, a digitized natural history collection data portal, and melanization was measured with ImageJ. We conducted a t-test using average apex melanization spot size and the latitude of their origin from 435 samples, and an ANOVA test on the average Cu2 melanization spot size and region of origin from 455 samples. Our linear regression analysis (p-value=0.0015) indicated statistical significance, however, an unexpected negative r-squared value, concluded a negative relationship between latitude and melanization spot size. Our ANOVA analysis (p-value=0.760) also indicated no significant relationship between Cu2 melanization spot size and region of origin. These findings may be attributed to climate change; rising temperatures offset the need for heat absorption, especially in higher latitudes where the effects of global warming are felt more dramatically. Unnaturally higher temperatures force butterflies to either migrate or lose their melanization.

This research was conducted as a CURE developed by the Biological Collections in Ecology and Evolution Network (BCEENET). BCEENET CUREs use digitized natural history collections data and free open source tools to increase accessibility to undergraduate research opportunities while also participating in innovative research.

Topic: *Population Genetics/Genomics*

A-565

Unveiling genomic patterns of climate adaptation in a widespread California scrub oak (Quercus berberidifolia)

Author: Jacqueline Holmes, Victoria Sork, Ryan Buck
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Human-induced climate change and land use changes are occurring so rapidly that numerous species risk local extinction unless they can adapt or relocate to suitable habitats. Woody plants are particularly vulnerable to environmental changes due to their sessile nature and life history traits, necessitating the need for research into the evolutionary and ecological factors driving local adaptation and their genetic adaptive potential. Characterizing adaptive molecular diversity across natural populations can guide conservation actions aimed at protecting and promoting woody plants. Landscape genomics assesses the regional distribution of adaptation through methods that identify genetic variants associated with environmental gradients using genotype-environment association (GEA) tests. Maladapted regions can be predicted through genomic offset models by quantifying mismatches between current GEAs and those expected under projected future climates. Many studies of tree species have used this approach to inform conservation management plans. However, similar research on shrub species is limited, despite their importance to many ecosystems. The overall goal of this talk is to assess where the endemic California scrub oak (Quercus berberidifolia) is vulnerable to climate change. The California scrub oak is found from Shasta County to San Diego County and into Baja California. This widespread species contributes more biomass than trees and dominates chaparral ecosystems, which are expected to expand under future climate warming. Using whole genome sequences (WGS), this project applies landscape genomic analyses and offset modeling to characterize the genetic diversity of 121 California scrub oak individuals, detect signatures of environmental adaptation, and determine regions of vulnerability under various climate scenarios. Preliminary principal component analysis (PCA) of genomic variation revealed two genetic clusters, while a Bayesian genetic structure analysis, ADMIXTURE, showed the most likely K to

be 1, although K=2 illustrates the same clusters found in the PCA. These clusters correspond to northern and southern scrub oak samples. We will conduct separate GEA tests of both clusters to identify regions of high and low genomic offset under future climate conditions, corresponding to vulnerable and resilient populations. This research will not only work to close a critical knowledge gap of how scrubs will respond to projected climate change but also inform conservation planning for chaparral species.

Topic: *Population Genetics/Genomics*

A-566

A Model for the Evolutionary Dynamics of Dioecy in Catopsis Griseb.

Author: Joshua Felton, Chelsea Specht
Affiliation: Cornell University

Plant reproductive systems are extraordinarily diverse, yet the evolutionary drivers and ecological consequences of mating system transitions, especially in spatially fragmented and stress-prone environments, remain poorly understood. Catopsis Griesb., a genus of clonal epiphytic bromeliads, offers a compelling system to explore these dynamics due to its patchy across the Neotropics and the presence of both hermaphroditic and dioecious sexual systems, observed across and within species.Catopsis nutans is one of the species in the genus that is polymorphic for sexual system across its range. I propose a model in which genetic mutations causing sterility and resulting in unisexual individuals provide the raw material for transitions between sexual systems. Ecological conditions, such as pollinator limitation and spatial isolation in the canopy then shape the distribution of these sexual systems across populations. Catopsis nutans is an excellent system to study dioecy as its epiphytic habit may amplify these pressures. Epiphytes are often isolated due to the discontinuous distribution of host trees, experience frequent stochastic mortality from branch fall, and must cope with variable water availability. By combining phylogenomic approaches across Catopsis with a phylogeographic study of C. nutans, my research aims to disentangle the interplay between genetic and ecological mechanisms in the evolution of dioecy.

Topic: *Education and Outreach*

A-567

Using Herbaria Data To Track Invasives: The Spread Of Bromus Tectorum In The Midwest

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Bromus tectorum is a cool-season, annual grass that grows well in disturbed soil and along roadways, invades habitats and crowds out native species. The noxious weed statutes of Minnesota were passed to combat the growth and proliferation of invasive species such as *B. tectorum* requiring areas prone to invasions to be inspected for and eradicated of noxious weeds and when found. If these noxious weed statues are being followed, then the spread of *B. tectorum* should be limited. Occurrence data from digitized herbarium specimens and iNaturalist observations from the Global Biodiversity Information Facility (GBIF) was used to estimate the spread of *B. tectorum* in the Midwest since its introduction with the first occurrence in Michigan in 1895. This occurrence data was plotted in ArcGIS Pro to visualize the area of occurrence of *B. tectorum*. Results indicated that both the number and area of occurrence of *B. tectorum* in the Midwest increased over time. Given our findings with *B. tectorum*, it seems that the noxious weed statutes passed in Minnesota have had little to no effect on the spread of noxious weeds. Future research could implement this method of evaluating the spread of invasive and nonnative weedy species using natural history collections to inform the management of species that threaten natural habitats.

This research was conducted as a CURE developed by the Biological Collections in Ecology and Evolution Network (BCEENET). BCEENET CUREs use digitized natural history collections data and free open source tools to increase accessibility to undergraduate research opportunities while also participating in innovative research.

Topic: *Population Genetics/Genomics*

A-568

The power to resolve relationships: identifying incongruence and precision of reduced-representation and genome-wide data in phylogenomics and population genomics

Author: Joshua Felton, Justin Scholten, Yana Rizzieri, Juliana Harden, Leland Graber, Chloe Jelley, Michelle Heeney, Chelsea Specht, Jacob Landis
Affiliation: Cornell University

Target capture of ultraconserved elements (UCEs) and taxon-specific probes are widely used in phylogenomics for their ability to consistently retrieve hundreds to thousands of overlapping loci across samples; with growing applications in population genomics. Meanwhile, declining costs and improved computational methods have made genome resequencing more accessible for nonmodel systems, enabling the generation of datasets that can address questions at both micro- and macroevolutionary scales. However, the extent of target capture to similarly address questions across different levels remains unclear. We assessed the congruence between reduced-representation methods and genome resequencing using public datasets from plants and animals.

We found that SNP retention was influenced by loci type and genome size, with genome-wide datasets retaining the highest proportions of single nucleotide polymorphisms (SNPs), while UCEs showed the lowest retention. Heterozygosity estimates varied by marker type; with Benchmarking Universal Single-Copy Orthologs (BUSCO) sequences inferring the lowest heterozygosity values, followed by genome-wide SNPs. UCEs had similarly low estimates while BUSCO plus supercontigs (flanking regions) and UCEs plus supercontigs exhibited intermediate heterozygosity values.

Phylogenetic analyses revealed lower bootstrap support for UCE datasets, while genome-wide datasets showed no significant differences from other loci. Population structure analyses frequently underestimated ancestral populations in reduced-representation datasets, often identifying one fewer population than genome-wide datasets and assigning samples to different clusters. These discrepancies underscore the challenges of relying solely on reduced-representation methods for robust inferences of genetic diversity, phylogenetic relationships, and population structure.

Topic: *Systematics & Taxonomy*

A-569

First report of the genus Micropsalliota (Agaricaceae) with the description of two new species from Pakistan

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The genus *Micropsalliota* Höhn. was originally described by Von Höhne in 1914, and later, Heinemann in 1956 and Pegler and Rayner in 1969 made amendments to it. The species of *Micropsalliota* are mainly found in the tropical and subtropical regions of Asia, Africa, and the Americas. These saprotrophic mushrooms are commonly found in groups in the soil of woodlands or along roadside verges. The members of this genus are characterized by dark spore prints, small to medium-sized basidiomata, ellipsoid to cymbiform basidiospores with an apical thickening in the endosporium, and frequently capitate or subcapitate cheilocystidia. The genus *Micropsalliota* is reported for the first time from Pakistan, with two new species identified through morphology and molecular phylogenetics (ITS and 28S). *Micropsalliota pakistanica* collected from district Swabi (humid subtropical climate) can be characterized by a white plano-convex pileus, free brownish lamellae, oblong to amygdaliform basidiospores, and utriform to lecythiform cheilocystidia. *Micropsalliota roseus* described from district Mandibahauddin (hot semi-arid climate) can be characterized by a dark reddish-brown, slightly umbonate pileus with cracked patches, amygdaliform to oblong basidiospores, and capitate cheilocystidia. Complete descriptions, colored photographs and detailed comparison from the closely related taxa have been provided. Morphological differences were supported by combined ITS-28S-based phylogenetic tree which also support the novelty of these species within the genus. Globally, *Micropsalliota* species are thought to number about 87, of which about 40 species from the tropical areas of Africa, America, India, Indonesia, and Malaysia. Previously, no species of this genus has been reported from Pakistan. The discovery of these two new species enhances our understanding of fungal diversity in Pakistan and highlights the importance of conserving natural ecosystems.

Topic: *Floristics*

A-570

Reconciling taxonomic change and taxonomic utility: a case study of the North American flora

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Taxonomic change is continuous through time, yet many uses of plant taxonomy depend on stability about what the taxonomic entities are (especially at the finest levels of species and infraspecies). How significant are the issues of taxonomic and nomenclatural disagreements, and how can we as taxonomists and floristicians move towards reconciling improvement and change in taxonomy treatments with stability and clear communication? We are developing a concordance of several major continental and regional floras in North America to study the nature and scale of the problem, by developing a concordance between the taxonomic concepts and names used in the Flora of North America north of Mexico (FNA) (1993 et seq.), the Flora of the Southeastern United States (FSUS) (2025), the Database of Vascular Plants of Canada (VASCAN) (2024), the Jepson eFlora (2024), the Biota of North America Program (BONAP) (2022), Plants of the World Online (POWO) (2025), the NatureServe database used in conservation planning at national and state/provincial levels (NS) (2024), and a diversity of other floras and systematic treatments. Even with most of these floras, checklists, monographs being "current" (since 2020), differences in species and infraspecies circumscriptions and names are obvious, affecting a major proportion of names in the North American flora. These are generated by differing scientific opinions about 1) ranks at the species rank and below (e.g. one source may recognize three species where another has three varieties or subspecies), 2) lumping and splitting (entitation or circumscription of taxa, e.g. one source may recognize one species where another has three species), 3) lumping and splitting at the genus level, such that a block of species is placed in a "sensu lato" genus or alternately in a "sensu stricto" segregate genus, and 4) nomenclatural disagreements and discrepances (i.e. orthography, genus gender, interpretation of name application based on type, etc.). Using a crosswalk of a large proportion of the North American flora, we examine the proportions of these discrepancies and present ideas for mitigating the negative impacts of taxonomic change on the variety of flora users.

Topic: *Conservation Biology*

A-572

Testing for hybridization in conservation collections at botanic gardens and arboreta

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As global biodiversity faces mounting threats, the conservation of rare and threatened species is critical to preventing extinction. Much like zoos protect endangered animals, botanic gardens and arboreta act as conservation repositories for rare and threatened plant species. These institutions play a vital role as sources for reintroduction efforts and as repositories for preserving/maintaining genetic diversity. Careful management of ex situ plant collections is essential for successfully reintroducing rare species and supporting their long-term survival. However, gardens and arboreta might not consider consequences of planting congeners together; especially if they are rare and threatened. Hybridization or gene flow between rare and common species can pose challenges for ex situ conservation, especially when seeds (or pollen) are used for restoration, reintroduction, or as source material for other gardens. This study seeks to understand if hybridization occurs between rare and common species at gardens and arboreta. We used three different tree genera (Magnolia, Oaks, and Walnuts) and included at least one rare/threatened species and several common congeners to investigate if removing geographic barriers increases the chances of hybridization. A targeted sequence capture approach was used to generate DNA sequences with the Angiosperm 353 (Oaks/Walnuts) and a Magnolia specific bait set. We reconstructed phylogenies, and applied Hybphaser and ADMIXTURE to survey for hybrid samples. Across all genera results suggested hybridization is occurring. Additionally, we found several mislabeled samples. Results are being used to inform holders of ex-situ collections and to make recommendations for managing rare and threatened plant species. This work is one of the first to investigate the potential for hybridization within conservation collections. As more species become threatened and are brought into collections, preventing hybridization and carefully handling rare and threatened species becomes critical to support future conservation and reintroduction activities.

Topic: *Pteridology*

A-573

Not a sterile hybrid, after all: a new look reveals a new species of Diplazium from southern Mexico

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Affiliation:, University of Vermont

Naturalist, agronomist, and longtime friend of John Mickel, Boone Hallberg spent more than half a century living in and studying the cultural and biological diversity of Oaxaca, Mexico. During decades working in support of Mickel's studies of Mexican ferns, Hallberg collected hundreds of important specimens, including types of numerous species that would be described by Mickel and colleagues. One of these important collections was of a *Diplazium* that Hallberg found along a streambed in rural north-central Oaxaca in December 1971. This fern is particularly distinct for having entire, equilateral, ternate pinnae with a proliferous bud at the pinnae base. Unlike anything that had been seen before, Mickel & Beitel (1988) and Mickel & Smith (2004) suggested this specimen was a putative sterile hybrid of *D. plantaginifolium* and *D. ternatum*, a species known from much higher elevations. This hybrid, now known as *D.* ×*subternatum* was subsequently described based on other, morphologically distinct specimens, leaving the true identity of Hallberg's specimen as an open question for pteridologists. Through a combination of morphological, molecular, and developmental data, we demonstrate that Hallberg's specimen is not a sterile hybrid, but instead it is a new and very rare species.

Topic: *Ecology*

A-574

A Long-Term Study of Changes in Vegetational Composition in an Suburban Forest in Southwestern Ohio

Author: Theresa Culley, Robert Tunison
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Many forests in the Ohio River Valley have historically been cleared for agriculture well over two centuries ago but some abandoned land fragments are slowly recovering naturally on their own or through active restoration efforts. These sites can revert back naturally over time to forests through successional change – often from herbaceous ruderal species to saplings and then to mature forest with a prominent shrub and herb understory. However the process of successional change in natural area fragments within an metropolitan matrix may be complicated by anthropogenic impacts amid greater climatic change. To examine the process of vegetational change within a suburban landscape, we conducted a long-term study of the Hazelwood Botanical Preserve, now known as the Harris M. Benedict Nature Preserve, a 65-acre forest located today within a residential and commercial matrix in northeastern Cincinnati, Ohio. The site was originally pasture and secondary forest when it was originally purchased in the early 1920's and since maintained with very little management by the University of Cincinnati as a botanical preserve. In 1999, the eastern third of the preserve was damaged by a F3 tornado, and increased grazing by white tail deer have continued to impact the vegetation, as well as the arrival of emerald ash borer. To quantify vegetational change over time, surveys were conducted in the western portion of the preserve in 1927, 1980, and 2010 along four transects to quantify plant species richness, abundance, and composition. Overall, plant species richness decreased from 1927 to 1980, when the forest overstory had largely recovered, after which point the number of species remained relatively consistent. In contrast, the number and dominance of invasive non-native species at the site substantially increased from 1980 to 2010. Although several herbaceous native species once viewed as glacial relics of the temperate deciduous forest may be extirpated today, the native tree flora persists, especially American beech, sugar maple, and oaks. This study indicates that although ecological processes may still be intact within this suburban site, the vegetation is also impacted by external factors within the metropolitan landscape, such as the introduction of invasive species. Active restoration of the botanical preserve will commence this coming year, involving university students, local high school students, nearby residents, and the township itself with the goal of protecting and enhancing biodiversity for future generations at this US National Natural Landmark.

Topic: *Paleobotany*

A-575

Late Cretaceous (Campanian, ~80 myr) permineralized mosses from the San Juan Islands, Washington State

Author: Cora Gehring, Alexander Bippus, Brian Atkinson, Mihai Tomescu
Affiliation: Cal Poly Humboldt, Klamath National Forest, University of Kansas

Late Mesozoic and early Cenozoic strata along the west coast of North America host permineralized fossil assemblages that have yielded - and continue to yield - a wealth of information on fossil floras ranging the whole gamut of plant diversity, from bryophytes to angiosperms. For bryophytes, these western North American floras have added, over the past two decades, new taxa that have increased the known fossil bryophyte diversity substantially. Ongoing exploration of these floras continues to reveal new fossil bryophyte occurrences and types. Here, we present recently identified bryophytes from the Cedar District Formation on Sucia Island (San Juan Islands, WA), dated to the Late Cretaceous, in the Campanian (~80 myr). The bryophytes are preserved anatomically in marine carbonate nodules that have yielded other plant fossils including ferns, gymnosperms, and angiosperms. One of the bryophytes is a relatively non-descript segment of thin (280 µm) gametophyte stem - probably moss - with incompletely preserved leaves. A second specimen is a moss gametophyte with 280 µm wide stem sheathed by 5-7 tightly appressed and overlapping leaves that cover about half of the stem's circumference at the base, with a ~160 µm wide and ~45 µm thick costa and unistratose lamina; maximum observed leaf width is ~800 µm. Cellular preservation in stem and leaves is incomplete, precluding taxonomic evaluation. A third specimen is a moss gametophyte with a thinner (~230 µm) stem with an incompletely preserved conducting strand. At the base, the leaves, >1.2 mm long and up to ~470 µm in width, are tightly wrapped around half of the stem's circumference, with a costa that is 130 µm wide and 40 µm thick. The costa widens to 190 µm (and 65 µm thick) with 140 µm wide unistratose lamina on either side. Distally, the costa narrows to <100 µm and bulging (possibly mammillose) cells or short lamellae are present adaxially. Toward the leaf tip, the lamina is 2-3 cells wide and the costa bears 5-8 adaxial lamellae up to 5 cells tall. Leaf anatomy places this fossil squarely among the polytrichopsid mosses. The fourth specimen is a moss gametophyte with 280-300 µm thick stem and densely inserted leaves >3.2 mm long. Stem and leaf anatomy is incompletely preserved due to taphonomic distortion, but a gemma cup is recognizable at the tip of the stem. The cup, ~600 µm wide, contains >17 gemmae. The gemmae are lenticular, ~100 x 80 µm, attached to the base of the cup by short, thin uniseriate stalks. Gemma cups are restricted, among mosses, to the Oedopodiopsida - Tetraphidopsida - Polytrichopsida clade, and uniseriate, rhizoid-like gemma stalks may be a synapomorphy of the Tetraphidopsida - Polytrichopsida clade. These Sucia Island fossils add another occurrence on the map of fossil bryophyte diversity and a 10th known occurrence of Campanian bryophytes. Two of these bryophytes probably represent new taxa for the fossil record, as their features differentiate them from previously documented fossil polytrichopsids, a lineage present in several other western North American fossil bryofloras.

Topic: *Macroevolution*

A-576

Synnovation and confluence explain disparities in species richness across the Andes and Hengduan- Himalaya Mountains

Author: Chih-Chieh Yu, Richard Ree
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Mountains harbor a disproportionate amount of terrestrial biodiversity, but the causes of this pattern, especially those promoting the origin of new species in mountains, remain poorly understood. Here, we studied the phylogenetically replicated radiations of Berberis (Berberidaceae) in the Andes (~ 109 spp.) and the Hengduan-Himalaya Mountains (HHM; ~ 247 spp.). We found that the greater species richness of Berberis in the HHM is not attributable to greater time for speciation or lineage immigration. Instead, the confluence of Oligocene cooling, functional leaf innovations (deciduousness and small, densely veined leaves), and expansion of high-elevation habitats progressively fueled net diversification, especially in one clade of high-elevation specialists in the HHM over the past 8–10 My. By contrast, the rate of diversification in the Andes was damped by the lack of functional leaf evolution and ecological opportunities. This case study of synergistic interactions between the evolution of traits and environments helps us understand the factors driving high levels of mountain biodiversity.

Topic: *Ecology*

A-577

Pyrodiversity and biodiversity; taxonomic and phylogenetic insights on post-fire forest communities

Author: Rebecca Wilcox, Becky Estes, Brent Mishler, Sarah Jacobs
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In the temperate forests of Western North America fire is a fundamental ecological process that structures species traits, community assembly, and biodiversity patterns on the landscape. Increasing pyrodiversity (spatiotemporal diversity in fire) has been identified as an important goal to help restore and promote healthy and resilient forests. However, much of the understanding of post fire conditions in conifer forests, while extensive, is restricted to the overstory, and there is a critical lack of similar knowledge for understory vegetation. Here, we use taxonomic (alpha and beta diversity) as well as phylogenetic metrics (alpha phylogenetic diversity, phylogenetic beta diversity, relative phylogenetic diversity, and local phylogenetic endemism) to explore how pyrodiversity influences forest understory plant community assembly dynamics and diversity patterns. Our study took place in mid-elevation conifer forest in the Eldorado National Forest located within the Central Sierra Nevada, California. Similar to the rest of the Sierra Nevada, the study area experienced fire suppression for the last century. However, in the past 15 years, the forest has experienced a diversity of fire ignition sources (lightning, prescribed, wildfire) and fire severities (low-high severity). Leveraging plant diversity surveys conducted pre- and post-fires, we asked: how does fire influence regional (watershed scale) and local (plot scale) plant community diversity and assembly dynamics? At the watershed scale, we found that compared to pre-fire conditions, both taxonomic and phylogenetic alpha diversity increase after fire, suggesting that restoring mixed-severity fire (fires within the natural range of variation for the region) can promote multiple aspects of understory plant diversity. At the watershed scale, we only observed significant local phylogenetic endemism (locally phylogenetically rare groups of species) post-fire. This suggests that fire may be an important mechanism driving landscape heterogeneity, by creating opportunities for local temporal phylogenetic endemism to occur during post-fire succession. At the plot scale, we found that topographic features (aspect or elevation) interacted with fire burn severity to influence post-fire species richness, phylogenetic beta diversity, and relative phylogenetic diversity. This suggests that local conditions interact with fire burn severity to influence post fire plant community diversity patterns. At the plot level, we also found evidence that environmental filtering was an important community assembly mechanism when burn severity was high, while competition was important when burn severity was low to moderate. Counter to expectations, we also found evidence of environmental filtering in unburned plots, which suggests that long unburned plots might present environmentally stressful conditions (i.e., low light availability, high fuels/ground cover) for fire adapted plant communities. Together these results help to provide a more holistic description of forest diversity and understanding of how plant communities respond to modern-era disturbance regimes.

Topic: *Biogeography*

A-578

C4 and CAM Dominant Regions of the World and their Shifting Distributions Under Projected Climate Change Scenarios

Author: Paul Markley, Barnabas Daru
Affiliation: Stanford University

Grasslands and deserts are primarily occupied by flowering plants with alternative metabolic pathways derived from C3 such as C4 photosynthesis or Crassulacean Acid Metabolism (CAM). These two pathways evolved in angiosperms in response to the increasingly drier and cooler temperatures of the middle to late Cenozoic for improving carbon capture from the then increasingly carbon depleted atmosphere. This enabled their proliferation across many different ecoregions. For example, many plants that express C4 or CAM photosynthesis can be widespread food stables such as corn (*Zea mays*) or as range restricted and culturally iconic as the Saguaro (*Carnegeia gigantica*). However, as anthropogenic climate change rapidly increases temperatures and creates novel ecological communities, the future climatic niches of these plants remain understudied and undetermined. Here, we present the distributions of C4 and CAM dominant regions of the world, and how they may shift and develop under projected climate scenarios. We used occurrence data from the Global Biodiversity Information Facility with climate projections from WorldClim v2.1 to create global

species distribution models of ~20,000 known plants that perform C4, and CAM. We calculated phylogenetic beta diversity using a dated megaphylogeny, and determined bioregions based on cluster differences using the phyloregion package. Preliminary findings suggest the near global expansion of C4 dominant areas, while CAM regions diverged, showing both increases and decreases in the number of grid cells classified into these regions as influenced by latitude and primarily between xeric and mesic environments. These results imply that of these two metabolisms, C4 photosynthetic plants, namely grasses, can take advantage of the climatic changes posed by increased concentrations of atmospheric carbon dioxide more so than CAM plants. There may be a greater risk of range reductions for CAM plants in the future despite previous studies regarding desertification if the rate of anthropogenic climate change continues at its current pace, while C4 plants may continue to expand their ranges.

Topic: Ecology

A-579

Adaptive Foraging in bees facilitates competitive release in a serpentine plant community

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Species competition is a central ecological process driving species coexistence, niche dynamics and community assembly. In plant-pollinator systems, understanding how pollinators respond behaviorally to competitive interactions is critical to identifying the mechanisms that shape pollinator niche breadth and the structure of plant-pollinator networks. While theoretical models have predicted that adaptive foraging mitigates floral resource overlap and facilitates coexistence in the presence of strong competitors, empirical tests remain limited. During adaptive foraging, individual pollinators are expected to modify their use of floral resources (niche expansion or contraction) in response to competition, enhancing the stability of pollinator communities. However, these individual-level and responses may vary across pollinator species due to differences in their life history strategy, level of sociality, foraging range and size. Here, we investigated adaptive foraging responses across three native bee species- Bombus, Osmia, and Andrena- in response to a natural fluctuation in the density of Apis mellifera, a dominant introduced competitor. The study took place in serpentine plant communities at the McLaughlin Natural Reserve in California where honeybee abundance declined significantly (~10%) Between 2021 and 2022, providing a unique opportunity to assess shifts in foraging behavior under reduced competitive pressure. We sampled pollen loads from 30-40 individual bees per species in each year and constructed individual-level networks to evaluate shifts in foraging specialization, individual degree, centrality and pollen load size and diversity, across bee species and years. Preliminary results suggest differences in pollen load size and diversity across bee species. We also found an increase in pollen load diversity but not size in when honeybee abundance was low, suggesting floral niche expansion with decreased competitive pressure. However, adaptive foraging responses varied by bee species. Overall, this work contributes to a growing empirical understanding of how competition shapes plant-pollinator networks and provides insights into the role of individual-level behavioral shifts in helping maintain plant and pollinator community resilience and stability.

Topic: Symbioses: Plant, Animal, and Microbe Interactions

A-580

Pests or pollinators: investigating the relationship between the composite thrips and an endangered Texas endemic

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Protecting habitat and mitigating climate change impacts are important and necessary steps for conserving plants, but for many species successful conservation will also depend upon understanding ecological relationships, such as their pollinator communities. *Hymenoxys texana* (Texas prairie dawn; Asteraceae) is a federally and state endangered annual species endemic to eastern Texas. Little is known about its reproductive ecology, but preliminary observations suggest that the composite thrips (*Microcephalothrips abdominalis*) could be a potential pollinator. Thrips (Thysanoptera) are more commonly known as pests, but they have been documented as pollinators for at least 85 plant species, including at least five species in family Asteraceae. This study aims to gather evidence for the role of *M. abdominalis* as a pollinator of *H. texana* by assessing the presence of *M. abdominalis* on blooming *H. texana* flower heads, determining the capacity of *M. abdominalis* to carry *H. texana* pollen, and evaluating the impact of *M. abdominalis* on the reproductive output of *H. texana*. In March 2025, we surveyed *H. texana* flower heads for *M. abdominalis* presence at five sites in Harris County, Texas. At the same five sites, we collected flower heads for thrips counts. We also set up insect exclusion trials with 15 flower heads in each of three treatments: white mesh bags to exclude flying insect visitors, red mesh bags to exclude flying insect visitors and deter thrips, and flower heads open to all insect visitation. We will then compare seed set ratios among treatments. Preliminary results indicate that *H. abdominalis* is commonly present on *H. texana* flower heads and can carry *H. texana* pollen. These findings point to an exciting new addition to the pollination potential of thrips and to the conservation of a rare plant species.

Topic: Phylogenomics

A-581

The origin and dynamic evolution of sex chromosomes in dioecious Asparagus lineages.

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A growing number of genome sequence assemblies are becoming available for dioecious seed plant species, enabling investigation of factors that might be influencing plant sex chromosome evolution. Earlier work on garden asparagus (*A. officinalis*) determined that two Y-specific genes - one suppreasor of gynoecium devopment and one promoter of pollen development - were responsible for sex determination. In this talk, we will present new data demonstartating origins of two distinct Y-chromosomes in separated dioecious *Asparagus* lineages and dynamic sex chromosome evolution in the dioecuous clade including *A. officinalis*. Variation in the structure and gene content among Y-chromosomes assembled for *A. officinalis* and three other asparagus species suggests multiple evolutionary paths from hermaphroditism to dioecy over the last 3 million years.

Topic: Ecophysiology

A-584

Maximizing hydraulic flow and stomatal conductance in the Gnetales

Author: Anju Manandhar, Scott McAdam, Talitha Soares Pereira, Daniela Aros Mualin
Affiliation: Purdue University

The high productivity of angiosperms compared to gymnosperms is only possible with a high stomatal conductance to water and CO_2. This high rate of gas exchange in angiosperms is because they have stomata that open by extreme mechanical displacement of neighboring epidermal cells which maximizes total possible stomatal pore area. Mechanical advantage is absent among the conifers, Ginkgoales, most ferns and lycophytes – except for some highly productive aquatic ferns. Gnetales, particularly *Gnetum*, are considered unique among the gymnosperms for having very high rates of stomatal conductance. We hypothesized that stomatal opening in *Gnetum* is supported by the presence of mechanical advantage, which allows *Gnetum* to capitalize on the highest xylem hydraulic conductance among the gymnosperms. Using gas exchange and anatomical measurements we found that *Gnetum* has convergently evolved mechanical advantage, whereby stomata open by lateral displacement into neighboring epidermal cells. We made comparisons with eight representative conifer species that like *Gnetum* are also adapted to low-light tropical forests, and found none of them have high rates of leaf gas exchange or mechanical advantage. Our results suggest that the evolution of mechanical advantage was critical for the evolution of high rates of leaf gas exchange and photosynthetic capacity in gymnosperms like *Gnetum* and presumably the common ancestor of angiosperms.

Topic: Population Genetics/Genomics

A-585

Arctic Willow Hybridization: Exploring Genetic Adaptation to a Changing Climate

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Climate change is rapidly transforming the Arctic landscape through disturbances, such as the shifting depth of permafrost in the tundra. This contributes to shrub encroachment, as plants that did not thrive in the tundra can now increase in abundance as warming continues. Willows (Salix species) are pioneer species that prefer disturbance to reproduce and are contributing to shrub expansion in the Arctic. Willows are widely-documented to have a high prevalence of hybridization and introgression, where hybrid vigor can occur, allowing hybrid offspring to potentially exhibit greater fitness than the parental species due to increased genetic variation. As warming-induced disturbance becomes more prevalent, new ecological niches will form or old niche space will shift in the Arctic and hybrid Salixmay be able to fill those niches, further promoting shrub expansion in the tundra. This study aims to investigate if there is admixture (gene flow between distinct populations) among Salix in the Arctic. Sampling was conducted through roadside collections from sites along a latitudinal gradient within Arctic ecosystems in Alaska. Genomic DNA was extracted, nuclear and chloroplast genes were amplified using PCR and ddRADtechniques were employed for a subset of samples and PCR was sequenced using Nanopore technology and ddRAD products were sequenced with Illumina. We expect to find evidence of hybridization events among Salix populations. This study will provide insight as to how the Arctic plant communities may change under increased disturbance fueled by climate change. By furthering our understanding on plants that contribute toshrub encroachment, we can further predict how organisms will shift distributions and adapt to changes so we can evaluate and anticipate future impacts.

Topic: Education and Outreach

A-586

BCEENET supports and assesses student learning in ecology and evolution using digitized natural history collections CUREs

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Supporting the development and implementation of Course-based Undergraduate Research Experiences (CUREs) in ecology and evolution is an important step in supporting equity in undergraduate research opportunities. Incorporating research directly into undergraduate coursework has been shown to reduce barriers to participation, such as time and financial limitations students may experience. Biological Collections in Ecology and Evolution Network (BCEENET) is a community of collections professionals, undergraduate educators, researchers, and data experts committed to increasing equity in undergraduate research experiences through CUREs. Here, we present four inclusive CUREs created by the BCEENET community using digitized natural history collections data, a unique and growing resource that can help to expand opportunities for research in ecology and evolution. BCEENET CUREs have been implemented at 53 institutions, including 12 community colleges and 18 minority serving institutions in online, hybrid, and in-person formats, engaging over 6,000 undergraduates in research experiences. We also discuss preliminary assessment results, support and resources for new BCEENET CURE implementers, and share opportunities to collaborate in assessment activities.

Topic: Phytochemical

A-587

Riding the Waves: Heatwave-induced shifts in metabolomic profiles of diploid and polyploid Duckweed (Spirodela polyrhiza) reveal differences in tolerance strategy

Author: Eric Yee, Tia-Lynn Ashman, Martin Turcotte
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We are in the midst of a global environmental crisis where extreme temperature anomalies like heatwaves have increased in duration, intensity, and frequency. Aquatic plant species are especially vulnerable to these extreme temperature events, as they have adapted to typically thermally stable freshwater ecosystems like lakes and ponds. However, some aquatic plants can be polyploid (containing >2 sets of chromosomes), often resulting in highly stress-tolerant phenotypes that can resist these sudden and extreme temperature shifts. Additionally, polyploid plants are known to contain higher basal metabolite concentrations and rates of biochemical activity, which may give them an advantage in surviving these increasingly severe, frequent, and long heatwave events. To investigate the heatwave response of polyploid plants, I have conducted a series of large-scale, controlled experiments using next-generation techniques to quantify the impact of heatwave duration and frequency on the metabolomic profiles of diploid and neoautotetraploid populations of duckweed (*Spirodela polyrhiza*, L. Schleid). I predict that 1) longer heatwaves will be more detrimental for diploids than polyploid duckweed, as polyploid plants have larger metabolite pools that lie closer to the activation thresholds for heat resistance, therefore minimizing damage, 2) more frequent heatwaves will decrease diploid survivorship as heat-related damage will occur before resistance metabolites can be upregulated, resulting in a trade-off between repair/survival vs. bet-hedging against future shocks, and 3) metabolomic diversity in polyploid plants will be greater because faster heatwave response enables them to divert resources to synergistic, alternative pathways and morphological responses that could confer long-term resistance. Here, I demonstrate that while resting metabolomic diversity of diploid and polyploids are similar ($p>0.05$), metabolomic diversity during heatwave events differs significantly between ploidies as heatwave duration increases. Specifically, diploid duckweed contained greater concentrations of essential amino acids (e.g., L-Tyrosine, L-Leucine), while polyploid duckweed contained greater downstream products associated with reactive oxygen species harvest (e.g., phenylpropanoids, vitexin, caffeinin, peroxidase products, etc.). Additionally, whole-organism biomass also exhibited significant changes with respect to ploidy and treatment length, where diploid duckweed exhibited a significant initial increase in response to heatwaves, while polyploid duckweed show minor biomass declines ($p<0.05$), until both polyploid and diploid populations crashed. Together, this suggests that diploid and polyploid duckweed employ different mechanistic strategies to tolerate heatwaves. Future directions aim to assess duckweed metabolomic profiles in response to cold spells.

Topic: Phytochemical

A-588

Floral trait variation and gene expression in Mimulus cardinalis across a range-wide latitudinal gradient

Author: Elenor Kennedy, Mikhaela Neequaye, Katie Wenzell, Hannah Gunn, Kelsey Byers
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Background & Aims: Pollinators play a crucial role in the evolution and diversification of flowering plants. However, intraspecific variation in floral traits occur frequently and likely reflect variable biotic and abiotic selection pressures. The hummingbird-pollinated species *Mimulus cardinalis* occurs across western North America, where geographic mosaics of selection have likely influenced its natural history, due to this wide species range. Processes driving early stages of divergence and speciation remain poorly understood, though theory predicts that trait divergence will be most likely at range edges. Within *M. cardinalis*, which is usually red-flowered and hummingbird-pollinated, two independent shifts to yellow flowers have occurred at the northern and southern range edges, including a population found on Cedros Island, off the coast of Baja California, Mexico.

Methods: This study characterises the local climatic variables of five accessions of *M. cardinalis* derived from central and trailing-edge populations. We use a variety of highly integrative methods in metabolomics and morphological analyses to characterise a

suite of pollinator-relevant floral traits across the *M. cardinalis* range. We use genetic tools such as transcriptomics and whole genome sequencing to study underlying genetic variation in two yellow-coloured, trailing-edge accessions.

Key Results: This study uncovers high levels of variation in morphology, nectar properties, pigmentation and scent profile across geographically diverse *Mimulus cardinalis* accessions. Cedros Island *Mimulus cardinalis*, a trailing-edge accession, is found to produce high volumes of nectar and scent. These changes may link to different pollination syndromes, or to different stages in an incipient pollinator shift. This work highlights the importance of considering suites of floral traits in studying intraspecific variation in relation to species range. Floral trait-underlying genetic differences between different *M. cardinalis* lines were also investigated, revealing potential mechanisms underlying floral diversification.

Conclusions: This work highlights the importance of interplay between floral traits in potential pollinator shifts, provides genetic insight into changes in these traits, and provides many future directions to study the early stages of pollinator-mediated trait-differentiation across a species range.

Topic: Comparative Genomics/Transcriptomics

A-589

Strategies for pangenome analysis of diploid and polyploid plant systems

Author: Adam Healey
Affiliation: HudsonAlpha Institute for Biotechnology

With multiple reference genomes becoming available for many different plant species, the need for tools and strategies that are capable of efficiently exploring pan-genomes is increasing. However, few pan-genome analysis tools were constructed with plant genome complexity in mind, where species are commonly repetitive, polyploid, and frequently undergo whole genome duplications and large-scale chromosomal rearrangements.

Using two plant species as an example- sorghum (Sorghum bicolor) and switchgrass (Panicum virgatum), we explore strategies for constructing plant pan-genomes, including uses, best-practices, as well as pitfalls and limitations. For both species, genetic diversity and population structure limit how much genomic variation can be explored using a single reference genome. For diploid sorghum, we constructed a 33 reference pangenome graph to capture the diversity of African landraces and cultivars using Minigraph-Cactus. The graph-based approach yielded improved short-read alignments, and a reduction in erroneous heterozygous variants. Further, we demonstrate how large structural variants identified from a graph can be quickly and accurately genotyped in short-read data using in-house analyses.

In tetraploid, outbred switchgrass, the whole-genome approach to graph construction is impractical due to genome complexity and population diversity. To remedy this, we instead focused on construction of local graphs (both iterative and all-vs-all) to identify novel structure and haplotypes within regions of interest related to switchgrass's utility as a biofuel crop. Together, these approaches showcase how plant researchers can use pan-genome construction and analyses to explore their own regions of interest within complex systems.

Topic: Pteridology

A-590

Do CAM ferns have inverted stomatal rhythms?

Author: Daniela Aros Mualin, Anju Manandhar, Scott McAdam
Affiliation: Purdue University

Crassulacean acid metabolism (CAM) photosynthesis has evolved independently multiple times as an adaptation to conserve water, with CAM plants opening stomata at night for CO_2 uptake, instead of the day. While CAM is well-studied in angiosperms, its occurrence in other plant groups remains underexplored. We examined whether CAM ferns, exclusively epiphytic and predominantly in Polypodiaceae, exhibit inverted stomatal rhythms. We also investigated potential mechanistic explanations for diurnal stomatal regulation in this group. We measured canopy conductance over a week under natural light conditions in 14 epiphytic Polypodiaceae species, and found that CAM ferns do not display fully inverted stomatal rhythms, like CAM angiosperms. Instead, all epiphytic ferns have stomata that are highly sensitive to vapor pressure deficit (VPD), with even minor increases in VPD leading to near-complete daytime stomatal closure. These results suggest that high VPD sensitivity, rather than an angiosperm-like, inversion of stomatal rhythms drives diurnal stomatal regulation in epiphytic ferns. The evolution of facultative CAM photosynthesis in epiphytic ferns may have been necessary for carbon gain in plants with stomata under such strong passive regulation by water status.

Topic: Systematics & Taxonomy

A-592

The Case of the Indistinguishable Species: Taxonomy of Amaranthus wrightii and Amaranthus torreyi

Author: Pankti Chavda, Danya Sumrein, Andrea Laine, Luis Figueroa Hernández, Andy Cabrera, Katherine Waselkov
Affiliation: California State University, Fresno, California State University

The genus Amaranthus includes about 75 species, including crops, weeds, and lesser-studied wild species. This research focuses on the morphological analysis of Amaranthus wrightii and Amaranthus torreyi, two species native to the southwestern U.S. These species may be taxonomically indistinct, with overlapping traits suggesting a potential misclassification. Clarifying whether A. wrightii is a distinct species is vital, as it has been identified as closely related to the invasive weed A. retroflexus, with implications for weed evolution. The analysis aims to identify morphological differences between the two species by collecting morphological measurements from herbarium specimens, focusing on key traits such as petiole length, leaf blade length, floral structures, and stem branching patterns. Principal Component Analysis (PCA) was used to assess variation in traits like petiole-to-blade length ratios and bract length. Additionally, species distribution models (SDMs) will be developed using MaxEnt to predict whether these species exhibit distinct or overlapping geographic ranges across the U.S., integrating herbarium records with previously collected field data. Initial data suggest the species share a similar geographic range and very similar habitats, as well as overlap in a variety of morphological characters, which may challenge the taxonomic classification of A. wrightii as distinct from A. torreyi. This study will clarify the taxonomic status of A. wrightii and A. torreyi, provide insights into their evolutionary relationships, and contribute to efforts to clarify the conservation status of A. torreyi. The results will also complement ongoing genetic studies in the lab, offering a comprehensive view of Amaranthus species diversity in the southwestern U.S.

Topic: Lichen and Bryophyte Diversity, Conservation, and Evolution in the Americas

A-593

Pyroenlichenment: Fire Drives Cladonia Presence, Abundance and Diversity in Florida Sugar Sand Scrub Habitat

Author: Seth Raynor, Scott Ward, Vivienne Sclater, Stephanie Koontz, Erin Manzitto-Tripp, Eric Menges
Affiliation: University of Colorado Boulder, Archbold Biological Station, Georgia Department of Natural Resources

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Topic: Systematics & Taxonomy

A-594

Inclusive approaches to taxonomy and classification of Convolvulaceae

Author: Lauren Eserman-Campbell, Ana Rita Simões
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Modern taxonomic and systematics research integrates a wide range of information from multiple disciplines including evolutionary biology, genetics, morphology, anatomy, conservation, ecology, and more. This integrative approach requires cooperation among researchers specializing in these research areas. To do this in a productive manner, the advancement of plant classification should incorporate the principles of diversity, equity, and inclusion to bring people together across the global plant community. Inclusive, collaborative research is especially important in widely distributed clades of plants. Some plant groups approach this through the establishment of global research networks (e.g. Convolvulaceae Network, Global Conservation Consortia). In this talk, the recently formed Convolvulaceae Taxonomic Expert Network (TEN) will be discussed along with recent advances in globally collaborative systematics research. By highlighting this work, we hope to bridge borders, create diverse partnerships, and advance research in systematics and taxonomy.

Topic: *Biodiversity Informatics & Herbarium Digitization*

A-595

Digitizing Boraginaceae: Unlocking lost herbarium data for a diverse plant family in California

Author: Hannah Porter, Camila Patino, Marina LaForgia
Affiliation: CSU Sacramento, California State University, Sacramento

The Borage family (Boraginaceae) is a diverse plant family with over 2000 species of shrubs, herbs, and trees. While this family is abundant worldwide, California has a uniquely high diversity of herbaceous Boraginaceae species (250) that primarily inhabit dryland and grassland habitats. Herbarium records across the state show nearly 90,000 specimens collected in this family from 44 different genera. The Sacramento State Herbarium has 435 specimens in this family from 22 different genera, however none of the data associated with these specimens have been catalogued and are therefore not currently included in online herbarium records. Given that most plants in our herbarium were collected in Placer County in the 70s, we hypothesize that our Boraginaceae specimens come predominantly from this area. Currently, only 440 of the state's 90,000 specimens are from Placer County, with only 200 of these specimens occurring prior to the region's development in the 1980s. We digitized and transcribed all Boraginaceae specimens in the Sacramento State Herbarium. We imaged specimens using a DSLR camera mounted on a lightbox and subsequently transcribed data associated with the labels of each specimen. Out of our collection of Boraginaceae, 103 specimens from 27 species were found to be from Placer County that have yet to be included in online records. By digitizing these specimens, we are updating our current understanding of the distribution of this family. Moreover, by uploading these data to the California Consortium of Herbaria's database, we are making these data freely available to researchers worldwide.

Topic: *Ecophysiology*

A-596

Effects of light availability on success of the invasive shrub European buckthorn (Rhamnus cathartica) in a temperate mixed forest

Author: Jeneva Tomaszewski, Brian Maricle
Affiliation: Saginaw Valley State University

A prominent invasive species in Michigan forests is European Buckthorn (*Rhamnus cathartica*), which occupies space in the understory and is especially successful along edges or other locations with good lighting. The goal of this experiment was to measure the physiological effects of light availability on *R. cathartica* and characterize its distribution in the Saginaw Valley State University Ecological Research Area, which is in the process of an invasion. Lighting and canopy cover were related to plant distribution and performance. There were trends for plant height and number of *R. cathartica* individuals per plot to increase with greater light availability. Photosynthetic light response curves were measured, indicating photosynthesis rates up to 77 percent higher and stomatal conductance up to 33 percent higher in *R. cathartica* plants in well-lit plots compared to heavily-shaded plots. Photosynthesis rates decreased during the transition to autumn, even with increased light availability as the canopy opened. It is important to understand the conditions under which invasive species establish and succeed in order to determine and predict the vulnerability of local ecosystems to the spread of invasives. Because lighting is of clear importance for the establishment of *R. cathartica* during an invasion, understanding the role of light and how it is used by *R. cathartica* might help in better understanding forest invasions in this and other systems.

Topic: *Education and Outreach*

A-597

The painter Hilma af Klint and botanical education in 1800s Sweden

Author: Lena Struwe
Affiliation: Rutgers University

The Swedish artist Hilma af Klint (1862 – 1944) is best known for her abstract paintings — a practice shaped by a life-long interest in spiritual explorations. An exhibition in May to September 2025 at The Museum of Modern Art (MoMA) in New York City, USA, features for the first time her Nature Studies, a portfolio of 46 drawings in MoMA's collection that demonstrates her close engagement with botany. Drawn in the spring and summer seasons of 1919 and 1920 near her home and studio on the island of Munsö outside of Stockholm (Sweden), these artworks present local Swedish flora, a few animals, and some cultivated plants. This talk discusses issues raised in the research for the exhibition, including the history of botanical education in Sweden during Hilma af Klint's youth - curricula, books, herbarium collections, etc. Women's roles in natural history education in late 1800s Sweden were not unsubstantial, since many teacher's posts were filled by women educated at female teacher's seminaries. It was also common for researchers active at universities and colleges to become adjunct teachers at the local elementary or secondary schools. The mid-to late nineteenth century saw the development of the Swedish school for all children ('folkskola', available for at least six grades levels since 1842). The natural history curriculum had a strong focus on local plants, crops, and animals at farms, and the use of herbaria collected by students during summer vacation and examined in the fall by teachers. Some of this tradition is still alive; for example, the pocket-sized Swedish student flora by botanists Thorgny Krok and Sigfrid Almquist was first published in 1883 and has since then been used by students and field botanists for over 100 years while continuously revised. This was the context for my research into Hilma af Klint's botanical background and experiences as a woman growing up in the late 1800s in Stockholm, attending public school, and becoming a painter of a wide variety of art forms, including botanical illustrations.

Topic: *Hybrids and Hybridization*

A-598

Survival heterosis in a montane wildflower varies with genetics and environment

Author: Cathy Rushworth, Gabrielle Sandstedt
Affiliation: Utah State University

Despite widespread support for heterosis, or hybrid vigor, in numerous domesticated systems, studies in wild systems are rarely performed. Yet numerous plant groups regularly hybridize and exhibit altered fitness, providing an unparalleled opportunity to study the genetic and phenotypic consequences of hybridization on fitness of wild organisms. One of these groups, the mustard genus *Boechera*, is highly self-fertilizing but known for widespread periodic hybridization. Herbarium studies have identified hybrids representing 400 unique combinations of parental species, most of which transition to asexuality, and hybrids have consistently higher overwinter survival than non-hybrids. We used genomic data and a reciprocal transplant experiment to compare heterozygosity and fitness in F2 and selfed lineages of the self-fertilizing wildflower *Boechera retrofracta*. We find that heterozygosity is concentrated in three genomic regions in both *B. retrofracta* and the ecological model system *B. stricta*. The transition to asexuality occurs in the F1 generation in interspecific hybrids, but at later generations in interpopulation hybrids. In the field, overwinter survival of interpopulation F2s is higher than selfed lineages, consistent with heterosis, and survival is predicted by genetic divergence between parents. Heterosis varies extensively by environment and genotype. Collectively, our results suggest that heterosis may underlie the unusually high frequency of hybridization in wild populations of *Boechera*.

Topic: *Paleobotany*

A-599

Into- or out-of-India? Early Eocene pollen and macrofossils from the Ghazij Formation in Balochistan, Pakistan test long-standing biogeographic hypotheses

Author: Edward Spagnuolo, David Shaw, Peter Wilf, Parker Przybylski, L. Alejandro Giraldo, Munir Ul-Haq, Scott Wing, William Clyde, Vera Korasidis
Affiliation: The Pennsylvania State University, Biostratigraphic Associates, Penn State University, Pennsylvania State University, Geological Survey of Pakistan, Smithsonian, University of New Hamshire, University of Melbourne

The Eocene collision of the Indo-Pakistan tectonic plate into Asia and resulting biotic exchanges hypothetically contributed to the immense biodiversity of Southeast Asia. However, pollen and macrofossil data with robust age constraints from pre-collision Indo-Pakistan are rare, limiting support for these hypotheses. Additionally, diverse mammal assemblages from the early Eocene (ca. 54 –50 Ma) Ghazij Formation in Balochistan, Pakistan previously showed a contrasting into-India dispersal pattern. The endemic mammal faunas of the then-tropical middle Ghazij were replaced by Holarctic taxa, found in the upper Ghazij, as the collision progressed. Here, we present a preliminary report on the first plant macrofossils, insect damage, and palynofloras from the same well-constrained strata of the Ghazij Formation that produced the mammalian faunas. The 39 palynological samples were collected from paleomagnetic sample splits through the lower, middle, and upper Ghazij. The macrofossils (15 sites, 420 specimens)

were concentrated in the upper Ghazij Fm. The palynofloras indicate an environmental transition from coastal or nearshore marine settings (lower Ghazij), to freshwater and coastal palm swamps (middle Ghazij), coastal peatlands, and increasingly terrestrial ecosystems that retain marine influence (upper Ghazij). Diverse dinocysts reaffirm the early Eocene age of the formation. We found several significant floral elements of the modern SE Asian flora as palynomorphs in the middle and lower Ghazij, including *Nypa*, *Barringtonia*, Euphorbiaceae, Fabaceae, Meliaceae, Moraceae, Dipterocarpaceae, and *Alangium*. *Croton*, Malvaceae, Polygonaceae, and Onagraceae are also found in the upper Ghazij. None of these groups are found in the leaf macroflora, composed of an estimated 42 species and dominated by Anacardiaceae and multiple Fabaceae and Arecaceae morphotypes. Rarer morphotypes include possible Menispermaceae, *Calophyllum,* and Araceae and the ferns *Acrostichum* and *Salvinia,* also recorded as spores. The diverse and abundant insect damage on the leaves records 47 damage types (DTs) of both generalized and specialized plant-insect interactions including nine hole feeding DTs, seven piercing and sucking DTs, 15 gall DTs, and three mines. The insect damage levels are some of the highest in the fossil record, although mining is rare, and comprise the only data of this type from the tropics during the Early Eocene Climatic Optimum (EECO). The presence of many significant Asian taxa as palynomorphs in the lower and middle Ghazij Fm., from a time of limited mammalian interchange with Asia documented from the same rocks, supports established hypotheses that these plant taxa were present in India before the main phases of the Asian collision and associated biotic exchange. A comprehensive review of the tropical Asian pollen record also suggests that many of the tree lineages found in the Ghazij Formation were present elsewhere on the Indian subcontinent before or during the India-Asia collision; however, the limited pre-collision deposits in other areas of South and Southeast Asia do not provide enough evidence to rule out their prior presence on the mainland. The abundant, well preserved, and stratigraphically well constrained macrofossil and microfossil records from the early Eocene Ghazij Formation highlight its importance as a reference point for future biogeographic and paleontological studies of the Asian tropics.

Topic: Biogeography

A-600

Quantitative biogeography and niche evolution in California Salvia

Author: Jeff Rose, Ricardo Kriebel, Kenneth Sytsma, Bryan Drew
Affiliation: The Ohio State University, California Academy of Sciences, University of Nebraska Kearney

Mediterranean-like biomes across the globe are biodiversity hotspots for both animals and plants. However, because such climates have only existed since the mid-Miocene, lineages adapted to Mediterranean-like biomes have diverged relatively recently, making it difficult to make robust inferences of phylogenetic relationships. Moreover, apparent abiotic niche conservatism within these lineages often leads to high levels of range overlap among species, potentially obscuring their biogeographic history. In particular, it is possible that pulses of expansion and contraction of suitable habitat throughout the Pleistocene, especially contraction towards the present, mimics a scenario of sympatric speciation when in fact speciation was primarily allopatric. In addition, the high levels of range overlap raise questions including how species boundaries are maintained, and if species that can hybridize are more ecologically similar than those that cannot. The California Floristic Province is the only area of Mediterranean-like biome in North America and is the center of diversity for the mint clade *Salvia* subg. *Audibertia*. Using a robustly-supported phylogeny, ecological niche models based on current and paleoclimate data, we test if the history of California *Salvia* better fit with an allopatric or sympatric model of diversification by testing if they show (1) divergence in ecological niche, especially among species which can hybridize, (2) are spatially clustered across the landscape, and (3) show past evidence for allopatric speciation followed by secondary contact, especially among hybridizing lineages. Our results provide important insights into the origin and maintenance of species diversity within Mediterranean-like biomes.

Topic: Phylogenomics

A-601

The value of visualizing phylogenomic assemblies, alignments, and trees in exposing errors and identifying patterns

Author: Rebekah Mohn, Ya Yang
Affiliation: University of Minnesota, Twin Cities

In an age of phylogenomic pipelines which take in data and produce the desired outputs, it can be tempting to trust the process and only evaluate summary statistics. We contend that visualizing a subset of the data each step of the way is critical to identifying both issues and interesting patterns. This will be illustrated with real data and real approaches to the visualization process.

Topic: Hybrids and Hybridization

A-602

Investigating the impact of cellular dynamics throughout development on floral size in Nicotiana polyploids of different ages

Author: Edie Russo, Timothy McGrath, Brooke Tillotson, Elizabeth McCarthy
Affiliation: SUNY Cortland

Pollination is dependent on the size of the flower tube, which ultimately determines which pollinators will be most efficient. For example, pollinators must have longer tongues to reach the nectar in flowers with longer tubes. Flower tube size is dependent on the cellular dynamics that underlie the tissue formation, which refers to cell division and elongation. We expect cells to divide early on in floral development and to elongate later on. To measure this, we look at cell length, width, and number across development. These measurements will help us understand how cells are changing and ultimately impacting floral tube size. Another factor that can influence flower size is polyploidy. Polyploids have duplicated genomes, and therefore, their cells may need to be larger than those of diploids to accommodate the additional genetic information. These larger cells may influence flower size, and it is known that young polyploids tend to have wider tubes because they have wider cells. We are working to understand if older polyploids display larger cells than diploids. Our study organisms are ~4-million-year-old *Nicotiana* section *Repandae* polyploids, first-generation synthetic *N. tabacum* lines, and their diploid progenitors. We stain flowers at different developmental timepoints (20%, 40%, 60%, 85%, 95%, and 100% of anthesis) with acid fuchsin and image them under a microscope to measure cell length, width, and number. These measurements allow us to understand the role that polyploidy plays in flower tube size differences in *Nicotiana* polyploids of different ages. Synthetic polyploids have wider cells compared to their progenitors. Surprisingly, our preliminary results show that older polyploids do not have larger cells than their diploid progenitors. We know that genome size tends to decrease as polyploids age. Intriguingly, we see a similar phenomenon with cell size as the polyploid age, which suggests that diploidization may occur at both the genomic and phenotypic levels.

Topic: Biodiversity Informatics & Herbarium Digitization

A-603

A deep learning approach for global species distribution prediction

Author: Yujing Yan
Affiliation: Harvard University Herbaria

The rapidly narrowing action window to reverse biodiversity loss has yield for more efficient methods to predict global species distributions using the Here we introduce a deep learning model to predict and interpolate global species distributions using imperfect biodiversity observations to more effectively model biodiversity. Trained on a large global dataset including ~34 million specimen occurrence records of terrestrial plants, our model demonstrates high precision and high speed in predicting full community distributions in random regions withheld from training data. It effectively interpolates species presence in areas with both abundant and sparse sampling. We envision that our model will be a powerful tool to improve global biodiversity assessments, guide conservation efforts, and contribute to basic and applied research in ecology and evolution.

Topic: *Crops and Wild Relatives*

A-604

Genotypic and geographical variation in stomatal traits in Tripsacum dactyloides L. (Poaceae)

Author: Paige Bostic, Allison Miller, Molly Hanlon, Isabella Vergara
Affiliation: Saint Louis University, Donald Danforth Plant Science Center, Danforth Plant Science Center

Variation is the foundation of evolution. By looking for heritable, intraspecific variation in a given trait, we expand the understanding of natural variation and identify potential targets of selection in breeding crops that support more sustainable agriculture. Understanding how plants tolerate different environmental conditions is critical in the changing climate. One consequence of climate change is worsening drought, and understanding how plants have evolved to tolerate arid conditions has applications in crop improvement programs that support agriculture in increasingly variable environments. Important indicators of drought tolerance in plants include stomatal density (the number of stomata across a given area) and stomatal conductance (the rate at which stomata carry out gas and water exchange with the environment). Here, we studied variation in stomatal traits in grass Tripsacum dactyloides L., a perennial relative of maize. At Shaw Nature Reserve in Gray Summit, Missouri, we grew and processed ~100 Tripsacum individuals representing at least two clonal replicates of 28 genotypes. We took stomatal samples by stripping imprints from T. dactyloides leaves, counted them in ObjectJ, and calculated density as the number of stomata per millimeter. We tested for differences in stomatal density across 28 genotypes. We measured photosythetic traits (list those traits here) using LICOR measurements taken at the end of the season and plotted stomatal conductance (gsw) across genotype. We observed significant differences in stomatal conductance across genotypes. These results suggest that genotype significantly influences stomatal traits in T. dactyloides. Future studies in T. dactyloides will focus on fitness-related traits under drought stress, such as biomass, height, and photosynthetic efficiency, and how these correlate with yield as well as below-ground traits.

Topic: *Population Genetics/Genomics*

A-605

Uncovering the Genetic History of Native Seeds to Inform Future Restoration

Author: Laura Meadows, Mitchell McGlaughlin
Affiliation: University of Northern Colorado

Ensuring the genetic alignment of native seeds within restoration areas is crucial for maintaining local adaptation and biodiversity in ecological restoration efforts. Restoration practices often utilize cultivar seeds that are grown in mass quantity and have been distributed throughout the landscape at an increased rate for decades, thus potentially diluting the genetic diversity of a plant population. The preservation of native plant populations is essential for their adaptation and survival; however, the genetic alignment of current restoration seed sources with historic native populations is underexplored. This study examines the genetics of native plants sampled from herbarium specimens collected 50 to 100 years ago, comparing them with seeds currently available from the USDA Germplasm Resources Information Network (GRIN) and commercial suppliers. Next Generation Sequencing (NGS) methods are used to determine how current seed stocks align with the genetic diversity of ancestral populations, answering questions about the potential loss of local genetic diversity and the use of local seeds for future restoration efforts. These findings highlight the need to assess seed sourcing practices to ensure the use of genetically appropriate materials in restoration efforts. This research offers insights into the genetic legacy of native plants and informs strategies to preserve local biodiversity amid rapid environmental change.

Topic: *Plant phenology in an era of rapid global change: new perspectives and frontiers*

A-606

From community science observations to phenological insights

Author: Daniel Park, Marisa Laitinen
Affiliation: Korea University, Purdue University

Community science, in which nonprofessional volunteers participate in the generation of scientific information and knowledge, has enabled data collection at unprecedented scales. In particular, the accumulation of community science observations and photographs have far outpaced the digitization of physical natural history collections online. It has been suggested that compared to, community science observations do not increase the spatial coverage of our knowledge of biodiversity beyond physical vouchered specimens. However, here we highlight how community science observations can extend our knowledge, particularly in the context of phenology, and complement physical specimens in this regard. We demonstrate how community science initiatives such as iNaturalist can greatly further our insight into how temporal interactions are responding to global change across multiple axes and show that collecting more of the same is a good thing for biodiversity science.

Topic: *Evolutionary history of the Gnetales*

A-607

The Gnetum gnemon genome provides insights into Gnetales evolutionary history and the development of salient morphological features.

Author: Veronica Sondervan, Cecilia Zumajo, Srividya Ramakrishnan, Dennis Stevenson, Melissa Kramer, Sara Goodwin, Samantha Frangos, Katherine Jenike, Olivia Mendevil Ramos, Gil Eshel, Damon Little, Manpreet Katari, Kranthi Varala, Sergios-Orestis Kolokotronis, Barbara Ambrose, Gloria Coruzzi, Michael Schatz, Robert Martienssen, W. Richard McCombie
Affiliation: New York University, New York Botanical Garden, Johns Hopkins University, Cold Spring Harbor Laboratory, Cold Spring Harbor, Purdue University

The position of Gnetales in the evolutionary history of land plants has been the subject of multiple studies, yet remains challenging due to unique molecular and morphological features and considerable contrasts among the three genera. In particular, Gnetum has caught the attention of botanists for its morphological peculiarities such as varied growth habit, lanceolate leaves, reticulate venation, and additional fleshy ovule envelopes; traits which are also found in many angiosperms. Indeed, the extensive morphological convergences between Gnetales and angiosperms have led to suggestions that these groups are sister clades. However, molecular data produces several conflicting topologies, with most recent analyses indicating Gnetales are sister to Pinales (“Gnepine” hypothesis).

We present a high-quality chromosome-level genome assembly of the tree Gnetum gnemon. We examine expression patterns and perform comparative genomics with 21 additional land plant species in order to study the evolution of gene families involved in key morphological traits such as ovule development and growth habit differences relative to the previously assembled vine Gnetum montanum. Among the genes supporting various Gnetales phylogenetic placements, conserved land plant ortholog groups, including ribosomal subunits and chloroplast genes, were more likely to support Gnetales as sister to the gymnosperms. In contrast, the Gnepine hypothesis was supported by mitochondrial genes and gymnosperm-specific ortholog groups. Repeat analysis also identified conifer-specific elements active in G. gnemon reproductive tissues, and fewer Copia-like elements in Gnetum than other gymnosperms. We believe a holistic approach involving different perspectives is required to better understand the complex relationships and evolutionary history of Gnetales.

Topic: Ethnobotany

A-608

ELONGATE DENDRITIC phytoliths as markers for cereal domestication and cultivation: A comparative analysis of 2D and 3D morphometrics

Author: Rosalie Hermans, Mao Li, William Brightly, Timothy Gallaher, Smagghe Wouter, Hannah Lee, Leticia Arco, Lara Stas, Perseverence Savieri, Luc Vrydaghs, Karin Nys, Christophe Snoeck, Caroline Strömberg
Affiliation: Vrije Universiteit Brussel, Donald Danforth Plant Science Center, University of Sheffield, University of Washington, VIB-UGent Center for Plant Systems Biology & Ghent University, University of Washington, Core Facility for Support for Quantitative and Qualitative Research (SQUARE)

Cereals have served as essential food sources for thousands of years. Reconstructing past agricultural practices through the study of crop domestication and cultivation offers valuable insights into the impact of agriculture on human societies. Phytoliths—microscopic silica bodies formed within plant tissues—provide a particularly useful line of evidence, as they preserve well in archaeological deposits and can be used to identify the cultivation of cereals.

A distinctive phytolith morphotype, Elongate dendritic, forms in the inflorescence bracts of many grass species in the grass subfamily Pooideae. It is commonly used as a marker for domesticated cereals (wheat, barley, rye, oats) in archaeological contexts, particularly when found in high abundance. However, its presence in non-cereal grasses, combined with potential morphological overlap between Elongate dendritic from cereal and non-cereal taxa, complicates its interpretation.

In this project, we examined the occurrence of Elongate dendritic in ≈350 modern grass specimens across the Pooideae. We found that Elongate dendritic production is likely an ancestral trait within Pooideae. High levels are largely confined to Triticeae (wheat, barley, rye) and *Avena* (oats) lineages—but these lineages include both wild and domesticated taxa. This means that the presence of Elongate dendritic in archaeological contexts—even in high abundance—should not be immediately linked to the presence of cereals.

We also evaluated the morphology of Elongate dendritic using both 3D and 2D approaches and investigated the potential factors driving morphological variation. We developed datasets including 91 species comprising 1,850 3D phytolith models obtained via confocal microscopy and 9,044 binary outlines from 2D images captured using standard light microscopy. We applied both traditional morphometric features and topological features derived from Persistent Homology (PH)—a powerful mathematical tool that is used to quantify the complex branching architecture of Elongate dendritic.

Genus-level classification produced modest results (accuracy=0.62; κ=0.49; no information rate (NIR)=0.27). While species- and subspecies-level classifications remain challenging (resp. accuracy=0.33; κ=0.32; NIR=0.06 & accuracy=0.30; κ=0.23; NIR=0.15). However, the presence of meaningful morphological variation suggests potential for future refinement. In general, high intra-sample variation complicates the distinction between taxa. The inclusion of topological features contributed to improved performance compared to using geometric features alone, supporting their value in enhancing classification efforts. Domestication status showed a measurable impact on morphology—domesticated forms tend to be larger and exhibit more compact, structurally solid forms—but again, high variability limits confident individual-level classification. No association was found between ploidy level (diploid, tetraploid, hexaploid) and morphology.

These findings offer important guidance for archaeologists and biologists studying crop domestication. By integrating 3D morphometrics, topological analysis, and machine learning, this study introduces a new approach to quantitative phytolith identification. Continued expansion of reference datasets, coupled with methodological refinement, will be essential for improving identification at finer taxonomic levels and unlocking the full potential of phytoliths in the study of domestication and cultivation practices.

Topic: Conservation Biology

A-609

Conservation genomics of the rare and endangered Santa Cruz Island Rockcress (Sibara filifolia) Brassicaceae

Author: May Roberts, C. Matt Guilliams, Kai Pessanha, Seth Kauppinen, Nicole Desnoyers, Kristen Hasenstab-Lehman
Affiliation: Santa Barbara Botanic Garden, US Navy

The Channel Islands archipelago, located along the Southern California coast, is often referred to as the "Galapagos of North America" due to the high number of species found nowhere else on earth. Sibara filifolia Greene (Brassicaceae) is one such endemic plant. This small annual, first described from Santa Cruz Island, is currently known to occur at a few restricted sites on San Clemente Island and Santa Catalina Island. It's rarity is, in large part, due to the long history of ranching and the introduction of non-native herbivores. To aid in archipelago-wide conservation and restoration efforts, we analyzed genomic data (ddRADseq) from over 200 individuals from across islands to determine 1) Are Sibara filifolia on the two islands different genetically? 2) What is the genetic health of the species where it occurs in terms of genetic diversity, levels of inbreeding, and patterns of gene flow within and between islands? Our analyses reveal strong evidence for taxon level differences between the two islands, and that both island populations have low genetic diversity and indications of moderate to high inbreeding. We found that gene flow is high on Catalina Island but very restricted on San Clemente Island. The results complement recent morphometric, greenhouse, and pollination studies which found significant differences by island. We present recommendations for land managers and restoration practitioners, demonstrate the functionality of genomics as a useful tool in conservation, and we also show that with more research in this region, there are likely more taxa waiting to be identified in this biodiversity hotspot.

Topic: Macroevolution

A-610

Life-history evolution across angiosperms

Author: Stephen Smith, Tom Carruthers, Indah Huegele
Affiliation: University of Michigan, University of Florida

I will present results from analyses of life-history evolution across land plants with particular focus on angiosperms.

Topic: Conservation Biology

A-611

Assessing Extinction Risk for the Flora of Eastern North America

Author: Diana Soteropoulos, Amanda Eberly, Nora Ventrella, Janel Johnson, Carl Nordman, Wesley Knapp
Affiliation: NatureServe, Center for Plant Conservation

NatureServe is a U.S. based nonprofit dedicated to unlocking the power of science to guide biodiversity conservation. NatureServe and its Network of member programs gather and maintain a unique body of detailed scientific information on the location, condition, and conservation status of plants, animals, and ecosystems of the United States and Canada. NatureServe Conservation Status Ranks, e.g. Global Ranks, indicate relative extinction risk from "Critically Imperiled, globally" (G1) to "Secure, globally" (G5). These Global Ranks inform conservation decisions in the United States and Canada. Updating plant taxonomy and maintaining a rank currency of 10 years is a formidable task, but NatureServe has made significant strides for the flora of eastern North America, which consists of over 11,000 native taxa. This has come via a major push to assess taxa without Global Ranks and with outdated Global Ranks through two workshops co-hosted by Atlanta Botanical Garden and NatureServe with broad participation from the Southeast Plant Conservation Alliance and diverse funding targeting the Southeastern U.S. (BAND Foundation), New England states (The Manton Foundation), and at-risk species on U.S. Forest Service Land (USFS). Without these efforts, many taxa in the eastern U.S. would remain unranked and may be overlooked for conservation prioritization.

Highlights from this recent work will be shared, including where we are for updating ranks of at-risk species in the eastern United States, the impact of ranking the entire flora of a region, and a brief look into a few genera with recently updated taxonomy and ranks.

Topic: *Education and Outreach*

A-612

"I don't have white privilege, but I definitely do have a Latino privilege": Beyond Monolithic Representations of Latinas in STEM

Author: Summer Blanco, Jessica Ortega, Tati Russo-Tait
Affiliation: University of Georgia

The STEM fields have received much attention because of the chronic underrepresentation of Black, Latino/a/e/x, and Indigenous students. Since the early 90's, Latino/a/e/x scholars have examined the experiences of Latinos/as/es/xs in education. This body of work, initially aimed at challenging deficit-based framings of Latinos/as/es/xs, has given voice to and documented the lived experiences of Latinos/as/es/xs in education, demonstrating the negative impacts of racist policies and racial discrimination on the Latino/a/e/x community. Much of this scholarship highlights the ways in which Latinos/as/es/xs challenge deficit orientations and resist racist policies. Latino/a/e/x education scholars illustrate that in response to exclusionary educational policies and practices some students engage in resistance that is motivated by social justice and offers a critique of social oppression. A growing body of work suggests that interventions that encourage students to reflect on the systemic nature of oppression improve career, health, and educational outcomes. Thus, developing a *critical consciousness* could be an *antidote* to combatting racism in higher education.

This study builds off findings from the first year of a three-year longitudinal study, where critical consciousness of sexism in a sample of racially diverse high school girls participating in an engineering outreach program was examined (Riegle-Crumb et al., 2023). The authors found that while most participants exhibited some understanding of systemic sexism, Black and Latina girls were more likely to name systemic sexism when trying to make sense of gender inequality in STEM. However, Black student respondents tended to be more critical when compared to Latinas, whose understandings were more heterogeneous. The authors hypothesized that the heterogeneity in responses amongst Latinas could be explained by these young women's intersectional social positions (i.e., SES, race, ethnicity, generational status, parent's education) and related lived experiences (Riegle-Crumb et al., 2023, p. 19). This study examined how the experiences of Latinas interested in pursuing a career in Engineering informed their view of themselves as racialized beings. We first explored participants' understandings of the way they are racialized in and out of STEM. We then identified discourses that participants encountered in formal and informal Engineering education spaces (i.e., relating to diversity and underrepresentation in Engineering). Finally, we show how the COVID-19 pandemic and social justice movements in 2020 nuanced participants' understandings of themselves as racialized beings, encouraged self-education on issues of social justice, and set in motion collective action. These findings provide insight on the ways that STEM education maintains the status quo of racial inequities and how social movements can offer marginalized STEM students a new lens to read the world.

Topic: *BSA Emerging Leader Lecture*

A-613

Place-based botany: Leveraging long-term data to produce impactful science and conservation in the Florida scrub

Author: Aaron David
Affiliation: Archbold Biological Station

Topic: *Paleobotany*

A-614

Exploring the phylogenetic position of the extinct family Cheirolepidiaceae in the conifer tree of life

Author: Ana Andruchow-C, Kelly Matsunaga
Affiliation: University of Kansas

The extinct conifer family Cheirolepidiaceae spanned from the Triassic to the early Paleocene, being particularly abundant in the Jurassic and Early Cretaceous. During that time, the family had a worldwide distribution and relatively high taxonomic diversity. Due to their abundance and their characteristic pollen grain, seed cone, and leaf morphologies, the fossil record of Cheirolepidiaceae is well documented. Previous works have proposed different taxonomic affinities for the family, associating them alternatively with the extinct order Voltziales, the living order Araucariales, and the living families Pinaceae and Araucariaceae. However, almost no phylogenetic analyses have included Cheirolepidiaceae with all other conifers, and so the affinities of this family remain untested in a phylogenetic context. We have built a total evidence matrix that includes members of all major conifer groups, sampling the six living conifer families, as well as members of the extinct orders Voltziales and Cordaitales. The taxon sampling also encompasses six of the most complete Cheirolepidiaceae known, including a new whole plant from the Lower Cretaceous of Arkansas. This total evidence matrix includes characters of leaf, seed cone, pollen cone, and pollen morphology, as well as DNA sequences. With this matrix, we conducted a series of phylogenetic analyses to try and answer the long-asked question of the affinity of this enigmatic conifer family. We performed total evidence analyses under maximum parsimony, varying character formulation (discrete vs continuous characters), treatment (ordered/unordered discrete characters, different standardization criteria for continuous characters), and weighting (equal weights versus extended implied weights with varying concavity constants). This variation of conditions allowed us to test the sensitivity of the results to different assumptions about the data. Further analyses were performed with Bayesian Inference, including both an undated analysis and a tip-dating analysis under the Fossilized-Birth-Death (FBD) model. The results of our parsimony and Bayesian tree-building analyses reflect the controversy in the cheirolepidiaceous affinities, with multiple possible positions for Cheirolepidiaceae. The most frequently recovered position, however, is as sister to the crown group of conifers, a placement also recovered by the FBD analysis. Overall, our analyses support the Cheirolepidiaceae as conifer stem group and potential morphological intermediate between the voltzialeans and the modern conifers. Additional sampling of living and fossil conifers may be necessary to resolve some of the remaining uncertainty. This nevertheless provides a phylogenetic framework for understanding character evolution in conifers and the origination of characters that define the conifer crown group.

Topic: *Systematics & Taxonomy*

A-615

Unidentified Flowering Objects (UFOs) from the Hengduan Mountains of China determined to be a new species of Astragalus (Fabaceae) through phylogenetic investigation

Author: Sarah Dayley, Abbigale Baum, Annika Wood, Amaya-Jean Roberts, Ashley Egan
Affiliation: Utah Valley University

Within the Harvard University Herbaria collection, two unidentified Fabaceae specimens were initially suspected to belong to the genus *Phyllolobium*. However, morphological investigation proved inconclusive due to the considerable overlap of diagnostic traits between *Phyllolobium* and *Astragalus*. To resolve their taxonomic placement, DNA was extracted from *Phyllolobium sichuanense*, previously not included in any phylogenetic analysis, and the two unidentified specimens and amplified for the internal transcribed spacer (ITS) region. The resulting sequences were added to 1,335 other *Phyllolobium* and *Astragalus* accessions from GenBank. Maximum likelihood and Bayesian phylogenetic inference indicate that both unidentified specimens belong to the same species and are nested within *Astragalus*, within the group A or Phaca clade with maxiumum support. The unidentified specimens did not group with any Astragalus species, but represented a separate lineage unto themselves. This, combined with a long branch length of its lineage, coupled with an inability to identify the specimens using any known *Astragalus* key, suggests the discovery of a new species. We discuss the morphological affinities of the new species in the context of named sections within *Astragalus*. Additionally, the *P. sichuanense* nested strongly within its genus.

Topic: *Comparative Genomics/Transcriptomics*

A-616

Exploring the Push and Pull of Patterning: the Diversification of the Epidermal Patterning Factor (EPF) Gene Family and its Potential Implications for Stomatal Patterning

Author: John Hodge, Andrew Leakey
Affiliation: University of Illinois Urbana-Champaign

Epidermal Patterning Factors (EPFs) are key signaling ligands which are best known for their role in facilitating stomatagenesis through the regulation of epidermal cell proliferation. EPF1/2s in Arabidopsis act as cell division inhibitors, reducing the

formation of stomatal precursors. EPF1/2s are in turn inhibited by their close relative, EPFL9 (STOMAGEN), which promotes cell proliferation and the formation of stomatal precursors. Despite being members of the same gene family and acting through the same signal transduction mechanism, efforts to reconcile how the relationships of EPF1/2s and EPFL9s to one another, as well as the other major clades of EPFs, have left knowledge gaps. We have generated a phylogeny of all extant EPFs representing over 40 tracheophyte genomes to identify how and when these genes diversified. Current evidence shows that the EPF1/2 and EPFL9 clades are sister to one another suggesting that the cell proliferation inhibitor (EPF1/2s) and its own interference inhibitor (EPFL9s) are the possible result of an ancient duplication of this gene family. Moreover, synteny analyses suggest that these core EPF clades generally maintain their genomic context through deep time although key cases can be found in which specific EPF1 or EPFL9 orthologs have been shuffled following key genomic rearrangements during angiosperm evolution. Taken together this work hopes to better resolve our understanding of how the modern EPF clades arose, how recent duplicates tend to diversify and acquire new functions, and ultimately resolve how these processes could drive variation in stomatal patterning.

Topic: Mycology

A-617

Evaluating the phylogenetic signal in the pathogenicity of fungal endophytes on seeds of two tropical pioneer species

Author: Nathali Jimenez Quiroga, Carolina Sarmiento, A. Elizabeth Arnold, James Dalling, Paul-Camilo Zalamea, Lindsay McCulloch
Affiliation: University of South Florida, University of Arizona, University of Illinois Urbana-Champaign

Plant-fungal interactions play a major role in shaping and maintaining biodiversity of tropical forests and their ecosystem services. Most plant-infecting fungi are likely polyphagous, with infection outcomes differing depending on host identity. For instance, more closely related plants often share similar responses to pathogens. It is less understood whether a phylogenetic signal is observed for pathogenicity across members of fungal communities on the same host species. Tropical plant disease ecology has focused primarily on foliar and root pathogens and their effects on seedlings or adult trees, with relatively little information regarding pathogens of seeds, a critical stage in plant life cycle. In this study, we evaluated how the phylogenetic distance among 58 isolates of ascomycete fungi relates to their pathogenicity on seeds of two tropical pioneer tree species: *Cecropia longipes* and *Ficus insipida*. Seeds were inoculated using mycelium from each isolate and incubated for 15 days. We measured seed mortality as a proxy of pathogenicity using 6-week-long germination experiments. Fungal phylogenetic signals were evaluated using Pagel's λ and Blomberg's κ. Pagel's λ indicated no phylogenetic signal for both *F. insipida* (λ = 0) and *C. longipes* (λ = 0). A likelihood ratio test showed that the models did not differ significantly from one in which λ was fixed at 0 ($p = 1$ for both tree species) but was significantly better than a model with λ = 1 ($p < 0.0001$ for *F. insipida*, $p = 0.0002$ for *C. longipes*). Blomberg's K indicated low phylogenetic signal for both *F. insipida* (K = 0.207) and *C. longipes* (K = 0.3). The observed variance in phylogenetically independent contrasts did not differ significantly from a randomized expectation (P = 0.87 for *F. insipida,* P = 0.59 for *C. longipes*), implying that closely related taxa do not resemble each other more than expected by chance. These results suggest that the trait of fungal pathogenicity relevant to seeds is structured less by evolutionary relationships of the fungi than by other factors, including environmental conditions or co-infection by other strains. Next steps include testing this hypothesis at a broader scale and continuing to elucidate the factors that impact the functional roles of fungi on their plant hosts.

Topic: Systematics & Taxonomy

A-618

Adaptive Compensation Following the Evolutionary Loss of Stamens in Mentzelia (Loasaceae)

Author: Paige Fabre, John Schenk
Affiliation: Ohio University

Infertile stamens, called staminodes, are common throughout Angiosperms and are often subject to abiotic or biotic selection pressures that lead to their functional cooption into novel structures. When fertile stamens are transformed into sterile staminodes, however, there is a disruption in pollen output and male fitness, potentially disturbing an optimal pollen-ovule ratio critical to effective reproduction. Flowers t hat evolve staminodes, therefore, may evolve compensatory strategies that preserve an optimal pollen-ovule ratio and reproductive output. We studied staminode evolution in *Mentzelia* section *Bartonia* (Loasaceae) to understand how the cooption of reproductive structures influences compensatory strategies of flowering plants. We hypothesized that compensation occurred following the functional cooption of stamens into staminodes. We predicted that compensation would evolve by (1) increasing pollen production of intact fertile stamens, (2) increasing the number of fertile stamens, or (3) decreasing the number of ovules. Using a newly inferred Angiosperms353 species tree, we performed phylogenetic comparative methods to evaluate evolutionary trends in stamens, pollens, and ovules for *Mentzelia* species with and without staminodes. We found evidence of compensation in staminode-bearing species, suggesting that flowers maintain an optimal reproductive output regardless of staminode presence.

Topic: Paleobotany

A-619

Evolution of tubers in Equisetum and the broader sphenophytes

Author: Jaemin Lee
Affiliation: University of California, Berkeley

Tubers are locally enlarged stem or root organs primarily functioning in carbohydrate storage, and many of them develop underground. Compared to the great taxonomic and morphological diversity of tubers among angiosperms, they are poorly known in gymnosperms and spore plants. Lateral stem tubers are found in *Equisetum*, the sole living genus of the once diverse sphenophytes, and the evolution of tubers in *Equisetum* and the broader sphenophytes is reviewed. *Equisetum* tubers are swollen rhizomal phytomers with increased storage parenchyma and reduced structures for water transport and aeration. They develop laterally from nodes of rhizomes that are high in starch concentration. To date, tubers have been described exclusively in members of the annually deciduous subgenus *Equisetum*, which may aid their early growth in the absence of persistent photosynthetic tissues. Tubers in *Equisetum* are morphologically variable in shapes, arrangements, and numbers. However, this variation reflects the plasticity in their growth forms and bears little phylogenetic significance among living taxa; therefore, tuber morphology may be ill-fitted as a diagnostic character of fossil taxa. Tuberous *Equisetum* fossils are exclusively known from the northern hemisphere, predominantly from the mid-high paleolatitudes of Cretaceous and Cenozoic deposits. This spatiotemporal distribution of fossil Equisetum tubers largely corroborates the reconstructed evolutionary history of the tuberous subgenus *Equisetum*. However, the oldest tuberous *Equisetites* from the latest Triassic-earliest Jurassic, separated by a 50-million-year gap from the other records, suggests that the lateral stem tubers may be plesiomorphic or have evolved more than once within the genus. Among the broader sphenophytes, disparate and nonhomologous types of stem tubers, whose tuberization occurs along the main plant axis via secondary growth, have been described from Archaeocalamitaceae and Calamitaceae. Such occurrences demonstrate that a greater diversity of stem tubers and tuberization mechanisms existed in the sphenophytes in the geologic past.

Topic: Floristics

A-620

The Flora of the Southeastern United States (FSUS): serving a constantly updating flora to a broad audience in multiple platforms

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At the Southeastern Flora Project, we aim to "reinvent the conventional Flora" to provide professionals and amateurs with sophisticated identification methodologies and current information on the >11,000 species in the region. In the 21st century, we embrace the idea that we can provide better tools to a diversity of users than we as a community did in a pre-digital world, when floras were updated very infrequently (and taxonomy became out-of-date), illustrations were necessarily limited, and identification technology consisted only of dichotomous keys. We develop the flora via a custom database system, FloraManager, allowing continuous updating, addition of new features, and customization of "flora products". We currently provide the flora in three main formats: pdfs/digital books, a web app, and three (with two more planned) installable mobile apps for subsets of the region. We provide all the features usual in a conventional "book flora", but with updatable taxonomy, extensive bibliography (> 7000 references),

tens of thousands of diagnostic photos at various phenologic states, geographically customized dichotomous keys by filtering, polyclave or multi-access key to all taxa (combined with on-the-fly decision trees generated when the number of taxa from the polyclave is reduced to ten or fewer), detailed habitat information, dichotomous keys featuring illustrations at critical decision points, comparison panels of similar taxa, trait data, links to iNaturalist, links to technical descriptions in Flora of North America, ecological and conservation metrics (Wetland status, Heliophily rating, Coefficients of Conservatism, conservation ranks such as NatureServe GRanks), and other features. We here describe these features and innovations, ask for ideas for future development, and solicit creative collaborations.

Topic: Crops and Wild Relatives

A-621

Which species are the wild progenitors of our future crops?

Author: Allison Miller
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There is no doubt that crop wild relatives (wild species that are interfertile with major crops) serve as a valuable resource for crop improvement. However, a relatively small number of wild plant species have entered the domestication pipeline and have evolved into crops. As a result, global grain agriculture is based on just a handful of highly optimized species. In the interest of developing more diverse, resilient agricultural systems to meet the needs of a growing population and changing environmental conditions, there is a need to broaden the base of species we consider to have actual or potential value for agricultural systems of the future. Scientists and breeders are already thinking about developing breeding pipelines for a broader variety of species, and for more diverse agricultural systems (cover crops, polycultures, etc.). The goal of this talk is to share a developing strategy to build the requisite foundation, and ultimately seed resources, required for the diversification of agriculture. One component of the diversification of agriculture includes perennial, herbaceous species grown for their hard seeds (perennial grains), which were never domesticated by early farmers but are drawing increasing attention as important components of future agricultural systems that mimic nature in perenniality and diversity. These species are at the early stages of domestication and making great progress. In this presentation, I will review pathways for development of future crops, targets of selection in breeding perennial grains, germplasm accessibility, and review an emerging list of candidate species, highlighting priority areas for future work. In doing this work, we hope to identify multiple species that are the wild progenitors of future crops, build germplasm resources, and initiate field studies to explore their potential utility and breeding prospects.

Topic: Symbioses: Plant, Animal, and Microbe Interactions

A-622

Variation of fungal resistance in Populus Hybrids: With both small and large scale drivers of presence

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Poplar trees (*Populus*) play a vital role providing ecosystem services for humans and are often critical species within the wide range of habitats they occupy. We were interested in the relationship of the fungal pathogen *Melampsora* spp., also referred to as rust, with natural hybrids of *Populus trichocharpa* (Black Cottonwood) and *P. balsamifera* (Balsam Poplar). Understanding contributors to rust is important as the fungus has been identified as a potential threat to proper development in many poplar species through infiltrating the mesophyll and impacting leaf physiology (Gortari, 2018). Our work is within a long-term common garden study at the University of Wisconsin - Eau Claire, which is part of the PopUp Poplar Network, a multi-year and multi-institution poplar research project. The PopUp Poplar Network as a whole is interested in how hybridization of *P. trichocharpa and balsamifera* leads to adaptive variability across five transects. Transects are natural hybrid zones across various habitats in Canada and Alaska. Cuttings from 47 poplar genotypes were collected across the five transects with 19 common gardens being supplied with 2 clones for each of the genotypes.

Our overall objective was to determine what factors might be influencing the prevalence of rust, both across the common gardens and within our focal garden. We first asked if transect, influenced the prevalence of rust (on a presence/absence scale) across all gardens. Secondly, we asked if the proportion of leaves affected by rust within the Eau Claire garden varied with individual leaf traits. We used ANOVAs and linear model tests to uncover any associations between rust and either transect or leaf morphology, ultimately, leaf width. For the multi-institution data we found that rust presence was significantly related to the original transect of the poplar hybrids. Also, for our Eau Claire data set, leaf width was positively and significantly related to the proportion of leaves affected by rust. The presence of variability in Poplar resistance to rust disease on the basis of original environmental variation and morphological variation is exciting for the larger Popup Network and encourages further investigation to other influential patterns in rust resistance. Understanding these driving factors further can provide knowledge into what adaptive traits are essential for Poplar fitness against fungal pathogens in a changing climate.

Cited: Gortari, F., Guiamet, J.J., and Graciano, C. (2018). Plant–pathogen interactions: leaf physiology alterations in poplars infected with rust (*Melampsora medusae*). Tree Physiology *38*, 925–935.

Topic: Conservation Biology

A-624

CATs out of the bag: Introducing RARECAT, a new tool to assist Conservation Status Assessments

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NatureServe's Conservation Status Assessments and Global Ranks are nearly comprehensive for vascular plants occurring in the United States and Canada. Like other methods of assessing extinction risk (such as IUCN Red List), NatureServe's method follows a general process that begins with selecting a taxon and defining its geographic scope, followed by research and data collection, the application of methods to those data to inform factors of rarity, threat, and trend, the recording of supporting information, review of the assessment and rank, and finally publication. Ideally, this process is repeated every ten years to keep pace with new information on threats and trends, and increasingly accessible digitized specimen data and expanding network of community scientists contributing high quality photo-based observations. NatureServe's RARECAT (Rapid Analysis of Rarity and Endangerment Conservation Assessment Tool) facilitates extraction and/or importation, vetting, and filtering of specimen and observation data, visualization of data quality and quantity over space and time, and calculation of the three fundamental factors of Rarity – Range Extent (also known as Extent of Occurrence/EOO), Area of Occupancy (AOO), and Number of Occurrences – for single taxa or multiple taxa concurrently. While RARECAT uniquely supports NatureServe' Conservation Status Assessment Methods, it also has broader applications. Examples of how this tool is being applied by NatureServe to facilitate global ranking efforts will be discussed, as well as future directions for RARECAT.

Topic: Biogeography

A-625

Niche Conservatism, Glacial Cycles, and Diffuse Co-evolution Shape the Continental Radiation of Cirsium (Carduoideae: Compositae) in North America

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A major goal of evolutionary biology is to understand how abiotic factors such as climate change, mountain uplift, and soil chemistry, and biotic factors such as pollinator preferences, shape the geographic distributions of lineages, promote diversification, and ultimately lead to speciation. These forces are best studied in groups that have undergone recent radiations, where patterns of lineage divergence and dispersal remain detectable. Compositae (Asteraceae) is among the most speciose and globally successful plant families, yet the drivers of diversification within younger North American lineages remain underexplored. *Cirsium* (thistles) presents a compelling model system to investigate these processes due to its recent, rapid radiation across the continent, ecological specialization, and presence in a range of heterogeneous abiotic environments. Using a time-calibrated phylogeny derived from Hyb-Seq data, we investigated how *Cirsium* diversification has been shaped by: (1) glacial–interglacial cycles and shifts in habitat structure, (2) niche conservatism in semi-arid environments, and (3) the emergence of hummingbird pollination syndromes. Our results indicate that *Cirsium* lineages primarily retained ancestral ecological preferences, with diversification occurring as species tracked suitable habitats across increasingly fragmented landscapes during the Pleistocene. Three main bursts of diversification occurring ~1.5–2 million years

ago coincided with glacial cycles and aridification, which created open habitats and reduced tree cover. These changes favored plants pre-adapted to low evergreen density and seasonal dryness, providing ecological opportunities for rapid thistle expansion. Approximately 10% of North American *Cirsium* species are primarily hummingbird-pollinated, which is a rare trait within North American Compositae. The transition to hummingbird pollination coincides with the onset of hummingbird diversification in North America (~2 Ma) and may represent a case of diffuse co-evolution. Hummingbird-pollinated species are often more fecund, potentially producing more seeds and increasing the likelihood of successful colonization of new or isolated habitats. Despite this, our trait-dependent diversification analyses suggest that these species exhibit near-significantly lower diversification rates, likely due to diminished ecological opportunity, reduced geographic space for expansion, and fewer opportunities for allopatric speciation in already saturated niches. Overall, our study demonstrates that *Cirsium*'s continental-scale radiation has been governed by niche conservatism, Pleistocene climate cycles, and limited but ecologically meaningful shifts in pollinator associations. These findings offer new insights into the evolutionary dynamics that have contributed to the success of Compositae in temperate regions and highlight the importance of integrating abiotic history and biotic interactions when studying plant diversification.

Topic: Floristics

A-626

Floristics on the Frontlines: A Flora of the Amargosa River Headwaters, Nye and Esmeralda Counties, Nevada

Author: Chloe Novak
Affiliation: California Botanic Garden

Baseline data on the diversity and distribution of plants is incomplete and inconsistent across much of the western continental U.S., despite this region accounting for a majority of the undeveloped land area in the country. Documentation has been particularly sparse in the state of Nevada, more than 80% of which is federally managed public land that may be subject to resource extraction and development. The headwaters of the Amargosa River in Nye and Esmeralda Counties is one such area where floristic documentation lags behind increasing proposals for major industrial land use change, which threaten both local biodiversity and the hydrological system upon which significant areas of endemism downstream depend within North America's most arid desert ecoregion. The study area encompasses approximately 2000 square kilometers and ranges in elevation from 790 to 2660 meters; it includes the Nevada portion of Death Valley National Park, the Grapevine Mountains Wilderness Study Area, extensive alkaline wetlands, the carbonate Bare Mountain, and volcanic Bullfrog Hills. This study aims to contribute the first comprehensive vascular flora of this critical area to directly inform land management and conservation efforts, while providing novel insights into the biodiversity and biogeography of the Mojave-Great Basin transition zone. Through systematic surveys and the collection of plant specimens, this study will produce a complete annotated checklist of vascular plant taxa along with biogeographic, physiographic, and conservation status assessments for rare plant taxa. Findings from preliminary fieldwork conducted in 2024 yielded the addition of at least 85 minimum rank taxa, including five rare plant species, one of which is a state record for Nevada. With diverse geology, topography, vegetation types, and contiguity with biodiversity hotspots at Death Valley and Ash Meadows, this research is likely to yield additional range extensions, new populations of rare plants, and previously undescribed taxa.

Topic: Disabled in Botany: Breaking Barriers in Plant Science Research

A-627

Broadening Participation in Botany: A Systematic Analysis of Undergraduate Plant Science Instructional Resources

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Despite the vast diversity of plants, estimated at over 370,000 species, botanical content is underrepresented in undergraduate biology education. This plant awareness disparity contributes to student disengagement and hinders understanding of plants' ecological and societal importance. To understand what plant science materials are currently available for undergraduate biology courses, we conducted a systematic analysis of published lesson-plans from 2000 to 2022 and identified 88 lessons that referenced plant content. All of these lessons are Open Educational Resources (OERs), which are freely available and modifiable teaching materials. The free-cost eliminates financial barriers and enables a broader range of implementation which can create more equitable learning environments, especially for students and instructors historically excluded from resource-intensive instruction. Using descriptive statistical analyses, we categorized plant taxonomic representation, teaching strategies, course context, and alignment with the Vision and Change in Undergraduate Biology Education Initiative core concepts and competencies. Most plant-focused lessons targeted biology majors and evenly spanned lower- and upper-division courses. The lessons were designed for a variety of course types including laboratory (40%), field (14%), and lecture (46%). The majority of lessons were created for class sizes (n<25 students), and used active-learning techniques such as peer discussion and group work. Our findings reveal opportunities to create new botanical curricula, particularly materials designed for large-enrollment, non-major courses, and those that intentionally scaffold accessible, field-based learning. By identifying content and pedagogical opportunities in current plant biology OERs, we aim to inform the development of resources that not only reduce plant awareness disparity but also dismantle barriers to participation in botany for both students and instructors.

Topic: Crops and Wild Relatives

A-628

How Perennial Plants Build Soil Quality and Implications for Agriculture

Author: Julia Erker
Affiliation: Saint Louis University

Humans have contributed to increased soil erosion, soil compaction, and disturbance of healthy soil structure, in part due to the replacement of native perennial plants with annual crop plants in agricultural landscapes. Annual crop plants tend to have lower root biomass than perennial plants, which as a result affect the surrounding soil structure. The reduction in root biomass in agricultural soils negatively impacts the development of physical soil properties, such as soil bulk density, soil porosity and water holding capacity. Studies have found that in comparison to annual crops, perennial plants improved bulk density as well as porosity due to abundant root growth. Though the ability of perennial plants to improve soil physical properties compared to annual species is well studied, it remains unclear whether certain emerging perennial crop species will be more effective at improving soil density, porosity and water holding capacity when compared to one another. This study aims to explore the species-specific impacts of two perennial plant species, Kernza and Silphium. We asked, what are the perennial plant species-specific effects on soil bulk density, soil porosity, and soil water holding capacity have been analyzed. From our findings we can answer questions like how can these perennial plant species have a positive restructuring effect on soil and where can their use be most beneficial. The findings of the study indicate that perennial plant species do vary in their effects on soil architecture and the use of certain perennial plant species could be more beneficial in certain areas. Specifically, it was found that Silphium retains more water and generally has larger pores than Kernza, suggesting that this species is adept at holding onto water at saturation. In addition, both species had consistent bulk density throughout their soil horizons, suggesting that there is a consistency present in liters of water per volume of soil throughout soil horizons in the two tested plant species.

Topic: Defining forces in fern evolution: Celebrating the contributions of Kathleen Pryer and Michael Windham

A-629

Seeing the forest for the ferns: Kathleen Pryer and the power of a broad perspective

Author: Eric Schuettpelz
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Over the past three decades, a dramatic increase in DNA sequencing has fundamentally shifted our understanding of phylogenetic relationships both among and within major fern lineages. This revolution can be traced, in large part, to a landmark 1995 study led by Dr. Kathleen Pryer, which provided the groundwork for discerning backbone relationships among extant fern families, while also illuminating character evolution across the group. In this and subsequent studies, Dr. Pryer uncovered the monophyly of heterosporous ferns, provided strong support for the leptosporangiate clade, and solidified the placement of horsetails among ferns, among many other major contributions. Throughout her career, Dr. Pryer has published extensively not only on fern phylogeny, but also on diversification, biogeography, life history, classification, molecular rate heterogeneity, and genomics. Much of this work has taken a broad perspective. With an

uncanny ability to focus on the big picture, Dr. Pryer has had a unique and lasting impact on our understanding of fern evolution. In addition to her scientific contributions, Dr. Pryer's legacy is bolstered by her remarkable commitment to excellence in training and her unwavering advocacy for early career scientists.

Topic: Bryology and Lichenology

A-630

Comparative Species Distribution Models of Structured and Opportunistic Lichen Collections in the Southern Appalachian Mountains

Author: Jeremy Howland
Affiliation: City University of New York

Biodiversity and ecological patterns are increasingly investigated through species distribution modeling (SDM), often relying on large-scale occurrence datasets like GBIF. However, many of these records are opportunistic, leading to sampling biases, redundancies, and geographic or environmental gaps. These limitations can affect the accuracy and reliability of models built to estimate habitat suitability and species presence across a region. In contrast, a large-scale, systematic, plot-based survey of lichens in the Southern Appalachian Mountains provides a unique, high-quality dataset that can be used to train and test more robust SDMs. By comparing structured and opportunistic datasets, both independently and in combination, this study investigates the geographic and environmental biases introduced by different sampling strategies. Outcomes of this will be used to investigate whether lichen biodiversity patterns are driven by environmental conditions alone or if the geographic isolation and extent are also shaping distributions.

Topic: Macroevolution

A-631

Genome Size Evolution in the African Ledebouriinae (Scilloideae, Asparagaceae)

Author: Boniface Ngarega, Cody Coyotee Howard
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Polyploidy and genome size variation are important drivers of plant evolution. Genome size has been shown to be positively correlated with the length of plant guard cells and negatively correlated with the density of stomata (big genomes = larger guard cells, less stomatal density). This suggests that genome size could act as a constraint on and/or affect stomatal architecture. Stomata help regulate gaseous exchange in plants, and therefore their size and density may reflect the habitat in which different species have evolved. Stomatal characteristics have ecological relevance as they directly affect water use efficiency, with smaller guard cells allowing for faster stomatal closing leading to decreased water loss in drier conditions. Geophytes, plants with resting buds positioned below the soil surface, have relatively larger genomes compared to plants with other growth habits, with considerable variation existing across geophytic taxa. It has been suggested that geophytes with larger genomes are found in more humid environments, while those with smaller genomes occur in more arid regions. This is hypothesized to be due to the drought sensitivity of species with larger stomata, as larger pores increase transpiration rates and require greater water availability to sustain photosynthesis. Here, we examine ploidy levels and genome size evolution across the Ledebouriinae (Scilloideae, Asparagaceae), a widespread group of geophytic, bulbous plants found across sub-Saharan Africa and beyond. We approximate ploidy levels and genome size using stomatal density and guard cell size using plants collected from across the southern African distribution of the Ledebouriinae (Namibia, South Africa, Zambia). We use a phylogenetic comparative approach to investigate the relationship between genome size and habitat. We test the hypothesis that species with larger genomes will exhibit fewer, larger stomata and will be associated with regions that are relatively more humid, while smaller genomes will correlate with drier habitats (e.g., Namibian taxa). Additionally, we assess whether shifts in ploidy coincide with biogeographic transitions into dry ecozones in Africa. Our study will provide insights into how genome size variation may influence historical ecology and biogeography.

Topic: Defining forces in fern evolution: Celebrating the contributions of Kathleen Pryer and Michael Windham

A-632

Myriopteris pryeriae: Integrating systematic approaches to expose a new fern species in North America

Author: Isabel Smalley, Max Botz, Amanda Grusz
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As the sister clade of seed plants, ferns are a pivotal source of information on the evolution of life on land. However, evolutionary relationships within the diverse fern lineage remain cryptic, especially at shallow taxonomic levels. The genus Myriopteris Fée (Pteridaceae) is one example wherein deep evolutionary relationships are well supported while species complexes, riddled with polyploidy, hybridization, and apomixis, remain poorly understood. Previous studies of Myriopteris reveal that cryptic cytotypes (i.e., morphologically similar taxa differing in chromosome number) are common. In this study, we leverage spore data to explore cytotype diversity among herbarium specimens assigned to the genus Myriopteris. In addition, Myriopteris covillei, a species that is frequently implicated as a parent of hybrids within this genus, is investigated, with a focus on the broader species complex. Our results suggest that the holotype of M. covillei (from the Panamint Mountains in Death Valley) represents a sexual tetraploid largely confined to the Great Basin. The extensive distribution of "M. covillei" outside the Great Basin (i.e., much of Arizona and California) is occupied by a cryptic diploid taxon that contributed half the genome of tetraploid M. covillei s.s. During my talk, we will reveal the identity of the missing diploid progenitor using spore data, geographic distribution, morphology, and DNA sequences generated using the GoFlag dataset. This study emphasizes the critical value of spores from herbarium specimens, especially type material, for clarifying taxon boundaries in reticulate species complexes. Alongside important taxonomic updates, this talk also emphasizes the important contributions of Drs. Kathleen Pryer and Michael Windham to fern systematics, illustrating the generational impacts of their research, mentorship, and training program.

Topic: Systematics & Taxonomy

A-633

Systematics and evolution of the true blueberries (Vaccinium sect. Cyanococcus, Ericaceae)

Author: Peter Fritsch, Andrew Crowl, Paul Manos
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The true blueberries (*Vaccinium* sect. *Cyanococcus*) are a monophyletic group of shrubs nearly endemic to eastern temperate North America, with one species extending to the northwest. This group served as a model system during the Modern Synthesis for examining the origins, prevalence, and diversification of polyploidy in nature and remains intensively studied because of its economic importance as a food crop. Nonetheless, its taxonomy and evolutionary history is still uncertain, particularly regarding the relative importance of allo- versus autopolyploidy in the evolution of the group, the extent to which levels of ploidy concord with species boundaries, and the utility of the morphological characters traditionally used for delimiting taxa. To address these knowledge gaps, we collected over 800 plants from natural populations with herbarium vouchers and photographs, ca. 550 of which were analyzed with flow cytometry to estimate ploidy. We examined thousands of herbarium specimens from key U.S. herbaria to examine morphology. A robust diploid phylogenetic estimate was generated for 36 samples of known ploidy with a target-enrichment phylogenomic approach. To this framework we added polyploids in several ways to test their evolutionary origins. Results suggest that autopolyploidy is the primary means of genome duplication in the clade. We also found a strong correlation of leaf and stem stomata size and density with ploidy throughout the group. With the knowledge gained from these studies, we have revised the taxonomy of the section to comprise 15 species. The revision differs substantially from prior work, e.g., "highbush" blueberry group as currently delimited by *Flora North America* has been repartitioned but not as in prior treatments; the taxonomy of two Southern Appalachian polyploids to which names have been extensively misapplied has been resolved; and a localized polyploid endemic currently buried in synonymy has been resurrected. We also discovered a morphological means to discern "rabbiteye" blueberry cultivars that have escaped from cultivation.

Topic: Systematics & Taxonomy

A-634

Using phylogenomics and morphometrics to evaluate the circumscription of the Channel Islands endemic Santa Cruz Island fringepod (Thysanocarpus conchuliferus Greene; Brassicaceae)

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*Thysanocarpus conchuliferus*Greene is a diminutive annual herb in the Brassicaceae, or mustard family. Known as the Santa Cruz Island fringepod, the species was thought to be limited to a global distribution of only 15 Element Occurrences on Santa Cruz Island (SCR), California. Due to its rarity, the species was listed as Endangered under the Federal EndangeredSpecies Act, and has been given the Rare Plant Ranking of 1B.2 by the California Native Plant Society. In 2008, plants identified as *T. conchuliferus* were collected on the mainland in the western Santa Monica Mountains (SMM), northwest of Los Angeles. Since that time, additional mainland SMM populations have been documented, which calls into question both the circumscription and distribution of this rare species. Here we use phylogenomics and morphometrics to evaluate the circumscription of *T. conchuliferus* and assess how plants from the SMM relate to *T. conchuliferus* and the other members of the genus. We collected and extracted genomic DNA from approximately 93 samples of *Thysanocarpus*. We used the ddRADseq technique to develop a DNA sequence dataset, which was analyzed using RAxML and IQtree. Samples of *T. conchuliferus* from the SMM form a clade with weak support (ML BS = 51) sister to a weakly supported clade (ML BS = 45) of *T. conchuliferus* samples from SCR. All *T. conchuliferus* samples form a clade with maximum statistical support (ML BS = 100). Support values throughout the rest of the *Thysanocarpus* tree are strong in general. The morphometrics dataset included measurements of 72 individuals of *T. conchuliferus*, 22 from SCR and 50 from the SMM. We measured eight characters (all in mm), including pedicel length, fruit length, distal wing depth at style, style length, fruit width, wing extent, seed chamber length, and seed chamber width at the widest spot. Plants from SCR and SMM were strongly statistically different in four characters, including distal wing depth at style, style length, seed chamber length, and seed chamber width. Although these results are preliminary, it appears that the plants from the SMM are genetically and morphologically distinct from *T. conchuliferus* from Santa Cruz Island and may warrant taxonomic recognition.

Topic: Paleobotany

A-635

A new genus of Podocarpaceae (Coniferales) from the early Miocene of New Caledonia

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The South Pacific archipelago of New Caledonia is renowned for its rich and distinctive flora, which includes many endemic angiosperms as well as an unusually high concentration of conifer species. The continental origin of the archipelago and the presence of notable relictual taxa has led many to suggest that Gondwanan vicariance played an important role in the formation of this flora. Geological evidence indicates that the landmass was submerged until the Oligocene, however, suggesting that the flora instead formed through relatively recent long-distance dispersal events. Recently discovered fossil floras provide a new window into ancient New Caledonian floras, potentially shedding light on the origins of this important biota. Here we describe one of the fossil plants contained in these floras, a new fossil Pododcarpaceae from an early Miocene deposit (~19 Ma) on the Pindaï Peninsula of western New Caledonia. The fossil material consists of fragmentary shoots covered in awl-shaped leaves, some of which are permineralized by iron oxides and preserve details of epidermal anatomy. The fossil leaves have narrow bands of paratetracytic stomata oriented parallel to the leaf axis, consistent with extant and extinct members of Podocarpaceae and particularly the genus *Dacrycarpus*. But stomata complexes in the fossils are tightly crowded and are not separated by epidermal cells, an arrangement unlike other living or fossil Podocarpaceae with comparable leaves. Hence, we assign this material to a new extinct taxon, *Dacrycarpoides neocaledonica*. The presence of extinct conifers on Miocene New Caledonia is consistent with floras from neighboring landmasses and highlights the role of extinction in shaping the modern flora of New Caledonia and other Australasian landmasses.

Topic: Symbioses: Plant, Animal, and Microbe Interactions

A-636

Order of arrival of microbial partners impacts the outcome of mutualism

Author: Ethan Groves, Madeline Green, Cristy Portales-Reyes
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Below ground plant mutualists offer many benefits to plant hosts, ranging from assistance in nutrient and water uptake to nitrogen-fixation. The relationship between plants and their mutualists depends on the resources traded and could result in different outcomes depending on the order of arrival of microbial mutualists. In addition, stressors can significantly impact plant growth and their ability to fix carbon needed for trading with microbial mutualists. Shade, specifically, limits photosynthesis and can impact carbon allocation to above and belowground structures. Here, we test the effects of order of arrival and shading on the outcome of mutualisms between plants, rhizobia, and arbuscular mycorrhizal fungi. In a full factorial greenhouse experiment, we manipulated shade, presence, and timing of inoculation with rhizobia and mycorrhizae for replicate Chamaecrista fasciculata individuals (shade x 2 + inoculum x 6 + 32 replicates = 384 individuals). We hypothesized that plants growing under ambient light would grow more and be better able to associate and benefit from interactions with microbial mutualists. Additionally, we expected plants growing with more than one mutualist to have greater biomass than those associated only with one. Using linear mixed effect models, we tested the impact of shade and inoculation type on aboveground and belowground biomass. Across all treatments, we find that plants grew less under shade. However, we found that when inoculation with rhizobia happened before or concurrently with mycorrhizae, the benefits of mutualism were greater than when plants were inoculated with mycorrhizae first. Shade and inoculating with AMF first decreased nodule count. Nodule size was larger for individuals inoculated with AMF first, but overall plant biomass was lower. Our results suggest that order of arrival in the rhizobia, mycorrhizae, and plant mutualisms impacts the outcome of the interaction.

Topic: Crops and Wild Relatives

A-637

Frequency of occurrence of the glyphosate resistance gene in feral alfalfa populations in hay-production areas and its potential impacts on pollinators and plant reproduction

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Gene flow of cultivar genes into wild plant populations has been demonstrated for many species. Alfalfa, the world's most important temperate forage crop, has been genetically modified for glyphosate resistance (GR) and deregulated without conditions since 2011. This deregulation has raised concerns regarding the spread of the GR gene not only into conventional and organic fields, but also into feral populations. Although wild alfalfa does not exist in the United States, the species can escape cultivation and become established as feral populations, which are commonly found along roadsides and in other unmanaged habitats in cultivated alfalfa-growing regions. While previous studies have documented the presence of the GR gene in feral populations in alfalfa seed-production regions, information is scarce regarding its frequency in hay-producing areas. Moreover, we have little information on the potential impacts of the GR gene on the plant's pollinators and reproductive traits. To address these knowledge gaps, we first determined the proportion of populations carrying the GR gene by bulk sampling 100 individuals per population. For populations testing positive, we individually tested 30 individuals in order to assess the proportion of GR individuals within each population. In populations with sufficient numbers of both GR and non-GR individuals, we compared pollinator foraging behavior and reproductive traits. Our findings revealed the presence of the GR gene in some hay-producing areas but not others. In certain counties, up to 42% of feral populations carried the GR gene, with as many as 80% of individuals within a GR-positive population testing positive. While bee species showed similar foraging

patterns on GR and non-GR plants, we observed some differences in plant reproductive traits. Ultimately, the relative seed output of GR versus non-GR plants will influence the spread of the GR gene in feral populations.

Topic: *Bryology and Lichenology*

A-638

Unseen and Unknown: Exploring Lirellate Lichens (Graphidaceae) in the Southern Philippines

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Documenting the remaining biodiversity persists as a challenge in this era of rapid extinction, particularly in regions with high species richness and endemism that are facing significant threats daily. This is particularly true for the Philippines, which is considered one of the megadiverse countries and a biodiversity hotspot. Lichens are among the most diverse yet understudied organisms, playing crucial ecological roles in nutrient cycling, air quality monitoring, habitat and food to wildlife, and providing sources of pharmaceutical uses to humans. Despite their significance, many lichen groups remain poorly understood with challenges in taxonomic classification. Among the most speciose lichen families is Graphidaceae, a diverse group of crustose lichens with approximately 2,000 species in 83 genera, and distinguished by its elongated ascomata (lirellae) and high species richness in tropical regions. While the systematics of Graphidaceae has been the subject of several studies, the Southern Philippines remains a largely unexplored area for lichen research, particularly in terms of the diversity and distribution of lirellate lichens. Studies have shown that undiscovered species richness is likely concentrated in highly diverse groups, as well as in remote areas with limited research opportunities, taxonomic expertise, and interest. The present research aimed at documenting the lirellate lichens of the Southern Philippines as part of the larger molecular systematics and evolution study of the group. Comprehensive field expeditions were performed in different areas in the Southern Philippines from 2019 to 2024, through several transect walks along different vegetation types. A total of 850 specimens of lirellate Graphidaceae were collected and identified through established protocols for lichen identification, which include morpho-anatomical examination, chemical spot tests, thin layer chromatography (TLC), and DNA sequencing. Preliminary results revealed the discovery of six possible new species within the genus *Sarcographa*, five new records for the Philippines, and the identification of hypoprotocetraric acid, a novel substance record for the genus. These findings underscore the rich, yet underexplored, diversity of Graphidaceae in the Southern Philippines, highlighting the critical need for continued taxonomic research in threatened and understudied regions. Given that this is still preliminary data and the first comprehensive study of this group in the region, further novel discoveries are expected. These findings will contribute to the revision of the taxonomic classification of lirellate Graphidaceae and play a significant role in efforts toward biodiversity conservation.

Topic: *Ecophysiology*

A-639

How is the energy use and dissipation in green-stemmed plants of the Mojave Desert and Colorado Plateau?

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Drylands cover 40% of Earth's surface and support over 1.2 billion people. In deserts such as the Mojave (MD) and the Colorado Plateau (CP), some plants utilize their stems to assimilate carbon, even when leaf photosynthesis is constrained by heat and drought. This ability to assimilate CO_2 helps them survive and remain functional under extreme conditions. This study was conducted in the dry season of 2024 in the Bonderman Field Station at Rio Mesa (CP) and the Lytle Nature Preserve at Beaver Dam (MD). To measure energy use and dissipation, we used a LiCor 6800 equipped with a Multiphase Flash™ fluorometer circular chamber and an LED light unit. This setup allowed us to assess fluorescence parameters—including maximal photochemical efficiency (Fv/Fm), electron transport rate (ETR), and non-photochemical quenching (qN)—in both leaves and photosynthetic stems of five individuals (n = 5) per species at each site. To determine the water status of plants, we measured predawn and midday water potential using a pressure chamber. Results showed no significant differences between organs at either site. However, Fv/Fm and ETR were 11% and 50% lower, respectively, in CP plants compared to MD plants, likely due to a 30% lower midday water potential in CP plants compared to MD plants. Despite this, energy dissipation (qN) was similar between the two sites. These findings suggest that although both locations experience high solar radiation, MD plants may exhibit adaptive traits that enhance their energy-use efficiency. In contrast, CP plants displayed characteristics of dynamic photoinhibition—a protective mechanism that helps prevent damage from intense radiation and supports survival under extreme environmental conditions.

Topic: *Bryology and Lichenology*

A-640

A (Lichen) Diamond Mine in a Gold Diggers State

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The high peaks and high plains of the Southern Rockies Mountain Ecoregion contain a biological mosaic of environments ranging from high elevation tundra and talus slopes and vast subalpine areas to riparian woodlands, semi-arid pinyon-juniper mesas, extensive short-grass prairie and sagebrush, and treeless high desert steppe. Colorado alone, with nearly 50% of its land in the public domain, 54 peaks exceeding 14,000 feet in elevation, and 637 peaks exceeding 13,000 ft., contains representation of these myriad ecosystems in a manner reflective of much of western North America. Despite this tremendous ecological variation, the lichens of Colorado remain woefully understudied, at least from any sort of broad-scale, regional perspective. In 2022, we launched a first-ever comprehensive inventory of the lichen biodiversity of the Southern Rocky Mountain Ecoregion, delimited by Colorado's state borders, and have been humbled by our early findings. To date, we have collected approximately 11,000 new museum voucher specimens, visiting nearly 1,000 new collection sites throughout the state. Our fieldwork and subsequent lichen identifications are quickly illuminating what appears to be a vastly understudied diamond mine (in a gold diggers state) of lichen biodiversity, with new state records, continental/hemisphere records, and new species being discovered on a near daily basis. In this talk, we highlight just a few of the many recent discoveries of lichen biodiversity in the Southern Rocky Mountain Ecoregion.

Topic: *Symbioses: Plant, Animal, and Microbe Interactions*

A-641

Metagenomic composition of Phoradendron leucarpum and host phyllospheres

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American mistletoe (Phoradendron leucarpum) is an aerial hemi-parasite that infects the vascular systems of trees. Instead of roots, it forms haustoria, which allow it to penetrate the host's xylem and redirect water and minerals to itself. Plant-associated microbes are known to shape plant health in ways such as facilitated nutrient acquisition and UV protection, but how microbes contribute to the unique ecology and life history of parasitic plants remains relatively unknown. In this study, we seek to characterize both the inner and outer leaf microbiome, or phyllosphere, of Phoradendron leucarpum. Given the interconnectivity of their vascular systems, the microbiome of mistletoe may be influenced by the microbiome of its host. Thus, we also sampled the phyllosphere of each host tree and performed a comparative, metagenomic analysis against that of the mistletoe growing on it. To describe both outer and inner phyllospheres, each host-parasite sample pair underwent two DNA isolations, with half of the materials being soaked in an 8.25% bleach solution to remove the external microbiome. Whole genomic DNA from the leaf tissue of each treated and untreated parasite as well as its host was sequenced with paired-end reads on an Illumina NovaSeq. Microbial taxa were determined using the MOSHPIT toolkit for the QIIME2 package for each sequenced sample and statistical comparisons were made in R. Further, we assembled plastomes for each individual mistletoe, which represent and control for the genotype diversity of the sample pool. Our work will extend insight into the assembly and function of microbiomes of parasitic plants, and broaden our understanding of how interactions between plants influence microbiome diversity.

Topic: *Systematics & Taxonomy*

A-642

Taxonomic revision of the tropical blueberries (Vaccinium L., Ericaceae) of the Philippines

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The tropical blueberries (Vaccinium L., Ericaceae) of the Philippines are key components of montane forests, serving as indicators of forest quality and providing essential resources for pollinators and frugivores. However, the taxonomic diversity in Philippine Vaccinium has been poorly understood. We addressed this knowledge gap by conducting a comprehensive taxonomic revision of the Philippine Vaccinium, utilizing data from fieldwork, community science, and herbarium specimens. We recognize 41 species of Vaccinium across the Philippine Archipelago, all but two of which are endemic to the country. Following the international code of nomenclatural for algae, fungi, and plants, lectotypes were designated for species with holotypes destroyed during World War II. Vaccinium bancanum, a widespread species in Indonesia and Malaysia, is excluded because of uncertainty in the identity of V. suluense, a synonym of V. bancanum described from a combination of unsatisfactory materials from Malaysia and the Philippines. Ten species were described as new to science, two were documented as new island records, and seven were rediscovered "lost species." Vaccinium species are found across all major Philippine islands except in Bohol, Catanduanes, Guimaras, Masbate, Siquijor, and Tawi-tawi. The islands of Luzon and Mindanao are both the centers of Vaccinium species diversity in the country. This study highlights the importance of a taxonomic revision in understanding species diversity, distribution, and conservation. Further, it builds upon our currently ongoing phylogenomic and biogeographic study of Asian blueberries within the tribe Vaccinieae. Additionally, this study underscores the critical role of natural history collections, herbaria, citizen science, and collaborative fieldwork in advancing biodiversity research. It is hoped that not only has this research increased species documentation in the Philippines, but it will also foster a deeper understanding of regional ecosystems for habitat protection and species conservation.

Topic: *Mycology*

A-643

Land-Use Type is a Driver of Arbuscular Mycorrhizal Fungal Community Composition in Eastern Washington Prairies

Author: Katherine Cole, Robin O'Quinn
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Arbuscular mycorrhizal fungi (AMF), belonging to the phylum Glomeromycota, are key to healthy, functioning terrestrial ecosystems worldwide. Associating with over 80% of all extant land plants, they play a pivotal role in nutrient cycling, contribute to overall plant health, and impact the structure and function of native plant communities. Given their significance to terrestrial ecosystems, AMF have a crucial role to play in the successful restoration of Eastern Washington's native prairies. However, AMF community composition is significantly altered by the commercial agricultural practices used extensively in this region for over 100 years. The Eastern Washington University (EWU) Prairie Restoration Project aims to restore ~120 acres of farmland to native prairie. This research will provide insight into the diversity of AMF communities in the region, helping to improve restoration efforts. We collected soil and root samples from a total of 37 sites across four distinct prairie land-use types: remnant native prairies (n=9), Conservation Reserve Program (n=10) lands, conventional-till farmland (n=11), and no-till farmland (n=7). AM fungal DNA extracted from soil and root samples, was amplified using the AMF-specific primer pair NS31-AML2, and sequenced on the Illumina MiSeq platform using 300bp paired-end sequencing. Sequences were quality filtered and grouped into amplicon sequence variants (ASVs) using QIIME2. Taxonomy for the recovered AMF lineages was assigned using the MaarjAM database. Preliminary analyses show that the community composition of AMF is significantly different across land-use types ($p<0.05$). AMF richness and diversity also differ across land-use types with prairie and CRP sites having significantly higher richness and diversity than conventional till sites ($p<0.05$), but not no-till sites. These results are an important first step towards restoring a native prairie AMF community to the EWU prairie restoration site.

Topic: *Biogeography*

A-644

Island colonization in flowering plants: Self-compatibility and establishment after "long-distance" dispersal

Author: Boris Igic, Annie Zell, Charlotte Miranda, Erin Grady, Dena Grossenbacher
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Among flowering plants, self-compatibility, long life span, and generalized pollination syndrome are each thought to increase the lifetime odds of finding a mate, particularly in isolated locales. An accumulated body of evidence supports the role of breeding system in island colonization, but less is known about the impact of other traits and their interactions during establishment. We employ a global dataset of flowering plant species to estimate the effects of traits on the probability of island occurrence. Our analyses additionally account for taxonomic relationships and assess the role of island arrival opportunity. Self-compatibility is strongly associated with island colonization. A longer life span and generalized pollination syndrome are also associated with increased island colonization, although this is primarily driven by their interaction with breeding system. Furthermore, the probability of island colonization is highly dependent on a metric of arrival opportunity. Mate limitation generally seems to depend on dispersal ability, perhaps at much finer scale than we examine here. We find that arrival opportunity and breeding system are the primary drivers of island colonization relative to other life history traits, lending additional support for the positive role of uniparental reproduction in establishment following long-distance dispersal.

Annie N. Zell, Charlotte H. Miranda, Erin L. Grady, Dena L. Grossenbacher, and Boris Igić. 2025. Island colonization in flowering plants is determined by the interplay of breeding system, lifespan, floral symmetry, and arrival opportunity. New Phytologist 245:420-432.

Topic: *Development and Structure*

A-645

Preformed contributions to total leaf development in seasonal woody plants

Author: Morgan Moeglein
Affiliation: Norwich University

Many perennial plant species preform leaves within resting buds during one growing season, undergo a period of dormancy, and then resume leaf development and maturation after bud break in the following season. To characterize how leaf preformation contributes to total leaf development, we imaged leaves within dormant buds, at bud break, and at the end of the growing season across 14 woody angiosperm species growing in a common environment. We found most leaves were initiated through preformation across species sampled while preformed leaf morphology was variable in its relationship to mature leaf form depending on the species. This suggests many seasonal woody plants invest in a certain number of leaves in the season before they mature, though the ultimate mature morphology of those leaves may be more or less influenced by preformation depending on the species.

Topic: *Conservation Biology*

A-646

Conservation genetics of critically endangered Gaultheria renjifoana (Ericaceae) from central Chile

Author: Anita Cisternas Fuentes, Glenda Fuentes Arce, Andrea Beltrán, Diego Alarcón, Patricio López Sepúlveda
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Genetic diversity is crucial for a population's long-term survival. Its loss can reduce population fitness, reduce the ability to adapt to environmental changes and increase extinction risk. Populations are susceptible to changes in their habitat especially those driven by human development. Such alterations can lead to a reduction in population size and limit the exchange of genetic material with other populations of the same species, thereby increasing differentiation between populations. Understanding how genetic diversity is distributed within and between populations—and the ecological factors influencing these patterns—is essential for identifying populations in need of protection and for understanding the threats to their long-term persistence.

In this study, we evaluated the genetic diversity and differentiation of four remnant populations of *Gaultheria renjifoana* using SNP data. *Gaultheria renjifoana* is classified as critically endangered in Chile due to its restricted distribution, small population size, and ongoing habitat changes in its native range.

Our results show that all populations exhibit similar genetic diversity parameters. However, the largest population, which is still surrounded by native forest, shows higher genetic diversity compared to the smaller and more disturbed populations. Genetic differentiation was high, with structure analysis assigning each population to a distinct genetic cluster. These findings highlight the need for an overarching conservation strategy that includes all populations of the species. Given the constant landscape changes and the frequent occurrence of wildfires in the area, we also recommend exploring *ex situ* conservation approaches as a complementary measure.

Ongoing research on the species will incorporate genetic analysis of three recently discovered populations. In addition, we will study the species' reproductive system and reproductive patterns to assess how fragmentation is affecting its biology and long-term viability. Ultimately, our goal is to preserve the species in its natural habitat by developing effective and realistic conservation strategies that maintain its genetic diversity.

Topic: *Functional Genetics/Genomics*

A-647

Generating transgenics to understand the role of YABBY5 in ultraviolet pigmentation polymorphism in yellow monkeyflowers

Author: Samantha Garcia, Jesus Martinez-Gomez, Quan Liu, Grace Johnson, Srinidhi Holalu, Benjamin Blackman
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Ultraviolet (UV) patterns on flowers serve to attract pollinators, increasing the likelihood of pollen transfer and thus increasing the likelihood of producing offspring. However, our understanding of how UV pigmentation patterns emerge during floral development is limited. Therefore we chose to investigate the genetic basis of natural variation in UV pigmentation patterns in the model system Mimulus guttatus (syn. Erythranthe guttata). This species exhibits population polymorphism in floral UV. Some populations express a bullseye pattern such that UV absorptive pigments occur only in the corolla throat, leaving the petal lobes UV reflective. Other populations express a runway pattern, where UV absorption occurs in the same area as the bullseye morph and also on the ventral petal lobe. Previous work in the lab highlighted the transcription factor YABBY5 as a potential candidate gene underlying this polymorphism. Using Agrobacterium-mediated plant transformation and tissue culture we have generated transgenic lines carrying a CRISPR/Cas9 construct targeting YABBY5 in bullseye and runway morph backgrounds. In CRISPR transgenic lines, we have observed a mutant phenotype that has both a visible and UV phenotype termed 'spotty dimmed': The visible phenotype is a spot of transparent floral tissue in the ventral lobe. The UV phenotype is a dimmed runway phenotype that is interrupted by the spot of transparent tissue that is fully UV reflective. Through further genetic and phenotypic analysis of these transgenic lines, we will gain insight into the genetic basis of an important plant functional phenotype.

Topic: *Paleobotany*

A-648

Updating the diversity of anatomically preserved zosterophylls of the Lower Devonian Battery Point Formation (Quebec, Canada)

Author: Bianka Rodriguez, Pénélope Claisse, Mihai Tomescu
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The Battery Point Formation of the Gaspé Peninsula in Quebec (Canada) hosts a high diversity of anatomically preserved plant fossils of Emsian age (~400 million years old). The majority of the plants described to date from this unit are euphyllophytes. Lycophytes – specifically, zosterophylls – are comparatively rare in the permineralized material and only one anatomically preserved species (*Crenaticaulis verruculosus*) has been formally described. Despite their overall scarcity, previous work by our group has identified several anatomically preserved zosterophylls and continued investigations are revealing additional specimens. Here, we summarize the data on 24 of these fossils, with a focus on their anatomical and taxonomic diversity. The fossils represent short segments of vegetative axes and are assigned to the zosterophyll group based on their exarch xylem and, where observed, *Gosslingia*-type tracheid wall structure. The state of preservation encompasses a broad range: from specimens with the full complement of tissues (xylem and in some cases phloem, cortex, and epidermis) to specimens consisting only of decorticated xylem strands and including a few charcoalified fossils. A few of the specimens have distinctive features, while others are either too incomplete or lack sufficient features for definitive classification. The size of the xylem strands, ranging 140–670 µm, overlaps well with the size range defined by the majority of previously described zosterophylls, with the smallest comparable to the xylem of *Zosterophyllum fertile* and the largest similar in size to *Deheubarthia*, *Stolbergia*, and *Euthursophyton*. The average diameter of the largest metaxylem tracheids of our specimens, ranging ~10-50 µm, falls in the lower third of metaxylem tracheid sizes documented in other zosterophylls, which can reach 150 µm. Our specimens are comparable in tracheid size to *Zosterophyllum*, *Crenaticaulis*, *Thrinkophyton*, *Ventarura*, *Gosslingia*, and *Trichopherophyton*; only two of them approach in size the larger tracheids of *Sawdonia deblondii*. Two of the axes possess unique anatomical features that suggest they may represent new species: one has a continuous monostromatic layer of cells with thickened walls located half-way between the central vascular tissues and the epidermis; the other has unusually large blister-like epidermal cells. Other specimens exhibit features not previously documented among zosterophylls: enlarged cortical cells with possible secretory function scattered throughout the cortex; large irregular club-shaped surface protrusions; and quadrifurcate planar branching. One axis, bearing a short branch with circinate tip, provides a first glimpse of the anatomy of such structures. Several of the axes that preserve phloem demonstrate that in zosterophylls this tissue formed a thin layer around the xylem consisting of elongated, thin-walled and very narrow cells (<10 µm), very similar to those of coeval euphyllophytes. Our survey of zosterophyll diversity demonstrates the presence of at least three previously unrecognized permineralized zosterophyll types in the Lower Devonian strata of Gaspé and adds new data to the range of anatomical features documented in zosterophylls.

Topic: *Lichen and Bryophyte Diversity, Conservation, and Evolution in the Americas*

A-649

Mobile Genetic Elements in Rare, Threatened, and Range-Restricted Lichenized Fungi

Author: Julianna Paulsen, Stephen Sharrett, Elaine Larsen, Devin Mumey, James Lendemer, Lalita Calabria, Jordan Hoffman, Eli Balderas, Jessica Allen
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Mobile genetic elements (MGEs) are genes that encode their own machinery to move within a genome. In fungi, MGEs have the potential to drive genome evolution by introducing mutations and causing structural instability, particularly under conditions like environmental or genetic stress. In this study, we investigated the connections between predictors of rarity, such as reproductive mode and distribution size, with MGE abundance in 29 species of lichenized fungi using a comparative phylogenetic framework. Twenty-two new reference genomes were generated with standard laboratory workflows, and MGEs were annotated using RepeatModeler2. MGEs accounted for 4.6–69.55% of the genome content in the species sampled, with a range of 1850–131,257 elements recovered in a given genome. Retrotransposons were the most abundant type of MGE, averaging 21.42% (±19.44) of the genome content in rare species and 16.34% (±8.2) in common species. Total MGE content followed a similar pattern, with means of 25.47% (±19.75) and 20.43% (±9.26) recovered for rare and common species, respectively. Several species were identified as outliers in the dataset, highlighting the need to better understand selection pressures driving genome evolution in single species. Analyzing intraspecific genomic data collected from different populations of the species with the highest MGE content, *Pseudocyphellaria rainierensis*, did not reveal significant differences in MGE content between individuals. The disproportionate distribution of MGEs, particularly retrotransposons, in rare, threatened, and range-restricted species may disrupt genomic stability, yet also create novel genetic diversity in isolated populations with limited gene flow. Investigation of associations between indicators of rarity and MGE expansions is essential to understand the potential implications that these genes have for extinction risks and species conservation.

Topic: *Ecology*

A-650

Native pollinator surveying and support on an organic herb farm in Washington State

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Trout Lake Farm (TLF) is a certified organic herb farm in North America. Located in Ephrata, WA, it is the main supplier of plant material to a leading nutritional supplement company. TLF's main crops include Coneflower (*Echinacea angustifolia* DC., *Echinacea purpurea* (L.) Moench), Catnip (*Nepeta cataria* L.), and Common Dandelion (*Taraxacum officinale* F.H.Wigg). TLF is beginning to adopt the principles of regenerative agriculture in addition to their organic system, including the documentation and support of biodiversity on the farm's property. This study builds off work carried out the previous year at the farm's sister location in Trout Lake, WA, where a round of native plant surveying was executed to establish a baseline understanding of pollinator habitat on farm property. The goal of this study was to document the pollinators using TLF property for nectar resources and habitat, to evaluate the extent to which they utilize the crops as nectar resources, and to support their populations on farm property using native plantings and nesting shelters. The methods included using random transects within crop fields and across farm property to survey foraging Lepidopteran (butterfly and moth), Hymenopteran (bee and wasp), and Dipteran (fly) pollinators. Results show that TLF crops supported a higher density of pollinators than surrounding native areas, but a lower diversity of pollinators in terms of families. The crops most utilized by pollinators include Nettle (*Urtica dioica* L.), Catnip (*N. cataria*), and Coneflower (*E. purpurea)*. The areas where the most diverse populations of pollinators were found were a native hillside on farm property and the Coneflower (*E. angustifolia)* field, with an equal number of families observed at each location. TLF has a uniquely supportive relationship with native pollinators compared to traditional staple crop agricultural systems due to the nectar resources provided by the crops throughout the growing season, and therefore has the potential to become a leader in the support of native pollinators in agricultural systems.

Topic: *Conservation Biology*

A-651

A Statewide Natural Heritage Survey for Colorado: Advancing Conservation through Comprehensive Botanical Inventory

Author: Jennifer Ackerfield
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The Colorado Natural Heritage Program (CNHP) is leading a transformative effort to complete the first-ever Statewide Natural Heritage Survey (SNHS). This survey is a comprehensive, multi-year biodiversity inventory designed to inform proactive conservation, climate resilience, and equitable planning across Colorado. Building on CNHP's 45-year legacy, this initiative combines targeted field surveys, herbarium records, geospatial modeling, and community engagement through iNaturalist to document the distribution, condition, and conservation status of Colorado's rare and imperiled plant species and ecosystems. This statewide initiative is driven by key objectives: enabling proactive planning for the conservation of at-risk species and anticipating climate change impacts; identifying wetlands that buffer communities from wildfire and drought; supporting biodiversity credit markets and recreation planning; and bringing equity to conservation by elevating data quality across all 64 counties. Already, recent bioblitzes in under-surveyed counties such as El Paso have uncovered rare plant species and previously undocumented wetland types, thus demonstrating the power of intensive inventory to reveal new conservation priorities. I will highlight some of these recent discoveries that reflect the richness and conservation value of Colorado's underexplored regions. I will also share anticipated outcomes, including the integration of digital data into Colorado's Conservation Data Explorer (CODEX) platform, the launch of a public-facing interactive story map and website, and the convening of a Statewide Natural Heritage Survey Summit in 2029. Together, these efforts aim to build a more inclusive, scientifically informed foundation for biodiversity stewardship across Colorado's landscapes.

Topic: *Conservation Biology*

A-652

Conservation genomics of Lithophragma maximum (Saxifragaceae), the San Clemente Island Woodland Star

Author: Caitlin Hazelquist, C. Matt Guilliams, Annie Ayers, May Roberts, Nicole Desnoyers, Kristen Hasenstab-Lehman
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Lithophragma maximum Bacig. (Saxifragaceae) is a narrow endemic, restricted to San Clemente Island, off the coast of Los Angeles, California. It is listed as Endangered under both the California Endangered Species Act and Federal Endangered Species Act. The plant is found in deep, cool, and moist canyons on the north side of the island. Previous greenhouse work has shown the plant requires a cold snap for successful germination. These life history traits, along with small population sizes may make this taxon especially vulnerable to warming and drying climatic trends. To assess genetic diversity of the species across its range we sampled eleven occurrences, and generated a large SNP dataset using double digest RADseq and high-throughput sequencing. Population genomic analyses reveal strong population structuring by watershed. Neighboring ravines generally exhibit a greater degree of genetic similarity than distant ones. All sampled locations exhibit a high degree of homozygosity, with some having moderate levels of inbreeding. For two large populations, Malo and Grove, all tagged individuals were genotyped. This will provide additional data that can be incorporated into ongoing demographic studies of these populations, and overall genetic management of the species.

Topic: *Conservation Biology*

A-653

Barriers to seed recruitment differ between disjunct populations of a threatened crop wild relative in the southeastern United States

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Affiliation: Atlanta Botanical Garden

Seed recruitment is critical to dispersal and maintenance of genetic diversity, influencing plant persistence under environmental change. This is especially paramount for rare plants that are more vulnerable because of their small and/or few populations. *Ribes echinellum* (Miccosukee gooseberry, Grossulariaceae) is a federally threatened and critically imperiled (G1) small perennial shrub, known from only two disjunct populations in the southeastern United States. While plants are abundant in both locations, seedling recruitment appears to be nearly absent. To investigate barriers to recruitment, we assessed seed production, seedling emergence, and herbivory. Seed viability was assessed with lab germination trials. Fruits were significantly more abundant in South Carolina (mean = 174 fruit/plot) than Florida (27/plot), but seed numbers per fruit were similar. In Florida, seedling emergence was high (44%), regardless of small mammal exclosures, suggesting low seed production limits recruitment. Observations of interannual boom-and-bust flowering patterns in Florida suggest weather-driven constraints. In South Carolina, seedling emergence was lower overall (6.3%), but especially low in uncaged plots (2.4%). For the South Carolina population, lab germination for fresh seeds was high, averaging 96% (SD=11%) under alternating incubation at 25/10°C (12:12h) following cold-moist stratification. This suggests herbivory may also play a role in limiting recruitment in South Carolina. Conservation strategies need to consider site-specific barriers to recruitment, including the mitigation of seedling herbivory in South Carolina and collecting seed in Florida during boom years. Future work will seek to understand factors influencing boom-and-bust flowering in Florida and environmental causes for low seedling survival in both states.

Topic: *Functional Genetics/Genomics*

A-654

A Review: Agrobacterium-mediated Gene Transformation in Phaseolus vulgaris

Author: Hannah Ratcliff, Joyce Onyenedum, Mira Anant
Affiliation: New York University, New York Botanical Garden, New York University, Stuyvesant High School

Vines exhibit a remarkable twining behavior, a circumnutating motion to help position themselves onto a support structure. These plants are able to secure their stems onto nearby objects through specialized tensile fibers called gelatinous fibers (g-fibers). Our

research seeks to investigate the molecular mechanisms underlying g-fiber development in the species *Phaseolus vulgaris* (common bean), focusing specifically on the genetic components that emerge following mechanical stimulation. Towards this aim, we are optimizing *Agrobacterium*-mediated gene transformation techniques to modify and study phenotypic expressions related to g-fiber formation during plant growth and development. Throughout this presentation, I will present our methodological approach, including optimization strategies to overcome transformation challenges specific to both *P. vulgaris*. Our findings hint at possible genetic pathways that may influence g-fiber development and point to a transformation approach that could be explored for use in other recalcitrant species.Understanding these mechanisms has broader implications beyond understanding the genes responsible for the twining motion in beans, as improved transformation protocols for *P. vulgaris* could benefit agricultural applications for this economically significant crop that serves as a crucial source of food for millions worldwide. We anticipate this work will serve as a valuable resource for researchers facing similar obstacles in genetic transformations.

Topic: Population Genetics/Genomics

A-655

Genome size, chromosome count, and cell size in the highly variable Claytonia virginica polyploid complex

Author: Brittany Sutherland, Krista Knieriem, Derek Anderson, Susan McLaughlin
Affiliation: George Mason University

Polyploid complexes—assemblages of related and potentially interfertile populations that differ in genome size and/or chromosome number—pose a challenge to the characterization of evolutionary history, interploidy reproduction, and population dynamics. One of the most widespread and yet poorly understood polyploid taxa in North America is the spring ephemeral, *Claytonia virginica*. This species presents a truly daunting degree of chromosome variation, with over 35 documented chromosome counts range from 2n = 12 to 2n = 191. This wide chromosomal variation, coupled with a life history that poses significant challenges to study, has left *C. virginica* and related eastern North American taxa poorly understood relative to their western North American congeners. Currently, data connecting genome size estimates to chromosome number are almost absent in this species—while numerous chromosome counts are published, only one genome size estimate is available, and that one lacks a corresponding chromosome count. To enable future research into this system, this study widely sampled *C. virginica* individuals throughout much of the range in spring 2025. All three presumed diploids (2n = 12, 14, 16) were sampled as well as multiple putative polyploids and aneuploids. For each sample, chromosome counts were performed on immature anthers, flow cytometry was used to estimate genome size of fresh leaf tissue, and guard cell size was measured. Genome size estimates varied somewhat with chromosome number, suggesting that chromosomal composition may differ throughout the range. While relatively weak, guard cell size did vary significantly with estimated genome size, and may serve as a useful screening tool for future large-scale studies of this system.

Topic: Systematics & Taxonomy

A-656

Phylogeography and conservation genomics in the endangered cycad genus Dioon (Zamiaceae)

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Cycads are one of the oldest living seed plant lineages and arguably the most endangered group of plants on the planet, with approximately 65% of all species threatened with extinction. Major threats to their survival include over collecting for trade and private collections and loss of habitat due to land conversion. Efforts to prevent further loss of cycad species include establishing reserves to protect habitat and, when this is not yet possible, growing plants ex situ in assurance colonies that will provide a source for reestablishment when reserves are possible. The long-term success of these efforts will depend on our understanding of the genetic diversity and structure within and among populations. In the near-endemic Mexican genus of *Dioon* (one species in Honduras), all but one of the 15 species included in the most recent IUCN Redlist assessment were considered Vulnerable or Endangered and all but one of those are decreasing in number. In the past ten years, there have been a number of new species described, as previous circumscriptions have been reevaluated and taxa split. This work has shown that species of *Dioon* can be extremely limited in their distribution and very similar in morphology, bordering on cryptic species in some cases, while other studies have shown that the contrary pattern also exists – relatively widespread species comprising multiple, isolated, but genetically similar populations. We are conducting a genus-wide study to characterize the population genetics, demographic history, and species delimitations in *Dioon* to better understand evolutionary history and patterns of diversification within the genus, as well as inform future conservation efforts. Here we report on our investigation of *D. tomasellii* populations from Jalisco and Nayarit states. These populations are widespread but relatively small and geographically isolated, to varying degrees. Observations during field explorations suggest that several morphotypes may exist and the geographic distribution suggests that gene flow may be limited among populations. We used data from a modified ddRADseq method to evaluate the genetic diversity and structure among these populations and infer their history of diversification and demographic dynamics, and morphological data to test for distinct morphotypes. We find separation among some populations in morphospace and identify the key characters that distinguish these populations. We also find that more distant populations are genetically isolated and are moderately differentiated, although this varies among populations. Relatively recent reductions in population size were also inferred for all populations. We will discuss the history of population divergence, potential species boundaries, and consequences for conservation, all in relation to what is known from other species in the genus.

Topic: Hybrids and Hybridization

A-658

Understanding the role of hybridization in North American diversification using pondweeds (Potamogetonaceae)

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The pondweed family (Potamogetonaceae) is one of the most species-rich submersed freshwater aquatic plant families in the world. Despite their ecological importance in maintaining freshwater ecosystems, there is a lack of basic biological knowledge for these plants. One of the largest barriers to further research is poor taxonomic resolution. Potamogeton has historically been one of the most difficult aquatic plant groups to describe due to high phenotypic plasticity and frequent hybridization; there are more described hybrids than discrete species. Despite the taxonomic complexity, the degree of hybridization in Potamogeton provides a unique opportunity to better understand the impact of hybridization as a macroevolutionary process. Interspecific hybridization has long been recognized as an important evolutionary mechanism by systematists, however the question of whether hybridization is an adaptive or restrictive force remains somewhat unresolved. North America has a similar number of discrete and hybrid species of Potamogeton (~30 of each) and will allow us to directly compare diversification through hybridization and discrete processes. Utilizing a newly designed, custom probe set for target sequence capture (Pondweeds350), we conducted the most in-depth phylogenetic study of Potamogetonaceae to date in an effort to resolve taxonomy and infer a robust phylogeny of North American pondweeds. We also generated time-calibrated phylogenies and paleoclimate models in order to better understand the history of hybridization and diversification in Potamogeton. Finally, we utilized the high degree of hybridization in Potamogeton to evaluate the impact of hybrid speciation on net diversification rates.

Topic: Biogeography

A-659

Understanding Species Relationships and the timing of an Eastern Asian - North American Disjunction in Amsonia (Apocynaceae)

Author: Dylan Cohen, Jeremie Fant, Norman Wickett, Krissa Skogen
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The Eastern Asian – Eastern North American disjunction has fascinated naturalists for centuries. Although separated by the Pacific Ocean, montane, and arid environments these two regions possess strikingly similar floras that include many genera, sister species, and even conspecific taxa found in both regions. While many studies have addressed the timing and dispersal patterns between Eastern Asia and North America, few have included groups that occur in mesic and arid areas outside this disjunction. *Amsonia* (Apocynaceae) is one such group that has the classical Eastern Asian – Eastern North American disjunction but is also found in arid regions of southwestern North America and mesic area in eastern Europe. This work seeks to understand species relationships, divergence times, and to test where *Amsonia* may have orientated, the

migration route used (Bering Sea Land Bridge or North Atlantic Land Bridge), and when dispersal may have occurred. To address these questions, we used a target capture sequencing approach with the Angiosperm 353 bait set to generate nuclear DNA sequences for phylogeny reconstruction. We then used BEAST with fossil and secondary calibration points to estimate divergence times followed by REVBAYES to estimate ancestral areas. We were able to include all known *Amsonia* species and most intraspecific varieties. Our results suggested that the European and Asian species are sister to all other *Amsonia*, with North American species placed into a western and eastern clade. *Amsonia* likely originated in temperate (mesic) Asia around 10 million years ago (mya) and dispersed to North America via the Bering Sea Land Bridge 4-6 mya and diversified into southeastern and southwestern clades recently. This work adds new knowledge to our understanding of a classical biogeographic disjunction and provides resources for future investigation into the evolution and conservation of *Amsonia*.

Topic: *Education and Outreach*

A-660

New research supporting the efficacy of the PlantingScience.org online mentoring program

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Plants are underrepresented in the curriculum of secondary schools in the US despite their crucial importance to the planet, human survival, and addressing challenges related to climate change (Balas & Momsen, Uno 2020, Stroud et al. 2022). Many students hold limiting preconceptions about plants and the scientists who study them. that can limit their motivation to study plants. One way to get more plants into classrooms and increase students' exposure to plant scientists is through student-teacher-scientist partnerships (STSPs). PlantingScience.org is an online STSP mentoring program for middle and high school teachers and their students established in 2005 by the Botanical Society of America and supported by multiple plant science societies and over 1000 volunteer scientist mentors from around the world. The program aims to improve secondary students' understanding of plant-related science concepts and practices, as well as improve students' attitudes about scientists and increase students' motivation to study plants.

Prior research established that the program's "Power of Sunlight" photosynthesis and cellular respiration module improved secondary student achievement (effect size = 0.284) and attitudes toward scientists (effect size = 0.280) (Taylor et al. 2022; Westbrook, Adams & Taylor 2023). A conceptual replication and extension of this research includes 66 high-school teachers from 33 US states and ~2000 of their students who have been randomly assigned to participate in the PlantingScience Power of Sunlight program or to learn the same key concepts in the traditional manner their teachers usually employ (Business-as-Usual or BaU). We will present preliminary data from this replication study to address several related research questions: 1) What words do students use to describe who scientists are and what they do prior to the intervention? 2) How does collaborative online work with a scientist mentor on a student-led plant science investigation influence students' attitudes about scientists? 3) Do students who participated in PlantingScience have higher motivation to study plants compared to those in the BaU condition? 4) How does participation in PlantingScience influence students' motivation to study plants?

Understanding a diverse set of US secondary students' attitudes towards scientists and motivation towards studying plants can help biology educators teaching undergraduates to better understand preconceptions their incoming students may hold about scientists and about studying plants. Students' insights about how PlantingScience mentors impacted their perceptions of scientists and their motivation to study plants can be helpful information for educators and scientists interested in understanding how students can be impacted by mentoring and science outreach.

Topic: *Education and Outreach*

A-661

Cultivating Collaboration: Enhancing Plant Science Education through Strategic Partnerships

Author: Kristine Callis-Duehl
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Public-private partnerships (PPPs) have emerged as influential mechanisms for fostering educational innovation and addressing gaps in resource availability in plant science education. This presentation highlights strategic collaborations the Donald Danforth Plant Science Center developed to enhance K-12 and undergraduate plant education. We demonstrate how PPPs can effectively bridge academia, industry, and community organizations by fostering dual enrollment programs associated with industry professionals and student-led and student-engaged science research programs with non-academic research, such as Course-based Undergraduate Research Experiences (CUREs). These partnerships have created authentic experiential learning environments, increased student engagement in plant sciences, and strengthened pathways into plant-focused careers.

Moreover, these collaborative efforts extend beyond plant and botanical sciences by incorporating expertise from other disciplines, notably education researchers. Education specialists contribute by overseeing rigorous assessments of program outcomes, providing researchers with training on effective student engagement strategies, and designing research programs that align with educational standards and developmental appropriateness for students. This interdisciplinary approach ensures comprehensive support for both students and educators, enhancing the efficacy and sustainability of educational programs.

Our ongoing research evaluates the impact of these collaborations on educational outcomes, student readiness for the workforce, and faculty pedagogical development. Initial findings indicate that PPPs significantly enhance students' practical skills, scientific identity, and career preparedness, while providing faculty with innovative teaching resources and professional growth opportunities. This presentation contributes to a broader understanding of collaborative educational models, emphasizing the systematic assessment of PPPs' roles in advancing plant science education and preparing future generations of plant scientists.

Topic: *Common gardens in the 21st Century: the intersection between evolution and ecology, science and management*

A-662

Across space and time: Incorporating multigenerational variance into GxE experiments using resurrection approaches

Author: Elizabeth M Lombardi, Julie Etterson, Briana Gross, Marissa Spear, Sophie Levi
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Common garden and reciprocal transplant experimental designs reduce the contribution of environmental heterogeneity to experimental studies of plant genotypic variability, but do not often directly measure changes in molecular or genetic changes across multiple generations. Genetic differentiation between groups is assumed to represent adaptive processes leading up to experimental conditions, and therefore the phenotype associated with each genotype is a proxy measure for adaptive processes across evolutionary time. This study of variance within a single generation of plants is not a fault of GxE designs, but developing methods that directly measure eco-evolutionary trends across generations within the framework of common garden design will improve the specificity of eco-evolutionary adaptation studies. This is especially true for isolating genetic variance in response to other evolving agents, like pathogens, which exert dynamic, sometimes cyclical selective pressure that differs from continuous or directional selection across environmental clines. Resurrection experiments, which isolate and measure genotypic change over time, provide an opportunity to explore recent evolutionary relationships between coevolving agents, and may be complementary to reciprocal transplant designs in order to study environmental context dependency in adaptation to biotic conditions. In this talk, I will review challenges, opportunities and resources for using resurrection approaches to directly measure genotype by environment interactions that are both spatially and temporally explicit. Specifically, I will present a study of urban sunflowers (wild *Helianthus annuus*) in which colleagues compared antecedent (resurrected) and modern genotypes. Results of this study suggest that microevolutionary processes in response to environmental change and introgression from crops led to divergent phenotypes in just 36 years. Building on this work, new research will isolate the consequences of pathogen pressure on native sunflowers by resurrecting and infecting antecedent and modern host genotypes from across the range of *Helianthus petiolaris* in order to tease apart plant and virus evolutionary trajectories. Sunflower resurrection research provides meaningful insight for both native and cultivated *Helianthus* congeners that are experiencing both drought and shifting biotic threats across North America, and exemplifies how resurrection and common garden designs can be complementary. Ultimately, this talk will provide an overview of resources and present a rationale for conducting common garden experiments with reciprocal design strategies that consider both environmental (home/away) and temporal (modern/antecedent) variables.

Topic: *Reproductive Processes*

A-663

Petaloid Staminodes Enhance Pollinator Attraction and Seed Set in an Arid-Adapted Plant

Author: Johan Ling, Paige Fabre, Natalie Kloss, John Schenk
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Staminodes are sterile stamens that are evolutionarily and functionally diverse across angiosperms, serving roles from visual attraction to pollinator facilitation. Although staminodes are often associated with increased male fitness because of their androecial origins, their influence on female fitness lacks consistent evidence across studies. This gap is especially relevant in species with brief anthesis in ecologically challenging environments, where efficient pollination is critical. Here, we tested whether petaloid staminodes influence pollinator behavior and reproductive success in *Mentzelia integra* (Loasaceae), an arid-adapted species with short-lived, evening-blooming flowers. Using a paired-choice experiment, we removed staminodes from one flower in each pair and assessed if pollinators preferred flowers with or without staminodes. To evaluate the effects on pollinator behavior and plant fitness, we measured visitation rate per flower per hour, first landing preference, floral constancy (i.e., transitions within and between flower types), visit duration, and seed set. Control flowers with intact staminodes received greater pollinator visitation and were consistently preferred as first landing sites across all observed bee taxa, suggesting a key role of staminodes in enhancing pollinator attractions. *Anthophora* and *Megachile* pollinators exhibited greater floral constancy between intact flowers, while *Perdita* showed no pattern, highlighting species-specific responses in how staminodes shape foraging behavior. Visit duration remained unchanged, implying that staminodes serve primarily as visual cues. Staminode removal led to a 33% reduction in seed set, revealing that they enhance female fitness. Our findings demonstrate that although staminodes increase male fitness by visually attracting more pollinators, the visual attractancy also benefits female fitness, underscoring their adaptive significance in arid environments, especially in species with a full whorl of staminodes.

Arid environment, evening anthesis, female fitness, floral evolution, male fitness, pollination, pollination limitation, seed production, Loasaceae, *Mentzelia*.

Topic: *Development and Structure*

A-664

Despite their morphological complexity, personate flowers in Penstemon evolved multiple times and have an oligogenic genetic architecture

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Adaptive radiations are characterized by the rapid evolution of novel traits making them excellent study systems to identify the genetic basis of adaptation. Floral adaptations often evolve rapidly as they are shaped by strong selective pressures imposed by pollinators. The wildflower genus *Penstemon* is a recent radiation displaying remarkable floral diversity including repeated origins of personate flowers. Personate flowers are characterized by an upward bulge in the lower lobe of the corolla tube which obstructs the floral passageway. Although this novel morphology has evolved multiple times across angiosperms, its ecological function and evolutionary mechanisms have not been previously studied. We combined phylogenomic analyses, Quantitative Trait Locus mapping, mating system studies, and pollinator observations to address these gaps. We found that personate flowers in *Penstemon* are produced by deep pleats in ventral petal tissue that curve the ventral petal surface upwards. Despite this complicated floral structure, our phylogenomic data revealed parallel origins of personate flowers in a focal *Penstemon* lineage. Using an F2 population, we identified two unlinked loci that account for 51% of the variation in personate shape, confirming a relatively simple genetic basis. We identified candidate genes under each QTL using an RNA-Seq experiment designed to detect differentially expressed genes between species in ventral tissue across multiple developmental stages. One historic hypothesis regarding the adaptive function of personate flowers is that they filter bees by size, however our pollinator observations found no support for this hypothesis. Instead, our controlled mating system study points to a potential role in reproductive assurance.

Topic: *Conservation Biology*

A-665

Thermal tolerance range for germination of a critically imperiled alpine endemic

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Climate change is an omnipresent threat to biodiversity, but impacts are more urgent in alpine environments where warming is happening faster than other terrestrial systems. While warming could benefit organisms in this harsh environment, there are also potential risks associated with thermal tolerance ranges and shifts in phenology. Robbins' cinquefoil (*Potentilla robbinsiana*, Rosaceae) is a critically imperiled (G1) herbaceous perennial endemic to alpine habitats in the White Mountains of New Hampshire. Trampling and overcollection contributed to the listing of this species as endangered in 1980 by the U.S. Fish and Wildlife Service. An integrated conservation effort followed, including protecting critical habitat, educating visitors, and collecting seed for outplanting and ex situ conservation. These efforts contributed to substantial recovery and the species was delisted in 2002 when the modeled minimum population size was met. While past threats have been successfully managed, rapid alpine warming represents a novel threat to this endemic species. To understand thermal sensitivity of seed recruitment for *P. robbinsiana* we conducted two germination trials reflecting current and future field temperatures: 1) a move-along (4 → 6 → 8 → 10 → 12 → 14 → 12 → 10°C, two weeks per temperature), and 2) a temperature gradient (4-14°C). Trials utilized fresh collected seed as well as banked seeds (15-23 years old). Seeds of all collections germinated in both trials following 12 weeks cold, moist stratification (4°C). In the move-along trial, germination began on week four at 6°C for all but one collection. Germination plateaued for most collections by weeks five to seven (8-10°C), but for a few continued until the end of the trial (14-16 weeks). In the temperature gradient trial, the lower thermal limit for germination was 8°C after two weeks of incubation. Germination increased with incubation temperature from 8 to 12°C for most collections, but over 12°C less seed germinated for several collections. Optimum germination temperatures ranged from 9-14°C. The oldest collections tested (>20 years) exhibited maximum germination of 80-100%, providing evidence that seeds of this species fare well under traditional seed banking conditions (15%RH, -20°C). Interestingly, no pattern emerged between collection year and germination, and results suggest that recruitment from the soil seed bank may demonstrate variable responses to warming depending on seed age. Less than half (41%) of seeds included in the experiment required one cold period to germinate, and results are forthcoming for ungerminated seeds which underwent a second stratification period. Complete results will provide important insights into the impact of thermal tolerance ranges for germination on seed recruitment dynamics, helping to inform conservation of this alpine endemic under climate change. While outside the scope of this study, future research should consider the impact of warming on pollination and other factors influencing seed set and maturation.

Topic: *Reproductive Processes*

A-666

Reproductive patterns in two endemic Chilean cacti Eriosyce litoralis and Eriosyce subgibbosa (Cactaceae)

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Understanding the reproductive biology patterns of endangered species is essential for their conservation, as it can help identify populations at risk. In self-incompatible populations, reproductive efficiency depends not only on the presence of pollinators but also on the amount of genetic diversity within the population. In this study, we evaluated natural reproduction and pollinator visitation rates in populations of two closely related endemic cacti species from the Chilean coast: *Eriosyce litoralis* and *Eriosyce subgibbosa*.

In five populations of each species, we assessed fruit and seed set from naturally pollinated flowers and conducted self- and cross-pollination experiments to evaluate the breeding systems of the populations using the self-compatibility index and measuring the extent of pollen limitation. Additionally, we performed pollinator observations to determine the frequency of pollinator visitation.

Our results show that pollen limitation was present in populations of both species, with *E. subgibbosa* experiencing slightly higher pollen limitation on average than *E. litoralis* (27% and 22%, respectively). Fruit set was also variable across populations; on average, fewer than 50% of flowers developed into fruits in both species. This may be related to

the low visitation rates observed. Both species are mostly self-incompatible, although leaky self-incompatibility was observed. *E. subgibbosa* had on average, twice the self-compatibility index of *E. litoralis* (16.4% compared to 8.3%).

Climatic conditions and the species' flowering periods—occurring in winter to early spring (June to October in the Southern Hemisphere)—may influence the low presence of pollinators. The species' most effective pollinators, hummingbirds, are either absent or present at low frequencies during this time. This temporal mismatch between pollinator availability and flowering may be influencing reproductive patterns and driving the evolution of leaky self-incompatibility in these populations as a mechanism to ensure seed production in the absence of reliable pollinators.

Topic: Pteridology

A-668

Comparing microclimate and physiological response in temperate fern gametophytes and sporophytes

Author: Riley Hopkins, Kylie Salinger, Gabriella Honda, Helen Holmlund, Donna Nofziger
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Ferns thrive in ecosystems around the world, including those with limited water availability. However, the charismatic adult fern (the sporophyte) is just one stage of the fern life cycle; fern sporophytes can only arise following the success of a small, independent gametophyte generation. The ability of fern gametophytes to survive dry or cold periods remains unknown in many species. While some epiphytic tropical fern gametophytes are desiccation-tolerant (capable of reviving after a period of desiccation), most terrestrial fern gametophytes cannot withstand desiccation. Fern sporophytes and gametophytes growing in the temperate forests of Switzerland experience periods of drought and freezing. We pose the following questions about the Swiss terrestrial fern Asplenium trichomanes: 1) Do fern sporophytes and gametophytes experience different microclimate conditions? 2) Are fern gametophytes desiccation-tolerant? We tracked dark-adapted chlorophyll fluorescence (F_v/F_m) and microclimate conditions (VPD_{leaf}, temperature) in adjacent gametophytes and sporophytes for six months. We found that fern gametophytes and sporophytes typically experienced different microclimate conditions, with gametophytes experiencing a lower (more humid) VPD_{leaf} ($p < 0.05$). Surprisingly, F_v/F_m showed different seasonal patterns in fern gametophytes and sporophytes. In mid- to late winter, the gametophytes exhibited higher F_v/F_m values than the sporophytes ($p < 0.05$). However, in the fall and spring, sporophytes exhibited high er F_v/F_m values ($p < 0.05$). Our results provide insight into the ability of fern gametophytes to thrive in seasonally dry and cold niches. Future studies might further illuminate the impacts of cold temperatures and desiccation on temperate fern gametophyte survival.

Topic: Hybrids and Hybridization

A-669

Husky Tomato Project: Cross breeding of Solanum lycopersicum for specific coloration patterns.

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In collaboration with the St. Cloud State University Community Garden, the Husky Tomato Project is focused on crossing different varieties of Solanum lycopersicum L. and using artificial selection to develop a red and black striped tomato to represent SCSU's school colors. Our work began in 2022 with cultivation of three varieties of striped tomatoes and one variety of a black tomato. The F2 offspring from these crosses that had some stripes and black mottling were selected for growing in the F3 generation alongside one additional variety of black tomato. Crosses were conducted in the Cargill Research Greenhouse using manual pollen extraction and pollination. Fruit from successful crosses is measured and phenotyped before seeds are collected. We report here on the result of 200 crosses to support development of the F4 generation. The fruits of the F3 generation are half black half red, black with red splotches, red with yellow orange stripes, black with red shoulders, completely black, or have faint black stripes down 50% of the fruit; the multicolored and striped phenotypes will be carried forward and crossed with the fully black or darker varieties to work toward the black and red striped pattern. It is likely that this work will continue for 10 or more generations but we expect that the culmination of this work will lead to a tomato with distinct red and black striped coloration and furthers research in ornamental horticulture.

Keywords: Tomato, artificial selection, cross breeding, morphology, phenology

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Topic: Bryology and Lichenology

A-670

Draft Genome Sequence of Nostoc (Nostocaceae) from the Metagenomes of Sticta deyana and Sticta beauvoisii and the secondary metabolic potential of lichen-associated Cyanobacteria

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Cyanobacteria produce a variety of unique secondary metabolites, many of which have potential use in pharmaceutical and other industries. While interest in their gene products has increased in recent years, there remains a paucity of annotated cyanobacterial genomes, including those that form symbiotic associations with lichenized fungi. Here we characterize two newly sequenced *Nostoc* Vaucher ex Bornet & Flahault genomes from the metagenomes of *Sticta deyana* Lendemer & Goffinet and *Sticta beauvoisii* Delise.

The *Sticta* metagenomes were sequenced on the Oxford Nanopore Technologies MinION platform. The *Nostoc* genomes were identified in the pool of contigs using blastn with the 16S sequence from *Nostoc* sp. '*Sticta* cf. *caulescens* AR124 cyanobiont' (NCBI KF 35968.1). The genomes were annotated using Prokka in the KBASE Narrative Interface. A phylogeny was constructed in Orthofinder to assess how the new genomes relate to other *Nostoc* genomes available from the National Center for Biotechnology Information. Biosynthetic gene clusters (BGCs) were identified and characterized using antiSMASH and compared with known gene cluster families (GCFs) using BiG-FAM.

The *Nostoc* sp. '*Sticta deyana* cyanobiont' and the *Nostoc* sp. '*Sticta beauvoisii* cyanobiont' genomes each assembled as one contig with 7,150,624 base pairs and 7,406,827 base pairs, respectively. They were identified in the phylogeny as members of the same clade of lichen-associated *Nostoc*. Each had 12 BGCs identified by antiSMASH, though much of the secondary metabolism appears to differ between the two genomes. Both had a BGC that shares 100% similarity with a known cluster, a region which codes for heterocyst glycolipids. One *Nostoc* sp. '*Sticta beauvoisii* cyanobiont' BGC had 100% similarity to a cluster which produces the terpene geosmin. Six *Nostoc* sp. '*Sticta deyana* cyanobiont' BGCs and five *Nostoc* sp. '*Sticta beauvoisii* cyanobiont' BGCs shared <50% similarity with known clusters. The remaining clusters in both genomes had no similarity to BGCs in the MIBiG database. Only three BGCs in the *Nostoc* sp. '*Sticta deyana* cyanobiont' genome and one in the *Nostoc* sp. '*Sticta beauvoisii* cyanobiont' had pairing distances of less than 900 from GFC models in the BiG-FAM database, making them core members of their respective families. The relatively low similarity of these genomes' BGCs to known clusters indicates they likely code for novel gene products.

Further research will be needed to elucidate the unique properties of these and other cyanobacteria. Cyanobacterial genomes are underrepresented in databases, and the role of their secondary metabolites in lichen symbioses remains poorly understood.

Topic: Plant phenology in an era of rapid global change: new perspectives and frontiers

A-671

Flowering phenology of a dioecious plant species, Northern spicebush (Lindera benzoin), and the response to climate change

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Anthropogenic climate change has significantly altered the timing of the seasonal life cycle events of plants (i.e., plant phenology) worldwide, such as flowering time in spring. These plant phenological shifts have substantial effects on their survival and reproduction and other species that interact with them. Variations in phenological shifts among species and their varied responses to climate change were reported in previous studies, and may lead to temporal mismatch under continuing warming in the future disrupting species interactions. Recent studies suggested the potential future phenological mismatch for dioecious plants which are dependent upon male and female individuals flowering synchronously. However, the impacts from climate change on dioecious plants phenology and reproduction are still understudied for most species. It is probably due to the lack of long-term observations on phenology with individually-identified sex information. Here in this study, we focused on a common

shrub species native in the United States, Northern spicebush (*Lindera benzoin*). We conducted ground phenology observation for randomly selected multiple female and male individuals for four populations in the eastern United States in 2024 and 2025. In addition, flowering phenology was extracted from community science observations mainly from over 30,000 iNaturalist research-grade records back to 2008 by annotating the occurrence of flowers and flower sex from the digital photos. Herbarium specimens were also used to obtain historical phenology records for male and female since 1901. Seasonal climate variables including winter temperature and precipitation were obtained for each observation site and year. Statistical models were developed to estimate the phenological sensitivity to warming in winter from male and female flowers across the species' geographic range. We did not find significant difference in flowering time between males and female flowers of four populations. But community science and herbaria observations suggested earlier flowering time of male flowers than female flowers, which may be driven by the sampling bias due to bigger and more visible male flowers than females. Preliminary results also showed similar sensitivities to warming in winter from male and female flowering time, which suggested a low risk of phenological mismatch in the future. This project will improve assessment of climate change impacts on dioecious plants and better predict the ecological consequences in the future.

Topic: Systematics & Taxonomy

A-672

Exploring patterns of diversity and evolution in an enigmatic genus of woody plants, Gymnanthemum Cass. (Compositae)

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With around 1,500 species and 130 genera, Vernonieae, also known as "the ironweed tribe," is one of the most species-rich tribes in the mega-diverse Compositae family. Vernonieae is often referred to as the "evil tribe" due to its large size, cosmopolitan distribution, and reliance on overly general diagnostic characters, which has complicated efforts to resolve relationships among subtribes and delimit genera. This complexity is particularly evident in the subtribe Gymnantheminae, especially in the genus *Gymnanthemum*. As the most species-rich genus among Eastern Hemisphere ironweed, *Gymnanthemum* has a center of diversity in Madagascar, a biodiversity hotspot, where approximately half of its species thrive. *Gymnanthemum* has been recognized based on only a few generalized characters, such as a woody habit and having phyllaries with broad and smooth shields. However, the subtribe Gymnantheminae was also defined using these same characters, which are shared among all its members. This has undeniably led to confusion regarding the circumscription of species within *Gymnanthemum*. Previous taxonomic work has focused on identifying specific traits that distinguish other genera from *Gymnanthemum* but not on establishing diagnostic traits unique to *Gymnanthemum itself*.

The main objective of this research is to apply integrative methods—combining molecular phylogenetic inference and comparative morphology—to investigate species diversity within *Gymnanthemum* and clarify its phylogenetic position within the tribe Vernonieae. Our current results, based on analyses of DNA sequence data from the nuclear ribosomal (nrITS) and chloroplast (psbA–trnH) loci, provide a preliminary phylogeny that helps understand species diversity within *Gymnanthemum* and their relationship within Vernonieae. These findings indicate that *Gymnanthemum*, as presently circumscribed, is non-monophyletic. This result underscores the need for an integrative taxonomic approach to re-evaluate the genus and identify more robust diagnostic characters. Beyond the impact of our work on advancing the systematic knowledge of *Gymnanthemum*, this research will also address broader questions regarding the biogeography and evolution of plant diversity in tropical Africa and Madagascar. Our findings will also contribute to the effective dissemination of taxonomic knowledge through the Global Compositae Database, an innovative public repository managed by the International Compositae Alliance (TICA), which is recognized by the World Flora Online as a Taxonomic Expert Network.

Topic: Reproductive Processes

A-673

Reproductive Rivals: Comparing glade and prairie habitat effects on the reproductive biology of Asclepias tuberosa

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Asclepias tuberosa is a milkweed found in both glade and prairie habitats that could be useful in supporting and restoring pollinator networks in Missouri. This study focuses on the native Missouri plant *Asclepias tuberosa* in both glade and prairie habitats found at Shaw Nature Reserve. This study also focuses on both abiotic and biotic factors of the two habits and how they impact *A. tuberosa*'s reproductive success and pollination system. Measurements of morphology (height, corolla span, umbel width, inflorescence number, and bud number) and habitat pH were collected. In addition to pollination observations, open and supplemental pollen tube experiments were conducted to determine if reproduction was affected by visitation differences. This study provides a new understanding of the adaptability of *A. tuberosa* to different habitats and helps evaluate its potential role as a supporter of diverse pollinator networks.

Topic: Biodiversity Informatics & Herbarium Digitization

A-674

Accelerating Phylogenomic Analyses: GPU Enhancement of the HybPiper Pipeline for Target Enrichment Data

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HybPiper is a widely used bioinformatics tool in botany, and its usage case is expanding to include increasingly large data sets, such as recovering Angiosperms353 loci from whole genome sequencing. Scaling workflows like HybPiper can pose substantial computational challenges and the feasibility of larger studies will depend on the efficiency of each step in the workflow. We investigated whether moving some of the functionality of HybPiper to Graphical Processing Units (GPUs) could improve computational efficiency. For example, we tested whether G-BLASTN, a CUDA-based graphics acceleration of BLASTN, would provide a speed increase with equivalent results. Preliminary testing showed an over 10-fold speed increase with G-BLASTN with modestly sized datasets, and we explored the usage of graphics-accelerated versions of Smith-Waterman and Needleman-Wunsch based alignment methods. These methods show promise, potentially overcoming existing bottlenecks in contig assembly and paralog processing. Our results suggest a partial or full CUDA-based graphics acceleration version of HybPiper will be beneficial for some users who have access to modern commercial and consumer graphics cards.

Topic: Floristics

A-675

Plant and lichen discovery in the Southern Philippines

Author: Peter Fritsch, Darin Penneys, Daniel Nickrent, Manuela Dal Forno, James Shevock, John Brinda, Fulgent Coritico, Victor Amoroso
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The Philippines contains a stunning level of plant and lichen species diversity. Nonetheless, this diversity is still poorly documented scientifically and severely threatened by habitat loss through human land use and climate change. We present the results of an NSF-funded seven-year project documenting the land plants and lichens of selected areas in the southern Philippines. The key partner institution was the Center for Biodiversity Research and Extension in Mindanao (CEBREM) at Central Mindanao University (CMU). The project core team was formed from representatives of institutions based in the U.S. and CMU, with contributions from researchers at many other Philippines institutions and international partners. The team focused primarily on central Mindanao, where most of the high peaks of the island occur but which remains inadequately explored. Examples of focal areas were dormant volcanic peaks, including Mt. Apo, the highest point in the Philippines; cloud forests, including "bonsai" vegetation, a unique assemblage of stunted trees; forest over limestone; ultramafic areas, which harbor rare and endemic plants from high levels of naturally occurring heavy metals in the soil; low-elevation coastal forests; and low-elevation dipterocarp forests, now nearly eliminated. Six major expeditions and various minor expeditions were conducted. Each

major expedition was one-month in duration and consisted of 30–40 team members, including senior researchers, graduate and undergraduate students, the leaders and staff of local partner government entities, community parataxonomists and guides, and local base camp support teams. Data and specimen collection generally constituted specimen collection numbers with duplicate sets, tissue collections dried in silica gel for DNA extraction, photographs of each vascular collection and many lichens and bryophytes, standardized data on habitats and specimen features recorded for collection labels, and photo- and video-documentation of expedition activities. An estimated 15,000 lichen, 14,000 bryophyte, and 6,700 vascular plant collection numbers were made, with the total number of specimens well over 100,000. Species new to science, new area records, and rediscovery of species known only from the type have been documented. Field guides and area species lists of various groups have been produced. The population of the data in searchable web portals is ongoing. The data on these portals include digitized images of the prepared specimens, live-specimen photographs taken in the field, and searchable label data. The project included an intensive training and outreach component, with three Filipino students obtaining their master's degree at U.S. institutions, and two students currently in U.S.-based Ph.D. programs. Project personnel also served on committees for five other graduate students obtaining their degree in the Philippines, and U.S. participant institutions hosted nine university faculty and students for training and collaboration during extended visits. Many Filipino students and local participants were trained informally in field methods and plant and lichen identification during expeditions. Five workshops and three symposia were delivered at Philippine institutions.

Topic: Paleobotany

A-676

Actinidiaceae fruits from the Late Paleocene Almont/ Beicegel Creek Flora, North Dakota, USA

Author: Kathleen Pigg, Melanie DeVore, Steffi Ickert-Bond, Soon Flynn
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Distinctive fossil fruits assignable to the family Actinidiaceae that represent a new genus are described from the Late Paleocene Almont/Beicegel Creek flora of North Dakota. The fossils occur in the Sentinel Butte Formation, Tiffanian 3 and pollen zone P5 of Nicholas and Ott. They are globose, radially symmetric, three (possibly five) loculate berries with a persistent calyx that contain around eight seeds per locule. Seeds fill the locules and are attached to a narrow central floral axis that lacks the large, pronounced placentae typical of *Saurauia*. Seeds have the characteristic hexagonal pattern on the outer seed coat with mostly vertical orientation of the facets and around 15 facets per one side of the seed. They are anatropous, elongate to subovate, broad to the outside and narrow toward the micropylar end with a vertically-oriented raphe. Seeds more closely resemble those of *Actinidia* morphologically and *Actinidia* and *Clemotoclethra* in details of seed coat anatomy. Together these features suggest a mosaic taxon occurring in the Late Paleocene in North America of a group known from the mesofossil *Parasaurauia* in the Late Cretaceous of Georgia, USA, and from seeds widely distributed in Europe up through archaeological times, and native today only to China (*Clematoclethra*), Asia (*Actinidia*), and the Paleo- and Neotropics (*Saurauia*).

Topic: Ecology

A-677

Dynamic Grasslands: Bison Wallows as Hotspots of Diversity and Vulnerability

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Affiliation: Kansas State University

Defaunation is among the earliest and most enduring human impacts on ecosystems. Over the last century, there has been concerted effort and interest to reintroduce large animals to try to understand and recreate the effects that large native animals had on landscapes. In this study, we focus on bison wallows—bare-soil depressions formed by repeated wallowing behavior—which likely numbered in the tens to hundreds of millions before colonization. Bison are generally attracted to recently burned areas, which used to be common, but spatiotemporally variable throughout the Great Plains. Our current understanding is that bison, congregating in large herds that would often move across the landscape, abandoning these wallows for months to years. This pattern likely produced a dynamic mosaic of patches differing in time since fire, grazing, and wallowing. At Konza Prairie Biological Station, we used a 35-year experiment manipulating fire and bison reintroduction, we attempted to mimic this historical pattern of migratory movement. We fenced 48 wallows and paired non-wallow prairie plots to mimic temporary abandonment and tracked taxonomic and phylogenetic diversity over four years. Plant diversity peaked during the growing season after exclusion and declined thereafter, suggesting a short-lived colonization window followed by competitive filtering. Gains were strongest in areas previously under intense grazing, highlighting the legacy of grazing pressure in shaping assembly trajectories. Unfenced control plots maintained stable diversity, except in grazing lawns, where drought triggered a spike in invasive *Bromus* spp. that persisted for at least a year—demonstrating that grazing pressure during climate stress can tip communities toward invasion. While modern bison are confined to fenced ranges, their historical migrations likely drove pulses of disturbance and recovery that maintained biodiversity at multiple scales. Wallows may once have functioned as ephemeral biodiversity hotspots, cycling between disturbance and recolonization, and shaping habitat structure for plants, insects, birds, and mammals alike. Though the full rhythm of these historical dynamics is lost to time, our results reveal a glimpse of a prairie once governed by movement, memory, and change—far more dynamic and ecologically complex than what remains today.

Topic: Ecophysiology

A-678

Hydraulic and allometric changes in Tsuga canadensis as it reaches its southern range limit in Wisconsin

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Eastern hemlock (*Tsuga canadensis*) is a characteristic species of mixed hardwood forests in northern Wisconsin. However, small, isolated relict populations of eastern hemlock exist in the more arid climate of southern Wisconsin. Given the wide climatic range of eastern hemlock in Wisconsin, we explored how this species' hydraulic and allometric traits vary with environmental conditions. While global trends allow predictions to be made at large scales, exploring intraspecific variation gives a deeper understanding of individual species and smaller-scale ecological trends. These insights can deepen understanding related to how local communities may change as the climate shifts and inform restoration efforts. We investigated how hydraulic and allometric adaptations vary with climate by examining five Wisconsin populations of eastern hemlock at different latitudes. In turn, we explored how drought conditions shape eastern hemlock growth in these populations. As latitude decreases, the populations had less negative P50 values, lower stem conductivity, and lower LA:SA. Our data suggests that as climates become more arid, the populations' stem hydraulic systems become less resistant to drought. We hypothesize that the southern populations have a decreased resistance to drought mainly obtained by reducing water loss through reduced allocation to leaf and branch tissue rather than adaptations in their stem's hydraulic systems. These data run counter to global ecological trends, highlighting the importance of exploring intraspecific variation. Our findings will be used to better understand the mechanisms of eastern hemlock as well as Wisconsin ecology, an increasingly important task as Wisconsin ecosystems become threatened with climate change.

Topic: Biogeography

A-679

Biogeographical History of Agalinis (Orobanchaceae): Interpreting Disjunctions and Identifying Radiations

Author: Pedro Pezzi
Affiliation: University of Arkansas

The highlands of South America serve as important hotspots of diversity and contribute to the remarkable plant biodiversity of the Neotropics. Agalinis (Orobanchaceae) occurs disjunctly between North and South America, and also between the two South American centers of diversity—the Andes and the campos rupestres in southeastern Brazil—offering a great opportunity to understand the spatial and temporal dynamics of Neotropical diversification. In this study, we constructed a dated phylogeny of Agalinis to investigate the genus' biogeographical history and migration patterns across the Americas, focusing on the two Neotropical biodiversity hotspots. We also examined the evolution of the hummingbird pollination syndrome and perennial life strategy in the genus and evaluated whether these traits are linked to increased diversification rates. Agalinis originated in the southeastern USA during the early Miocene and rapidly diversified. It migrated to South America in the Late Miocene or Early Pliocene, and we propose two possible routes for the colonization of South America: either through the Andes or via the Brazilian lowland grasslands (Chaco, Cerrado, Caatinga), using

grassland corridors for dispersal within the continent. Moreover, we found that the Agalinis lineage that colonized the campos rupestres in the southeastern mountains of Brazil originated from nearby diverse species pools, such as the Cerrado and Atlantic Forest biomes, rather than from distantly located highlands, such as the Andes. After colonizing the South American highlands, the genus underwent rapid diversification. State reconstruction analyses indicated that the genus had a bee-pollinated ancestor and that hummingbird pollination evolved only once, with multiple reversals back to bee pollination. In contrast, the perennial life strategy evolved at least three times within the genus, including once in the ancestor of all South American species. Our results show that Agalinis is a clade that refutes the tropical conservatism hypothesis and the "out-of-the-tropics" model, having originated in North America and later migrated to South America. After colonization, it rapidly diversified—an example of "dispersification." These high diversification rates were, in part, associated with Quaternary climatic oscillations and the emergence of both the hummingbird pollination syndrome and the perennial life strategy.

Topic:

A-680

Northern shift in the geographic distribution of the southern flying squirrel

Author: Paullina Ruiz, Janice Krumm
Affiliation: Widener University

Glaucomys volans, also known as the southern flying squirrel, is found in the eastern half of the United States and Mexico. They often live in forests and mountainous areas. We hypothesized that their distribution is impacted by changes in climate over time. In this study, we compared the range of these squirrels pre-1980 and post-1980 to determine if the average latitude of their localities shifted north. Using *G. volans* occurrence data from the Global Biodiversity Information Facility, we excluded occurrence records from fossil specimens, records missing year of collection, decimal latitude, decimal longitude, or georeference uncertainty. We then reviewed and excluded all records with georeference uncertainties greater than 50km. When the occurrence records were mapped using QGIS, we did not visually detect a northern range expansion. However, when we compared the average latitude of specimens collected pre-1980 and post-1980, the latitude of records collected post-1980 were significantly higher compared to specimens collected pre-1980, suggesting a northward shift in the species distribution. This suggests that global warming may be shifting the range of this species northward. Climate change may be affecting the distribution of *G. volans* on smaller scales as well, so additional research on habitat usage would be recommended.

Topic: Hybrids and Hybridization

A-681

Phenotypic Differentiation, Environmental Adaptation, and the Genetic Architecture of Divergence Between Mimulus glaucescens and Mimulus guttatus

Author: Quinn Evans, Henry Arenas-Castro, Jennifer Coughlan
Affiliation: Yale University, Yale

How species are maintained in secondary contact is a fundamental question in evolution, and one with important consequences for biodiversity. Finescale ecological divergence is one mechanism of co-existence which requires the evolution of functional traits. Understanding the genetic architecture of divergence can allow us to assess how rapidly this divergence can occur. In this study, we used a pair of sympatric Californian monkeyflowers which differ in ecology and several putatively adaptive phenotypes to explore genetic divergence. We conducted a large common garden experiment with parental species as well as F1 and F2 hybrids and measured 10 reproductive, anatomical, and morphological traits. In contrast to the typically water-dwelling Mimulus guttatus, Mimulus glaucescens (which inhabits drier habitats) flowered early, reproduced via self-fertilization more often, produced fewer and larger stomata, produced epicuticular waxes, and exhibited a unique fused bract at reproductive nodes. By quantifying trait distributions in the F2 generation, we find that a diversity of genetic architectures underlie trait divergence, with many traits appearing largely quantitative. These findings suggest that ecological divergence may have required many mutational steps to achieve. Some traits exhibited strong genetic correlations, suggesting that they share a genetic basis and may represent evolutionary tradeoffs. Abnormal trait distributions and trait combinations in hybrids may have significant implications for selection against hybrids in the field, which may also contribute to species maintenance. This work contributes to a growing literature that suggests that species identity can be maintained in secondary contact, even with complex genetic architectures.

Topic: Paleobotany

A-682

Leaf abscission in arborescent lycopsids

Author: Michael D'Antonio
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A striking feature of late Paleozoic arborescent lycopsids is the presence of leaf scars, set within leaf cushions, that blanket the trunk and branches in regular spirals. Whether these scars represent leaf loss through senescence and decay or leaf loss through the regulated developmental process of organ abscission has been a longstanding question in paleobotany—one marked by a notable absence of evidence. Here we investigate permineralized leaf cushions of *Sigillaria approximata* with and without articulated leaves in longitudinal section under microscopy. The developmental anatomy of *Sigillaria* cushions and leaves indicates leaf loss through abscission. The stages of leaf abscission documented here, including the development of an abscission zone and a separation layer, as well as scar differentiation, correspond to well-characterized stages of organ abscission in living angiosperms, though the timing of several stages could not be assessed in *Sigillaria*. This finding suggests convergent evolution of abscission—in distantly related vascular plants, separated in time by 300 million years—resulting from a shared constraint on wound healing associated with the beneficial loss of unnecessary organs.

Topic: Pteridology

A-683

Homoploid hybridization and animal dispersal in the Texas endemic rock quillwort (Isoetes lithophila)

Author: Lisa George, Sylvia Kinosian, Jacob Suissa, Alejandra Vasco
Affiliation: Botanical Research Institute of Texas, University of Arizona, The University of Tennessee

Recent state-listing of the Texas endemic rock quillwort (*Isoetes lithophila*) has spurred research into its taxonomic delineation, population dynamics, and ecological interactions. *Isoetes lithophila* is found in rock pools within the Llano Uplift, a geologic region in central Texas characterized by granite domes rising hundreds of feet above the surrounding area. Specimens traditionally referred to as Isoetes lithiophila include plants of two morphologically similar taxa (*I. lithophila* and *I.* aff. *melanopoda*) and their hybrids. These diploid hybrids are morphologically distinct and inhabit microhabitats different from their parents. It is unclear if the homoploid hybrid Isoetes are fertile, but their environmental persistence and spore morphology suggest they may be. To understand the population structure and hybrid dynamics of the Texas rock quillworts, we sequenced almost 200 individuals from eight sites and dozens of rock pools using reduced representation sequencing. We found evidence for substantial gene flow among plants in different rock pools and discrete rock outcrops within a limited geographical area (about 5 miles distance). At distances greater than 10 miles, we found genetic differentiation between Isoetes lithophila populations and concomitant morphological and phenological variation. This pattern of genetic substructure is consistent with observations of potential mammalian dispersal agents identified in camera trap data. These unexpected findings should help expand our expectations of quillwort biology and better conserve this and other quillwort species.

Topic: Overcoming the barriers to on-going Castilleja research: From botanical enigma toward an emerging model system

A-684

Floral trait variation, selection, and ecological interactions of Castilleja sessiliflora

Author: Evan Hilpman
Affiliation: Oberlin College

Species in the genus *Castilleja* exhibit striking diversity in floral morphology and color, volatile organic compound (VOC) profiles, and ecological interactions, making them an increasingly valuable system for studying the evolution of plant traits in response to both mutualists and antagonists. Across multiple studies, we examined how floral traits vary

among and within *Castilleja* species and how populations are affected by interspecific interactions. In a multispecies field study across four sites in the Sierra Nevada, we quantified floral morphology, scent emission, and visitation across five co-occurring *Castilleja* species. Morphological traits broadly aligned with pollination syndromes, but substantial variation existed among populations, particularly within the hummingbird syndrome. Volatile profiles also showed some species-level differentiation but did not consistently predict floral visitor assemblages. These results suggest that classic pollination syndromes oversimplify the ecological dynamics in this group.

Focusing on a single widespread species, *Castilleja sessiliflora*, we conducted phenotypic selection analyses within a large population exposed to both pollinators (hawkmoths and bees) and pre-dispersal seed predators (plume moths). We found support for directional, stabilizing, and correlational selection amongst floral and plant traits, but it appeared that selection on floral scent was limited to less abundant compounds, while the compounds that contributed most to the total floral emissions showed no significant association with fitness. Seed predation reduced reproductive success by over 50% and contributed to selection favoring shorter flowers and reduced β-myrcene emission, indicating antagonists play a significant role in shaping floral trait evolution.

Together, these studies illustrate that *Castilleja* floral and plant traits are subject to multiple, and sometimes conflicting, selective pressures across space and time. However, these ecological interactions represent a tiny fragment of the biotic interactions that affect *Castilleja*; from the root parasitism of host plants, to the many insects that live on and within these *Castilleja,* it remains unclear the extent to which plant traits mediate and are mediated by these interactions. These findings underscore the importance of integrating community-level ecological context, including antagonistic interactions, into studies of floral trait evolution.

Topic: *Phylogenomics*

A-685

Phylogeny and phylogeography of eastern North American milkweeds (Asclepias, Apocynaceae) inferred from plastome phylogenies

Author: Shannon Straub, Carl Wagner, Claudia Kalina, Lindsey Balman, Nataly Vargas, Mark Fishbein
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The eastern North American milkweeds (*Asclepias*, Apocynaceae) comprise a clade of 20 species including familiar plants of prairies, forests, roadsides, and gardens, such as common milkweed (*A. syriaca*), butterflyweed (*A. tuberosa*), and poke milkweed (*A. exaltata*). Importantly, the species also include the most widely used host plants of the monarch butterfly (*Danaus plexippus*). The species from a subclade representing about half of the large Temperate North American clade of milkweeds, a rapidly diversifying lineage for which phylogenetic relationships remain unclear. Here, we expand on previous work that used a single exemplar plastome sequence of each species and partially resolved the phylogeny by increasing intraspecific sampling per species to 2-34 individuals (in most cases about 20), representing the full geographic range of each species. The increased sampling allowed us to evaluate 1) the plastidic monophyly of each species, 2) evidence for incomplete lineage sorting (ILS) of plastomes, 3) evidence of introgression of plastomes, 4) plastidic variation within species, and 5) phylogeneographic histories of widespread species. Using maximum likelihood analysis of partitioned plastome sequences, we found monophyly of most species, including some of the most widespread species, indicating minimal impacts of ILS and introgression on recovering interspecific relationships. For the most part, interspecific nodes were highly supported, providing an increased understanding of species relationships, notwithstanding evidence for plastome capture revealed in previous studies. In some cases, multiple plastome lineages were found that did not form clades, best explained by introgression. These include two lineages of *A. exaltata* and *A. amplexicaulis* and three lineages of *A. lanceolata* and *A. rubra*. For the latter pair of species, individuals were somewhat intermixed in each clade, suggesting that both ILS and introgression may have been involved in the evolution of these species. For the widespread and densely sampled *A. syriaca* and *A. tuberosa*, there was little geographic structure to plastome variation and, in the case of *A. tuberosa*, no support for the three recognized subspecies forming distinct lineages.

Topic: *Macroevolution*

A-686

Phylogenetics of the Australiasian showy mistletoes (Loranthaceae): Testing hypotheses of biogeography and host mimicking

Author: Matthew Vandal, Rayan Aissi, Margaret McNally, Daniel Nickrent, Sarah Mathews
Affiliation: Louisiana State University, Cornell University

Australasian showy mistletoes are members of the Gondwanan family Loranthaceae, and comprise the largest mistletoe clade in Santalales. The three radiations of the family, in Australasia, Africa, and the Americas, remain poorly studied in the absence of detailed species phylogenies. Biogeographic studies so far have been unable to discriminate between an origin for the family in East or West Gondwana. Further, data have been insufficient to document patterns of biotic exchange between Sunda and Sahul, and determine the origins of endemic Australian genera and species. Mistletoe evolution is shaped by the interactions of mistletoes with their hosts, avian pollinators and dispersers, specialist butterflies and ants, and generalist herbivores. These interactions remain to be investigated in a phylogenetic framework, along with key traits relating to phenology, floral morphology, haustorial structures, and phenotypic similarity between mistletoes and their hosts (putative mimicry). With a focus on the Australasian members, we are assembling plastid and nuclear phylogenomic data sets to obtain the phylogenetic framework needed to characterize the evolution of species, traits, and ecological interactions and their relationships to climatic and floristic change.

Topic: *Floristics*

A-687

Floristic diversity of the Avocado Belt of northern Michoacán, Mexico

Author: Victor Steinmann, Carlos Cultid Medina, Alberto Pérez Pedraza, Brenda Bedolla García, Gabriel Sánchez Ken
Affiliation: Instituto de Ecología A.C.

The Mexican state of Michoacán is renowned for its avocado production, and 30% of the avocados consumed in the world and more than 80% of those eaten in the United States are grown there. Nearly all this production occurs in the pine-oak and cloud forests of the northern part of the state, an area comprising approximately 20,000 km^2 and referred to as the Avocado Belt. Soaring demand over the past 20 years has triggered a massive conversion of native forests to the monoculture of a single cultivar, the Hass Avocado. As a result, there are significant environmental challenges, including water depletion, pollution, loss of biodiversity and increased ailments among the local population due to widespread use of pesticides. The PERSEA Project, funded by the Mexican government, is a multidisciplinary endeavor determined to resolve these challenges, and one of its major components is the first floristic inventory of all vascular plant taxa occurring spontaneously in the Avocado Belt. The premise is that only by understanding the composition and distribution of the phytodiversity can effective conservation efforts can be implemented in the region. Based on herbarium records, iNaturalist observations, and fieldwork in different portions of the Avocado Belt, more than 3200 species have been documented from the early 1800s to present. More than 90% of these are native, including various species endemic to the area. Ferns comprise 6 % of the diversity, gymnosperms < 1%, and angiosperms 93 %. 180 families are present, the largest being Asteraceae, Fabaceae, Orchidaceae, and Poaceae. Together they possess 35 % of the phytodiversity. Although avocado orchards are a monoculture, they house moderate diversity, and more than 250 species, the majority native, can be found growing within them. Very few taxa of the Avocado Belt have been formally assessed for their conservation status, but among those evaluated for the IUCN Red List are *Balmea stormiae* (endangered) and *Bursera madrigalii* (critically endangered). Much more work remains to been done and future efforts will focus on exploring under-collected areas, formally assessing rare taxa, and proposing conservation plans.

Topic: Defining forces in fern evolution: Celebrating the contributions of Kathleen Pryer and Michael Windham

A-688

Reticulate evolution in Ynesmexia (Pteridaceae): phylogenomics reveal homoploid hybrids, polyploidy, and evidence for chloroplast capture

Author: Blake Fauskee, Sungsik Kong, Michael Windham, Kathleen Pryer
Affiliation: Duke University, University of Wisconsin-Madison

Ynesmexia (Pteridaceae) is a newly described genus of cheilanthoid ferns comprising five species displaying such remarkable morphological diversity that they were previously assigned to disparate genera (occasionally to different families). By employing a robust phylogenomic approach using 376 phased nuclear loci and full chloroplast genomes, our analyses combined maximum likelihood tree inference, multispecies coalescent species tree estimation, phylogenetic network estimation, and tests of introgression to capture both bifurcating and reticulate patterns of evolution in *Ynesmexia*. Our complementary approaches reveal extensive hybridization within the two well-supported subclades of *Ynesmexia*. In the *subcordata* subclade (*Y. subcordata, Y. fournieri,* and *Y. ×gryphus*), *Y. ×gryphus* is shown to be a homoploid hybrid—a rare event in ferns—between *Y. subcordata* and *Y. fournieri*. *Ynesmexia ×gryphus* maintains interfertility with both progenitors, resulting in the detection of ongoing introgression between *Y. subcordata* and *Y. fournieri*. The plastid phylogeny fails to resolve relationships in the *subcordata* clade, forming a polytomy consistent with chloroplast capture. In the *seemannii* subclade (*Y. seemannii* "*seemannii*" and *Y. seemannii "lozanoi"*), hybridization between the two "morphs" is coupled with ploidy variation inferred from spore measurements, suggesting that additional undescribed entities exist in this group. Finally, *Y. skinneri* s.s. is revealed to be an allotetraploid hybrid between the two major subclades. The phylogenetic placement of *Y. skinneri* suggests either unsampled progenitors or a hybrid origin preceding the full diversification of *Ynesmexia*. Our findings demonstrate *Ynesmexia* has undergone extensive reticulate evolution, underscoring the value of integrating phylogenomics and network-based approaches with careful morphological studies to resolve complex species radiations.

Topic:

A-689

Seasonal Variation in Occurrence Records in the American Red Squirrel

Author: Kamiyah Brunson, Makiyah Brunson, Janice Krumm
Affiliation: Widener University

The American red squirrel (*Tamiasciurus hudsonicus*) is native to North America, inhabiting boreal coniferous forests and relying on seeds and cones from evergreen trees for survival. We hypothesized that behavioral changes across seasons in red squirrels would affect the spatial distribution of occurrence records in this species. We downloaded over 72,000 *T. hudsonicus* occurrence records from the Global Biodiversity Information Facility (GBIF), and removed records without latitude and longitude, without collection year and month, and records outside of the native range of *T. hudsonicus*. We categorized the remaining 13,497 occurrence records by collection season: spring (March-May), summer (June-August), fall (September-November), and winter (December-February). We mapped the occurrence records using QGIS, an open access mapping and spatial analysis program, and compared seasonal patterns. Our results showed fewer specimen records during winter compared to summer records, potentially due to behavioral changes including increased energy conservation in winter and increased resource availability in summer. It is likely that the decrease in records in the winter months was also impacted by reduced collecting efforts. We also found a significantly greater mean latitude of occurrence records in summer, likely due to more severe winter conditions in the northern part of the red squirrel range. These findings enhance our understanding of how seasonal factors influence the ecology of the American red squirrel. Future research should investigate the factors driving reduced winter occurrence records, focusing on shelter use, food availability, and energy expenditure.

This research was conducted as a CURE developed by the Biological Collections in Ecology and Evolution Network (BCEENET). BCEENET CUREs use digitized natural history collections data and free open source tools to increase accessibility to undergraduate research opportunities while also participating in innovative research.

Topic: Functional Genetics/Genomics

A-690

Laser-Induced Transcriptomic Analysis in Sunflowers

Author: Daniel Frimpong, Jennifer Mandel, Luis Cabrera, Judy Bowen, Teresa Flores-Reyes, Alejandro Ponce-Flores
Affiliation: The University of Memphis, University of Memphis

Laser-induced technologies have revolutionized molecular biology by enabling high-precision cellular treatments and gene expression analysis without physical contact. While zinc (Zn) is essential for enzymatic processes, photosynthesis, and plant stress resistance, its uptake mechanisms in sunflowers (*Helianthus annuus*) remain poorly understood. This study investigates whether laser-induced selective removal of the wax cuticle enhances foliar Zn fertilizer penetration and uptake, ultimately influencing plant growth and reproductive parameters. With this, this study specifically aims to address the following queries: (i) Will wax cuticle removal using lasers enhance zinc sulphate absorption among the sunflower genotype? (ii)Will the absorbed zinc fertilizer influence specific growth and reproductive parameters in control versus laser-treated samples? and (iii) Will the laser-induced selective ablation of the leaves alter gene expression patterns in control versus laser-treated samples after RNA sequencing?

To achieve this, Laser-Induced Breakdown Spectroscopy (LIBS) and Inductively Coupled Plasma Optical Emission Spectroscopy (ICP-OES) will be employed to track Zn distribution in sunflower leaves. An RNA sequencing experiment will be conducted to identify differentially expressed genes in control versus laser-treated plants. Using a completely randomized design, 36 Sunrich Gold Hybrid F1 sunflowers will be divided into control (foliar Zn application without laser treatment) and experimental (Zn fertilizer applied post-laser treatment). Growth parameters such as plant height, stem girth, and specific leaf area, as well as reproductive traits including flower diameter, hundred seed weight, and biomass, will be evaluated. Chlorophyll content and Zn accumulation will be analyzed through ICP-OES, while LIBS will visualize Zn spectral peaks across treatments. Differential gene expression analysis will be performed using HISAT, StringTie, and DESeq2 in R, with principal component analysis (PCA) clustering to assess transcriptional changes. This research will help unravel Zn-responsive genes and nutrient transport mechanisms while optimizing agrochemical application methods for sustainable agriculture.

Topic: Development and Structure

A-691

Investigating the anatomy of Torreya californica (Taxaceae) seed cones

Author: Aspen Avelar, Kelly Pfeiler, Austin Nguyen, Kelly Matsunaga
Affiliation: University of Kansas

The conifer family Taxaceae consists of 6 extant genera and 30 species of trees and shrubs that are predominantly distributed throughout the Northern Hemisphere. Ovulate cones of Taxaceae, with the exception of *Cephalotaxus*, comprise a single terminal seed that is fully or partially enclosed by an aril. The evolutionary origins of this derived cone morphology are poorly understood. While the aril is not usually considered to be homologous to the ovuliferous scale of other conifers, the evidence of its homology remains mixed. After pollination the aril arises from the subtending axis and grows to enclose the seed, becoming fleshy to attract seed dispersers. Teratological specimens suggest the aril may be derived from two fused bracts. Expression patterns of the C-class MADS-box gene *AGAMOUS* imply possible ovuliferous scale homology but could alternatively represent novel gene function for fleshiness. The polarity of vascular bundles may provide additional clues to the identity of the aril since ovuliferous scales in conifers are vascularized by inverted bundles (adaxial phloem and abaxial xylem). However, Taxaceae arils are only known to be vascularized in the genus *Torreya*. Published accounts from the early 20th century suggest aril bundles in *Torreya* are inverted, but this observation has not been corroborated in the recent literature and no published figures exist. Here we describe the anatomy of mature *Torreya californica* cones to investigate prior reports of inverted bundles in *Torreya* arils. A mature seed cone of *Torreya californica* was fixed in FAA and then embedded in paraffin wax for sectioning. Sections were stained using a modification of Sam's (1983) quadruple stain protocol. Prepared sections were studied with light microscopy. This study adds to our knowledge of Taxaceae cone anatomy and may help us to better understand the evolution of conifer seed cones.

Topic: *Macroevolution*

A-692

The origin and genetics of rare plants in the California Floristic Province, the case of Clarkia lingulata (Onagraceae)

Author: Oscar Vargas
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Biodiversity hotspots are characterized by having high indices of endemism. Rare endemics are important components of biodiversity hotspots because they are found to make around one third of the species composition in these areas. Therefore, elucidating the genetic diversity and the origin of rare endemics is pivotal to our understanding and conservation of biodiversity hotspots. *Clarkia lingulata* (Onagraceae) is a rare endemic with only two known populations in the California Floristic Province. It has been hypothesized that *C. lingulata* originated via budding speciation from *C. biloba*. I used the Angio353 target-sequencing-set to test the aforementioned hypotheses. Reciprocal monophyly does not support a budding speciation scenario. Genetic variation is discussed in the context of management and conservation for this rare species.

Topic: *Lichen and Bryophyte Diversity, Conservation, and Evolution in the Americas*

A-693

The implications of the "liverwort way" of being a land-plant and on their evolution and our research

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Liverworts are a lineage of land plants that have maintained an independent evolutionary trajectory for more than 400 million years. Since then, they have independently resolved ecological and evolutionary challenges, allowing them to be successful in a wide range of environments, from forest canopies to deserts. As a result, liverworts have evolved unique morphologies and life strategies compared to other land plants. In this talk, I will argue that the unique liverwort ways of being land plants is not only a fascinating biological subject, but also highlights the need for special considerations while conducting conservation and evolutionary research in this group. To exemplify this at two contrasting evolutionary scales, I will discuss recent research in liverworts in the family Aytoniaceae. At a fine taxonomic scale, I studied the population structure of the widespread West-coast endemic *Calasterella californica*---a clade that diverged from its closest extant relative ca. 100 Mya---using genomic data. In this project I studied the genetic structure of this lineage across California to understand whether the often-assumed high dispersal ability of liverworts can maintain gene flow across spatially distant populations. Instead, we found strongly divergent populations that follow a geographic pattern, challenging our understanding of the taxonomy in this group. At the larger taxonomic scale, I will explain some of the challenges that arise when studying the biogeographic evolution of a very old lineage, such as Aytoniaceae. Solving some of these challenges required the implementation of a newly developed model ("PAw GeoSSE +J") that accounts for the possibility of long-distance dispersal and changes associated with missing speciation events. When applying this model to this cosmopolitan family, we found that even for groups hypothesized to be extremely good dispersers, long-distance dispersal is five times more likely to lead to speciation than short-distance dispersal. The ultimate goal of this talk is to encourage discussion about the many avenues of research in bryophytes that continue to arise as more bryophyte basic knowledge---such as the world checklist of liverworts, and genomic data for a broad number of species---becomes available. Considering the uniqueness of bryophyte biology when conducting evolutionary and conservation studies will enhance our ability to make fair assessments of bryophyte diversity, as well as framing the outstanding disparity in morphology and life cycles that bryophytes bring to the table when studying land-plants evolution.

Topic: *Population Genetics/Genomics*

A-694

Genomic Insights into Population Differentiation and Structural Variation in the Rare Gaviota Tarplant (Deinandra increscens subsp. villosa; Asteraceae)

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Many plants have small and fragmented ranges, where each population may harbor locally adaptive variation but also face elevated risks of local extinction. This is especially true for annual, self-incompatible plants, where demographic stochasticity and limited mate availability increase the potential for reproductive failure. To inform conservation efforts for one such species of concern — the Gaviota tarplant (*Deinandra increscens* ssp. *villosa*) — we resequenced 842 individuals spanning its narrow coastal range in California. We find that populations at discrete localities are genetically differentiated, with each representing a unique combination of ancestry components. The Sudden Peak/Tranquillon Mountain locality, which consistently has the largest census population, also possesses the highest genomic heterozygosity. However, smaller and more peripheral populations also harbor distinct genetic variation, particularly the Gaviota Coast locality, which occupies the hottest, driest, and most southeasterly portion of the species' range and shows genome-wide differentiation. In addition, we uncover widespread structural variation across the genome and detect introgression into the demographic center from a yet-unidentified, more genetically diverse lineage. Ongoing work will compare modern and historical demography and explore how genomic differentiation — including structural variants and introgressed regions — may contribute to local adaptation in this rare, fragmented taxon.

Topic: *Population Genetics/Genomics*

A-695

Using a population genomic pilot study to inform a rangewide landscape genomic assessment of the imperiled clonal shrub Neviusia alabamensis (Rosaceae)

Author: Maia Jones, Wenhsi Kuo, Jordan Hathaway, Jordyn Riehn, Noah Dell, Brad Delfield, Burgund Bassuner, Allison Rea, Maura Collins, Georgia Thomas, Rebecca Sucher, Ivan Jimenez, Matthew Albrecht, Christy Edwards
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As we face a global biodiversity crisis, it is critical to strategically assess and manage threatened plant species. For exceptional species, which cannot be preserved in conservation seed banks, living collections are a valuable way to protect their genetic and phenotypic diversity ex situ and propagate germplasm for restoration of wild populations. However, space and resources for living collections are often limited, so it is important to design optimized ex situ collections that efficiently conserve both neutral and adaptive genetic variation as well variation in phenotypic traits that may enhance the survival of the species. *Neviusia alabamensis* is an imperiled clonal shrub native to the southeastern United States. Although it produces flowers, this species has not been observed to set seed in the wild and instead reproduces asexually via root divisions, making it a candidate for ex situ conservation in living collections. We designed a pilot study to assess genetic and phenotypic diversity and the extent of clonality in four populations from Arkansas, and use our results to inform our main study, which uses population and landscape genomics to inform an ex situ collection that includes individuals from throughout the entire species' geographic range. We generated 2bRAD data and collected phenotypic and phenological data from wild-collected root divisions growing in a common garden setting. We found that each of the four populations represents a single clonal group, or genet, and that phenotypic traits did not vary significantly within or among populations. These results informed our strategy for sampling populations in the remainder of the range, and we have collected root divisions from across the species' range, which are now is now being propagated in our common garden. We plan to generate 2bRAD libraries for the remainder of our collections, and collect phenotypic and phenological data on these individuals in a common garden setting. These genomic and phenotypic data will be combined with environmental data to conduct genotype-environment and phenotype-environment associations to identify neutral and adaptive alleles. These results will inform collection management decisions by assessing whether tradeoffs exist in the ability to conserve neutral and adaptive variation in genetic and phenotypic traits. This research will help to design an efficient, optimized ex situ collection to ensure the conservation of instraspecific variation in this species.

Topic: *Paleobotany*

A-696

A synangiate structure with novel morphology from the Early Devonian of Gaspé (Canada)

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The Battery Point Formation of the Gaspé Peninsula (Quebec, Canada) hosts the most diverse Early Devonian assemblage of permineralized plant fossils currently known. The majority of the fossils discovered in these Emsian (~400 myr) strata represent vegetative plant parts. Sporangia, comparatively rare, have almost exclusively typical trimerophyte morphology – fusiform, paired, and twisted around each other. A recently discovered fertile structure, representing a synangium containing spores, strays from this norm. The synangium is detached from its subtending structure, of which no evidence is preserved. The synangium is ovoid, ca. 2 mm long and 1.5 mm at its widest point, and has complex morphology. Transverse sections in the median section of the synangium reveal six markedly convex lobes separated by dehiscence lines located in the deep grooves between the lobes. Toward the synangium apex, the six lobes become progressively less convex with no dehiscence separating them. Toward the base of the synangium, the cross-sectional geometry is gradually inverted – the six lobes develop median longitudinal grooves that deepen gradually until each lobe becomes a concave structure and the dehiscence lines run along the resulting six protruding ridges formed by the margins of the six dehiscence lines. The wall of the synangium is one-cell thick, with large cells that decrease in size slightly at the dehiscence lines. The periclinal walls of the synangium wall cells are differentially thickened: in the convex parts the outer periclinal walls are thicker, whereas in the concave parts, the inner walls are thicker, consistent with hygroscopically effected dehiscence. Parenchyma cells are present internal to the outer cell wall layer in the basal portion of the synangium. An incomplete partition consisting of 1-2 layers of very thin tubular cells is present at the center of the synangium, in its basal half. Due to the minute size of the cells, the partition is incompletely preserved and distorted. Nevertheless, we observed it is triradiate at the center, with each of the three rays probably bifid. This, along with the consistent presence of six dehiscence lines along the synangium, suggests a hexasporangiate organization. Numerous spores are present inside and around the synangium. They are ~25 µm in diameter, with fine trilete marks and a thin sporoderm that consists of an internal smooth later and a thin outer layer that holds minute raised "islands" of varied shape with coralloid morphology. This synangiate structure represents a new type of reproductive structure with no known equivalent in Early Devonian floras. Its anatomy suggests a complex dehiscence mechanism. We hope that future discoveries will clarify whether it belongs to one of the early tracheophyte species already reported from the Battery Point Formation or to an entirely new species.

Topic: *Ecophysiology*

A-697

ABA peaking-type dynamics drive plant water use during seasonal drought

Author: Jessica Guo, Cade Kane, Aabhas Senapati, Scott McAdam
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Plant water use strategies are often characterized by empirical changes in water potential, stomatal conductance, or transpiration under drought, which is exacerbated by climate change. Abscisic acid (ABA), long known to mediate plant drought response, has diverging temporal trends associated with water use strategies. Under drought, ABA rising-type species rely on sustained ABA production to maintain stomatal closure, while ABA peaking-type species utilize ABA for initial stomatal closure but then maintain stomatal closure with turgor loss. In both gymnosperms and angiosperms, ABA peaking-type behavior is associated with anisohydric species that tolerate very low water potentials. However, connecting physiological and phytohormone determinants of water use strategies have yet to be demonstrated under field drought conditions. Here, we investigated *in situ* stem water potential and foliar ABA dynamics in *Larrea tridentata* at the NEON-SRER site near Tucson, Arizona. Daily predawn water potentials were measured via stem psychrometry on six shrubs from April to October 2023, which encompassed the premonsoon drought and monsoon recovery periods. Manual chamber measurements were taken every 2 weeks, during which 10-12 leaves were sampled for foliar ABA. Extraction, purification, and quantification of ABA were performed by ultra-performance liquid chromatography tandem mass spectrometry with an internal standard. In total, foliar ABA was sampled 14 times between late April and mid-August.

Predawn water potentials were -2 MPa in April and declined nearly uniformly until -7.4 MPa on July 19, which demarcated the start of the monsoon. Thereafter, predawn water potentials varied with monsoon precipitation pulses and achieved a maximum of -1.5 MPa following the largest event of the season (9.1 mm). While field-collected foliar ABA showed high variability between shrubs, mean foliar ABA (n = 6) stayed high until June and then decreased until the onset of the monsoon on July 19, indicating ABA-peaking behavior consistent with *Larrea*'s tolerance of low water potentials. During the premonsoon drought, ABA and predawn water potential were significantly correlated ($p = 0.008$, $R2 = 0.613$). Furthermore, ecosystem-scale evapotranspiration (ET) and predawn water potential were weakly correlated ($p = 0.058$, $R2 = 0.543$), suggesting that stomatal closure and the concomitantly reduced transpiration were associated with loss of turgor rather than high foliar ABA. While previous studies have shown ABA peaking-type behavior under experimentally imposed drought, we believe this is the first instance of angiosperm ABA peaking-type behavior in response to natural drought conditions. Furthermore, we demonstrate the importance of phytohormone and physiological mechanisms in underlying patterns of ecosystem water flux.

Topic: *Conservation Biology*

A-698

Gaps in the conservation of phylogenetic diversity in the Chilean vascular flora

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Setting conservation priorities of plant genetic resources requires botanical knowledge as well as an assessment of what is so far under protection. However, a strategy based on species in general implies that every unprotected species would be of equal priority. Using phylogenetic diversity as a guideline may allow setting priorities on those species that will maximally increase the representation of the tree of life in the conservation network. In this work we assessed the representation of both species richness (SR) and phylogenetic diversity (PD) in the Chilean protection network, both *in-situ* and *ex-situ*. To this end we compiled plant lists of Chilean protected wilderness areas (PWA: *in-situ* conservation units) from the literature. We also compiled lists from Chilean seed banks, botanical gardens and arboreta (ECU: *ex-situ* conservation units) as a collective effort of the curators. We then harmonized all lists into one taxonomy following the updated version of the Catalogue of Vascular Plants of the Southern Cone. While estimating SR amounts to counting the species in each conservation unit (CU), estimating PD needs a phylogenetic tree. We used the lists of all Chilean native plants to build a phylogenetic tree using the R-package U.PhyloMaker which imputes species absent from a backbone tree of the vascular plants based on their generic or familial affiliation. PD was then calculated using the R-package picante. We compiled information for 49 PWAs and for 23 ECU. As a whole, the Chilean conservation network (both *in-situ* and *ex-situ* CUs) protects 60% and 70% of the Chilean SR and PD, respectively. PWAs alone protect 48% and 63% of SR and PD, while ECUs alone account for 36% and 47% of SR and PD. Thirteen PWAs and six ECUs show significant phylogenetic overdispersion, while four PWAs and three ECUs show significant phylogenetic clustering. Marginal contribution to SR and PD of most areas is less than 1%, indicating that the Chilean conservation network is resilient in conserving SR and PD. However, the loss of one ECU (namely the INIA seed bank at Vicuña) would represent a loss of 8% SR and 4% PD from the whole conservation network. On the other hand, the great majority of the protected species are conserved in only one CU. Therefore, if these CUs are lost, the overall percentage of conserved flora may be minimally affected, but there will be an immediate loss of conservation for specific species, for which there is no backup in other CUs. There is a notable gap in the botanical knowledge of the Chilean *in-situ* conservation network,

with over 50% of the PWAs without a plant checklist. Future efforts to assess the effectiveness of the Chilean conservation network should be aimed at cataloging vascular plants inside PWAs.

Topic: Biodiversity Informatics & Herbarium Digitization

A-699

A computational and targeted sequencing approach for mixed plant DNA identification with Angiosperms353

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The identification of plant species from mixed samples is crucial in various fields, including food and drug safety. Traditional methods face challenges due to the high costs of DNA sequencing, inefficiencies in computational workflows, and incomplete sequence databases. This study introduces a novel approach using the Angiosperms353 target capture sequencing kit for efficient identification of angiosperm DNA in mixed samples. Our method assembles short pair-end reads using existing workflows to assemble contigs from enriched DNA (HybPiper) for each mixed sample. Using a reference database of exemplar Angiosperms353 sequences from 871 taxa, we apply phylogenetic inference to categorize contigs and variance in phylogenetic distance across genes to identify the presence of likely taxa in mixed plant samples. We demonstrate a high precision and accuracy in identifying unknown taxa from a set of mixed samples including 160 *in silico* mixes of reads (up to 10 species in a single mix), and 11 libraries with 54 species constructed from known mixed DNA. The pipeline reaches 98.1 to 99.6% accuracy, 92.9 to 100% precision for in-silico mixes, and 90.7% accuracy and 98.0% precision for artificial real mixes, with proper parameter choices. We explored the parameter cutoffs of the pipeline to offer an empirical range for different applications.

The Angiosperms353 and HybPiper assembly proved effective in sorting mixed plant DNA samples. Our method shows potential for efficient and accurate scientific and practical applications in plant species identification.

Topic: Conservation Biology

A-700

Integrating Genomics and Phenotypic Data to Understand Adaptive Intraspecific Variation in the Threatened Floodplain Species, Boltonia decurrens

Author: Wenhsi Kuo, Matthew Albrecht, Brad Delfield, Noah Dell, Meg Engelhardt, Jordan Hathaway, Maia Jones, Rebecca Sucher, Christy Edwards
Affiliation: Missouri Botanical Garden, Washington University in St. Louis

The decurrent false aster (*Boltonia decurrens*) is a threatened perennial plant endemic to the dynamic floodplain ecosystems of the Illinois River Valley, distributed over approximately 220 km in a narrow latitudinal range. Historically maintained by regular flooding, these habitats have been heavily modified by anthropogenic activities, including damming, channelization, and agricultural expansion. As a result, *B. decurrens* populations have declined significantly due to altered hydrology, reduced disturbance regimes, and increased competition from invasive species. These threats, compounded by rapid climate change, highlight the urgency of effective *ex situ* conservation strategies that can preserve the species' evolutionary potential and support future restoration efforts.

Successful ex situ conservation depends not only on the ongoing survival of a species but also on capturing the genetic diversity underlying adaptive traits that confer long-term sustainability and resilience in heterogeneous and dynamic environments. However, general guidelines for evaluating intraspecific variation — particularly in categorizing neutral and adaptive genetic variation — remain underdeveloped. To address this, we established a living collection of *B. decurrens* comprising over 450 individuals from 18 natural populations. This collection is a valuable resource for exploring both neutral and adaptive variation under common environmental conditions.

We generated a high-quality, chromosome-level genome assembly using PacBio HiFi long-read sequencing and Hi-C scaffolding. This assembly provides a genomic foundation for population-level resequencing and downstream analyses of both demographic history and adaptive evolution. We conducted whole genome resequencing for all individuals in our living collection, and have initiated genome-wide scans for identifying polymorphisms potentially under selection.

In the first year of common garden phenotyping, we quantified key life history traits, including vegetative growth rate, bolting time, flowering phenology, and stem height. We observed substantial phenotypic variation across populations. Notably, the timing of bolting and flowering varied widely, and we found a significant negative correlation between flowering time and the latitude of source populations. This latitudinal cline, despite the relatively narrow geographic range, suggests that potential selective pressures have shaped phenological traits, likely in response to microclimatic gradients or differences in disturbance timing across the floodplain. Moreover, populations varied in whether they flowered in the first year, suggesting genetic differentiation in life history strategies between annual and perennial tendencies. Variation in flowering stem height may reflect adaptive trade-offs related to floodwater levels or energy allocation under varying disturbance regimes.

Ongoing analyses include genotype–phenotype associations, landscape genomics, and genomic scans for selection (e.g., FST outliers, Tajima's D, XP-CLR), with the goal of identifying candidate adaptive loci. By comparing patterns of adaptive and neutral genetic structure, we aim to inform guidelines for ex situ sampling that preserve both genetic diversity and adaptive capacity. This research will not only support the long-term conservation and restoration of *B. decurrens* but also contribute broadly to understanding how local adaptation operates in dynamic floodplain systems and how genomic tools can guide conservation planning for rare and endemic plants.

Topic: Development and Structure

A-701

Ovule development in the "living fossil" Wollemia (Araucariaceae)

Author: Ormary Alvarez, Cecilia Zumajo
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TheAraucariaceaefamily isamongst the gymnosperms and first appeared in the Mesozioc era and consists of thegenera: *Araucaria*, *Agathis*, and *Wollemia*. The genus, *Wollemia* consists of one species: *Wollemia nobilis* (commonlyknown as the 'wollemi pine', here after *Wollemia*) it was thought to be extinct until it was re-discovered in Australia in 1994. *Wollemia* presents the typical ovule morphology of a gymnosperm: one integument surrounding the nucellus andorthotropous orientation. As most of the studies on ovule development have been focused on flowering plants, most of what we know is from an ovule with two integuments and anatropous orientations, with studies that have been focused on morphologically-different gymnosperm ovules, such as *Ginkgo biloba* that presents fleshy integument or Gnetalesovules that have extra envelopes surrounding the ovule. Thus, studies in *Wollemia* provide the perfect framework to understand how ovule development has evolved across seed plants.

To understand how ovule development occurs, we identify the homologs of canonically known genes and we perform *in situ* hybridization in*Wollemia* cones. This allows us to pinpoint exactly when and where specific genes are expressed, and to determine their evolution. We analyzed integument developmental genes including *WUSCHEL (WUS)*, and *BELL1*homologs, as well as mega- micro- spore developmental genes such as *SPOROCYTELESS/NOZZLE (SPL/NZL)*. We have found that some of these genes share the same expression patterns with angiosperms and other studied gymnosperms, like in the case of *WUS*, while others differ, for instance one of the *BELL1* homologs. This study provides more insightsinto the evolution of the ovule genetic network and contributes to our understanding on the evolution of ovules and seeds, from a molecular approach.

Topic: Biogeography

A-702

Diversity and drivers of alpine plant community structure in western North America

Author: Hannah Marx, Joseph Kleinkopf
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High-alpine summits remain botanical mysteries. Due to their extreme environments and remote nature, documenting diversity in alpine ecosystems has historically been challenging. Alpine peaks largely lack baseline biodiversity data essential for providing context about how plant communities are changing over time. What we do know from a few well-studied alpine communities is that despite abiotic conditions that push the physiological limits of plant life, mountain summits harbor a higher-than-expected floristic diversity within them, high turnover between regions, and high rates of endemism. They are also currently experiencing dramatic environmental changes that are impacting the flora and therefore are critical to understand as sentinels of change. Here,

we present the first results from a multi-institutional collaboration to coordinate collections-based biodiversity surveys of alpine plant communities across western North America. From this detailed biodiversity dataset, we are testing specific hypotheses about processes driving the patterns we observe today to better understand how they will change in the future.

Topic: Ecophysiology

A-703

Side Hustle: Zinnia elegans Flowers Photosynthesize to Bloom on a Budget

Author: Amelie LeTierce, Jessica Savage
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Developing flowers must expend carbon for growth and maintenance in exchange for reproductive function, leading to the assumption that flowers are dependent on carbon translocated from leaves via the phloem. However, photosynthetic carbon assimilation by floral tissues may partly offset floral carbon demand, especially for long-lived flowers late in development, after carbon allocation to growth declines. In this study, we surveyed the growth and physiological maintenance of *Zinnia elegans* flowers to understand the contribution of floral photosynthesis to carbon balance across development. Plants from six horticultural varieties with differently colored flowers were grown in a growth chamber at the University of Minnesota, Duluth. Developing flowers were studied as buds and blooming flowers. To show that flowers assimilate carbon, we conducted a survey of CO_2 gas exchange in the dark and at net photosynthetic capacity (measured at 600 umol photons / m^2 / s). All buds and blooms responded to light and exhibited gross photosynthetic carbon assimilation, even if they had a negative net carbon assimilation at photosynthetic capacity. Dark respiration and gross photosynthetic capacity varied by variety and the highest gross photosynthetic capacity was observed in blooms of apparently green varieties. Variation in dark respiration explained little of the variation in photosynthetic capacity, showing that blooms varied greatly in photosynthetic performance traits. A second cohort is being grown to follow growth in terms of biomass and projected surface area. We will sample buds and blooms from this cohort to determine floral tissue carbon content and estimate carbon accumulation in developing flowers. Finally, we will use a mathematical modeling approach to estimate cumulative phloem carbon import to show how phloem demand changes over development and how floral photosynthesis may result in differential phloem import.

Topic: Biogeography

A-704

Tracking the insular radiation of Kadua (Rubiaceae) across the Hawaiian conveyer belt

Author: Isaac Lichter-Marck, Michael Landis, Felipe Zapata, Bruce Baldwin, Nina Ronsted, Sarah Swiston, Fabio Mendes, Warren Wagner, Kenneth Wood
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Island plants are ideal systems for the study of fundamental evolutionary processes such as dispersal and diversification, but our understanding of insular plant radiations has long been limited by the difficulty of estimating robust phylogenetic relationships and tracking the timing of island evolution in the absence of fossils. We use target capture sequencing with Angiosperms353 baits to reconstruct the evolution of a fascinating, yet understudied lineage of Hawaiian endemic plants in genus Kadua (Rubiaceae). We densely sample Kadua from all major Hawaiian islands and infer relationships using concatenated and pseudo-coalescent (ASTRAL) approaches. We then jointly infer rates of dispersal and diversification, colonization and divergence times, as well as gather relative support for key biogeographic hypotheses using TimeFIG, an innovative model of biogeography implemented in RevBayes. A unified spatio-temporal framework based on phylogenomic and paleogeography-aware approaches provides an exciting path forward for studying insular radiations despite uncertainty caused by unresolved phylogenies and lack of fossils.

Topic: Phytochemical

A-705

Root-derived phenylpropanoids are necessary for normal growth of Arabidopsis

Author: Chase Hearn, Fabiola Muro-Villanueva, Clint Chapple, Josh Widhalm
Affiliation: Purdue University

In vascular plants, phenylpropanoid metabolism is essential for the deposition of lignin, a polymer comprised of hydroxycinnamyl alcohol subunits that fortifies cell walls and facilitates water transport. Attempts to manipulate subunit composition have raised new questions surrounding the role of lignin in plant development. Dwarfism induced by lignin modification is often attributed to impaired vascular development, however, the occurrence of some lignin-modified plants with intact vasculature suggests an unexplored role linking phenylpropanoids to plant growth regulation. *Arabidopsis* mutants that deposit lignin either comprised exclusively of sinapyl alcohol or hydroxycinnamaldehyde subunits have enhanced saccharification potential without severe growth penalties. In contrast, combining these mutations severely compromises growth, and perturbs lateral root and root hair development. We found that supplying this mutant with exogenous coniferyl alcohol or its lignan dimer, pinoresinol, complement these phenotypes with high specificity. We also observed complementation with dimethylpinoresinol, which cannot be incorporated into lignin, suggesting pinoresinol acts independently of lignification. To further investigate the origin of these phenotypes, we performed grafting experiments and found that wild-type roots are sufficient to fully restore the growth of mutant shoots, and that mutant roots can impose dwarfism on wild-type shoots. Metabolic profiling revealed mutant roots are depleted in coniferyl alcohol and pinoresinol, suggesting these phenylpropanoids may have uncharacterized roles in plant development. Together, our results provide evidence for phenylpropanoids in the regulation of plant growth and development.

Topic: Ecophysiology

A-706

Beauty is Skin Deep: Obscured Chlorophyll is Photosynthetic in Zinnia elegans Flowers

Author: Amelie LeTierce, Monica Ruuska, Jessica Savage
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Chlorophyll is central to light harvesting for photosynthesis in leaves, but its functional role in flowers, particularly in visually non-green tissues, remains ambiguous. In this poster, we present findings from a comparative study of floral color, pigment content, and photosynthetic performance in six horticultural varieties of *Zinnia elegans*, a species with wide variation in flower color. Developing flowers were studied as buds, bursts, and blooming flowers. We found that floral chlorophyll content was similar in buds and bursts of all varieties, but varied in blooms. In blooms, chlorophyll was concentrated in petals and present in all varieties, including those without visibly green petals. In non-green varieties, flavones and carotenoids were abundant, perhaps obscuring chlorophyll reflectance. Net photosynthetic capacity (measured at 600 umol photons / m^2 / s) was positively correlated with petal chlorophyll content across and within varieties, demonstrating that petal chlorophyll is functionally related to floral photosynthesis. Apical bloom flowers had the highest petal chlorophyll content and net photosynthetic capacity. These results reveal that floral pigmentation is continuous rather than discrete, with petals showing varying levels of chlorophyll regardless of dominant visible color. This variation illustrates an ecological trade-off in petal color between contrast for pollinator attraction and chlorophyll content for light-harvesting and floral photosynthesis. Thus, petal color reflects a balance between reproductive strategy and physiological function in Zinnia elegans.

Topic: Physiology

A-707

The role of ethephon and gibberellic acid on fruit maturation of the cut-leaf Monkeyflower

Author: Aidan Van Dalen, Allison Yee, Jesus Martinez-Gomez, Benjamin Blackman
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Plant hormones regulate all aspects of plant growth and are important for environmental plastic response. Previous work in our lab has shown that gibberellic acid – a plant growth regulator responsible for elongation and flowering – can modulate fruit maturation rate

in the cut-leaf monkey flower Mimulus laciniatus (Erythranthe laciniata). Endemic to the Sierra Nevadas, the rate of fruit maturation in this plant is dependent on the narrow flowering season. Ethylene is another hormone that is known to play an integral role in the flowering and ripening of fruits in plants, such as bananas and avocados. This study aims to understand if ethylene also plays a role in fruit maturation and test if there is cross-talk between the ethylene and gibberellic acid pathways during fruit maturation. We grew M. laciniatus in cold growth chamber conditions to mimic the plants' native habitat. Following germination, the plants were sprayed twice a week after being split into four hormone treatment groups: water control, a "low" ethephon solution, a "high" ethephon solution, and a combined group treated with a "low" ethephon solution and gibberellic acid. To determine the effects of these hormones, the dates of three key developments were monitored: floral anthesis, onset of fruit maturation and completion of fruit maturation. Preliminary results indicate that plants treated with even "low" ethephon treatment twice a week for three weeks failed to flower, ultimately resulting in senescence and death. This indicates that ethylene perception may be age dependent; in ongoing experiments we are applying ethephon at later developmental timepoints. This experiment provides insight into whether or not ethylene activates independently of gibberellic acid, revealing if the two hormones share the same pathway in fruit maturation.

Topic: *Systematics & Taxonomy*

A-708

Phylogenomics of the Hemiparasitic Genus Cassytha (Lauraceae)

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Parasitism has evolved in angiosperms at least 12 times, resulting in similar morphological, cellular, and genetic changes in these organisms. One such example is *Cassytha*, the only parasitic genus of Lauraceae. *Cassytha* is a vine-like twining obligate hemiparasite, that attaches to its host and uses its haustoria to graft to the vascular tissue of the host to acquire nutrients and water. *Cassytha* is nearly endemic to Australia, where 18 out of 20 currently accepted species are found. One species, *C. filiformis*, is also found circum-equatorially, and two species are found disjunct, in southern Africa. The delimitation of species within *Cassytha*, their phylogenetic relationships, and the position the genus within the family remains poorly understood. Previous molecular work on *Cassytha* has used one to few placeholder species in broader phylogenetic work conducted on Lauraceae. Our prior work used a combination of target plastid and nuclear non-coding sequences on an extensive sample of *Cassytha* individuals, to delimit species and construct a species-level phylogeny. We have used that molecular analysis to guide our sampling of the genus to capture as much diversity as possible, and currently, have sequenced 60 individuals (including within *Cassytha* and green Lauraceae outgroups) through Next Generation Sequencing methods to assemble and annotate complete plastid genomes, nuclear ribosomal arrays, and near-complete (protein-coding) mitochondrial genomes as a comprehensive dataset to assess backbone structure within Cassytha. Our work also has reinforced the exact position of *Cassytha* within Lauraceae, as well as uncovered the initial split as well as phylogenetic relationships within the genus. Furthermore, a complete library of annotated plastids provided the opportunity to conduct substitution analyses (dN/dS) to assess the variance of selective pressures between different gene families, and as well as between different taxa. This provided a springboard to investigate structural differences in the plastid genome in the genus and uncover multiple instances of structural diversity present in *Cassytha*.

Topic: *Molecular Ecology*

A-709

Green Signals: eDNA and Canopy Signatures Track Biodiversity Across the Western Cape's Managed and Disturbed Landscapes

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Traditionally, plant community research has relied on field surveys and on-ground measurements of environmental variables. Modern remote sensing now provides high-resolution data at the global scale, detecting a wide range of plant traits and geochemical features. However, remote sensing primarily captures canopy-level information, missing smaller ecosystem components. Combining remotely sensed traits with ground-based biodiversity measurements presents an opportunity for large-scale, less labor-intensive biodiversity studies. Yet, we do not understand how locally measured biodiversity metrics and remotely sensed diversity metrics relate to each other and which relationships are relevant for monitoring and management.

The BioSCape program is a collaboration between U.S. and South African agencies and institutions. Using the Greater Cape Floristic Region as a study system, the project aims to understand the organization of biodiversity, and its function and importance for ecosystem health and services. Our BioSCape project, one of many funded projects under BioSCape, forges a connection between hyperspectral imagery and an emergent method of biodiversity quantification: environmental DNA (eDNA) sampling. The Berg and Eerste Rivers, two watershed systems sharing headwaters and surrounded by diverse land uses including agriculture, wine farms, urban areas, and pristine reserves, were surveyed using airborne data from AVIRIS-ng and PRISM imagers in 2023. 540 eDNA samples were gathered from these river systems, and DNA metabarcoding libraries were built to assess holistic biodiversity from across the entire tree of life. We ask 1) Do functional and taxonomic biodiversity relate to each other along the Berg and Eerste River? 2) How does biodiversity organize itself along these rivers? By which dimensions? How does human intervention affect biodiversity? 3) How do invasive plant species affect non-visible facets of biodiversity?

We find that taxonomic and functional diversity are related to each other across the Berg and Eerste River systems. Further, we find that biodiversity, both visible and non-visible, organize by dominant plant community type, human modification index, and by distance from the headwaters. Invasive plants were found to have an effect on local microbial and fungal biodiversity. This holistic view of the earth has broad applications for restoration monitoring, understanding food webs and communities, and understanding the effects of natural resource management.

Topic: *Molecular Ecology*

A-710

Abiotic and hormone factors can modulate fruit maturation plasticity in an endemic Monkeyflower

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Plasticity – the ability for a single genotype to produce different phenotypes in response to environmental conditions – is a common mechanism employed by non-motile organisms to survive in a changing environment. Two sister species in the yellow monkey-flower clade *Mimulus* (syn. *Erythranthe*) exhibit a plastic response to cold temperature that is novel compared to their closest relatives. In cold conditions, *M. laciniatus* and *M. nasutus* exhibit a phase of delayed development between flowering and senescence where fruits form but do not fully mature in a phenotype termed the cold-dependent developmental delay (CDDD). In this study, we test whether additional abiotic or biotic stress and hormones trigger an exit from CDDD, prompting normal seed maturation under cold conditions. We performed two experiments. In the first, we grew *M. laciniatus* and *M. nasutus* in cold growth chamber conditions to induce CDDD. Once individuals enter CDDD we split the plants into experimental treatments designed to mimic natural environmental stressors: drought conditions, heat, and herbivory. To measure CDDD progression, we tracked the number of buds, flowers, and fruits on each individual weekly and calculated the rate of fruit maturation. Our results show that simulated herbivory and high temperatures are sufficient to promote normal fruit

maturation only in the mountain-endemic *M. laciniatus* but not in the wider-ranging *M. nasutus*, indicating that this plastic response may be an adaptation to high elevation environments for *M. laciniatus*. Interestingly, drought, an important environmental factor for these plants, did not promote CDDD exit and rapid fruit maturation in either species. In the second experiment, we investigate the role of hormones – specifically gibberellin – in CDDD. Using a similar method from above, we induced CDDD in *M. laciniatus* and applied GA to treatment 3 groups: applications of gibberellin to the apical meristem, designed as a global application; applications of gibberellin directly to fruits, designed as a local application; and a control group. Our results showed that both global and local applications of gibberellin are sufficient to increase rates of fruit maturation in *M. laciniatus*, thereby overriding CDDD. These findings will build our understanding of how plants use plastic traits to contend with and adapt to environmental fluctuations.

Topic: Biodiversity Informatics & Herbarium Digitization

A-711
Yes, Barnard College Has A Herbarium of Her Own

Author: Hilary Callahan
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In 2025, we revived, digitized and analyzed Barnard College's 19th century herbarium of ~4,000 specimens (BCBL). From the College's founding in 1889, this resource flourished alongside the 1891 chartering of the New York Botanical Garden and the subsequent 1896 transfer to NYBG of Columbia University's many botanical books and approximately 400,000 specimens. By 1900, both Barnard College and Columbia University had relocated from midtown to northern Manhattan, with only Barnard bringing along "a herbarium of her own." Then, this herbarium supported botany curricula designed by Dr. Emily Gregory, the first Barnard faculty member appointed by Columbia, to teach Barnard students exclusively. She and her successor Dr. Herbert Maule Richards emphasized experimentation and research while also respecting natural history and systematics as foundational. Today, the physical and digital BCBL herbarium supports instruction about systematics and collections-based research while also enlivening lessons and projects about biogeography, ecological genetics and biodiversity conservation on an urbanized and changing planet.

Components of the herbarium include: (i) specimens collected and prepared pedagogically, (ii) ex siccatae that connected instructors and students with a wider network of collectors, (iii) over 900 specimens from the extensive, high-quality personal herbarium of an ambitious botanical amateur, Sarah Louisa Clarke, and (iv) collections curated and donated by leading botanists of the day, some members of the Torrey Botanical Club or on staff at NYBG, and others at institutions in the mid-Atlantic or beyond. These latter portions of the collection are a useful demonstration of the pacing and spatial details of collecting in the greater New York area between the mid-1800s and early 1900s, and a basis for comparison with NYBG's ongoing New York City Eco-Flora project. Beyond supporting botanical pedagogy and urban plant conservation, the BCBL herbarium was and is a site of collaboration, class negotiation, and feminist resistance, all situated within the history of environmental knowledge production and women's education in the United States.

Topic: Phylogenomics

A-712
Non-monophyletic Compositae: investigating phylogenomic conflict in different target-capture datasets of the sunflower family

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The once considered indisputable boundaries of the Asteraceae, one of the largest angiosperm families, have recently been called into question in light of recent phylogenomic results. Uncertainties arise in the relationships between the family Calyceraceae, Asteraceae subfamily Barnadesioideae, and the remaining Asteraceae, marked by weak branch supports and topological conflicts. In the context of phylogenetic classifications, this could have implications for the classification of Asteraceae and Calyceraceae, thus warranting careful consideration of the phylogenomic results. Despite the recent spotlight, reports of confusing relationships among these three clades have consistently arisen with the use of large nuclear, target-capture datasets and coalescent-based phylogenetic methods, and seen with at least two different bait sets, the Angiosperm353 and Compositae1061 sets. Here, we reanalyze data from multiple studies using these two bait sets, focusing on disentangling the incongruences in the relationships between these three clades and obtaining a deeper understanding of these datasets.

Topic: Ecology

A-713
The National Ecological Observatory Network (NEON) Data Source and Species Richness Examples

Author: Marian Lea
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The National Ecological Observatory Network (NEON) is a large-scale, 30-year ecological data collection program fully funded by the U.S. National Science Foundation. NEON generates over 180 data products at 81 sites distributed throughout 20 eco-climatic domains across the U.S. These data encompass broad spatial and temporal scales to enable understanding of the key drivers and responses of environmental change across the USA. The observatory became fully operational in 2019, though some data collection began as early as 2012. Over ten years into data collection, and in the sixth year of full operations, we use the plant presence and percent cover data product to explore the spatial and temporal scales that make NEON so unique.

Looking at all the NEON plant presence data, 81% of taxa recorded are to species or lower, ranging from 53% to 94% among sites. Species richness tends to be lower at high latitudes, and peaks around 35°N. Plots in the east generally have more species than those in the west, with a peak around 85°W. Looking at NLCD class, cultivated plots have low richness (mean = 46 species), as do NLCD classes only present in NEON plots in Alaska (dwarf scrub mean = 37, sedge herbaceous mean = 48), and emergent herbaceous wetland plots also have low richness (mean = 34). Grasslands (mean = 92), including pasture hay (mean = 97), tend to have higher species richness, as do non-evergreen forests (deciduous forest mean = 102, mixed forest mean = 106, woody wetland mean = 107). Average richness per plot ranges from 27 species at the Konza Prairie Agroecosystem (cultivated crops) to 232 average species across all NLCD classes at the Jones Center at Ichauway (cultivated crop mean = 128, deciduous forest mean = 246, evergreen forest mean = 253, mixed forest mean = 261).

Focusing on one site as a simple demonstration of how change can be observed with NEON Plant Diversity data, we explore pre- and post-burn community characteristics at the Soaproot Saddle site in California, many of which were impacted by the 'Creek Wildfire' in 2020. Mean species richness of the plots burned in 2020 was historically higher than in unburned plots, but does show a decrease after the fire and then a substantial rebound in the following years. Shannon diversity has similar trends. Principal Components Analysis of relative abundance of plant family cover shows distinct post-fire grouping of plots impacted by the fire compared to plots that did not burn. This initial exploration is a starting point for exploring which families vary consistently in response to fire at this site.

Topic: Biodiversity Informatics & Herbarium Digitization

A-714
The SEINet Network of herbarium specimen data

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The SEINet Network is an online database for over 24 million herbarium records from more than 460 herbaria across North America. Herbaria can share snapshots of locally-managed data or use the web portal as their central database of record, taking advantage of built-in tools for duplicate harvesting, data cleaning, and more. Collections in SEINet are organized into regional consortia–such as the Consortium of Midwest Herbaria or the Texas and Oklahoma Regional Herbarium Consortium–that are accessed through different websites but share a central database. This shared data commons allows herbaria to leverage tools that minimize duplication of effort (e.g., batch georeferencing) and maximize access to and use of the data. The SEINet Network includes taxon pages, checklists, and other tools that enable researchers, educators, land managers, and the public to search, view, map, download, and analyze herbarium specimen data from multiple sources in one place. Data in SEINet conform to international data standards (e.g., Darwin Core) and are highly findable, accessible, interoperable, and reusable (FAIR), making them ready for research across multiple botanical disciplines, from taxonomy to ecology and applied plant science.

Topic: Systematics & Taxonomy

A-715

Exploring the rapid evolution of a mega-diverse clade in Africa and Madagascar: A case study from Vernonieae (Asteraceae).

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Vernonieae is one of the most species-rich tribes in the sunflower family and notable for its challenging taxonomic history. A key challenge for taxonomists who work with this group has been characterized by what is referred to as "The Vernonia Problem", which refers to a large and poorly-defined core genus. Throughout much of its taxonomic history, *Vernonia* was considered among the largest plant genera on Earth; however, it was significantly reduced in 1999 to comprise only 20 species from the Americas. Despite significant taxonomic revision for this tribe in North and South America, more than 300 species from the eastern hemisphere (largely Africa and Madagascar) remain in the genus *Vernonia* that await recircumscription and placement into an alternative, segregate genus. Vernonieae is currently represented by 12 subtribes and 66 genera across its range in the eastern hemisphere. A critical priority for advancing systematic knowledge of this group is a concerted integrative taxonomic effort that combines a well-resolved phylogeny and detailed comparative morphological analyses. This study highlights important advances in developing a well-resolved, infratribal phylogenetic framework to test the monophyly of genera currently recognized in Vernonieae from the eastern hemisphere and to guide subsequent taxonomic revision. We present results from a comparative phylogenetic analysis that includes the largest taxonomic sampling to date of species of Vernonieae from across the range of this tribe in the eastern hemisphere. We highlight the taxonomic implications of the results from these analyses as well as priorities for future sampling to guide this integrative taxonomic work going forward.

Topic: Comparative Genomics/Transcriptomics

A-716

Phylogeny and Comparative Genomics of Plastids in the genus Lobelia in the Mexican Transition Zone

Author: Miguel Perez Perez, Laura Lagomarsino, Arturo Castro-Castro, Richie Hodel, Tina Ayers
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In Mexico alone, there are approximately 100 species of *Lobelia* (Campanulaceae), of which 83 are endemic to the Madrean-pine-oak woodlands of the five principal mountain systems known as the Mexican Transition Zone (MTZ). These 100 species represent about 23% of the 435 total *Lobelia* species worldwide. *Lobelia* is circumscribed in 18 sections based on morphological characters. The "Mexican lobelias" belong to five of the eighteen sections: sect. *Cryptostemon*, sect. *Homochilus*, sect. *Lobelia*, sect. *Stenotium*, and sect. *Tylomium*.

Using 43 species of *Lobelia*, including 20 endemic species from the MTZ, we assembled and annotated new plastomes, generated a plastome phylogeny focused on the five sections of *Lobelia* that occur in the MTZ, and analyzed and compared the chloroplast genomes to identify differences in their genomic structure.

A phylogeny using 44 coding genes supported the monophyly of four of the five sections of the Mexican lobelias. Most Mexican *Stenotium* species were sister to the sections *Cryptostemon, Homochilus*, and *Tylomium* but a few Mexican *Stenotium* were early diverging members of sect. *Lobelia* or nested in taxa recognized as the genus *Diastatea*.

Some Mexican lobelias exhibited complex rearrangements in their chloroplast genomes, with inversions primarily occurring in the invert repeat (IR). Additionally, we found evidence of IR reduction in a few species of *Lobelia*. Our preliminary findings indicate that the chloroplast genomes within the Lobelioideae subfamily present an exciting new avenue for exploring and understanding the intricate evolution of chloroplast genomes.

Topic: Conservation Biology

A-717

Conserving intraspecific variation in endangered Dalea foliosa by optimizing ex situ collection design

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The establishment and maintenance of ex situ populations can play a pivotal role in safeguarding imperiled plant species from extinction. In order for ex situ conservation efforts to be as effective as possible, these populations must be designed to efficiently capture and conserve a representative sample of the intraspecific variation present within naturally occurring populations. Traditionally, ex situ collections have emphasized the inclusion of individuals from geographically disparate portions of a species' native range, or, more recently, have attempted to maximize putatively neutral genetic variation. However, as populations of a given species face variable selective pressures based on differences in their local environments, local adaptation can give rise to genetic and phenotypic variation which is adaptive in nature, conferring fitness benefits under certain selection regimes. Designing ex situ collections which aim to maximize adaptive intraspecific variation may prove key to preserving species' evolutionary potential, leaving them better suited to adapt to rapidly changing natural environments. In this study, we investigated neutral and putatively adaptive genetic and phenotypic intraspecific variation within *Dalea foliosa*, with the goal of informing ongoing conservation efforts for this species. We propagated individuals representing 244 unique wild-collected maternal lines from seeds from across the species' native range and cultivated them under standardized conditions in a common garden design. We collected a wide variety of phenotypic data aimed at capturing differences in seed germination rate, seedling establishment, growth rate, survival, and flowering phenology. We also developed a reference genome and conducted whole genome resequencing for each individual in our study. Analysis of our data showed that some genetic loci and phenotypic traits showed associations with environmental conditions, potentially indicating adaptation of populations to their local environments. We then use variation in both neutral and adaptive genetic and phenotypic traits to design efficient and effective ex situ collections of *D. foliosa*. The results of this study have important implications for the ex situ conservation of not only *D. foliosa*, but also other species of conservation concern which exhibit fragmented distributions over highly variable environmental ranges.

Topic: Plant genome skimming: special uses and future potential

A-718

Ultrabarcoding in the classroom for teaching genomics and plant evolutionary biology

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Teaching and research are often treated as distinct duties competing for an academic's time and resources. However, bringing research into the classroom combines these aims, with many benefits for teachers and students alike. Plant organellar genomes are an excellent way to introduce numerous genomic concepts and tools, including population genetics using a reference genome, *de novo* genome assembly, annotation, comparative genomics, and data submission to GenBank. I discuss a set of student-generated resources, projects and publications resulting from Course-Based Undergraduate Research Experiences (CUREs) involving organellar genome assembly and comparison of low-coverage whole-genome shotgun datasets. These projects have resulted in important biological findings, valuable new resources, and a demonstrable track scientific track record for students to build a career on. I'll highlight projects looking at sunflowers, lichens, Cannabis, barn swallows and flax.

Topic: *Ecology*

A-719

Ecological diversification of the oaks: tests of adaptive evolution across environmental niches using reflectance spectra and spectrally-derived traits

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Topic: *Macroevolution*

A-720

Biogeographic History and Diversification of Orobanchaceae: Host specificity and Continental shifts as Drivers of Evolutionary Adaptation

Author: Emmanuel Chukwuma, Maribeth Latvis, David Tank
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Orobanchaceae represents the largest clade of parasitic plants with 106 genera and ~2300 species. The family exhibits complex evolutionary trajectories driven by host specificity and ecological adaptation. This study employs dense taxonomic sampling to refine our hypotheses related to biogeographic history and diversification patterns, while incorporating host preference as a potential key driver of diversification. We employ Bayesian methods to reconstruct the family's historical lineage divergences, determine transition rates, and assess the impact of geological and climatic events on species distribution. We further evaluate how host specificity influences lineage diversification, ecological range shifts, and adaptive responses across parasitic strategies. We posit that host specificity has influenced phylogenetic divergence patterns, with generalist taxa exhibiting broader geographic ranges compared to specialist lineages, which may demonstrate more constrained dispersal events. Findings from our study provide insights into a broader understanding of the evolution of parasitic plants, how they adapt to range shifts, and respond to historical geological transformations.

Topic: *Phylogenomics*

A-721

Phylogeny and Biogeography of the genus Lobelia in the Mexican Transition Zone

Author: Miguel Perez Perez, Laura Lagomarsino, Laymon Ball, Arturo Castro-Castro, Richie Hodel, Tina Ayers
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The five major mountain ranges in Mexico, the Mexican Transition Zone (MTZ), provide a unique opportunity to study the relationships of closely related species restricted to a single range. These mountains are a transition zone because they have a mix of organisms from the temperate parts of the Americas and the tropics. Here, we focus on the angiosperm genus *Lobelia* (Campanulaceae). There are approximately 100 *Lobelia* species in the MTZ; 83 are found only there. Most species have small, blue flowers and nectar guides consistent with insect pollination, but six have large, red flowers and lack nectar guides consistent with hummingbird pollination. Both groups have species with a unique floral feature, a complex nectar spur. We present preliminary results on molecular data gathered from a nuclear probe set developed for *Burmeistera* (subfamily Lobelioideae). We built a comprehensive phylogenetic framework for *Lobelia*, focusing on Mexico's highly diverse and endemic lineages. This framework addresses broad evolutionary questions about pollinator shifts, hybridization, and biogeography. Shifts in pollinators from insects to hummingbirds have occurred in at least two different lineages of Mexican lobelias. We identified one recently described species that most likely resulted from recent hybridization. We present a time-calibrated tree to test specific biogeographic hypotheses in the MTZ, including 1) geographic barriers between lineages, 2) long-distance dispersal between mountain ranges, and 3) biogeographic patterns associated with pollination syndrome or the presence of nectar spurs.

Topic: *Evolutionary history of the Gnetales*

A-723

Fossil history, geological antiquity, and structural relationships of gnetophytes

Author: Gar Rothwell
Affiliation: Ohio University; Oregon State University

Among the five clades of seed plants with living representatives, gnetophytes are second in complexity only to flowering plants. The fossil record documents that both clades underwent their initial evolutionary radiations during the Early Cretaceous, but that gnetophyte diversity diminished thereafter, while flowering plants continued their explosive evolution to become the dominant living land plant clade in both species richness and percent cover. A critical evaluation of fossils attributed to gnetophytes reveals that while species as ancient as the Permian are assigned to the group by some authors, specimens with synapomorphies that allow for confident placement among Gnetales occur only from the Late Jurassic onward. The oldest evidence for putative gnetophytes consists of polyplicate, boat-shaped pollen from the Permian. Convincing gnetophyte megafossils occur first in the Late Jurassic, and evolutionary diversification of the clade is represented by an increasing diversity of fossils during the Lower Cretaceous. A review of paleontological evidenve reveals that there is a frustrating paucity of fossils with convincingly gnetalean diagnostic characters, prompting the expectation that far more paleontological evidence will be required to critically test phylogenetic hypotheses developed using nucleotide sequence data.

Topic: *Phytochemical*

A-724

Anthocyanins in Viola sororia identified by LC-MS-MS

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The North American common meadow violet, *Viola sororia* Willd., is a blue-purple flowering plant part of the Violaceae family. *V. sororia* is natively found in the greater eastern region of the United States, Canada, and Mexico. The vibrant colors of *V. sororia* are attributed to a class of flavonoid molecules called anthocyanins. Anthocyanins are a common type of plant pigment characterized by a flavylium skeleton modified with hydroxy, methoxy, and sugar substituents. These molecules also undergo more complex modifications such as acylation with organic acids. The degree of hydroxylation on the aglycone, or core structure, corresponds to absorption at higher wavelengths and results in different petal colors. The types of and relative amounts of athocyanins and other factors such as pH, copigmentation, or modifications contribute to the observed color of the flower. The enzymatic pathways that produce anthocyanins are highly conserved among plants and are characterized, however, the exact identity of the anthocyanins within *V. sororia* were not yet identified.

This poster presents the 16 anthocyanins and 2 flavanol derivatives found in *V. sororia* using methanolic extraction and using liquid-chromatography and tandem mass spectrometry. Positive and negative mode electrospray ionization was used to differentiate between anthocyanins and flavanols, which share the same precursor ion and fragmentation patterns. The two main anthocyanins were cyanidin and delphinidin-based derivatives with hexose, rhamnose, rutinose, and acetyl groups as the main substituents. In addition, myrcetin-based derivatives were also identified with the same main substituents. This poster demonstrates a robust qualitative method to investigate the anthocyanins in *V. sororia* which can be applied to other species.

Topic: *Conservation Biology*

A-725

Toward a Global Strategy for the Ex-Situ Conservation of Cactaceae in the Face of Climate Change

Author: Tania Hernandez (Sanders)
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Cactaceae has recently been recognized by the IUCN as one of the most threatened plant families globally. Climate-based extinction risk models suggest an even more severe outlook, with projected increases in aridity and prolonged drought posing critical threats to species survival throughout the Americas. These escalating environmental pressures are straining the capacity of botanical gardens and conservation institutions to sustain living collections, making *ex situ* conservation increasingly difficult. The

situation is particularly urgent for Cactaceae, whose highest levels of diversity are concentrated in developing countries—regions often limited by scarce financial resources, institutional instability, and vulnerability to political, economic, and climate disruption. *Ex situ* conservation efforts, in particular, are further hindered by extremely stringent international regulations that restrict the collection, export, and exchange of plant material, creating significant barriers to both research and global collaboration.

In this context, we propose a collaborative and technology-forward framework to improve global outcomes for the *ex situ*conservation of Cactaceae. A central element of this strategy is the creation of an institutionalized metacollection—a coordinated, global database of living cactus collections. This tool will allow us to assess the current genomic representation of species in botanical collections, perform GAP analyses, and collectively prioritize geographic areas and taxa for new collection efforts. We propose that this initiative be coordinated through a new BGCI-led Global Conservation Consortium for Cactaceae, modeled after existing consortia for other high-risk plant groups. Such a structure would also facilitate the legal and ethical exchange of germplasm, including seeds, DNA samples, and herbarium material, among participating institutions.

In parallel, we emphasize the need to develop, share, and standardize workflows for genomic and genetic research in Cactaceae, which present unique DNA extraction and sequencing challenges due to the prevalence of polysaccharide mucilage, secondary metabolites, and latex in many species. Partnerships with local institutions are essential to obtain local collecting permits, perform in situ HMW DNA extractions, and support capacity building in source countries. The development and transfer of specialized protocols will expand global participation in Cactaceae conservation science and help overcome current barriers in resource-limited regions.

Finally, we explore the potential of emerging conservation technologies for Cactaceae. Cryopreservation of seeds and pollen appears particularly promising, given the family's adaptation to dry conditions and the relative ease of transporting desiccated reproductive material across borders. Additionally, tissue culture—particularly in the form of callus propagation—may offer a dual benefit: generating sufficient clean tissue for DNA extraction from small, rare, or single-individual accessions, and providing a medium that can be exchanged internationally with fewer restrictions than live plants. Tissue culture lines can also be cryopreserved and banked for future sequencing efforts or propagation technologies.

In conclusion, the future of Cactaceae conservation will depend on cross-border collaboration, the use of innovative technologies, and equitable partnerships with institutions in the regions where these plants naturally occur. By building a shared infrastructure for research, propagation, and information exchange, we can ensure a more resilient and coordinated response to the urgent threats facing this iconic plant family.

Topic: Hybrids and Hybridization

A-726

Population genetics of the Southwest Texas red oaks: characterizing North America's most elusive oak

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Successful conservation efforts require species to be clearly delineated in order to locate individuals on the landscape and properly concentrate resources to help threatened populations. Hybridization and admixture can complicate efforts to determine species boundaries, and hybrid individuals are often regarded as abnormal or unimportant in a conservation context. This is despite many examples demonstrating how hybridization can be a crucial strategy for adaptation, especially within plants. Here, we describe our research delineating species boundaries in a group of red oaks found in the Chisos and Davis Mountains of southwest Texas, with a focus on *Quercus tardifolia* C.H.Muller (1936), the late leafing oak, which was thought to have gone extinct in 2011 before the discovery of a tree in Big Bend National Park in 2022 and other locations thereafter. Using restriction-site associated DNA sequencing (RADseq), we genotyped 166 red oaks, including 10 individuals identified as *Q. tardifolia* or *Q. aff. tardifolia* (7 wild, 3 herbarium specimens), individuals of two other rare species endemic to the Chisos (*Q. graciliformis* and *Q. robusta*), individuals from more widespread species (*Q. gravesii*, *Q. hypoleucoides*, and *Q. emoryi*), and other taxa. Sequences were quality controlled and aligned to the *Q. rubra* reference genome before loci were called and filtered using Stacks. We then ran STRUCTURE clustering analyses, calculated population genetic statistics in putative hybrid and parental taxa, and modeled hybrid lineages using the phylogenetic Species Networks applying Quartets method (SNaQ). Our results across analyses consistently inferred all sampled wild *Q. tardifolia* individuals to be hybrids of lineages composed primarily of *Q. gravesii* and *Q. hypoleucoides*, with genetic patterns most resembling those of an F1 hybrid class. Admixture was also observed in other taxa, but more analyses and more extensive sampling efforts are required to better characterize the relationships in this group of red oaks. While these findings suggest that *Q. tardifolia* may not be a distinct species, we maintain that the entity *Q. tardifolia* remains a set of potentially important populations in this species complex.

Topic: Macroevolution

A-727

Do rates of phenotypic evolution scale with body size among eucalypts?

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Measuring and characterizing variation in evolutionary rates is critical for understanding the factors driving disparities in levels of biodiversity across different taxa (e.g., angiosperms vs gymnosperms) and regions (e.g., temperate vs tropical habitats). Biologists have long recognized that body size is intimately related to an organism's life history, though there are conflicting hypotheses concerning how evolutionary rates scale with body size. On one hand, the generally smaller population sizes and longer generation times associated with large organisms should lead to relatively slow accumulation of genetic/phenotypic diversity. At the same time, stronger genetic/phenotypic drift in small populations could also cause larger organisms to exhibit relatively fast evolutionary rates. Accordingly, while both larger animals and plants tend to exhibit slower rates of molecular evolution, rates of phenotypic evolution instead appear to be faster among larger animals in some vertebrate clades. Notably, relationships among body size and rates of phenotypic evolution remain generally understudied—particularly among plants. Here, I leverage a recently-published phylogenomic framework along with continuous stochastic character mapping—a novel phylogenetic comparative technique—to test whether body size is associated with variation in rates of leaf/flower evolution among eucalypts (genera *Angophora*, *Corymbia*, and *Eucalyptus*). Eucalypts are an iconic Australian radiation of trees and shrubs ranging from about 1 to 100 meter in height, thus constituting a fantastic "natural experiment" for investigating relationships among body size and evolutionary rates among plants.

Topic: Biodiversity Informatics & Herbarium Digitization

A-729

Conservation Gap Analysis of Artocarpus (Moraceae)

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In response to *in-situ* threats to plant biodiversity, germplasm repositories such as botanic gardens and kin institutions have demonstrated substantial capabilities for conserving a variety of threatened and other special status taxa in a typically *ex-situ* context. Seed banking, for one, has emerged as a popular and (importantly) often cost-effective conservation method for most plant species. Many tropical taxa, though, are considered "exceptional"—their seeds cannot be stored this way long term under standard conditions. As a result, although alternative technologies and systems are under development (e.g., micropropagation or cryopreservation), maintenance of full-scale living collections continues to be a critical strategy to conserve such clades' biodiversity outside of the wild. Such collections, especially individually, are commonly challenged by logistical, permissions, and funding constraints. For example: complexities of data access and transmission, captive population "lifecycles", or basic spatial limitations—this last issue being an especially significant consideration when dealing with large, long-lived, woody species. Formation of decentralized, collaborative networks can counteract some issues by facilitating the sharing of data, plant materials, and fiscal and other resources. However, managing collective holdings still necessarily involves balancing of the representation of and investment into inter- and intra-specific botanical diversity. Drawing on work especially in research around crop wild relatives (CWR), as well as studies exploring the effectiveness of environmental and geographic surrogates for genetic variation, plant conservation scientists have increasingly taken up a strategy of "gap analysis" to try and address these entangled obstacles of data integration and collections management in conservation planning and prioritization. As a wholly exceptional, speciose, and variably distributed clade of trees—one encompassing crops and CWR, as well as taxa facing several different levels of extinction

threat—the genus *Artocarpus* (breadfruit, Moraceae) is an ideal candidate for this type of study. I will here be presenting on the results of a corresponding conservation gap analysis for this genus: by synthesizing global collections and occurrence data to quantify existing *ex-situ* representation and *in-situ* conservation coverage for *Artocarpus* species, this work aims to facilitate identification of targeted opportunities for future conservation action among different regions and taxa.

Topic: Conservation Biology

A-730

Resilient Restoration: Drought Resilience Amongst Southern California Quercus agrifolia Populations on Tribal Lands

Author: Alexandra Hoff, Lluvia Flores-Rentería, Megan Jennings
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The Coast Live Oak (*Quercus agrifolia*) is a model species to investigate the global problem of climate change-induced mortality of culturally significant trees as it is facing threats such as drought, and high temperatures. As a foundational species, *Q. agrifolia* provides shelter and food for a variety of species and is culturally significant to our tribal partners and native peoples throughout the species' range. This species has a large distribution throughout coastal California and northern Baja California, populated by its two varieties: *Q. agrifolia* var. *agrifolia* and *Q. agrifolia* var. *oxyadenia*. The latter having more tomentose leaves and a more southern, inland distribution compared to *Q. agrifolia* var. *agrifolia* which could be anadaptation to drought and higher temperatures. We collaborated with local tribal communities to promote tribal resilience by researching climate impacts on this culturally significant plant, amongst others. Our first objective was to identify which variety and populations perform better under drought conditions. Our second objective was to assess levels of conservation concern through population genetic estimates. We predicted that trees from within the distribution of *Q. agrifolia* var. *oxyadenia*, where there is a hotter, drier climate, would be more resilient to drought. We expected genetic differentiation between the two varieties. We also hypothesized that the variety and populations with higher genetic diversity would be more tolerant to drought conditions (populations in *Q. agrifolia* variety *oxyadenia)*. With the permission of our tribal partners, we sampled *Q. agrifolia* acorns and leaf material from 8 populations across southern California, including tribal reservation lands, and leaf material from 18 populations for genetic material. In a greenhouse drought experiment, we grew these acorns and measured physical responses of plant performance such as survival, growth, and stomatal conductance. Our results did show significant differences based on variety, and we were able to identify poplations with higher performance. The differences in genetic diversity also varied significantly by variety, the populations were structured in three genetic clusters. These findings will be used by our tribal partners to inform conservation decisions and the drought-tolerant trees that survived the drought experiment were rematriated are being replanted to restore the tribal lands they were collected from.

Topic: Pteridology

A-731

Perine evolution in the fern group Elaphoglossum sect. Lepidoglossa (Dryopteridaceae)

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Ferns exhibit an incredible variation in the surface structure of their spores. This micromorphological diversity has proven useful for resolving taxonomic challenges—such as distinguishing morphologically similar species and defining larger groups within complex genera. In this study, we investigate spore micromorphology in the fern genus Elaphoglossum, with a focus on section Lepidoglossa —the most species-rich section of the genus, comprising over 200 species distributed across tropical regions. Members of this section are characterized by scaly laminae and scales with acicular marginal cells. Using scanning electron microscopy (SEM), we analyzed the perine structure of 100 species of sect. Lepidoglossa. Of these, 20 species were newly imaged and have not been previously published. Based on the SEM images, we scored six discrete morphological characters of the perine and built a character matrix for comparative analysis. Character evolution was optimized using the software Mesquite and an unpublished plastid phylogeny that includes approximately 72% of the species diversity within the section. We found that perines of species belonging to sect. *Lepidoglossa* typically have broad, continuous folds. Spiny perines evolved independently at least four times, and perforations at least five times within the section. Our character evolution analyses suggest that in general perine ornamentation in the section evolved from spines to irregular deposits to rough surfaces. Perines of the *E. muscosum* clade are morphologically distinct, having low spherical or hemispherical deposits called papillae —a character not observed elsewhere in the section. Our findings suggest that perine characters can provide meaningful phylogenetic signal within Elaphoglossum *sect. Lepidoglossa*.

Topic: Bryology and Lichenology

A-732

Rare and common lichenized fungi adapt to light availability, stand maturity, anthropogenic landscape impacts, and climate

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Rarity is an emergent trait arising from species' life history traits and environmental interactions. Lichens — long-lived, sessile symbiotic assemblages of fungi, algae, and bacteria — exhibit a high incidence of rarity. This study investigates the drivers and consequences of rarity by comparing the population genomics of three pairs of lichenized fungi with contrasting range sizes, morphologies, and life history traits: the common species Punctelia rudecta, Lepraria finkii, and Usnea strigosa, and their rare congeners P. appalachensis, L. lanata, and U. subfusca. We sampled 924 individuals from 36 sites from the southern and central Appalachian Mountains of eastern North America. Population genomic datasets for each species were generated by aligning short-read whole-genome shotgun sequences to high-quality reference genomes assembled from long-read sequences. Coding and noncoding sequences were separated and quality-filtered before downstream analyses. Recombination rates varied by genus and corresponded to observed reproductive morphology with the lowest rates observed in *Lepraria*, which reproduces asexually, and the highest rates observed in the included *Usnea* species both reproducing via sexual spores. Allelic richness was consistently higher in rare species than in common species. Isolation-by-distance, inferred from significant positive correlations between geographic and genetic distance using Mantel tests, was observed in all three rare species but absent in their common congeners. We used latent factor mixed models (LFMM) to perform genotype-environment association (GEA) analyses.

Topic: Biology of mycoheterotrophic and parasitic plants

A-734

Genomic, morphological, and fungal host variation in the mycoheterotrophic Corallorhiza maculata species complex

Author: Hana Thixton-Nolan, John Freudenstein, Craig Barrett
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Mycoheterotrophic plants exploit fungi for most to all nutritional needs, providing compelling model systems to study population-level variation across their known ranges. Previous research suggests that non-photosynthetic, fully mycoheterotrophic plant species predominantly display high host specificity, but few studies exist that quantify host associations across entire geographic ranges and if these associations are influenced by plant genotypes. Additionally, research regarding population structure, gene flow, and morphological differences has focused on a few populations which limits how we can develop conservation strategies for rare or endangered species. We are using the widespread *Corallorhiza maculata* complex to address questions of genomic and morphological variation across the geographic range from Mexico to northern North America. This complex contains *C. mertensiana, C. bulbosa, C. macrantha,* and *C. maculata* (*senso lato*), the latter with three varieties (*maculata, occidentalis,* and *mexicana*). These taxa vary in flowering time, floral morphology, geographic distribution, and fungal associations, but their degree of taxonomic and ecological distinctness are not well characterized. Our goal is to quantify genomic, morphological, and fungal host variation of the *C. maculata* complex across North America. Using a combination of reduced representation sequencing of nuclear DNA, floral morphometrics from 17 characters, and fungal ITS metabarcoding, we have found preliminary evidence that contradicts the distinction for the *C. maculata* complex based on earlier studies with microsatellite data. However, this lack of distinction is supported by prior research using plastid restriction site analysis and floral morphometry on a smaller sampling

size. For floral morphology, we identified clustering patterns from multivariate analysis for *C. maculata* vars. *maculata* and *occidentalis* suggesting that they may not be as morphologically distinct despite differences in flower shape and phenology. These two varieties are known to co-occur with overlapping ranges, and the differences noted may not be significant enough to differentiate the two varieties. We generated over 19,000 SNPs after filtering and linkage thinning and identified low F_{ST} between *C. maculata* vars. *maculata* and *occidentalis*. This suggests that they share recent common ancestry and lack a strong pattern of genetic differentiation, further supporting that these two species may not be genetically distinct as previously thought. The pattern between the two varieties was further supported by multivariate analysis with overlapping clusters. Furthermore, in our phylogenetic tree the two varieties did not form monophyletic groups and supports the lack of genetic differentiation but there were notable patterns of clustering. Our findings somewhat contradict previous research in the complex, suggesting that *C. maculata* vars. *maculata* and *occidentalis* are not completely distinct based on nuclear data. We expect to see distinct fungal taxa being targeted by *C. mertensiana*, *C. maculata* var. *maculata*, and *C. maculata* var. *occidentalis*, providing support for the ecological distinctness among the three entities. We are testing the hypothesis that fungal host specificity is under genetic control, which may explain clustering patterns. The outcomes of this study will identify fungal host diversity, plant-fungal associations, and quantify plant diversity, expanding what is currently known for fully mycoheterotrophic plants and their hosts.

Topic: Biodiversity Informatics & Herbarium Digitization

A-735

Standardizing author citations in nomenclatural databases.

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An essential component of any biodiversity portal is a well-maintained and comprehensive taxonomic "backbone" or set of tables that will include all the names needed for serving information about the relevant taxa. Those of us who work with organisms treated under the International Code of Nomenclature for algae, fungi, and plants (ICN) are fortunate in having several valuable nomenclatural resources to draw on for this purpose. There is a tendency in discussing such resources to focus primarily on the scientific name itself, but resources often differ in the author citation, not the name itself. The differences may be slight to the human eye but computers are fussy. Brummitt and Powell addressed the problem in 1992, publishing "Authors of plant names". The book includes an indexed list of the names of people who have authored names of "flowering plants, gymnosperms, pteridophytes, bryophytes, algae, fungi and fossil plants". For all the authors, it lists their full name, dates of birth and death when known, recommended abbreviations and groups for which they published names. Since 1992, Kew has maintained and updated an online version of author abbreviations, at least for vascular plants. This presentation reflects the first step in designing software that will make it relatively simple to update the author citations in a taxonomic list to conform to the IPNI standard. In it, we examine the taxonomic table for the *Aspleniaceae* in the Pteridoportal.

ICN recommends, but does not require, following the standard abbreviations. The proposed software will not address the objections of those who dislike the standard abbreviations, but it will make it easier for those who wish to start using them, to do so, whether in a database or manuscript.

Topic: Overcoming the barriers to on-going Castilleja research: From botanical enigma toward an emerging model system

A-736

Genomic Evidence for Widespread Hybridization in Castilleja

Author: Malia Santos, Sarah Jacobs, Maribeth Latvis, Sean Harrington, David Tank
Affiliation: University of Wyoming, California Academy of Sciences, University of Arkansas

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Topic: Ecophysiology

A-737

Cold tolerance during germination in an invasive spreading northward

Author: Jordan Goodrich
Affiliation: Christopher Newport University

Phyllanthus urinaria is an annual invasive weedy species originating from the tropical regions of Asia. Phyllanthus urinaria is distributed throughout the Gulf Coast of the United States, ranging from Texas to North Carolina. Recently, P. urinaria appears to have moved up the Atlantic Coast and was first reported in Virginia in 2018. This study examined P. urinaria seeds collected from specimens growing at the Virginia Living Museum in Newport News, Virginia. We hypothesized that germination would be highest in 25° in full light conditions because of the tropical origins of P. urinaria, and its appearance locally in mid-summer.. Phyllanthus urinaria is also more prevalent in warmer temperatures and grows in disturbed habitats where it is exposed to high light. We found that germination was 78.8% at 25° in shade, and only 0.4% at 15° in full light. Our findings indicate that P. urinaria will continue to germinate well in warmer temperatures, in shade conditions. Additionally, any germination at 15° could indicate P. urinaria continuing to adapt to colder conditions as it moves north. Additional experiments that simulate increasing temperatures across the season will help us determine whether P. urinaria could continue to spread into more northerly regions in the United States.

Topic: Biogeography

A-738

What do population genomic analyses and ecological niche modeling tell us about the phylogeography of Conradina canescens (Lamiaceae) in the North American Coastal Plain?

Author: Jillian Cieslik, Steve Orzell, Brock Mashburn, Christy Edwards
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Conradina is a monophyletic genus with seven species of fire-dependent subshrubs, all endemic to the southeastern USA. *Conradina canescens* is endemic to the North American Coastal Plain (NACP), a biodiversity hotspot, and occurs in both coastal and inland sites with xeric sands substrates that support fire-prone ecosystems of recent to Holocene (coastal) and Plio-Pleistocene (inland) age. Throughout its range in the Florida panhandle, *C. canescens* exhibits genetic discontinuities and morphological variation that raise questions about its evolutionary history and the historical forces that gave rise to these patterns of variation. In this study, we employed both genetic analysis and species distribution modeling to reconstruct the phylogeography of this species. We collected samples from across the range of *C. canescens* and genotyped them using 2b-RADseq. We analyzed population structure and conducted demographic modeling using Approximate Bayesian Computation. In addition to these genetic approaches, species distribution models (SDMs) were constructed to predict the habitat suitability of this species since the last glacial maximum. SDM results indicate that coastal and inland populations of *C. canescens* occupy distinct climatic niches. Analyses of genetic structure also revealed genetic discontinuities between inland and coastal populations. Specifically, populations from a three-county inland region of Plio-Pleistocene sandhills formed a distinct genetic cluster and occupied a unique environmental niche. Demographic modeling also provided insight into the evolutionary and geographic drivers behind the genetic and morphological discontinuities exhibited by the species. On a broader scale, this study contributes to the growing body of work elucidating the phylogeographic patterns of the endemic Southeastern United States and allows for future research comparing these patterns among species with similar ranges.

Topic: Development and Structure

A-739

Cellular retooling in organ body plan elaboration

Author: Sunil Kenchanmane-Raju, Kenneth Birnbaum
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Adult plant growth centers, called meristems, produce a variety of organs, including roots, stems, and floral meristems, all made up of many anatomically similar cell types. The diversity of meristems in plants allows us to pose a fundamental question in multicellular organisms: how does a single genome construct organs with different functions from similar cell-type components? In this study, we conducted a comparative analysis of single-cell transcriptomes from maize primary, seminal, lateral, and crown roots, as well as highly divergent inflorescence meristems. We find that the transcriptional differences among even similar organs, like those in the root system, are often driven by the significant divergence of specific cell types. In contrast, a subset of regulatory genes has similar expression environments in highly divergent meristems, which is a hallmark of a core meristem regulator. One such transcription factor, grassy tillers1—an important regulator of branching in the shoot—demonstrated a conserved cellular expression pattern between shoot axillary meristems and lateral roots. We illustrate that, similar to its role in shoots, gt1 regulates lateral root outgrowth, a key trait in nutrient and water uptake. Overall, the cell-by-cell comparative approach from divergent meristems has the potential to identify core growth regulators and uncover mechanisms that confer specialized functions to organs.

Topic: Ecophysiology

A-740

From Form to Function: Trait Variation in a Giant Rosette Across California Deserts

Author: Gabrielle Moneymaker
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Giant desert rosettes are a distinctive growth form common in arid environments, yet few studies have evaluated how their traits vary across environmental gradients. Gradients in arid environments can be especially acute because even subtle climatic shifts can provoke outsized impacts, and many species may exist near their ultimate range limits. Yucca schidigera, a widespread giant rosette in California, spans both semi-arid (Mojave Desert) and hyper-arid (Sonoran Desert) regions, making it a useful model for assessing morphological and physiological responses to aridity. We measured morphometric traits, leaf water relations, chlorophyll fluorescence, stable isotope composition, and environmental variables across six populations of Y. schidigera along a precipitation gradient. Our results reveal a trade-off between structural traits associated with water conservation and traits supporting photosynthetic performance, challenging the assumption that drought-adapted species universally maximize water-saving traits. These findings offer insight into how arid-adapted growth forms mediate resource allocation under environmental stress and contribute to broader questions of trait evolution and resilience in dryland systems.

Topic: Biodiversity Informatics & Herbarium Digitization

A-741

Late-flowering phenology shifts in Witch-hazel, Hamamelis virginiana

Author: Edward McAssey, Katie Mercado, Karolina Heyduk
Affiliation: University of Connecticut

Climate change is affecting plant species by changing temperature and precipitation regimes at faster than historical rates. In response, some species are able to adjust their phenotypes in response to changing abiotic conditions via plasticity and/or adaptation. Spring conditions (warmer temperatures) are arriving earlier, which has been shown to accelerate flowering time in several species. Less well studied is the observation that fall conditions are extending deeper into the year. Some species, such as witch-hazel, *Hamamelis virginiana*, take advantage of being one of the last, and only, plants flowering during the late fall season. We sought to understand whether witch-hazel has shifted to flowering later in response to extended warmth in the fall season. We analyzed digitized herbarium sheets to document flowering across a century of collections, then correlated flowering with year to determine whether recent climate change is shifting flowering to later in the season. We additionally used GPS coordinates and a principal component analyses of Bioclim environmental variables to better understand how environmental change over time is impacting phenology. To increase our sample size from the last few decades, where herbarium collection numbers decreased, we used iNaturalist observations to complement our initial herbarium-based analysis. Our preliminary analyses indicate witch-hazel appears to be undergoing a slight phenological shift in the northeastern US. While this particular analysis cannot distinguish phenotypic plasticity from genetic adaptation, future work could further dissect this question by using population genomics and common garden studies of trait variation.

Topic: Bryology and Lichenology

A-742

Metagenomic exploration in Dictyonematinae: First insights into the genomes of lichen-forming fungi in Basidiomycota

Author: Manuela Dal Forno, Yelyzaveta Kriukova, Eric Schuettpelz, Paul D'Agostino
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The study of lichens, a diverse group of symbiotic organisms integral to terrestrial and even some aquatic ecosystems, is essential for advancing our understanding of fungal nutrition and biodiversity. Despite their widespread occurrence, lichens have traditionally been understudied, and foundational knowledge such as species identification, geographic distribution, and phenotypic variation remains limited. However, herbarium collections around the world, which house millions of lichen specimens amassed over centuries, represent invaluable resources for both traditional taxonomic work and modern molecular research. These collections offer a unique opportunity to explore undescribed species and expand our understanding of lichen genetics and genomics, particularly within groups like the subtribe *Dictyonematinae* (Agaricales), the most species-rich clade of lichenized fungi in the Basidiomycota.

Historically, limited insight into the true species diversity and evolutionary relationships among basidiolichens has hampered both basic and applied research, creating substantial taxonomic challenges. To address this gap, our project aimed to generate novel genomic data from 15 basidiolichen samples, including two historical herbarium specimens and one species from the order Lepidostromatales. This approach enabled a direct comparison of genomic data between contemporary and preserved specimens, demonstrating the utility of herbarium collections in genomic research.

In addition to genome sequencing and quality assessment, we employed a suite of bioinformatic tools to analyze and compare the data and its potential outcomes. One such tool, BUSCO (Benchmarking Universal Single-Copy Orthologs), was used to evaluate the completeness and quality of metagenome-assembled genomes (MAGs). Analyses were conducted on MAGs derived from both fungal (mycobiont) and cyanobacterial (photobiont) partners, as well as from other organisms present in the samples, regardless of their partnership status. Our results show that even specimens collected over four decades ago can yield high-quality genome assemblies. Notably, in our analyses, the total number of sequencing reads (in GB) was a stronger predictor of genome completeness (as measured by BUSCO) than the initial read quality. BUSCO scores for mycobiont MAGs varied considerably, while cyanobacterial MAGs showed consistently high completeness (87–97%), with only a few exceptions.

To further investigate the biosynthetic potential of these lichens, we utilized tools such as fungiSMASH and antiSMASH, which identify biosynthetic gene clusters (BGCs) in fungal and bacterial genomes, respectively. These analyses revealed putative genes involved in the production of secondary metabolites — compounds central to the ecological functions and chemical defenses of lichens. The detection of BGCs in both fungal and cyanobacterial genomes highlights the biochemical complexity of these symbiotic systems.

While the origin of lichenization in the Ascomycota remains a subject of ongoing debate, there is strong evidence that lichens in Basidiomycota evolved multiple times in at least three orders of Agaricomycetes. This study is a step towards a better understanding of how this nutritional mode has risen in Fungi, especially among basidiomycetes.

Topic: *Hybrids and Hybridization*

A-743

Molecular basis of transgressive segregation of flower color in monkeyflowers (Mimulus)

Author: Rong-Chien Lin, Yaowu Yuan
Affiliation:, University of Connecticut

Transgressive segregation, the production of extreme or novel phenotypes in hybrid populations, is frequently observed in nature. Theoretically, transgressive segregation can be achieved through complementary gene action, epistasis, or/and single-locus overdominance. However, little empirical data is available to elucidate the molecular mechanisms underlying transgressive segregation. To address this problem, we have studied transgressive segregation of flower color in the hybrids of *Mimulus lewisii* and *M. parishii,* two closely related monkeyflower species bearing light pink flowers due to low concentrations of anthocyanin pigments. Previously we have shown that the light pink color of *M. lewisii* and *M. parishii* flowers are due to high expression level of *ROI1*, an inhibitor of anthocyanin production, and low translation efficiency of PELAN, an activator of anthocyanin biosynthesis, respectively. This leads to our hypothesis based on complementary gene action that *PELAN* and *ROI1* in *M. lewisii* act as a strong activator and a strong repressor, respectively, whereas in *M. parishii*, as a weak activator and a weak repressor. Accordingly, the dark pink hybrids can result from the combination of a strong activator and a weak repressor, and the opposite is true for extremely pale hybrids. Although our preliminary results support the action of *PELAN* and *ROI1*, our hypothesis can only explain ~70% of color variation observed in F_2 individuals, indicating additional factors in the transgressive segregation of flower color. Through creating near isogenic lines (NILs) and transgenic characterization, we identified two additional genes contributing to flower color variation in the hybrids. Our findings suggest that transgressive flower color in *Mimulus* is likely caused by a mixture of complementary gene action and epistatic effects.

Topic: *Paleobotany*

A-744

Permineralized cymes with epigynous flowers from the Eocene Appian Way Locality, Vancouver Island, British Columbia, Canada

Author: Ruth Stockey, Gar Rothwell, Graham Beard
Affiliation: Oregon State University, Ohio University; Oregon State University, Vancouver Island Paleontology Museum

Fourteen permineralized inflorescences have been identified in the calcium carbonate concretions from the Appian Way Locality, south of Campbell River on the east coast of Vancouver Island in British Columbia, Canada. Sediments are currently dated as Eocene on the basis of invertebrate paleontology, palynology and stratigraphy of coccoliths. Concretions were slabbed on a rock saw and surfaces prepared for study using the cellulose acetate peel technique. Inflorescences are determinate, flat-topped, and appear to be cymose with a central flower and two lateral flowers attached to each side on a short peduncle. While flowers appear to be in alignment, tracing the position of bracts and the arrangement of flower bases indicates that they were actually produced helically. A large number of elongate trichomes are produced between the flowers in some specimens. Remnants of what appear to be petals and immature stamens are present above the floral cup. Stamens appear to be immature with elongate filaments and short anthers. Fruit wall is composed of compact, small diameter sclereids with a row of larger idioblasts in the outer pericarp. Contents of the carpels are variable with some cellular tissue and in one case what might be two young or aborted seeds.

Topic: *Overcoming the barriers to on-going Castilleja research: From botanical enigma toward an emerging model system*

A-745

Paintbrushes and Printmaking: Investigating diversification dynamics in Castilleja and communicating biodiversity science to broader audiences

Author: David Tank, Malia Santos, Erin Bentley, Maribeth Latvis, Sarah Jacobs
Affiliation: University of Wyoming, University of Arkansas, California Academy of Sciences

In this talk, I will discuss my research investigating the radiation of the paintbrushes (*Castilleja*; Orobanchaceae), and how we have used this group to foster public engagement with herbaria and the biodiversity sciences. *Castilleja* is notorious for its species-rich nature and taxonomic complexity, where rapid diversification, polyploidy, and reticulate evolution are all likely contributors to this complexity. Here, I will discuss our phylogenetic studies of the patterns and processes of speciation in this young, species-rich group, where even delimiting species boundaries can be extremely challenging. I will then transition to discussing Kaleidoscope Science – a novel outreach program born out of a science/art collaboration with the Visual Arts Department at the University of Wyoming – that uses screen printing as a medium to increase public awareness and knowledge of *Castilleja* diversity, the Rocky Mountain Herbarium, and the role of natural history collections in the biodiversity sciences.

Topic: *Pteridology*

A-746

A morphometric analysis of western sword fern (Polystichum munitum) pinnae and pinnae scales across the coast redwood forest ecological gradient

Author: Lacey Benson
Affiliation: San Jose State University

Ferns are an integral component of biodiversity and productivity in the coast redwood understory and canopy. Given that summer fog is expected to decrease and winter precipitation patterns are predicted to change it is vital to understand the role of microclimates and adaptation strategies utilized by ferns in the coast redwood ecosystem in order to gauge how the distribution, community dynamics, and reproductive success of ferns will be affected in the coming decades. Researchers have found ferns display signs of shifting climate patterns through leaf traits such as number of fronds, size of fronds, foliar uptake capacity and leaf water retention. By studying morphological and physiological changes to ferns scientists can get a more rapid understanding of how community dynamics and slower growing species such as the coast redwood will be affected by future changes to climate. The aims of this study are (1) to compare western sword fern (Polystichum munitum or POMU) pinnae size traits (length, width, and length:width ratio) to environmental variables such as precipitation, fog frequency, and temperature; (2) to quantify pinnae scale density to compare with climate data; and lastly (3) to collect, mount, and enter POMU specimens and redwood associate species into the Carl W. Sharsmith Herbarium at SJSU. To achieve these objectives, we utilized digitized herbarium accessions as well as personal collections to measure pinnae in ImageJ and count scales on both pinna surfaces. Analyses compared latitude and climate variables and found significant differences in scale density across the ecological gradient. This study greatly informs our understanding of the landscape scale variety of morphological and physiological traits within POMU and adds to previous research on POMU foliar water uptake capacity and leaf water retention abilities.

Topic: *Population Genetics/Genomics*

A-747

Genomic vulnerability of the Saguaro cactus under climate change

Author: Eddy Jesus Mendoza-Galindo, Piero Foncerrada-Elizondo, Pedro Andrade, Tram Vi, Michelle Guerra, Michiel Pillet, Diana Martinez-Lona, Antonio Hernandez-Lopez, Francisco Molina-Freaner, Tania Hernandez (Sanders)
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The Saguaro cactus (*Carnegiea gigantea*) is an iconic plant species native to the Sonoran Desert in the western United States and northwestern Mexico. It is known for its distinctive, colossal appearance and cultural significance. Like many other cacti, the Saguaro is threatened by habitat loss, urbanization, and climate change. Previous studies predict a decline in the Saguaro's habitat due to climate change. Nevertheless, little is known about the adaptive potential of the species. In this work, we genotyped several populations across the Saguaro's distribution, aiming to understand the adaptive potential of natural populations from a genomic perspective. First, we found that the Saguaro is divided into two distinct genetic groups based on geography: North and South. Second, we found that the environment is a strong predictor of the Saguaro's genetics, accounting for around 30% of the genetic variation. Third, we mapped the genome–environment interaction to 18 genes, which are promising candidates for explaining its physiological strategy of local adaptation. Then, we predicted the genomic vulnerability of natural populations under climate change scenarios, observing a differential requirement for adaptive changes between Northern and Southern populations. Finally, we observed that the phenotypic health of current populations can serve as a predictor to identify the most vulnerable populations under climate change. Overall, we found that Southern populations are critically endangered compared to Northern populations. This work is essential to identify the actions needed to prevent the extinction of the Saguaro, the most iconic cactus in the Sonoran Desert.

Topic: *Comparative Genomics/Transcriptomics*

A-748

Cell-type-specific ortholog regulation during chilling stress response

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The increased frequency of extreme weather events poses a significant threat to the productivity of major crop species. Developing climate-resilient crops requires a mechanistic understanding of plants' responses to environmental changes. *Zea mays* (Maize), an important crop for food security, is susceptible to low temperatures owing to its tropical origins. In contrast, *Tripsacum dactyloides*, a wild relative of maize, withstands low temperatures and many of the abiotic stressors facing the US corn belt. Both maize and Tripsacum share a whole genome duplication (WGD) event after their split from *Sorghum bicolor*. Polyploidy associated with a WGD increases genetic variation for environmental adaptation, however, differences in duplicate paralog evolution could drive differential adaptive advantages for organisms with shared WGD events. Previous studies have shown that Tripsacum orthologs of the phospholipid biosynthesis and stress response pathways are regulated differently in response to chilling stress compared to maize and sorghum. Here we integrated transcriptome and chromatin accessibility datasets in maize, sorghum, and Tripsacum leaf tissues to explore the role of cis-regulatory element (CRE) variations in functional divergence of duplicate paralogs under chilling stress response. However, different cell types may exhibit different molecular responses, and such gene responses can be masked by conventional transcriptomic studies using bulk RNA sequencing. We further employed a comparative analysis of single-cell transcriptomes from maize, Tripsacum, and sorghum to reveal key cell types critical for chilling stress variation across these species. Specifically, GDSL esterase was found to be upregulated in maize epidermis upon cold stress. CRE evolution between these species will inform cell-type-specific environment-responsive gene regulation. With their genetic similarity and shared whole-genome duplication, Tripsacum's cold stress response gene regulation provides precise orthologous editing targets in maize to improve its low-temperature resistance. This precise cell-type-specific gene expression information allows engineering climate resilience in major crops without pleiotropic effects on growth and other developmental processes.

Topic: *Population Genetics/Genomics*

A-749

Domestication and genetic diversity in Agave tequilana Weber

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Agave tequilana Weber blue variety, commonly known as "agave azul," is the sole species and variety authorized by the guidelines of the Tequila Regulatory Council for the production of Tequila. The establishment of the Tequila Appellation of Origin (DOT) and the intense international demand for this beverage have led to intensified clonal reproduction of "agave azul." This practice drastically reduces the genetic diversity of crops and contributes to the loss of varieties that do not meet producers' expectations or regulatory standards, resulting in the loss of critical natural diversity found in other varieties not authorized for the production of the spirit. Previous studies have relied on traditional genetic markers such as AFLPs and microsatellites to examine the genetic diversity of this iconic agave. In this study, we aim to harness the potential of the Genotyping-by-Sequencing (GBS) method, using the sequenced genome of the *A. tequilana* Weber blue variety as a reference to obtain a pool of high-resolution Single Nucleotide Polymorphisms (SNPs). This high-quality dataset helped us investigate and document the genetic diversity present in *A. tequilana* Weber crops across the territories permitted by the most recent DOT, as well as in nearby areas and botanical collections. This project aims to better understand the genetics underlying the cultivation, propagation, and domestication processes of this species of high cultural value. We conducted fieldwork in search of wild relatives or sister landraces previously reported in the literature. Unfortunately, we observed that other varieties of *A. tequilana* have virtually disappeared and are extremely difficult to locate, even in botanical collections. Our findings on the genetic diversity of "agave azul" contradict previous studies that utilized traditional markers. Contrary to earlier reports, we found significant variation despite it being a clonal cultivar. *A. tequilana* forms a cohesive group, well-differentiated from other species within the angustifolia complex (*A. angustifolia* and *A. rhodacantha*), belonging to a lineage of richer, more diverse groups of Agave in the region.

Topic: *Functional Genetics/Genomics*

A-750

Developing Gilia yorkii and Gilia capitata as Genetic Model Organisms

Author: Amanda Lavelle, Elise Johnson, Clinton Whipple
Affiliation: Utah Valley University, Brigham Young University

Gilia yorkii and *Gilia capitata* are closely related members of the Phlox family that are interfertile yet have distinct differences in morphology. *G. yorkii* is endemic to the Sierra foothills east of Fresno, CA while *G. capitata* is broadly dispersed through California and Mexico. Previous work outlines the morphological differences between these species and demonstrates the ability to further develop *G. yorkii* and *G. capitata* as model organisms due to their morphological diversity, ecological diversity, and hybridization capabilities. To further develop *G. yorkii* and *G. capitata* as a genetic model, we are developing a protocol for tissue culture and *Agrobacterium tumefaciens* mediated transformation to facilitate functional studies in these species. Currently, we are able to produce flowering plants via hypocotyl tissue culture using a callus initiation media followed by a root promoting media and subsequent transfer to soil substrate. The transformation protocol is under development and shows great potential for success. Future work will focus on functional studies to examine genes critical to differences between these two species.

Topic: *Common gardens in the 21st Century: the intersection between evolution and ecology, science and management*

A-751

Common gardens in the 21st Century: the intersection between evolution and ecology, science and management

Author: Jeannine Cavender-Bares, Steven Augustine, Beth Fallon, Clarissa Fontes, Brett Frederickson, Mariana Hernandez-Leal, Matthew Kaproth, Laura Ostrowsky, José Ramírez-Valiente, Lucy Rea, Heather McCarthy, Andrew Hipp
Affiliation: Harvard University, National Park Service, BeZeroCarbon, University of Minnesota, Minnesota State University, Instituto de Ciencias Forestales, University of Oklahoma, The Morton Arboretum

Common gardens and reciprocal transplant experiments are a classic and critical means for integrating ecology and evolution. By disentangling genetic and environmental variation, they enable tests of adaptive evolution across environments, local adaptation, plasticity and adaptive plasticity. Common garden experiments come in many forms: they can include greenhouse experiments with environmental treatments, field experiments that span latitudinal gradients encompassing broad climatic variation, or field experiments that include natural environmental gradients coupled with environmental treatments, such as imposed drought or added rainfall. In doing so, they provide us with the means to evaluate the potential of populations to adapt to environments in the future. Common gardens can incorporate a variety of designs that span the hierarchy of the tree of life from genomically identical individuals, pedigreed families, populations, species and lineages. In this talk, we synthesize results across a series of oak common gardens encompassing both intraspecific and interspecific variation. We explain their potential to integrate physiological, molecular, and quantitative genetic approaches to test for adaptive variation and plasticity within and among families, populations and species. In particular, we provide evidence for co-gradient plasticity and adaptive evolution in response to drought, seasonal temperature, and freezing that help to reveal the functional shifts involved in diversification and to explain the dominance and coexistence of the oaks in North America. In the face of rapidly changing environments, these experiments represent an important means to evaluate the potential of assisted geneflow and migration to foster forest resilience.

Topic: *Biogeography*

A-752

Spatial Phylogenetics of the Sri Lankan Angiosperms: Uncovering Patterns of Endemism, Ecology, and Conservation Priority

Author: Malith Viduranga Weerapperuma Achchi Athukoralage Don, Daniel Spalink
Affiliation: Texas A & M university, Texas A&M University

Quantifying diversity across landscapes is essential to interpreting how ecological heterogeneity and the history of clades contribute to the foundation, dispersal, and establishment of biodiversity. The spatial phylogenetics concept is a key element that can be used to analyze the assembly of the flora, with special emphasis on processes of dispersal and niche evolution linked to spatial patterns of phylogenetic diversity. This preliminary study was aimed at exploring how evolutionary features of the vascular flora of Sri Lanka are distributed across the landscape. Using a phylogeny at the species level covering 95% of the Sri Lankan flora, and geographic locations retrieved from traditional sampling, herbaria, digitized records, and online databases, we calculated spatial variation in species richness and phylogenetic α and β diversity across environmental gradients. Distribution models for species that have occurrence data were developed to infer fine-scale variation in potential diversity, phylogenetic distance, and interspecific range overlaps. Significant levels of phylogenetic diversity (PD) relative phylogenetic diversity (RPD), and phylogenetic endemism (PE) were calculated to understand total evolutionary history, range-restricted unique lineages, and deviations from expected phylogenetic structure. Bioregionalization and categorical analysis of neo and paleo-endemism were performed to establish conservation priorities. The application of phylogenetic metrics revealed significant phylogenetic clustering across the island, with the southwestern region exhibiting the greatest concentration of species richness and endemism. Categorical analysis of neo- and paleo-endemism (CANAPE) indicated that the predominant concentrations of PD occur beyond the extent of currently established conservation areas, underscoring potential gaps in protection protocols. The areas highlighted as conservation priorities in this study are essential for broad-scale planning in Sri Lanka, especially in the context of evolutionary history preservation.

Topic: *Biogeography*

A-753

Identifying individuals of a threatened oak species, Quercus brandegeei, using UAS Imagery

Author: Angelina Wang, Anjin Chang, Tayyibe Gunduz, Daniel Wblesther Perez Morales, Christian Silva Bejarano, Kate Good, Chai-Shian Kua, Silvia Alvarez-Clare
Affiliation: The Morton Arboretum, Tennessee State University, Independent, Centro de Investigaciones Biológicas del Noroeste S.C.

Quercus brandegeei is an endangered species of oak that is endemic to Baja California Sur, Mexico. It is a medium-sized evergreen tree that is found in sandy soils near ephemeral stream beds. Due to their restricted range, inaccessibility to water, consumption by domestic animals, and habitat degradation, only *Q. brandegeei* adult individuals remain. Since 2016, The Morton Arboretum and partners have collected genetic, phenological, and ecological data on *Q. brandegeei* to determine specific threats and identify conservation and management priorities. However, questions remain regarding the population size of mature individuals and its exact habitat. UAS (Unmanned Aircraft Systems) or drones are becoming increasingly popular to utilize for conservation purposes. In November 2024, we collected aerial photographs using multispectral and RGB (Red, Green, and Blue) sensors at six sites in the Cape Region of Baja California Sur: three sites with known *Q. brandegeei* individuals and three previously unexplored sites. Across these six sites, we collected over 20,000 images that have been processed and used to program the AI detection model, YOLO (You Only Look Once). The trained AI detection model will be applied to aerial images of sites to test positive detection rates of *Q. brandegeei*. We are also comparing the accuracy of the AI detection model to visual image recognition in order to determine which methodology is better suited for this study species. Next steps include applying this model to more previously unexplored sites throughout the species range to quantify the population size of the remaining mature individuals and as well as creating a methodology to apply this technology to other species.

Topic: *Macroevolution*

A-754

Does divergence time estimation improve understanding of plant evolution?

Author: Tom Carruthers
Affiliation: University of Michigan

Phylogenetic inference and divergence time estimation are prone to error. This error can undermine inferences of trait evolution, diversification, or biogeography. Further, even when tree topologies and divergence times are accurately inferred, limitations in the models used and information content of phylogenetic trees can critically undermine inferences. Through analyses of simulated and empirical datasets, this talk will explore when and why these issues occur in plants, and how they are influenced by the type of data, taxonomic expertise underpinning the dataset in question, and analytical choices.

Topic: *Biogeography*

A-755

Biogeography and Biome Shifting in Lonicera: A Tale of Two Clades

Author: Mansa Srivastav, Michael Donoghue
Affiliation:, Yale University

Lonicera (Caprifoliaceae) is a clade of ~140 species that are distributed widely around the Northern Hemisphere. Its species occur in temperate forests in the major centres of endemism, but also in several regions that are not as often associated with temperate Laurasian clades, including cold deserts and alpine areas of Central Asia, and circumboreal and Mediterranean regions. We analyzed the biogeography of *Lonicera* using a greatly expanded restriction-site associated DNA sequencing (RADSeq) dataset that includes nearly 80% of the species. A well-supported tree identifies clades corresponding to the traditional subgenera *Periclymenum* and *Chamaecerasus*, and three sections of *Chamaecerasus* (*Nintooa*, *Coeloxylosteum*, and *Isoxylosteum*). As in a previous RADSeq phylogeny, the fourth and largest traditional section of *Chamaecerasus*, *Isika,* was found to be paraphyletic. Only three of the 23 previously recognized subsections were found to be monophyletic. Through a series of dating and biogeographical analyses we infer that crown *Lonicera* likely began diversifying in East

Asia some 40 million years ago. We reconstructed the evolution of a number of traits of potential relevance to biogeography (biome type, plant habit, leafing strategy, fruit color, ploidy, ovary fusion, and flower color change) and found that while there are noteworthy geographical patterns, these are not directly associated with the major disjunctions or biome shifts. The two major clades show strongly contrasting patterns of evolution. Crown *Periclymenum* dates to ~15 mya and its species occupy chapparal habitats in Mediterranean regions and temperate forests in Europe and North America; only a few species are native to Asia. *Chamaecerasus*, on the other hand, began to diversify ~37 mya, and mostly occupies Asia, with just five and four more recent entries into Europe and North America, respectively, none of which yielded a substantial radiation. None of the lineages within *Chamaecerasus* occupy Mediterranean climates, but they have shifted from temperate forests into cold deserts, alpine areas, wetlands, and taiga. Hence, the overall biogeographic history of *Lonicera* reflects the fact that its two constituent subclades have followed very different evolutionary trajectories.

Topic: *Phytochemical*

A-756

Root-derived phenylpropanoids are necessary for normal growth of Arabidopsis

Author: Chase Hearn, Fabiola Muro-Villanueva, Clint Chapple, Josh Widhalm
Affiliation: Purdue University

In vascular plants, phenylpropanoid metabolism is essential for the deposition of lignin, a polymer comprised of hydroxycinnamyl alcohol subunits that fortifies cell walls and facilitates water transport. Attempts to manipulate subunit composition have raised new questions surrounding the role of lignin in plant development. Dwarfism induced by lignin modification is often attributed to impaired vascular development, however, the occurrence of some lignin-modified plants with intact vasculature suggests an unexplored role linking phenylpropanoids to plant growth regulation. *Arabidopsis* mutants that deposit lignin either comprised exclusively of sinapyl alcohol or hydroxycinnamaldehyde subunits have enhanced saccharification potential without severe growth penalties. In contrast, combining these mutations severely compromises growth, and perturbs lateral root and root hair development. We found that supplying this mutant with exogenous coniferyl alcohol or its lignan dimer, pinoresinol, complement these phenotypes with high specificity. We also observed complementation with dimethylpinoresinol, which cannot be incorporated into lignin, suggesting pinoresinol acts independently of lignification. To further investigate the origin of these phenotypes, we performed grafting experiments and found that wild-type roots are sufficient to fully restore the growth of mutant shoots, and that mutant roots can impose dwarfism on wild-type shoots. Metabolic profiling revealed mutant roots are depleted in coniferyl alcohol and pinoresinol, suggesting these phenylpropanoids may have uncharacterized roles in plant development. Together, our results provide evidence for phenylpropanoids in the regulation of plant growth and development.

Topic: *Functional Genetics/Genomics*

A-757

Developing Gilia yorkii and Gilia capitata as Genetic Model Organisms

Author: Elise Johnson, Clinton Whipple, Amanda Lavelle
Affiliation: Utah Valley University, Brigham Young University

Gilia yorkii and *Gilia capitata* are closely related members of the Phlox family that are interfertile yet have distinct differences in morphology. *G. yorkii* is endemic to the Sierra foothills east of Fresno, CA while *G. capitata* is broadly dispersed through California and Mexico. Previous work outlines the morphological differences between these species and demonstrates the ability to further develop *G. yorkii* and *G. capitata* as model organisms due to their morphological diversity, ecological diversity, and hybridization capabilities. To further develop *G. yorkii* and *G. capitata* as a genetic model, we are developing protocols for tissue culture and *Agrobacterium tumefaciens* mediated transformation to facilitate functional studies in these species. One challenge we faced developing the tissue culture protocols was promoting root formation and subsequent transfer to soil substrate. With the tissue culture protocol near completion, the transformation protocol is under development and shows great potential for success. Future work will focus on functional studies to examine genes critical to differences between these two species.

Topic: *Symbioses: Plant, Animal, and Microbe Interactions*

A-758

Microbial Diversity and Stress Physiology in Biological Soil Crusts of a Temperate Sand Barren with high Nitrogen deposition

Author: Elena Lopez Peredo, Caitlin Morrison, Rachel Kulp, William Goyette, Michael Weintraub, Fernando Rodriguez
Affiliation: Rochester Institute of Technology, The University of Toledo

Biological Soil Crusts (BSCs) provide a range of essential ecosystem services, including increased soil stability, nitrogen (N) fixation, water retention, and prevention of erosion. These crusts form through the complex interplay of bacteria, cyanobacteria, fungi, green microalgae, diatoms, and mosses, which bind soil particles into cohesive surface layers. BSCs are especially critical in arid and nutrient-poor ecosystems, where they are often the primary form of soil cover. However, their composition and functional capacity in temperate systems remain underexplored.

In this study, we investigated the microbial diversity, metabolic capacity of microbial communities from BSCs found on a sand barren in the temperate Oak Openings at the Kitty Todd Nature Preserve in Northwest Ohio. Contrasting with other areas rich in BSCs, this area is characterized by elevated nitrogen deposition from nearby agricultural and urban sources. In addition, we isolate and explore the stress tolerance of green microalgae from isolated from these BSCs.

During the summer of 2024, we collected triplicate BSC samples from seven locations along a transect at the Kitty Todd Nature Preserve. To examine microbial diversity, we employed a dual approach. We assessed the prokaryotic community structure through 16S rRNA gene amplicon sequencing (targeting the V4–V5 regions), and further characterized functional potential via shotgun metagenomic sequencing. This allowed us to link taxonomic diversity to biogeochemical function. Previous research in this region has shown that BSCs here may perform both nitrification and denitrification even at low soil moisture resulting in gaseous nitrogen loss. This is unusual among crusts, which typically reduce leaching and conserve nitrogen. Of particular concern is the potential release of nitrous oxide (N_2O), a potent greenhouse gas. Understanding the microbial taxa and pathways involved is therefore crucial to predicting the net ecological impact of these crusts under elevated N input scenarios.

We also explored the diversity and physiological resilience of green algae isolated from these temperate BSCs. Although often associated with aquatic systems, unicellular green algae (Chlorophyta) are common soil microbiota, and are of special interest due to their close evolutionary relationship with Embryophytes plants. We established single isolate cultures of multiple algal taxa under common garden conditions, exposing them to elevated nitrogen levels and controlled desiccation stress. Algal taxonomy and phylogenetic placement were determined using barcode genes, and their photophysiological responses to desiccation were measured using chlorophyll fluorescence (Fv/Fm) as a proxy for photosynthetic efficiency.

Topic: *Conservation Biology*

A-760

Using landscape genomics to inform management practices for increasing climate resilience in a Californian foundation species, blue oak (Quercus douglasii)

Author: Ryan Buck, Scott Butterfield, Elizabeth Hiroyasu, Jeanette Howard, John Knapp, Zachary Principe, Brooke Rose, Victoria Sork
Affiliation: UCLA, The Nature Conservancy, San Diego State University

Climate change is adversely impacting biodiversity across the globe. Long-lived tree species are especially susceptible due to their sessile nature and expected adaptational lag to historic temperatures. The blue oak tree (*Quercus douglasii*) is a foundation species in California that supports thousands of other species; therefore, knowing how it will respond to climate change can inform our predictions of how long-lived forest species and entire ecosystems will respond. Our goals are to 1) identify regions of vulnerability and resilience of blue oak populations using landscape genomics, 2) determine if landscape genomic predictions align with ecological niche model predictions 3) develop seed sourcing strategies for three focal sites managed by The Nature Conservancy. We used whole genome sequences (WGS) from 163 individuals across blue oak's range and performed genetic-environment association analyses with ten fine-scale environmental and soil variables via univariate latent factor mixed models and multivariate partial redundancy analyses. Genomic offset, a metric of maladaptation, was calculated through gradient forest models and eight future climate scenarios by contrasting current

patterns of climate-associated adaptive genetic variation with the adaptive patterns needed under future climate scenarios. Predictions were then compared to habitat suitability change models for the same climate scenarios. The resilience of seed sources identified through three methods - landscape genomics, local, and random – were compared to determine the best method for restoration management. Our results show that blue oak will be more vulnerable along the Sierra Nevada basin and in the northernmost extent of its range, with patches of resilience along the central coast of California. When compared to habitat suitability change, increase in genomic offset was correlated with a decrease in suitability at a range-wide scale, but that pattern broke down at the focal preserve scale, suggesting that genomic and ecological predictions may align at landscape scales but not always at finer resolutions. Seed sources identified through landscape genomic methods increased planting site resilience significantly more than choosing nearby seeds or random seeds within a preserve. Our study found that large swaths of blue oak range may be vulnerable in future climate regimes, aligning with ecological niche model predictions, but site resilience can be increased through the use of landscape genomics to identify seed sources.

Topic: Population Genetics/Genomics

A-761

Landscape genomics provide evidence of different historical gene flow dynamics between widespread Arctic sedge and shrub species in Alaska

Author: Elizabett Stunz, Luis Pallares Solano, Ned Fetcher, Stephen Escarzaga, Christine Bacon, Michael Moody
Affiliation: University of Gothenburg, The University of Texas at El Paso, Wilkes University, University of Texas at El Paso

The Arctic covers ~14% of the Earth's land area, and its vegetation history has been shaped by recurring patterns of geological formation, glaciation, and environmental shifts. An increase in relative abundance of shrub species such as birch and willow (*Betula* and *Salix* spp.) is a response to ongoing environmental change in tundra ecosystems. *Eriophorum vaginatum* is a tundra sedge, whose potential decline due to competition from shrubs may affect ecosystem stability in the Arctic. Here, we compare the genetic diversity, population structure, and gene flow of four widespread Arctic plant species that form part of a shared community in the Arctic. This includes two long-lived tussock forming sedges (*Eriophorum vaginatum* L. and *Carex bigelowii* Torr. ex Schwein) and two shrubs (*Betula nana* L. and *Salix pulchra* Cham.). These taxa were sampled over a ca. 400 km latitudinal gradient in Alaska using thousands of genomic markers obtained from double-digest Restriction Site-Associated DNA sequencing. Further, we examine the mechanisms of isolation by distance, by environment, and by resistance to determine how they influence the spatial distribution of allelic variation across the Arctic landscape. Adaptation and refugial isolation followed by resistance of an ecological barrier of forest cover or ecotone, has shaped the genetic structure for *E. vaginatum* and *C. bigelowii*. For the shrubs, both *B. nana* and *S. pulchra* show a general lack of population structure, potentially due to more recent and rapid population dispersal, lack of multiple refugial origins, or contemporary widespread gene flow. A lack of genetic structure and local adaptation could facilitate a competitive advantage for these developmentally plastic shrubs, while isolation by resistance due to forest cover and local adaptation can create obstacles to gene flow of potentially better-adapted sedge ecotypes to migrate northward under rapid environmental change. These findings have implications for long-term community structure involving these widespread Arctic plant species, which could lead to modifications in ecosystem function.

Topic: Reproductive Processes

A-763

Modeling Transitions to Wind Pollination in Angiosperms

Author: David Timerman, Deren Eaton, Spencer Barrett
Affiliation: Columbia University, University of Toronto

The evolution of wind pollination from animal pollination is a major transition in angiosperm reproductive biology, having occurred independently across numerous lineages. Although often considered inefficient compared to animal-mediated pollination, its repeated evolution suggests important selective advantages under certain ecological conditions. While transitions between pollination systems generally are well documented empirically, theoretical frameworks linking ecological pressures to evolutionary outcomes remain surprisingly underdeveloped, especially for transitions from animal to wind pollination. This lack of theory is striking given that many aspects of plant reproduction, such as sex allocation, the evolution of selfing, and the origin of dioecy, are grounded in robust mathematical models. Yet pollination mode itself is rarely treated as an evolving trait in formal models, leaving a major component of reproductive evolution poorly understood.

We present a comprehensive mathematical framework to address this theoretical gap by modeling the selective pressures and evolutionary dynamics driving transitions between pollination systems. The model integrates resource allocation trade-offs, physical constraints on pollen transfer, and ecological factors influencing reproductive success. A central component is how plants allocate limited resources among ovule production, pollen production, and investment in attractive traits that promote animal pollination. Animal-pollinated species typically produce modest amounts of sticky pollen and invest heavily in floral traits such as large petals and nectar rewards. In contrast, wind-pollinated species forgo these investments, producing large quantities of dry, aerodynamic pollen and simplified, exserted floral structures that enhance wind dispersal. These divergent strategies create trade-offs and functional interference: traits that increase success via one mode can reduce effectiveness via the other. For example, large petals can obstruct airflow, while pollen adapted for animal vectors performs poorly in wind dispersal. Our model incorporates these trade-offs alongside ecological parameters such as pollen limitation, population density, and pollinator availability, which shape the relative fitness payoffs of different pollination strategies.

By allowing both wind and animal pollination to contribute to reproductive success, the model explores the potential for ambophily, pollination via both vectors, to evolve and persist. Though often viewed as a transient state, ambophily may represent an evolutionarily stable strategy under certain ecological conditions. Using a game-theoretical framework, we identify evolutionarily stable strategies across a range of scenarios and evaluate possible pathways linking animal pollination, ambophily, and wind pollination. We ask: Under what ecological conditions can wind pollination evolve from animal pollination? Can ambophily function as a stable reproductive strategy rather than a transitional state? And how do factors such as pollen limitation, population density, and pollinator availability shape the selective landscape driving these evolutionary outcomes? This integrative model generates testable predictions about the conditions favoring transitions in pollination mode and provides a theoretical foundation for understanding a major shift in angiosperm reproductive evolution.

Topic: Conservation Biology

A-764

A Biotechnological Framework for Scaling Up Zostera marina Restoration Through In Vitro Propagation and Regeneration

Author: Elena Lopez Peredo, Grace Dixon, Sarah Merolla, Agustin Moreira-Saporiti, Liam Culhane, Mirta Teichberg, Fernando Rodriguez
Affiliation: Rochester Institute of Technology, Marine Biological Laboratory

Zostera marina L., a foundational seagrass species in temperate coastal environments, functions as a critical ecosystem engineer by stabilizing sediments, enhancing water quality, and providing essential habitat for fisheries and invertebrate communities. Despite its ecological importance, *Z. marina* meadows across the northeastern United States, including in Cape Cod (MA), have declined dramatically in recent decades due to a combination of elevated water temperatures and nutrient pollution linked to anthropogenic activities. Restoration initiatives to re-establish lost seagrass beds face challenges derived from limited seed availability, low recruitment rates, and seasonally restricted access to viable propagules. To address these limitations, we developed a multipronged approach for the propagation and regeneration of *Z. marina* that integrates seed germination, scalable micropropagation, and explores the initial steps towards callus-based somatic embryogenesis.

Our first objective focused on optimizing in vitro germination of field-collected seeds. We used seed collected during 2024 from 13 donor populations in southeastern Massachusetts. Seeds were sterilized and cultivated in axenic controlled conditions using either biphasic or liquid basal f/2 media, with and without aeration (via bubbling or orbital shaking). Germination rates in culture reached up to 85%, and seedlings achieved substantial biomass and leaf development within four weeks, with individuals producing up to three leaves and reaching a maximum leaf height of 4.5 cm. Comparisons between in vitro and seawater aquarium conditions demonstrated that axenically grown seedlings perform well and show high survivability when transferred to non-sterile environments. This step confirmed that seeds from diverse populations can be effectively germinated under sterile conditions and that cultured seedlings can withstand acclimatization, making them suitable for restoration deployment.

To accelerate and scale up material production independently of seasonal seed availability, we established a micropropagation chain using seed-derived material grown axenically. This approach supports rapid and continuous multiplication of planting stock under controlled conditions and eliminates the dependency on repeated field collections. Micropropagation provides a powerful tool for producing large quantities of genetically diverse material year-round, overcoming one of the key bottlenecks in current restoration practices.

In parallel, we explored the regenerative potential of *Z. marina* through callus induction and somatic embryogenesis. Axenic seedlings and wild explants were exposed to varying types and concentrations of plant growth regulators in agar media. Preliminary trials demonstrated early callus formation in both root tissues and immature seeds, opening the door to the use of somatic embryogenesis for the regeneration of whole plants from a single founder seed. This capability would enable the propagation of clonal lines with desirable traits and provide a novel entry point for additional biotechnological applications in seagrass biology.

Collectively, our integrative strategy advances the development of propagation and restoration pipelines for *Z. marina* by combining classical plant cultivation techniques with modern plant biotechnology. This work contributes foundational knowledge and applied tools for restoring seagrass meadows and protecting vulnerable coastal ecosystems in the face of rapid environmental change.

Topic: Population Genetics/Genomics

A-765

Population Genomics of Natural and Restored Halodule wrightii in Tampa Bay

Author: Bethany Burns
Affiliation: University of South Florida

Global conservation efforts are becoming increasingly important as human-driven impacts like climate change and coastal development continue to rise significantly, impacting ecosystems such as seagrass meadows. In monospecific ecosystems such as seagrass beds, biodiversity in the form of genetic diversity is important, and even a small increase in genetic diversity can enhance ecosystem services such as invertebrate habitat, increased primary productivity, and nutrient retention. *Halodule wrightii* is commonly used in many seagrass restoration projects due to its quick colonization with rhizome growth and wide tolerance to environmental conditions. Our objective was to determine the extent of successful restoration by analyzing patterns of genomic diversity. We collected *H. wrightii* from 10 populations in the Tampa Bay region in Florida, representing four restored populations, five natural populations, and one natural population outside of Tampa Bay that is currently used for ongoing restoration projects. We used double digest restriction-site associated DNA sequencing (ddRADseq) to examine a reduced representation of the genome of *H. wrightii* populations. We aimed to (1) compare genomic diversity in restored and natural *H. wrightii* beds, (2) determine how environmental conditions affect the genetic composition of *H. wrightii* populations, and (3) identify potential specific target genotypes for restoration in the future. Our findings could help indicate genotypes that are particularly well-suited to restoration and are associated with a suite of environmental conditions that will be useful in future restoration projects.

Topic: Conservation Biology

A-766

Genomic insight into Agave utahensis vars. eborispina and nevadensis

Author: Paola Moreno, Carrie Kiel, Naomi Fraga
Affiliation: California Botanic Garden

Agave utahensis vars. eborispina and nevadensis are rare desert plants facing threats from climate change and illegal harvesting. Using ddRADseq, this study explores the genetic diversity, evolutionary relationship, and population structure to determine their uniqueness and trace possible poaching origins. Findings reveal two primary genetic groups of minimal gene exchange and evidence inbreeding, particularly in the Spring Mountains. Genetic data also assures the concerns that poached individuals may originate from specific wild populations. This research enhances conservation efforts and supports the potential listing of A. utahensis under CITES protection

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Topic: Ecology

A-767

How does floret variation in Gaviota tarplant (Deinandra increscens subsp. villosa; Asteraceae) connect to its range, windfarm development, and genetic structure?

Author: Dorian Scheim, Kristen Lehman, Rachel Meyer, C. Matt Guilliams, Emma Steigerwald
Affiliation: University of California, Santa Cruz, Santa Barbara Botanic Garden, University of California Santa Cruz

Gaviota tarplant, Deinandra increscens subsp. villosa (Asteraceae), a federally endangered annual herb endemic to a small and highly fragmentary range along the Central Coast of California, is a species of strong interest to conservation practitioners, making developing an understanding of potential adaptations to the discrete patches in which it occurs critical as a result. We chose to focus on characterizing counts of ray and disk florets, a diagnostic feature in Gaviota tarplant, which are variable within this species and are typically heritable quantitative traits. The ratio of ray to disk florets represents an established tradeoff in other aster systems between energetic investment in pollinator attraction (ray florets) and reproductive output (disk florets)–a dynamic that is highly influenced by the surrounding environment. We are dissecting flower heads from almost 200 herbarium specimens collected from across the tarplant's range and over the course of the last century to count ray and disk florets per inflorescence. We will analyze these traits in relation to environmental variables hypothesized to play an important role in Gaviota tarplant's local adaptation, including fog cover and soil moisture. We will also assess how these phenotypic traits may have changed over time. Our results will provide conservation managers with important data about a fitness-relevant trait in this endangered plant, and may further aid in guiding and interpreting a large ongoing project exploring genotype-by-environment associations in this species.

Topic: Comparative Genomics/Transcriptomics

A-768

Integrating Environmental Drivers, Phenology, and Gene Expression to Understand Flowering and Seed Production in Zostera marina

Author: Fernando Rodriguez, Elena Lopez Peredo, Agustin Moreira-Saporiti, Sarah Merolla, Grace Dixon, Mirta Teichberg
Affiliation: Rochester Institute of Technology, Marine Biological Laboratory

Zostera marina, commonly known as eelgrass, is a marine monocot that plays a foundational role in coastal ecosystems worldwide. Eelgrass meadows provide essential habitat and food sources for numerous ecologically and commercially important species. Beyond their ecological significance, seagrasses help to stabilize coastlines against erosion, improve water quality by filtering excess nutrients, and serve as long-term carbon sinks. However, eelgrass populations are experiencing global declines due to increasing pressures from eutrophication, coastal development, and rising nearshore water temperatures associated with climate change. In particular, warming events and marine heatwaves have pronounced negative effects on eelgrass health and survival, contributing to large-scale population losses.

Restoration of these critical ecosystems is challenging and typically involves harvesting rhizomes or seeds from donor populations for transplantation. This approach can inadvertently reduce the effective population size of donor beds. Furthermore, a key limitation in restoration efforts is the lack of detailed understanding of *Z. marina* reproduction under natural conditions. Although this species reproduces sexually on a seasonal basis, there is limited data on its flowering and fruiting patterns, the environmental drivers that influence them, and the gene expression responses in wild populations.

To address these gaps, we adopted a comprehensive approach to characterize reproductive patterns in *Zostera marina* by combining phenological observations with transcriptomic analyses across multiple sites. From March to September 2023, we established five permanent stations across seven seagrass meadows in Cape Cod, capturing data before, during, and after the flowering period. At each site and station, we recorded environmental variables and measured the density of reproductive shoots and seed yield. Reproductive shoots began developing in mid-to-late April, and the data series suggests that temperature plays a significant role as a triggering factor for flowering.

In parallel, we conducted RNA-seq-based gene expression analysis at each site to examine molecular changes associated with flowering and seed maturation. Sequencing reads were aligned to the *Zostera* genome version 3, and differential

expression analysis was performed using DESeq2. Over 160 vegetative tissue samples were collected throughout the reproductive season and used for transcriptomic profiling to identify gene expression patterns linked to the onset and progression of flowering. We identified a sharp decrease in genes traditionally associated with the inhibition of flowering, alongside an increase in the expression of genes that regulate the cascade of flowering signals. Additionally, RNA-seq was used to analyze different developmental stages of reproductive material, from fertilized flowers to mature seeds, to gain a deeper understanding of the gene expression changes that regulate reproductive transitions in *Z. marina*.

Topic: *Education and Outreach*

A-770

Teaching students to "see" plants in the experience of everyday life: the power of botanical vision

Author: Robert Noyd, Hannah Grover
Affiliation: U.S. Air Force Academy

All instructors strive to help their students apply classroom learning to their personal and/or professional lives and to take their knowledge beyond the classroom. Botany instructors, in particular, have the advantage that plants are woven into the everyday experiences of their students as food on their plates, in the clothing they wear, the towels and paper products they use, as part of the landscapes in which they travel, and the flowers they give or receive to express feelings. This ubiquity provides endless opportunities to apply the knowledge from class to the plants they encounter daily or the plants of their past or future life. But we must ask: are we effectively leveraging this relevance, concreteness, and familiarity that plants offer? If so, how is instruction designed to explicitly support the transfer of botanical knowledge to new, real-world botanical encounters? What instructional practices support and promote the awareness of plants? While awareness of the presence of plants is a start, we can take our students deeper into their application of their classroom learning; we can push them to develop what I call "botanical vision." From their awareness of plants, botanical vision also includes the power to apply and fluently use botanical terms to describe plants they *see* both morphologically and anatomically, to name the plants they *see*, and to *see* the underlying complexity of their physiological, developmental, and evolutionary processes. This presentation will introduce several targeted instructional strategies designed to cultivate botanical vision – tools that help students carry classroom learning into the rich botanical landscapes of their everyday lives.

Topic: *Molecular Ecology*

A-771

Microbial Ecology and Environmental Stress Responses of Green Microalgae in Retention Ponds of the Genesee River Basin- Lake Ontario watershed

Author: Francesca Molee, Maleah Sena, Fernando Rodriguez, Elena Lopez Peredo
Affiliation: Rochester Institute of Technology

Extreme rainfall events in the U.S. are projected to become 20% more severe and occur 200% more frequently in the coming decades due to climate change. This is concerning for the health of aquatic systems, as runoff from precipitation events is a major source of aquatic pollution. Urban runoff can carry harmful chemicals such as herbicides from landscaping and deicing salts from road maintenance, which impact the overall health of nearby water bodies. Applied fertilizers also create nutrient-rich waters, fueling Harmful Algal Blooms (HABs). HABs have severe effects on aquatic organisms and community structure, and pose health risks to humans and megafauna alike through the production of cyanotoxins.

Retention ponds are constructed to catch and hold this polluted runoff, mitigating both pollution and flooding. While successful in runoff management, this strategy creates runoff-fed ecosystems that expose organisms, including photosynthetic microbial communities, to high levels of pollutants. This can lead to altered community dynamics and selection for organisms with increased chemical tolerance. These systems can therefore be used to explore the ecological consequences of urban and suburban pollution pressure by examining microbial communities in water and sediment, with a focus on those often linked to HABs, such as cyanobacteria and eukaryotic algae.

In this research, we combine high-throughput prokaryotic sequencing of the 16S ribosomal gene, algal isolation methods, and in-lab chemical stress testing under common garden conditions to investigate the physiology of photobionts and the community structure and diversity of microbial communities in retention ponds heavily impacted by urban runoff in the greater Rochester area (NY). This includes contrasting these communities with those from ponds that are relatively unaffected by anthropogenic pollution. In addition, we explore the role of seasonal fluctuations and pollutant levels in our results. Samples collected in early spring are fed by saltier water with high concentrations of deicing road salts following the winter thaw, while samples collected in early summer contain excess nutrients from lawn fertilizers and herbicides commonly used in urban areas. Bacterial communities in polluted sites are enriched for taxa traditionally linked to human activities. Intriguingly, we did not observe an increase in cyanobacteria—often linked to HABs—in the polluted sites.

Over 150 algal strains were isolated and used in common garden experiments to evaluate their tolerance to pollution. Our results indicate that members of the green algal community tolerated low concentrations of deicing salts, but were highly susceptible to the presence of higher concetrations of NaCl and $MgCl_2$ road salt (marketed as a "safer" salt). Excess nutrients from fertilizer also impaired growth. However, stress response varied greatly by individual isolate, and some taxa thrived in conditions equivalent to those in polluted waters. The common herbicide Roundup Weed & Grass Killer inhibited algal growth completely, even at extremely low concentrations. We did not identify any eukaryotic algae capable of tolerating the herbicide.

Topic: *Phycology*

A-773

Impact of Salt Stress on Growth and Astaxanthin Production in a Suite of Algae within the Scenedesmaceae

Author: Maleah Sena, Francesca Molee, Elena Lopez Peredo
Affiliation: Rochester Institute of Technology

Microscopic green algae in the Chlorophyta are cosmopolitan unicellular organisms that can thrive in a diverse range of environments, including both terrestrial and aquatic systems. Due to this, they exhibit a broad tolerance to environmental conditions, ranging from high light, temperature swings, low humidity of terrestrial environments, to the low-light, nutrient-rich waters of seasonal pools. This ability to colonize a variety of habitats, some cases even among members of the same genus, makes them ideal candidates for the study of responses to environmental stressors, including drought and salinity.

Tolerance to water loss is an essential trait for adaptation to terrestrial environments and is often accompanied by the triggering of other protective mechanisms such as responses to oxidative stress and high light. Additionally, exposure to high salt concentrations is often a consequence of drought, meaning that salt and water-loss stress are likely intertwined and may also influence the production of secondary metabolites. The response to excess salt plays a crucial role in shaping the physiological and biochemical stress responses of green algae, impacting both growth and secondary metabolite production.

Here, we examined a suite of algae within the Scenedesmaceae—Tetradesmus obliquus (UTEX 72), Tetradesmus deserticola, Enallax costatus, Fletchneria rotunda, T. obliquus (UTEX 393), and Tetradesmus bajacalifornicus—to compare their physiological responses to water loss and changes in salinity. We used UV/Vis spectroscopy to measure both overall algal growth and color changes indicative of pigment production. Additionally, we used flow cytometry to assess oxidative stress, chlorophyll fluorescence, and astaxanthin content in algae under these stress conditions. We demonstrate that exposure to sodium chloride (NaCl) and magnesium chloride ($MgCl_2$) significantly affects the production of carotenoid pigments, including astaxanthin, a ketocarotenoid known for its antioxidant properties.

Finally, we explored the genetic basis of pigment production under stress by analyzing transcriptomic signatures associated with pigment biosynthesis in algae subjected to desiccation. We analyzed a dataset of slowly desiccated algae to examine the expression of astaxanthin-related genes. The aim of this analysis is to identify potential candidate genes as biomarkers for astaxanthin production under other conditions, such as salt stress. Given the close relationship between salt and drought stress, we predict that gene expression patterns (upregulation and downregulation) will be similar for both conditions.

The importance of this research lies in the biofuel potential of algae within the Scenedesmaceae. By triggering the production of additional valuable compounds while maintaining high growth rates, we can optimize the economic yield of algal biofuel production systems.

Topic: *Physiology*

A-774

Transcriptome and chromatin dynamics during water-limitation and recovery in switchgrass

Author: Yuvraj Chopra, Sahar Ghahramanloo, Nate Emery, Chad Niederhuth, Sunil Kenchanmane-Raju
Affiliation: University of California, Riverside, Michigan State University, University of California Riverside

Renewable energy offers a long-term solution to rapidly depleting conventional energy sources. Plant tissues enriched with lignocellulosic biomass represent a significant renewable energy source for biofuels. An upsurge in the prevalence of extreme weather patterns challenges the sustainability of agriculture. Water limitation among all abiotic stresses has a profound effect on the vegetative biomass, threatening bioenergy crops. Switchgrass (Panicum virgatum), a perennial C4 grass, represents a valuable bioenergy model crop, particularly due to its energy efficiency and tolerance to water limitation. Insights into the mechanisms driving water-limitation tolerance in switchgrass could highlight specialized response strategies. To this end, this study integrates transcriptome and chromatin accessibility datasets from leaf tissues of Kanlow and AP13 genotypes to explore conserved and genotype-specific transcriptomic responses to water-limitation and recovery with emphasis on cis-regulatory elements (CRE) controlled trait variation. Plants from both genotypes were subjected to water limitation, 24-hour recovery, and a 3-week recovery period. Our results show that Kanlow had an earlier onset of transcriptome changes and significantly more differentially expressed genes than AP13 across all treatments. Transcriptome analysis showed differences in expression of photosynthesis, stress-responsive, and amino acids biosynthesis related genes under water limitation. To identify genes with regulatory divergence between the genotypes, differentially regulated gene expression analysis was performed. Physiological data suggest that AP13 has better tolerance to water limitation, whereas Kanlow has superior recovery. Overall, the results suggest that water-limitation and recovery responsive genes exhibit altered chromatin dynamics, highlighting the potential role of CRE variation in differential response between the genotypes. Findings from this study provide a molecular foundation for understanding mechanisms of responses to water limitation and recovery in switchgrass.

Topic: *Population Genetics/Genomics*

A-775

Genomic diversity of a subspontaneous Criollo cacao population in Belize

Author: Holly Brabazon, Jacob Marlin, Lenardo Ash, Elmer Tzalam, Erick Ac, Mark Canti, Meg Staton, DeWayne Shoemaker
Affiliation: University of Tennessee, BFREE

Theobroma cacao L. (cacao) is a tropical fruit tree that produces the raw beans used to make chocolate. Using whole-genome sequencing of 389 cacao trees, we investigated the genomic diversity of a population of cacao found at a research station in Southern Belize. Population genomic analyses, including fastSTRUCTURE, measures of Hardy Weinberg Equilibrium, Tajima's D, observed vs. expected heterozygosity, estimates of effective population size, and kinship analysis, were performed to determine the population demography and evolutionary history of this unique population. Results suggest a small number of trees established this population, resulting in high relatedness and low genetic diversity and provide additional context to the evolutionary history of Criollo cacao in Central America.

Topic: *Evolutionary history of the Gnetales*

A-776

Ephedra as a model clade for gymnosperm evo-devo

Author: Veronica Di Stilio
Affiliation: University of Washington, Seattle (WA)

Genomic and transcriptomic resources are rapidly expanding; hundreds of plant genomes, including representatives from all major land plant lineages and their algal relatives, have been sequenced—and the pace continues to accelerate. Yet, as "omic" data accumulates faster than we can interpret it, the need to experimentally validate gene function becomes more urgent.

To meet this need, the strategic development of model systems must continue—ideally expanding to include entire model clades for evolutionary and ecological studies. Despite increasing interest in genotype-phenotype connections, model organisms remain rare and unevenly distributed across the plant tree of life. Notable gaps exist in early-diverging vascular plants (lycophytes and ferns), early angiosperms, and especially gymnosperms. Filling these gaps is essential for building a "functional" tree of plant life. Developing model systems at key phylogenetic nodes enables robust ancestral reconstructions of gene function. As the sister clade to angiosperms, gymnosperms are critical for reconstructing ancestral gene regulatory networks in seed plants. However, challenges such as long life cycles and large genomes have hindered the development of gymnosperm models. *Ephedra* (Gnetales) offers a promising solution, with relatively small genomes, shrubby growth habits, and shorter life spans—suitable for greenhouse cultivation and laboratory experimentation. These features position *Ephedra* as an emerging model clade for gymnosperm evolutionary developmental biology (evo-devo).

Established and emerging plant models are already informing evo-devo themes such as deep homology, gene network co-option, and functional divergence of orthologs. For this symposium, I will discuss how *Ephedra* is advancing as a model clade, supported by a growing toolkit that includes an advanced draft genome for *E. tweediana*, virus-mediated gene silencing, and RNA-seq applications. These tools and resources, developed through collaborative research, are helping to unravel the origins of plant morphological diversity.

Topic: *Systematics & Taxonomy*

A-777

A Threefold Increase: Revealing Circinaria Diversity in Western North America

Author: Virginia Bassett, Elizabeth Perry
Affiliation: Brigham Young University

The lichen-forming fungal genus *Circinaria* (Megasporaceae)—commonly known as manna, crater, or dung lichens—occurs broadly across the Intermountain West of North America. Globally, *Circinaria* comprises ~40 species, but only ~13 species have been documented in North America. To better characterize species-level diversity of *Circinaria* in western North America, we sampled over 150 specimens from populations throughout the Intermountain West. These were assessed within an integrated taxonomic framework, combining molecular, morphological, and ecological data. The fungal DNA barcoding marker (ITS) was amplified through PCR. The newly generated sequences, coupled with additional sequences retrieved from GenBank, were analyzed using phylogenetic inference to delimit species hypotheses (SHs). Morphology and ecological features of DNA-based SHs were assessed, particularly in relation to currently described species. Our results revealed greater species-level diversity in western North America than expected, documenting over 30 distinct species/species-level lineages in the region. Several of the candidate species circumscribed here can reasonably be described as new to science based on the data on hand. The threefold increase in species-level diversity recognized in western North America underscores the need for further taxonomic research and emphasizes the importance of formal species descriptions, which can further our understanding of *Circinaria* distributions, inform conservation efforts, and contribute to regional lichen ecology.

Topic: *Biodiversity Informatics & Herbarium Digitization*

A-778

Herbariograph: a deep–learning tool to classify specimen images

Author: Fabio Andres Avila Castillo, John Park, Leanna Feder, Damon Little
Affiliation: New York Botanical Garden

Herbarium specimens are the physical evidence of plant diversity worldwide and a rich research data source. With about 400 M items distributed in 3.5 k registered herbaria in 185 countries, it is estimated that approximately 10% have associated digital images. Despite this low proportion, information in these images facilitates numerous avenues of research aimed at understanding the hidden complexity and variation of plants. The first step in harvesting this information is to sort images by the types of items represented within them. To address this challenge, we present Herbariograph, a new open image dataset, and deep-learning model designed to automatically recognize all image types commonly stored in collection databases. The dataset comprises 17 image categories, with 12,288 images per category gathered from 43 institutions. A VisionTransformer (ViT) with a novel image tokenizer (Trident) was trained on the Herbariograph dataset.

The trained model produces a test macro F1 score of 0.9581. Herbariograph will help to automate specimen image processing to make targeted dataset creation faster, better, and more accessible.

Topic: *Biodiversity Informatics & Herbarium Digitization*

A-779

Pressing Forward and Cultivating Engagement: The Duke Herbarium's Social Media Strategy for Public Outreach and Institutional Reflection

Author: Kathleen Pryer, Kaylee McKinzie, Erin Heyeck, Yuchen Chen, Nicolas Zepeda, Matthew Cicanese, Hannah Jacobs, Andrew Griebeler
Affiliation: Duke University

Early in 2024, an announcement from Duke University sent shock waves through the global botanical community. Citing a reorientation of funding priorities during its centennial celebration, Duke broadcast a top-down decision to divest its 100-year-old herbarium and to disperse this world-renowned collection of nearly 1M specimens (herbarium.duke.edu). The extraordinary nature of Duke's decision was reflected in the outrage and dismay with which it was met by natural science leaders from around the world (tinyurl.com/497kzz6y), and by Duke's own community. In response to this crisis, a Duke developed a social media-based digital humanities project to document, educate, and commemorate this significant collection. Here we report how, through strategic social media storytelling, they transformed pending institutional loss into a public engagement opportunity. Their Instagram account @bluedevil.herbarium is a digital archive and educational platform, featuring high-resolution photographs, videos, 3D models, historical narratives, and community memories. Content focuses on highlighting herbarium specimens, digitization efforts, and seasonal or thematic posts that invite dialogue between science, community, and culture. Informed by the broader campus discourse on sustainability and environmental justice, this social media presence also gestures toward conversations on climate, stewardship, and transparency within academic institutions. Initial outcomes demonstrate significant public impact, with 750 followers gained in the first four months. Notable metrics include reaching 40,000+ unique accounts within ninety days, and multiple testimonials from around the world expressing the importance of herbaria and of this project's value in preserving institutional memories and advancing scientific literacy. This project presents a case study in how herbaria can leverage social media not only to promote their collections but also to situate them within pressing ecological and institutional narratives. The Duke Herbarium model may serve as a flexible framework for other collections seeking to enhance their visibility, foster community engagement, and thoughtfully participate in broader environmental conversations.

Topic: *Reproductive Processes*

A-780

What are you doing in my swamp? How urbanization impacts the reproductive success of Missouri native species Iris virginica

Author: Sara Wuerstl, Franceska Isufaj, Kyra Krakos
Affiliation: Maryville University

Plant-pollinator networks can be negatively impacted by habitat loss with one of the main contributors being urbanization. Comparing the differences found in the rural and urban habitats can be important in restoring the highly urbanized areas and protecting the existing rural ones. To compare the potential impacts of habitat on reproductive success, *Iris virginica* was studied in a rural population at Shaw Nature Reserve and in an urban population at Litzsinger Road Ecology Center. In this study, *I. virginica* is analyzed by examining morphological differences and the pollination system based on the habitat location. Morphological measurements for height of plant, corolla span, and stamen length. Nectar collection was done hourly to demonstrate if the plant was able to replenish nectar levels. Nectar levels are expected to decrease throughout the day with little replenishment due to nectar robbing. Soil samples were collected from each habitat to determine pH. Pollination observations were done at twenty-minute increments combined with insect pollen loads to determine the main pollinator. Hand pollination treatments were done at each population. Pollen tubes were counted from each treatment to determine if *I. virginica* was pollen limited. After data collection was complete, it was determined that the urban habitat in 2024 was significantly shorter. Nectar production also increased this year but still followed the same trend of decreasing nectar levels throughout the day. This study addresses how abiotic environmental factors, morphology, nectar production, and pollination rates impact the reproductive success of *I. virginica* in its wetland environment. The information from this study can be further applied to restorative efforts.

Topic: *Phytochemical*

A-781

Medicinal Succulent, Molecular Mystery: Assessing the role of Abiotic stress in Mesembrine Alkaloid Production in Kanna (Sceletium tortuosum)

Author: Elena Foust, Karolina Heyduk
Affiliation: University Of Connecticut (UCONN), University of Connecticut

Kanna (*Sceletium tortuosum*) is a medicinal succulent indigenous to the Cape Provinces of South Africa. Mesembrine-type alkaloids, primarily found in this species, are responsible for their mood-elevating properties. Despite growing interest in its pharmacological potential, there remains little known about how environmental factors influence mesembrine alkaloid biosynthesis and accumulation. Only one previous study has examined how soilless media impacts mesembrine alkaloid concentration. Abiotic stress is known to enhance secondary metabolite production in many medicinal plants, often through the upregulation of biosynthetic genes. However, the absence of a reference genome for *S. tortuosum* has limited genetic and metabolic insights, leaving the regulation of mesembrine biosynthesis under stress largely unexplored. The intensity of dry environments, UV-B exposure, and temperature are increasing due to climate change, and understanding stress responses is essential to assist with conservation efforts, ensuring this plant continues as a medicinal resource. As a member of the Aizoaceae family, *S. tortuosum* is believed to exhibit facultative Crassulacean Acid Metabolism (CAM), performing C3 photosynthesis under favorable conditions and switching to CAM under stress such as drought to reduce water loss. However, its photosynthetic pathway has not been definitively characterized. Furthermore, limited research has examined how CAM-performing species respond to monochromatic blue light, which is known to stimulate stomatal opening independently of photosynthesis. Gas exchange measurements were collected for plants grown under normal, drought stress, and blue light treatments using a portable photosynthesis LI-COR system, providing data on photosynthetic efficiency. LC-MS metabolite profiling will detect structural and quantitative changes in alkaloids in response to stress conditions. Gene expression analysis under both control and stress conditions will help to identify key regulatory genes involved in alkaloid biosynthesis. Correlating gene expression patterns with alkaloid concentrations could ultimately guide efforts to enhance the pharmacological potential of *S. tortuosum* through both cultivation and engineering strategies. Leveraging abiotic stress to optimize the accumulation and concentration of these alkaloids could ultimately reduce the need for large-scale harvesting of wild populations and support sustainable cultivation practices. This approach can potentially strengthen the economic value of *S. tortuosum* while contributing to the development of more effective plant-derived antidepressants. This study investigates the influence of abiotic stress in the form of drought, monochromatic blue light, and UV-B radiation on mesembrine alkaloid accumulation in *S. tortuosum*. There is an emphasis on understanding the physiological and molecular responses related to the photosynthetic efficiency and plasticity of this medicinal

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Topic: *Bryology and Lichenology*

A-782

An Analysis of the Accuracy of Photo-Based Plant Identification Applications on Bryophytes of British Columbia

Author: Philippa Stone, Kody Forsyth, Connor Wardrop, Mari Wilson, Janet Ngo
Affiliation: University of British Columbia

In recent years a number of different photo-based plant identification applications (apps) have become available to download and use. These apps enable anyone with a smartphone to attain basic identifications of plants, and are widely used as an educational tool and act as a major resource for community science projects. Multiple studies have questioned and quantified the accuracy of these apps' identifications showing that the proportion of correct identifications varies widely between apps and across taxonomic groups. However, so far these studies have only been carried out on vascular plants and no study of the accuracy of these apps' identification of bryophytes exists.

Fieldwork was conducted in the Canadian Cascades in E.C. Manning Provincial Park, British Columbia. We took over 400 photos of 50 species of mosses, liverworts, and hornworts with smartphone cameras to analyze using photo-based plant identification apps. We took photos of each bryophyte with just the smartphone camera, and with a hand lens held up to the smartphone camera lens to increase magnification. We used six of the most popular photo-based plant identification apps; Seek by iNaturalist, PlantSnap, Pl@ntNet, PictureThis, Apple Visual Look Up, and Google Lens.

We found that Seek by iNaturalist was the most accurate at identifying bryophytes to species, followed by Apple Visual Look Up, and Google Lens. Seek by iNaturalist also left the highest percentage of bryophyte photos unidentified. Pl@ntNet was the only photo-based plant identification app that failed to identify any bryophyte photos correctly at the species level, and also failed to identify any photographs to the correct genus, or family. Use of a hand lens significantly increase the proportion of bryophytes correctly identified to species level when using Seek by iNaturalist, but did not significantly increase or decrease the proportion of bryophytes correctly identified to species level using any of the other apps. Overall, plant identification accuracy of bryophyte photos was much lower than has been reported for similar studies testing the accuracy of photo-based plant identification apps vascular plant identifications.

Topic: Paleobotany

A-783

Temporal patterns in gymnosperm seed size evolution

Author: Stepfan Huntsman, Andrew Leslie
Affiliation: Stanford

Modern seeds are extremely variable in size, ranging over 11 orders of magnitude by mass. A substantial fraction of this variation is due to angiosperms, however, with extant gymnosperms showing less variation. Angiosperms also appear to have a more dynamic history of seed size evolution, with a dramatic rise in seed size in the Paleocene that may be a response to the emergence of closed-canopy rainforests. By contrast, gymnosperms are widely thought to have exhibited similar sizes over much of their history, following an initial rise in the Carboniferous, but detailed patterns in their seed size evolution are unclear, particularly in the Mesozoic. We compiled a database of fossil gymnosperm seeds, including dispersed seeds and those found in reproductive structures, spanning the Devonian through the Paleogene. The data set includes around 700 fossil seeds from which we recorded linear measurements. We also compared these data with compilations of modern gymnosperm and angiosperm seed sizes (835 and 6545 species respectively). Our data show a notable decline in gymnosperm seed sizes from the Permian through the Triassic, with relatively small sizes prevalent over the Mesozoic. Gymnosperms do appear to show a rise in seed size from the Paleogene through the modern, but unlike angiosperms, where size shifts are found throughout clades, gymnosperm patterns are often clade specific. For example, the extreme size of Carboniferous seeds is primarily due to Medullosan pteridosperms, and the Cenozoic rise in seed size is more pronounced in Araucariaceae and Podocarpaceae than other lineages. It is notable, however, that these are tropical conifers most likely to interact with closed-canopy angiosperm forests. In general, we find that Mesozoic gymnosperm seeds are comparable to those of modern temperate woody angiosperms, while the modern gymnosperm size distribution is more similar to that of tropical woody angiosperms. These patterns suggest that the emergence and extinction of specific lineages plays a prominent role in gymnosperm seed size history, but at least some clades have responded to global trends in the same manner as the Early Paleogene rise in angiosperm seed size.

Topic: Ecology

A-784

Four Decades of Vegetation Change and Land Use Management on Three Mile Island, Lake Winnipesaukee

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In the late 1970s, a team of ecologists and conservation-minded campers established a long-term vegetation monitoring study on Three Mile Island, a 43-acre mixed conifer-deciduous forest on Lake Winnipesaukee, New Hampshire. The study followed the implementation of a land use plan that divided the island into four zones—urban, compromise, productive, and protective—to balance recreation and conservation. In 2021, we resampled 19 permanent vegetation plots, adding a fifth decade of data to a rare long-term dataset. We analyzed changes in species richness, abundance, and evenness to assess how vegetation has responded to differing land use intensities. Overall, we observed directional shifts in both understory and overstory composition. A notable overstory trend was the decline of Betula papyrifera (paper birch) and concurrent increase in Acer rubrum (red maple), along with increasing prevelance of overtopped and intermediate canopy species, suggesting successional dynamics and shifting forest structure. Compromise and productive zones exhibited similar vegetation trajectories, while urban and protective zones showed more distinct changes. These findings highlight both the resilience and sensitivity of island vegetation to recreational land use and will inform revisions to the island's land use plan. The results also contribute to broader understandings of ecological succession, management impacts, and community engagement through long-term ecological research in small, insular New England ecosystems.

Topic: Hybrids and Hybridization

A-785

Assessing the Long-term and Immediate Consequences of Allopolyploidy on Flower Size in Nicotiana

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Allopolyploidy describes hybrid organisms that have experienced a whole genome duplication. This can lead to changes that result in immediate or long-term consequences. These consequences can be phenotypic, including flower tube length and width. Coevolution with flowers and their pollinators can drive the patterns observed in flower size evolution. It is known that younger polyploids tend to have wider tubes than their diploid progenitors, but the patterns of flower size evolution across polyploid speciation compared to diploid speciation has not been explored. *Nicotiana* section *Suaveolentes* were used to observe flower size evolution among allopolyploid species. There are ~90 species in the section, which emerged ~six million years ago from one allopolyploidization event. We spent a month at Kew Gardens, UK to gather photos from 35 species. There were between one and five plants of each species and five flowers from each plant were photographed. Each flower had five photos looking down the flower tube to measure width, and five photos of the dissected flower to measure tube length. These photos were then incorporated into introductory biology labs where students measured them using FIJI, including three replicates of each flower photo to ensure the dataset was robust. A phylogeny of the species was used in tandem with the data to create ancestral state character reconstructions. The difference between the measurements for both length and width respectively between adjacent nodes from the reconstructed tree were calculated to generate evolutionary trajectories which were then compared to diploid data, observing the effects of polyploidy on flower size evolution. In addition to flower size evolution, long-term consequences of polyploidy from *Nicotiana* section *Suaveolentes* were compared to synthetic lines of *N. tabacum*, representing the immediate consequences of polyploidy. *N. sylvestris* and *N. tomentosiformis* were used to create hybrid *N. tabacum*, generating the F_1 lines. These hybrids were then induced to become polyploids, creating the S_0 lines. Photos of these flowers were measured to obtain length and width data using the same methods as above. Trajectories were created and indicated that the S_0 lines are significantly bigger in length and width compared to their respective F_1 lines. It can be predicted that this may be due to the difference between the genetic information in their genome contributing to bigger cell size, therefore their size is overall larger. The study allows us to compare long-term and immediate consequences of polyploidy and effects of polyploidy on flower size evolution.

Topic: Evolutionary history of the Gnetales

A-786

Exploring Ephedra in the Atacama: Phylogenetic Diversity, Conservation Priority, and Vulnerability in the World's Driest Desert

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Ephedra is the only genus of the Gnetales present in Chile. With only 6 known species in the country, it inhabits mainly dry habitats in the north and central areas, with one of the species also found in Patagonia. Even though two endemic species have been described for Chile, *E. trifurcata* has recently been declared extinct, leaving only *E.*

gracilis as a strict endemic. The remaining 4 species are shared with neighboring countries. Ephedras are sturdy plants, adapted to live in some of the most inhospitable environments, such as the Atacama Desert, the driest in the world.

Ephedra has been studied by the EDGE of existence initiative, which considers species that are evolutionary unique and endangered with extinction (according to the global IUCN Red List), as priorities for conservation. At the global level, the species of the genus *Ephedra* have low rankings, not qualifying as priority species for the EDGE program. From the species present in Chile, four appear in the EDGE list, meaning that they have been globally assessed by IUCN. However, important discrepancies between the global list and the local assessment have been found. The most dramatic one is *E. trifurcata*, considered extinct in Chile (and globally since it was endemic) and listed as data deficient for the global IUCN list.

There are two problems with the EDGE assessments for this group of species. First, the phylogeny used to generate the global EDGE scores considered all extant gymnosperms. Even though this makes sense from a phylogenetic point of view, because of the age of most crown groups of extant gymnosperms, the clades that are "newer", remain obscured by the much higher branch lengths of the oldest relatives. In Gymnosperms this is particularly important since crown nodes of some of the groups, date as far back as the Jurassic or even further as in *Ginkgo*. The other problem has to do with the lack of communication between local Red Lists and the global IUCN Red List from where the data for EDGE is sourced. This is especially relevant in the case of endemic species, whose conservation is the sole responsibility of one government. A clear illustration of this is the case of *E. trifurcata* previously mentioned.

To overcome this, we did a study based on local flora, in which all species of *Ephedra* in Chile were studied, using as a proxy for conservation assessment, the current and future distribution of the species in the country, and calculating both EDGE as well as the Relative Evolutionary Distinctness index RED (Ramirez et al 2019).

Using models of species distributions, we found that all species of *Ephedra* in Chile are expected to lose more than 50% suitable habitat, being the most affected the strict endemic *E. gracilis*, in the Atacama Desert. Considering this, new data for current threat and for expected loss of evolutionary diversity has been generated, hoping to aid in the conservation of this important and unique group of plants.

Topic: Bryology and Lichenology

A-787

The overlooked succession: how lichen and moss communities respond to fire in a post-agricultural prairie

Author: Mariana Cardenas Henao, Maowei Liang, Troy Mielke, Daniel Stanton
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Lichens and mosses are regularly overlooked in ecological assessments, particularly when studying ecosystems in which these organisms are not dominant elements of the landscape, such as prairies. When included at all, they are often treated as a monolithic category that ignores the diversity and nuances of their biological communities. This study used the iconic platform of the Old Fields experiment at Cedar Creek Ecosystem Science Reserve, MN —a post-agricultural chronosequence spanning 8 to 97 years of abandonment in a prairie ecosystem. In this field experiment, half of each field is burned every 4 years, while the other half remains unburned. We explored how succession time and fire affect ground lichen and moss community attributes —such as cover, richness, and alpha diversity—, as well as their beta diversity patterns. In each field, we characterized both lichen and moss communities in 48 0.5 m x 0.5 m plots in each fire treatment. Overall, we found more moss and lichen species in the non-burned areas compared to the burned areas (mosses: S = 16 and S = 8 in unburned and burned areas, respectively; lichens: S = 16 and S = 10 in unburned and burned areas, respectively). However, lichen and moss community attributes behave differently in this secondary successional system. Moss cover, richness, and diversity significantly declined from early to late stages of succession in both treatments, although the burned treatment generally exhibited higher average values across all plot-scale attributes. In contrast, lichen community attributes displayed more dynamic patterns. Lichen cover in unburned areas followed a quadratic trend, peaking around 50 years of succession, while in burned areas it remained relatively stable over time. Lichen richness also showed a quadratic pattern, with peaks around 40 years in burned areas and 50 years in unburned areas. Lichen diversity increased linearly with time in unburned areas, whereas in burned areas it rose until approximately the 50-year mark. When examining beta diversity, dissimilarity in community composition between burned and unburned areas increased over time for both moss and lichen communities, suggesting a gradual divergence between the two treatments. However, this divergence was not statistically significant. On average, moss communities were significantly more similar in burned areas than in unburned ones, indicating that fire led to more homogeneous moss assemblages. In contrast, the dissimilarity in lichen communities was not statistically different between burned and unburned areas. We concluded that lichen and moss communities follow different successional patterns in both fire treatments, with fire acting as a stronger limiting factor for lichens than for mosses, likely due to the presence of ruderal moss species such as Ceratodon purpureus. This study also highlights the importance of considering lichens and mosses as unique categories in long-term ecological assessments, since they can provide different perspectives on ecosystem development.

Topic: Development and Structure

A-788

Genetics of Floral UV Pigmentation of Bullseye Morph in Monkeyflowers

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Pigmentation that absorbs light in the ultraviolet (UV) spectrum is produced by some plants around their reproductive organs. UV pigmentation generated in this way serves the function of attracting pollinators and protecting the plants' gametes from mutations due to UV radiation. Mimulus guttatus (syn. Erythranthe guttata) has been proven to be a good system to study the genetics of UV pigmentation. The species is polymorphic for its floral UV pigmentation patterning, and the two most common morphs are a bullseye pattern and a runway pattern. Prior work in our lab has implicated the candidate gene YABBY5 in underlying UV pigmentation differences between these morphs. Our lab has shown that transgenic lines carrying CRISPR/Cas9 constructs targeting YABBY5 in the runway morph background produce two UV phenotypes: dimmed runway and spotty dimmed. The dimmed runway phenotype is characterized by a noticeable reduction of UV pigmentation in the distal portion of the ventral lobe. Similarly, the spotty-dimmed phenotype has loss of UV pigmentation across the ventral petal in addition to exhibiting cells that lose yellow pigmentation. In this study we investigate if YABBY5 is also involved in regulating UV pigmentation in M. guttatus in the bullseye morph background. Preliminary results show that the CRISPR/CAS9 transgenic lines have a four-base-pair lesion in the YABBY5 gene which introduces a premature stop codon. We qualitatively phenotyped floral UV pigmentation of the plants and quantified the intensity of UV absorption using a UV camera. Transgenics exhibit slight loss in floral UV in the floral tube of the ventral lobe. We also observe that trichomes lack UV pigmentation. This indicates that YABBY5 may also potentially play a role in regulating the UV pigmentation patterning of the bullseye morph. This work will help us understand how patterning polymorphisms arise in nature.

Topic: Phylogenomics

A-789

Using Synteny-Aware Phylogenomics Approaches to Describe Homoeologous Exchange in Grass Genomes

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Affiliation: The University of Alabama

Whole-genome duplication (WGD) is a major force in plant evolution, resulting in extra copies of the organism's genome. With this genetic surplus, some genes may take on new functions, while others become redundant and are eventually lost (fractionation). Over time, WGD can drive speciation by creating genetic barriers between populations or contributing to the evolution of novel physiologies and morphologies. Aside from gene loss through fractionation, the genes duplicated through WGD may undergo homoeologous exchange, resulting in the movement of copies with different evolutionary histories to opposite subgenomes. As part of this process, genes maintained in duplicate may be derived from the same parental genome, though they are found in divergent subgenomes resulting in a shift of the perceived evolutionary history of these paralogous genes. This process can make estimating the impact of WGD events on the evolution of lineages difficult and may lead to misconceptions about the evolutionary timing of polyploid events. The grass family Poaceae has had multiple polyploid events occur throughout its history with one, the *rho* event, occurring prior to the diversification of the family. Some studies using gene tree phylogenies have identified signal for additional potential WGD events occurring between the divergence of the Pharoideae subfamily and the BOP and PACMAD clades. Synteny analysis shows no evidence supporting these independent polyploidy events, suggesting that they may be anomalies and not

signal of distinct WGD events. Understanding the extent to which HE influences WGD detection is critical for reconstructing plant evolutionary history accurately. To address this, we conducted a comparative genomic study of 63 pseudomolecule-scaffolded genomes from grasses and other members of the Poales. Using both gene tree and syntenic (GENESPACE) approaches, we trace gene duplication patterns over time and identify genome rearrangements that could provide clues about past duplication events. Our goal is to determine whether the putative unique gene duplications seen in a subset of grass genomes, are a result of HE rather than the evidence of a distinct WGD event. By integrating phylogeny with synteny approaches, we aim to clarify the role of HE in shaping plant genomes and its implications for polyploidy detection.

Topic: *Hybrids and Hybridization*

A-790

Examining patterns of homeolog bias across subsets of genes associated with floral phenotypes in Nicotiana allopolyploids of different ages

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Allopolyploidy includes both interspecific hybridization and whole genome duplication, and has been a driving force in the evolution of angiosperms. Allopolyploids can display homeolog bias, where one progenitor copy of a gene is expressed at a higher level than that of the other progenitor. Patterns of homeolog bias across the entire transcriptome can lead to subgenome dominance if one progenitor is consistently expressed at a higher level than the other. Here, we investigate whether patterns of homeolog bias vary across subsets of genes that control different floral phenotypes—including flower color, flower size, flower symmetry, and flower organ identity—compared to overall patterns of homeolog bias across the transcriptome. We hypothesize that allopolyploids that share floral phenotypes with one progenitor will have biased expression towards that progenitor in the genes controlling that phenotype. However, we predict that the homeolog bias in allopolyploids will be less drastic than the bias observed between progenitor species. We will also explore whether patterns of homeolog bias change with allopolyploid age and expect to find that older polyploids show stronger homeolog bias than younger polyploids. To answer these questions, we will analyze transcriptomes from corolla tissue from 60%, 85%, and 95% of anthesis length buds from first-generation synthetic *Nicotiana tabacum* lines, from natural *N. tabacum* allopolyploids (which arose ~0.6 million years ago), and from *N.* section *Repandae* allopolyploids (which arose ~4 million years ago) and their diploid progenitors. This study will provide insight into whether reciprocal homeolog bias may drive the evolution of floral phenotypic differences in allopolyploids from the same origin.

Topic: *Systematics & Taxonomy*

A-791

Using the Boechera Microsatellite Website (BMW) to resolve notorious taxonomic complexities within the genus: The case of Boechera bodiensis

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As currently circumscribed, *Boechera* (rock cress; Brassicaceae) is a largely western North American genus comprising ~75 sexual diploid taxa and ~355 genetically distinct hybrid lineages. Most of the hybrid lineages are capable of reproducing via apomixis, creating a level of evolutionary and taxonomic complexity rivaling that of more familiar "problematic" genera such as *Taraxacum, Hieracium, Poa,* and *Rubus*. Using new data and analytic tools provided by the *Boechera* Microsatellite Website (BMW), we document recent progress in untangling the complex evolutionary web that is *Boechera*. The establishment of a continuously curated database available through the BMW; (windhamlab.biology.duke.edu) has been crucial to this effort. The BMW has multiple functions and capabilities, including the ability to: 1) Infer ploidy (and reproductive mode in taxa with sufficient sampling); 2) identify likely hybrids and estimate the amount of divergence among their parents; 3) develop hypotheses regarding potential parental lineages (PPLs) of hybrids; 4) elucidate the complex evolutionary pathways by which apomictic triploid and tetraploid hybrids arose; 5) circumscribe clusters of genetically similar individuals in the database to serve as operational taxonomic units (OTUs) for a broad range of analyses (morphological, geographical, ecological, etc.); 6) assess levels of genetic diversity within OTUs and categorize the likely sources of this variability (i.e., diversification of a single hybrid lineage vs. multiple hybrid origins); 7) resolve nomenclatural issues by linking OTUs to microsatellite-identified type specimens; and 8) provide a new, more solid foundation for continued progress on understanding hybridization in *Boechera*. The functionality of the BMW is demonstrated through an analysis of *B. bodiensis*, a rare species endemic to the western Great Basin, USA.

Topic: *Conservation Biology*

A-792

Exploring the demographic, spatial, and environmental traits of the climate relict Arroyo Oak to investigate water dependency

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The arroyo oak (*Quercus brandegeei*) is an endangered oak species endemic to Baja California Sur, Mexico (BCS). This species is likely a climate relict as it is composed of populations that persist in isolated areas of suitable climate surrounded by intolerable conditions (microrefugia). Indeed, the species is named after the arroyos (small ephemeral riverbeds), which it is restricted to. Previous work found that individuals of the species tend to occur in clumps. However, we wanted to investigate factors influencing the spatial and geographic distribution of size-classes more finely for this climate relict. In particular, we evaluated the relationship between ecogeographic, demographic, and spatial data at both individual (n=667 trees across 3 populations) and population scales (n=19 populations across the range). We expected water availability to be a primary determinant of tree distribution and size within populations and across BCS. As expected, we found that within populations, arroyos influenced the location of the trees, and soil-based proxies for water availability (e.g. water content, sand %, and clay %) are significantly positively associated with the size of trees. However, topographic and spatial proxies for water availability (distance to arroyo, aspect, and slope) were not significantly associated with tree size. We also found that, based on soil proxies (e.g. sand % and clay %), arroyo oak populations have higher water availability than random points across BCS. These results affirm the importance of water availability in the per

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Topic: *Population Genetics/Genomics*

A-793

Assessing the Origin and Population Structure of a Great Lakes Region Disjunct Species, Agoseris glauca (Asteraceae)

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Small, isolated populations often have low genetic diversity and low potential for adaptation in response to environmental changes. Alternatively, isolated communities are often more likely to display local adaptations and over time speciate. The Great Lakes Region is home to over 50 vascular plant species that are disjunct from the species' core populations. *Agoseris glauca* (Asteraceae) is a Great Lakes disjunct and Michigan state threatened species geographically isolated from its core range by 900 km. This study uses Genotyping by Sequencing to assess the population genetics of *A. glauca* for two Michigan disjunct populations and five western populations in the core range of the species. Specific goals were to 1) determine the amount of genetic variation in Michigan populations of *A. glauca* and several populations throughout the primary range of the species; and 2) determine whether the Great Lakes populations of *A. glauca* survived the last glaciation in a glacial refugium, are present due to pre or postglacial vicariance, or are the products of more recent dispersal. Cluster analysis and hierarchical F statistics were used to assess relationships among all seven populations. In all models, populations in Montana and Utah were different from all populations east of the Rocky Mountains. Two South Dakota populations and the Minnesota population were closely related to each other, and the Michigan populations were likewise closely related. Michigan populations show genetic distance from the South Dakota and Minnesota populations in our pairwise F_{ST}, and at K= 4 form their own cluster. At K=3 these Michigan populations cluster with South Dakota and Minnesota populations. Future studies will be carried out to determine approximate time of divergence and possible local adaptations in the threatened Michigan populations.

Topic: *Development and Structure*

A-794

Gilia as a novel model for evo-devo: QTL fine-mapping

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Identifying causative loci responsible for morphological evolution across species boundaries is a major challenge for the field of evo-devo. While candidate gene approaches are common, too often these fail to move beyond suggestive correlations. Forward genetic analysis through QTL mapping can identify causative polymorphisms underlying natural variation. However, these powerful genetic approaches are limited to strains that are interfertile. Unlike most animals, fertile hybrids form across species boundaries frequently in plants, opening a direct route to find loci contributing to dramatic evolutionary shifts in morphology. A few such interfertile species complexes have been developed as novel evo-devo models, but more are needed. Here we describe our progress towards developing species of the genus *Gilia* (Polemoniaceae) new model for plant evo-devo. We show that morphologically distinct species *G. capitata* and *G. yorkii* form a fertile hybrid and that QTL for key distinguishing traits can be mapped. Aided by a chromosome-scale genome assembly, we demonstrate that high resolution mapping of a flower color QTL is possible. Multiple changes at a Flavanol 5' 3' Hydroxylase are responsible for a blue white polymorphism associated with changes in the anthocyanin delphinidin. Progress towards transformation of *Gilia* promises to further establish this emerging model.

Topic: *Phylogenomics*

A-795

Exploring the Genomic Diversity of Dudleya (Crassulaceae) using a Genome Skimming Approach

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Affiliation: Yale University

Dudleya (ca. 51 spp.) is one of the most speciose succulent plant clades endemic to North America, and the group has been demonstrated to be recalcitrant to phylogenetic approaches based on classical genetic markers, implying a complex evolutionary history. While *Dudleya* displays diversity in vegetative and floral morphology, edaphic endemism, and physiology, comparative studies on this group have been limited by the lack of resolution in its phylogeny, and its evolution from the genomic perspective remains largely unexplored. Genome skimming has emerged as a powerful phylogenomic approach for non-model plant groups due to its minimal wet lab requirements, relatively low cost, and compatibility with a wide range of tissue types. In this pilot study, we leverage genome skimming data at a high coverage of six representative species across all three traditionally circumscribed subgenera of *Dudleya*, aiming to survey the genomic diversity of this group, including estimates of genome size, heterozygosity, and repeat fraction. We also explored the promise of this sequencing approach to recover low-copy regions *in silico* that could be potentially useful for improving phylogenetic resolution of this group. Our data and analyses provides insights on the features of genomic diversity of *Dudleya* the and sets a foundation for future phylogenomic and comparative research of this group.

Topic: *Systematics & Taxonomy*

A-796

The 'Yucca queretaroensis Problem' and Darwin's Most Wonderful Case of Fertilization: Determining the correct placement of a rogue taxon resolves the age of Yucca

Author: Christopher Smith
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Yucca is a genus of woody, new world monocots that contains roughly 50 species, with range that extends from southern Mexico to the northern Great Plains. Their strict reliance on yucca moths for pollination, and the moths' extreme host specificity have made them a textbook example of coevolution. Darwin referred to their pollination as, "The most wonderful case of fertilization ever published". Many workers have speculated that yuccas' specialized pollination might have spurred increased rates of speciation and diversification, but testing this hypothesis has been difficult due uncertainty about the placement of a rogue taxon, *Yucca queretaroensis*. Multiple previous studies, using different morphological and genetic data sources, have placed this species in different positions, either falling within Yucca section Sarcocarpa, or as sister to all other species in the genus. These alternative placements have produced starkly different age estimates for the genus, from as much as 25 million years, to as young as four million years. Determining the correct placement of this rogue taxon has been challenging because the material available study is exceptionally limited. This rare, highly endangered endemic from the Sierra Gorda of central Mexico is exceptionally difficult to find in its native habitats, and collections in herbaria and botanical gardens are exceptionally limited. Indeed, all previous molecular studies have relied on the same three samples collected in the 1990s, and so the 'Queretaroensis problem' has remained unresolved for decades. To finally solve the mystery, I collected new material from a dozen sites within the plants' native range and generated new data from all samples included in previous studies and all individual growing in botanical gardens within Mexico. I generated sequence capture data for 353 nuclear genes and all coding regions from the chloroplast genome. With these data I reconstructed species trees and re-estimated the age of the genus. The results suggest that *Y. queretaroensis* is closely related to other species within the genus, falling in the section Sarcocarpa. The past difficulties in identifying the correct placement of this taxon appear to be the product of multiple laboratory errors, mistakes in field identification, and frequent hybridization with co-distributed taxa. The 'queretaroensis problem' offers a cautionary tale that reveals the continued importance of traditional botanical tools, including vouchering and preparation of herbarium specimens, even in the era of metagenomes.

Topic: *Biodiversity Informatics & Herbarium Digitization*

A-798

Climatic Niche Divergence and Predictive Biogeography in Claytonia (Montiaceae): Insights from 25,000 Curated Observations

Author: Thomas Stoughton, Emma Terry, Diana Jolles
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The genus Claytonia (Montiaceae) includes approximately 45 taxa distributed across North America, grouped into three major taxonomic sections that reflect distinct life history strategies and perennation structures. While high rates of edaphic endemism have been suggested in this group, the extent to which climatic factors alone can explain species distributions remains uncertain. We analyzed ~25,000 georeferenced and hand-curated Claytonia observations from iNaturalist to assess patterns of climatic niche divergence both among species and among sections. Using ecological niche modeling and species distribution modeling approaches, we tested how accurately species and sectional identity could be predicted from climatic data alone. Our results show exceptionally strong predictive accuracy at the sectional level, and fairly strong accuracy at the species level, even among species with overlapping geographic ranges. These findings suggest that climatic differences play a key role in shaping broad biogeographic patterns within Claytonia, providing a valuable alternative to the traditionally emphasized role of soil specialization. This study highlights the utility of curated community science datasets in testing hypotheses about niche evolution and diversification in widespread temperate plant lineages.

Topic: *Reproductive Processes*

A-799

Pollinator-mediated interploid reproduction in a Campanula rotundifolia contact zone

Author: Brittany Sutherland, Krista Knieriem, Derek Anderson, Susan McLaughlin
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Although whole genome duplication is widely recognized as a source of reproductive isolation between diploids and polyploids, the reproductive dynamics between different polyploid cytotypes are less well understood. Work to date suggests that not only may different polyploid cytotypes continue to reproduce, but that their hybrid interploid offspring likewise retain some fertility. The circumboreal perennial wildflower, *Campanula rotundifolia*, exhibits ongoing reproduction between sympatric tetraploid and hexaploid individuals, and their pentaploid hybrid offspring exhibit some reproductive success. However, the extent of prezygotic isolation, specifically pollinator mediated barriers, has not been characterized in this system. Using a less-lethal sampling technique to identify pollinators and collect pollen loads, this study determined differences pollinator assemblage visiting tetraploid, hexaploid, pentaploid, and aneuploid plants. Flow cytometric analysis performed on burst pollen samples estimated the proportions of intra- and interploidy pollen deposition. By combining these pollen composition estimates with seed set and offspring cytotypes, we can construct a more complete picture of reproductive barriers at play in this mixed-ploidy contact zone.

Topic: *Biodiversity Informatics & Herbarium Digitization*

A-800

Identifying the collector practices that shape spatial, temporal, and taxonomic bias in herbaria

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Natural history collections (NHCs) are essential for studying biodiversity. While spatial, temporal, and taxonomic biases in NHCs affect analyses, the influence of collector practices on biases remains largely unexplored. We utilized one million digitized specimens collected in the northeastern United States from 237 herbaria and analyzed contributions from ~10,000 collectors. We investigated (a) similarities and differences between more- and less-prolific collectors, and (b) how these practices influence spatial, temporal, and taxonomic biases. We identified six common collector practices, or collection norms: collectors generally collected (a) different species, (b) from multiple locations, (c) from sites sampled by others, (d) during the principal growing season, (e) species identifiable outside peak collecting months, and (f) species from species-poor families and genera. Some norms changed over decades, with different taxa favored during different periods. Collection norms have increased taxonomic coverage in NHCs, however, collectors typically avoided large, taxonomically-complex groups, causing their underrepresentation in NHCs. Less-prolific collectors greatly enhanced coverage by collecting during more months and from less-sampled locations. We assert that overall collection biases are shaped by shared predictable collection norms rather than random practices of individual collectors. Predictable biases offer an opportunity to more effectively address biases in future biodiversity models.

Topic: *Ecology*

A-801

Investigating Landscape-Scale Drivers of Silicon Accumulation in Grasses (Poaceae)

Author: Lillian Chao, William Brightly, Luziana Cohen, Elijah Cole, Caroline Strömberg
Affiliation: University of Washington, University of Sheffield

In the past two decades, the role of silicon accumulation in terrestrial plant biology and ecology has begun to receive considerable attention. Grasses (Poaceae) are a clade well-known for high degrees of silicification, which has been found to confer resistance to both abiotic and biotic stresses, including drought, heat, and herbivores. Past hypotheses have often used herbivore defense as an explanation for the high degree of silicification in grasses, although recent studies point towards more complex drivers of silicification in grasses, with considerable focus being placed on environmental factors such as temperature and precipitation. However, the origins and drivers of silicification in grasses, as well as explanations for the variation found across and within clades, remain hotly debated. It is often difficult for hypotheses to adequately explain the scale at which mechanisms operate. High temperatures, for example, may correlate with high silicon accumulation due to adaptations promoting silicon accumulation in warm-climate clades. Alternatively, high temperatures may correlate with high silicon concentrations due to local effects, such as increased evapotranspiration. We aim to identify drivers of silicon accumulation in grasses and determine whether species or local-level variations are better predictors of silicon accumulation. To do this, we are using silicon concentration data collected from phylogenetically and geographically diverse grasses (200 species across all 12 subfamilies), combined with occurrence records from online databases (WorldClim, GBIF). We then identified the realized temperature and precipitation niche for each sampled species, allowing for comparisons of the relationship between a species climate niche, individual growing conditions, and silicon concentration to be made. Each sample, originating from herbarium collections, will be georeferenced, allowing for local climate conditions to be compared with the broader species niche. Preliminary results show no correlation between silicon concentration and broader species climate niche. However, past studies illustrate significant intraspecific variation in silica concentrations based on growing conditions. Therefore, we predict that local climate conditions may best explain variations in silicon accumulation seen in grasses. Other preliminary results show promise for further study. We found that most grasses range 0 - 10% Si by weight, high silicon accumulation seems to have evolved independently multiple times, and ancestral grasses likely had intermediate silicon concentrations of about 2.6%. A stronger understanding of the drivers of variation in silicon accumulation in grasses can help to recontextualize past studies and provide insights into the evolution of silicon accumulation. Additionally, these analyses can form links between climate change, ecosystem dynamics, and global silicon and carbon cycling.

Topic: *Development and Structure*

A-802

Genomic and molecular bases of pollination syndrome evolution in monkeyflowers

Author: Tianyu Cui, Yaowu Yuan
Affiliation: University of Connecticut

Many flowering plants have evolved a suite of floral traits that enable specialized associations between the flower and the pollination agent, recognized as the pollination syndrome. As an evolutionary transition between pollination syndromes requires coordinated changes of multiple floral traits, with each trait controlled by multiple genes, one would predict that it should happen infrequently. Yet these switches occur rapidly in nature and have been extensively documented. As such, the evolution of pollination syndromes is one of the most intriguing examples of polygenic adaptation in plants.

Identifying the genes and mutations of adaptive traits is crucial for understanding phenotypic evolution under natural selection. This study aims to systematically dissect the genomic and molecular bases of floral trait variations among three closely related monkeyflower (*Mimulus*) species, which display three distinct pollination syndromes (hummingbird-, self-, and bee-pollination). The bee-pollination syndrome represents the ancestral state in the *M. lewisii* species complex. The hummingbird-pollinated *M. cardinalis* and the self-pollinated *M. parishii* represent two independent pollination syndrome switches. To reveal the loci underlying these switches, we constructed two sets of NILs that cover the entire genome in the *M. lewisii* background (representing the ancestral bee-pollination syndrome), each one differing from wild type *M. lewisii* for a known chromosome fragment introgressed from *M. cardinalis* or *M. parishii*. Each set of NILs is produced through marker-assisted serial backcrosses to *M. lewisii*.

By comparing the differences between the NIL and the parental line, these NILs helps us to assess the phenotypic effect of each chromosome region in a homogeneous genetic background. They can then be used as starting materials for fine-scale mapping. Different NILs related to the same component trait (e.g., pistil length) can be crossed together to test the phenotypic effects of interactions among loci. Combined with stable transgenic experiments and other techniques, the NILs construction provides a highly effective way to functionally characterize the causal genes the mutations under each component trait of pollination syndrome.

These NILs are also used to test how floral trait variations influences pollinator responses in a common garden environment. They allow us to mimic the effects of single-locus changes that may represent a step in the adaptive walk toward the optimum during pollinator shifts in nature. By observing how introgressed loci alter floral traits related to pollinator attraction, reward, and efficiency, we aim to gain a deeper understanding of the evolution of pollination syndromes and polygenic adaptation in general - whether through the gradual accumulation of many small effect mutations or through a few loci with large effects.

Topic: *Reproductive Processes*

A-803

Association between self-fertilization and habitat marginality

Author: Elena Meyer
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Plant populations are increasingly forced to exist in marginal habitats due to human influences such as climate change and fragmentation of species' ranges. Self-fertilization has been hypothesized to be evolutionarily advantageous in situations where finding a mate would be challenging, such as in marginal environments. It is possible that levels of self-fertilization could change rapidly in response to these pressures. Rates of selfing and outcrossing are often not consistent across a species and often already vary within populations. Using species distribution models, we generated estimates of habitat suitability for a number of species for which estimates of within-species selfing rate variation already exist (here, quantified as the multi-lous outcrossing rate, tm). Using these models, we looked for an association between selfing rate and establishment of populations in marginal habitats, with the hypothesis that selfing would be higher in areas of more marginal habitat suitability.

Topic: Reproductive Processes

A-804

Picky pollinators: how floral spatial distribution and coloration impacts Nymphaea odorata pollination

Author: Sara Wuerstl, Kyra Krakos
Affiliation: Maryville University

Plants such as *Nymphaea odorata* can be keystone species for the wetland environment due to their role in gas exchange and by acting as a habitat for other aquatic species. This study focused on the Missouri native aquatic plant *N. odorata* in a wetland habitat found at Shaw Nature Reserve in Gray Summit, Missouri. Spatial distribution and various environmental conditions can impact plant reproductive biology. In this study, *N. odorata* is analyzed by examining morphological differences and the pollination system based on the placement and coloration of the plant (pink center, pink bank, white center, white bank.) Morphological measurements for height of inflorescence, corolla, stigma pad, and stamen length for each of the four populations were collected. Nectar collection was completed in the morning to determine if nectar levels differed between color and location. Inflorescence height is expected to differ between each of the populations based on prior years. To determine if *N. odorata* was pollen limited, hand pollination treatments were completed, and seed number counts were recorded. After data collection was completed, it was determined that the pink bank populations had higher nectar levels and seed counts but were shorter in height compared to the white populations. The pink center populations had the highest total visitation rates, however, it was the only population that was pollen limited. More population sampling is needed to understand the dynamics of spatial distribution and color of inflorescence effects on the plant pollinator network for *N. odorata*. This study provides an in-depth analysis of the wetland aquatic habitat with both biotic and abiotic factors being considered. Given the high biodiversity found in these ecosystems, this project will help better understand interspecies relationships. The information from this study can be further applied to restorative efforts.

Topic: Education and Outreach

A-805

Plants X Tech: Affordably Accelerating Plant Science

Author: Mason McNair
Affiliation: Michigan State University

As research, education, and outreach become increasingly resource-intensive, the need for affordable, scalable, and accessible approaches has never been greater. The Plants X Tech lab at Michigan State University's approach bridges biology, engineering, and pedagogy to democratize access to affordable tools. Our approach prioritizing affordability drives innovation, accelerates discovery, improves reproducibility, and fosters broader participation in science, especially in resource-limited settings. Emphasizing collaboration between researchers, educators, and students from different disciplines allows the co-creation of tools to fit real-world needs. Borrowing from the "maker" community's open-source and DIY approach, we have successfully incorporated computer aided design, 3D printing, robotics, phenomics, and genomics to bridge disciplines like pedagogy, material science, entomology, conservation, horticulture, taxonomy, and of course, botany. Here we showcase multiple case-studies from past, current, and future projects demonstrating the versatility of this approach.

Topic: Botanical History

A-806

Herbarium as Autobiography: A Chronology of 19th Century New York Botanist Sarah Louise Clarke

Author: Hilary Callahan
Affiliation: Barnard College

The collector Sarah Louise (Rogers) Clarke, S.L. Clarke, is as enigmatic as she was ambitious. Despite her collections being cited in dozens of publications, she left no field notebooks or correspondence. In 2025, digitization of the Barnard College Botanical Laboratory herbarium revealed 900+ specimens she collected, more than doubling the 671 previously databased by herbaria at the New York Botanical Garden (NY), University of Washington (WTU), University of Colorado (UC) or Univerity of Michigan (MICH). Born in 1852 in suburban London, Clarke was the eldest and only surviving daughter of an American couple who had returned to the United States some time in the 1860s. It is unknown how she was educated prior to her 1879 wedding to Samuel B. Clarke, a Harvard educated and socially prominent attorney. The Clarkes had a daughter Edith (b. 1881), a son Roger (b. 1884). By 1890, S.L.C. had moved into a new "apartment-hotel" called The Beresford, near the then-new American Museum of Natural History. She initiated a personal herbarium and joined the Torrey Botanical Club. All of this conincides with founding of the NY Botanical Garden and Barnard College. Clarke's early collecting was mostly in and near New York. The decade from 1894-1904 is prominent in Barnard's collections, revealing that her daughter likely accompanied her during some of her extensive summer travel to high-elevation localities throughout Europe: Switzerland in 1894, 1896 and 1897, France in 1898, Norway in 1899, Austria in 1900, Italy in 1902 and 1904, and the United Kingdom in 1903. In the springs, autumns and winters of those years, Clarke traveled to the Adirondacks, to Georgia and Florida, and to Canada. She undertook adventurous expeditions to Colorado and the rugged White Mountains of New Hampshire. The Social Register of 1904 indicates an affiliation with Barnard College, but she was a 37-year-old mother at the time of Barnard's founding and is not an alumna. Her participation there was likely limited to its active and well-connected Botany Club. Clearly, Clarke was a zealous botanist who adeptly prepared aesthetically outstanding vouchers, detailed labels, and a meticulous index to her collection (perhaps employing others with compatible skills to perform this work across more than a decade.) We attempt to align Clarke's chronology with those of other contemporary botanists, to learn where and when she traveled or collected with others. In sum, herbarium work greatly enriches an otherwise skeletal biography of a woman who allocated time, labor and personal resources to plant science, diversifying more stereotyped narratives about wealthy New York women of her class and era. Clarke died in 1906 at aged 53, coming to rest at the Clarke family grave site in the Grove Street Cemetery in New Haven, Connecticut.

Topic: Conservation Biology

A-807

Insights into the evolution, biogeography, and conservation of frailejones (Espeletiinae, Asteraceae)

Author: Mauricio Diazgranados, Clara Morales-Rozo, Maria Pinilla Vargas, Martha Kandziora, Roswitha Schmickl, Andrea Simbaqueba
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Páramos, located above the timberline in the Tropical Andes, are outstanding examples of sky islands and are widely regarded as some of the most diverse and rapidly evolving high-elevation ecosystems in the world. Frailejones—a common name referring to all species within the subtribe Espeletiinae (Asteraceae)—are the most iconic plants of the páramos. With approximately 144 recognized species, most of which are endemic yet locally abundant, frailejones serve as a model group for understanding biogeographic and phylogenetic patterns in sky islands, as well as the conservation challenges they face in the context of a global environmental crisis. We present the current state of knowledge on these aspects. Recent phylogenetic analyses using *Hyb-Seq* on 1,269 nuclear loci support the hypothesis of two major clades—a Venezuelan clade and a predominantly Colombian clade—that diverged and radiated over the past 2.5 million years, initially from Venezuela into Colombia and more recently into Ecuador. The delimitation of previously established genera remains contentious, complicated by frequent interspecific hybridization. Regarding conservation, a recent assessment of Colombian species indicates that 55 of the 90 species found in the country (61%) are threatened, with 40 species (45%) classified as endangered. Efforts are underway for both in vitro and in situ propagation of several species. Utilizing a comprehensive dataset of 5,560 georeferenced records covering 138 species, we applied the Important Plant Areas (IPAs) approach at a resolution of 100 km^2. This analysis identified 176 potential IPAs based on the distribution of globally threatened species (59 species) and 51 IPAs based on species richness (76 species). However, only 27% of these potential IPAs currently fall within established protected areas, while 73% face significant human disturbances. These findings offer critical guidance for prioritizing the conservation of these keystone species in the páramos of the northern Tropical Andes.

Topic: *Education and Outreach*

A-808

A course-based genome assembly project for undergraduate students: genome assembly and annotation of Carya glabra (pignut hickory)

Author: Shengchen Shan, Edgardo Ortiz, Huiting Zhang, Pamela Soltis, Alex Harkess, Douglas Soltis
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As part of the American Campus Tree Genomes (ACTG) initiative, this Course-based Undergraduate Research Experience (CURE) class provided undergraduate students with hands-on experience in genome assembly and annotation of *Carya glabra* (pignut hickory), a native tree species found in McCarty Woods on the University of Florida campus. This project gave students a unique opportunity to contribute to the first organellar and nuclear genome assemblies for this species while developing practical skills in bioinformatics, genomics, and scientific communication. Throughout the semester, students participated in every stage of the genome assembly pipeline – from evaluating raw sequencing data (PacBio HiFi reads and Illumina Hi-C reads), performing genome profiling analysis to estimate genome size and heterozygosity, to assembling the nuclear genome and assessing quality metrics such as N50 and BUSCO scores. The students also analyzed Hi-C data to aid chromosome-level scaffolding and used visualization tools including Juicebox for manual genome curation. In addition, organellar genomes were successfully assembled and annotated. By combining real-world data with active learning, this project promoted student engagement across a range of disciplines — including Biology, Data Science, Engineering, and English — and emphasized programming, collaboration, critical thinking, and scientific writing. The students presented their work at the University of Florida's Undergraduate Research Symposium, further developing their science communication skills and gaining experience in sharing research with a broader audience. They also worked together to prepare a manuscript for publication. Beyond building bioinformatics skills, students gained insight into the process of scientific research and the role of genomics in understanding biodiversity and evolution. A set of teaching tools is available on request.

Topic: *Biodiversity Informatics & Herbarium Digitization*

A-809

Bryophyte and Lichen Imaging Workflow at the Claude E. Phillips Herbarium (DOV)

Author: Zachary Shamblin
Affiliation: Delaware State University

The Claude E. Phillips Herbarium (DOV) at Delaware State University contains over 200,000 specimens of plants and is the largest herbarium on the Delmarva peninsula, an area containing Delaware and the eastern shores of Maryland and Virginia. Within this collection is a small collection of Lichen and Bryophyte specimens. Currently, DOV is engaged in a multi-year initiative to digitize the remaining plant specimens, which includes both the Bryophyte and Lichen specimens. These specimens are mainly contained within packets with the label adhered to the front. This presents a challenge when imaging, as the specimen must be removed from the packet to image both the specimen and the label, potentially damaging the specimen. A workflow was developed in which the label, along with a corresponding barcode was imaged. As time was limited, only the label was imaged and not the specimen itself. While it was originally estimated that there were about 40,000 Bryophyte and Lichen specimens were to be imaged, after processing this collection for duplicates, approximately 2,000 Lichen and 12,000 Bryophyte specimens were imaged. With the developed workflow, we were able to obtain a peak imaging rate of 100 specimens per hour, however, efforts were hampered by the need to remove specimens from packets when a label was not adhered to the front of the packet. Currently, the images from the Bryophyte and Lichen collection at DOV have been uploaded to Mid Atlantic Herbaria portal. The work performed in this project, highlights the ability of herbaria to quickly image collections like the Bryophyte and Lichen collections at DOV. These small collections are important overall in the wealth of data that they may provide to researchers.

Topic: *Systematics & Taxonomy*

A-811

Evolution of the Viburnum dentatum species complex

Author: Anthony Baniaga, Carlos Maya-Lastra, Patrick Sweeney, Erika Edwards, Michael Donoghue
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The *Viburnum dentatum* species complex of Eastern North America (Dipsacales, Adoxaceae) has long been a source of confusion, and this is reflected in widely varying taxonomic interpretations over the past two centuries. From 1-12 taxa have been recognized, with the most recent treatment accepting seven. Based on our extensive collections of populations throughout the range of the complex, we present new evidence on phylogenetic relationships, chromosome numbers and genome sizes, leaf morphology, and geographic ranges. Our analyses of these data support a new classification in which we propose to recognize six species. They also highlight a perplexing pattern with respect to the evolution of chromosome numbers and genome sizes, in which populations with lower numbers/smaller genomes (4X *V. recognitum* with 2N=36 chromosomes) appear to have been derived from ancestors with higher numbers/larger sizes (12X *V. scabrellum* and *V. ashei* with 2N=108; 8X *V. dentatum*, *V. venosum*, and *V. carolinianum* with 2N=72). Leaf morphology and pubescence, though highly variable, show significant phylogenetic and geographic patterns. Overall, our work provides a solid framework within which more focused studies can further clarify the evolution of this widespread, highly variable, and ecologically significant group of plants. To facilitate further research on these plants we are establishing a replicated set of vouchered accessions, collected from across the eastern US range of the *V. dentatum* complex, in both the Marsh Botanical Garden at Yale University in New Haven, Connecticut, and the Oak Spring Garden in Upperville, Virginia. We encourage anyone interested in using these resources to contact us for further information.

Topic: *Pteridology*

A-812

Ferns of Colombia: what we know, what we've learned, and what remains to be discovered

Author: Alejandra Vasco, Michael Sundue, Susana Vega-Betancur, Sarah Morris, Lucia Vargas, Kimberlie Sasan, Weston Testo
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Colombia has the highest diversity of ferns of any country in the Americas, but by many measures its fern flora remains understudied and poorly known. Supported by NSF and in collaboration with partners at numerous Colombian institutions, we have sought to advance knowledge of Colombian ferns through fieldwork, herbarium study, generation of genomic resources, student training, and public outreach. This project has dozens of participants, and to date has resulted in the collection of more than 12,000 specimens, revision of thousands of more in herbaria, and generation of target-capture sequence data for hundreds of species. Dozens of species new to science or previously not recorded for the country have been added to the flora of Colombia; these have been found both in the field and in herbaria. Along with these discoveries, this project has provided ample opportunities for training students and engaging with communities in the USA and across Colombia. In this talk, we reflect on what we have learned, examine what work lays ahead, and consider opportunities for continued discovery and collaboration.

Topic: *Paleobotany*

A-813

Zingiberalean Fossils from the Late Paleocene in Beicegel Creek (McKenzie County), western North Dakota, USA

Author: Kathleen Pigg, Laura Griffin, Melanie DeVore
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The monocot order, Zingiberales, is composed of two major groups; the bananas and the gingers. The families that make up this order include Musaceae, Lowiaceae, Strelitziaceae, Heliconiaceae, Costaceae, Zingiberaceae, Cannaceae, and Marantaceae. There is an abundance of these families represented in the fossil record.

Observing siliceous plant material from Beicegel Creek (McKenzie County), western North Dakota, USA, it is believed that there are specimens that represent a family of this order dating back to the Late Paleocene (57 MYA). Samples of extant plants to represent each of the families was used to carry out a morphological and taxonomic study to further identify the fossil remains to possibly a family. Such specimens collected include *Musa acuminata* (Musaceae), *Heliconia psittocorum* (Heliconiaceae), *Strelitszia nicollai* (Strelitziaceae), *Canna indica* (Cannaceae), *Hedychium coronarium* (Zingiberaceae), and a specimen of the Marantaceae family. Cross sections were made of the leaves and particularly the stem due to the fossils seeming to be of what once was a pseudostem. Stomatal comparisons between the families were also compared to the fossil record of leaf material known as *Zingiberopsis*. Through analyzing extant specimens of this order to the fossil material in this study, as well as character mapping and the geological time scale of North America during the Paleocene, the fossils presented are believed to be of the Musaceae, specifically close to the genus *Ensete*.

Topic: *Pteridology*

A-814

From morphology to microhabitat: Exploring cryptic diversity in Woodsia mollis (Woodsiaceae)

Author: Bryce Hegstrom, Amanda Grusz
Affiliation: University of Minnesota Duluth

Woodsia mollis (Kaulf.) J.Sm. is nested within a small clade belonging to the Woodsiaceae and is notorious for being difficult to identify, with the extra complication of exhibiting variable genome copy number (i.e., ploidy) and reproductive mode (sexual versus apomictic). In this study, I leverage herbarium specimens of W. mollis to determine what morphological differences within the species most contribute to this taxonomic confusion. I also examine specimens for reproductive mode (sexual versus apomictic), conduct spore counts, assess perispore morphology, gametophyte/sporophyte morphology, and perform geospatial analysis of environmental variables to further resolve cryptic diversity within W. mollis. To this end, I surveyed herbarium specimens (N = 412) from major North American herbaria (ASU, BRIT, DUKE, MICH, MO, NY, VT, UC, and WIS); of specimens surveyed, 107 were fertile and were included in my analyses. Collection dates of sampled specimens spanned 1888 to 2010, and roughly half of the specimens exhibited signs of asexual reproductive mode. My results build on a growing body of work focused on the small Woodsiaceae clade, including, a recent investigation of the sister species, Woodsia montevidensis Hieron., that revealed multiple understudied cytotypes comprising this widespread South American taxon (Ponce et al., 2025); as well as recent work to resolve taxonomic ambiguity within the closely related Woodsia scopulina D.C Eaton. species complex (Zenzen, 2021).

Topic: *Reproductive Processes*

A-815

Pollen Limitation in Urban Orchards: Insights from Multi-Year Experiments on Pollinator Dynamics

Author: Emma Siegfried, Franceska Isufaj, Sara Wuerstl, Nathan Muchhala, Aimee Dunlap, Nicole Miller-Struttmann, Sabashton Tabor, Harriet Seelam, Nathan Eades, Kyra Krakos
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Urban agriculture is growing globally to reduce environmental impacts and address food insecurity. Urban orchards, or "edible forests," are notable for their diverse tree species and pollination strategies, which complicate effective pollination since no single pollinator can meet their needs. However, key knowledge gaps remain regarding pollen transfer dynamics, pollinator behavior, and socio-environmental influences on pollination services. The full study aims to address two key questions: (1) How does the socio-environmental context of urban orchards influence pollinator diversity and pollination success? (2) How do targeted interventions to enhance native bee diversity and abundance affect orchard yields? Leveraging a network of 36 urban orchards across St. Louis, Missouri, this research employs observational and experimental approaches to test the ecological intensification hypothesis. Methods include pollen supplementation experiments, single-visit pollen deposition and removal assays, and analyses of pollen tube growth to quantify pollination success. Pollinator behavior and fidelity are assessed through video analysis and pollen load composition. Preliminary findings from multi-year (2022-2024) pollen limitation experiments reveal that smaller urban orchards are more prone to pollen limitation, with spatial factors and resource diversity playing critical roles in pollinator retention. High conspecific pollen loads on stigmas indicate pollinator fidelity, further supported by insect sampling data. The pollen limitation results are a critical component of the larger project aimed at understanding and optimizing pollination dynamics in urban orchards to enhance fruit production. Pollen limitation, which occurs when insufficient pollen transfer reduces seed or fruit production, serves as a key indicator of the effectiveness of pollination services in these systems. The full study highlights the potential of urban orchards to serve as productive agricultural systems through enhanced pollination services and provides actionable insights for urban agriculture practitioners. By integrating ecological, behavioral, and socio-environmental perspectives, this research advances understanding of pollination dynamics in urban ecosystems and offers strategies for sustainable urban food production.

Topic: *Dryland Floras*

A-816

Evolution, life history, and CAM photosynthesis in the dryland-clade Cistanthe

Author: Anri Chomentowska, Pauline Raimondeau, Lan Wei, Ellie Jose, Sophie Dauerman, Virginia Davis, Andrés Moreira-Muñoz, Iris Peralta, Patrick Sweeney, Erika Edwards
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Cistanthe (Montiaceae; Caryophyllales) is a quintessential dryland herbaceous lineage. Many of the species are distributed across xeric habitats of Northern Chile—including those that paint the Atacama Desert magenta pink during "superblooms". We know that both perennial and annual *Cistanthe* species can facultatively utilize Crassulacean acid metabolism (CAM) photosynthesis, an adaptation to drought that confers increased water use efficiency. Particularly, we were interested in the dynamics of how desert annuals might make use of this facultative ability to CAM in response to exogenous stressors like drought or endogenous stress like flowering throughout their short life cycle.

As a foundation for comparative research, we inferred the phylogeny of the genus *Cistanthe* (as well as across the larger clade of Cistantheae) using next-generation sequencing. To test the impact of drought and life stages on the photosynthetic behavior of a desert annual, we assayed pre- and post-flowering CAM activity and analyzed gene expression in *Cistanthe cachinalensis* (a desert annual species that can be easily cultivated) under drought and fully-watered conditions. Additionally, we sequenced, assembled, and annotated the genome of *C. cachinalensis* to be used as a reference for both the phylogenetic and transcriptomic sequences.

We found that life history is evolutionarily labile, with repeated transitions between annuality and perenniality; however, both annual and perennial *Cistanthe* species exist in desert environments, often in sympatry.This suggests that, even among very closely related species, there is no "one way" for herbaceous species to adapt to xeric habitats. We also saw a lack of phylogenetic resolution in one clade of Atacama *Cistanthe* annuals, with evidence of significant introgression. CAM assays in *C. cachinalensis* confirmed upregulation of CAM upon drought conditions. When under fully-watered conditions, flowering individuals showed slightly higher CAM activity as compared to pre-flowering plants. Moreover, analyses of differential gene expression suggest possible co-regulation of CAM expression and reproduction.

Topic: *Systematics & Taxonomy*

A-817

Phylogenomics and Floral Morphometrics of Western Australian Darwinia (Myrtaceae)

Author: Patricia Chan, Bing Li, Jacob Landis, Matthew Barrett, Ashley Hamersma, Thomas Givnish
Affiliation: University of Wisconsin-Madison, Cornell University, James Cook University, University of Florida

We are using a variety of approaches to analyze the relative importance of various drivers of species diversification in the large, relatively young, morphologically diverse genus *Darwinia* (Myrtaceae) from Western Australia. This group is ideal for such a study given the narrow endemism of many species, the sky-island biogeography of several taxa, the apparent lack of long-distance seed dispersal across the group, and the striking diversity of inflorescences and associated pollinators, with the latter including birds, marsupials, and several groups of insects. We developed a *Darwinia*-specific bait kit for target sequence capture, and analyzed several hundred single-copy nuclear loci, and obtained greater resolution and support than had been possible using traditional

approaches employing sequences for just a few genes. We are extending these studies to construct and date nuclear and plastome phylogenies, to reconstruct relationships, character-state evolution, species diversification rates, and historical biogeography in *Darwinia*. We are also investigating the reproductive ecology and pollination syndromes of several representative *Darwinia* species through studies of pollinator behavior, floral morphometrics, and floral volatile and nectar chemistry. Data resulting from these studies will be integrated into analyses of the drivers of taxonomic and morphological diversification in *Darwinia*. This research will shed light on speciation, endemism, adaptive radiation, coevolution, and convergence in a large, threatened clade from the Western Australia biodiversity hotspot based on research by collaborators at the Western Australian Herbarium, Australian Tropical Herbarium, King's Park Botanic Garden, and the University of Wisconsin-Madison.

Topic: *Pteridology*

A-818

Comparing environmental niche within and between sexual and apomictic lineages of Myriopteris Feé (Pteridaceae)

Author: Max Botz, Amanda Grusz
Affiliation: UMD, University of Minnesota Duluth

The drought-driven hypothesis for the origin of obligate meiotic apomixis in ferns (Grusz et al., 2021) emphasizes the possible involvement of abiotic factors in the formation of diploid spores and the development of apogamy. Here, we examine two case studies in the xeric-adapted genus *Myriopteris* Fée (Pteridaceae) to assess whether sexual diploid (2n = 2x) and apomictic triploid (2n = n = 3x) lineages occupy unique environmental envelopes. To this end, we assessed soil and satellite data along with genetic and reproductive traits. In the first case study, we examined *Myriopteris lindheimeri*, which is polymorphic for reproductive mode and includes both sexual diploids (N = 17) and apomictic triploids (N = 30) ranging from central Mexico to the southwest United States. We also examined *Myriopteris gracilis*—a wide-ranging apomictic triploid (2n = n = 3x) with multiple evolutionary origins—leveraging the data set of Wickell et al. (2017; N = 643). Our analyses of *M. lindheimeri* and *M. gracilis* integrate genetic, morphological, cytogenetic, and environmental traits to determine: What, if any, abiotic factors are associated with reproductive mode (sexual versus obligate apomixis) in *Myriopteris*?

Topic: *Education and Outreach*

A-819

Restoration and Digitization of the Historic College of Saint Scholastica Herbarium (CSS)

Author: Max Botz, Jace Bartell, Mikaela Hetchler, Amanda Grusz
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The College of Saint Scholastica Herbarium (CSS) collection contains samples predating the college and the monastery's founding, including specimens dating back to as early as 1905. This historic collection of ~3000 specimens, ranging from angiosperms to bryophytes, provides insights into the history of the college through specimen collection localities. Additionally, the CSS collection tells the story of the predominant collector, Sister Alice Lamb, who is credited for the collection's earliest documented specimen and a vast bulk of the collection. Through our digitization efforts, we have begun cataloging, imaging, and digitizing these specimens so that they can be integrated into the Minnesota Biodiversity Atlas online, making them available to the public and scientific community alike. Funding for this project, including the CSS digitization, has been generously supplied by the Olga Lakela Herbarium (DUL) endowment at the University of Minnesota Duluth.

Topic: *Reproductive Processes*

A-820

Blooming Resilience: The Impact of Winter Drought on Phlox pilosa

Author: Franceska Isufaj, Kyra Krakos
Affiliation: Maryville University

Drought winters can impact reproductive biology and plant-pollinator networks, potentially altering ecosystem dynamics. This study investigates the impact of drought winters on the reproductive biology of *Phlox pilosa*, a native Missouri flowering plant located at Shaw Nature Reserve, an area that experiences drought winters. Specifically, we addressed four key questions: (1) Does the morphology of *P. pilosa* differ between drought and non-drought winters? (2) Who are the primary pollinators during drought and non-drought winters? (3) Is there a correlation between display size and pollinator visitation rate? (4) Are *P. pilosa* pollen limited in drought or non-drought winters? From 2021 to 2024, morphology, pollinator visitation, and pollen limitation were assessed. Results revealed that in the extreme drought winter of 2024, *P. pilosa* exhibited significant morphological changes, including reduced plant height and corolla size and increased floral tube opening. Halictid bees were identified as the primary pollinators in most years, but during the drought winter, pollination rates dropped, and a broader range of visitors contributed. No correlation was found between floral display size and pollinator visitation. Despite these changes, supplemental hand-pollination experiments demonstrated that *P. pilosa* was not pollen-limited, showcasing its reproductive resilience. These findings suggest that while drought winters impact the morphology and pollination dynamics of *P. pilosa*, this species remains robust under changing climatic conditions. Its resilience highlights the potential of *P. pilosa* as a valuable resource for pollinator conservation in the face of climate change. Future research is needed to explore its role in supporting pollinator diversity in ecosystems impacted by climate change.

Topic: *Bryology and Lichenology*

A-821

Bryophytes influence forest succession in a northern temperate rainforest

Author: Carrie Woods, Olivia Brech
Affiliation: University of Puget Sound

In northern temperate rainforests, gap-phase dynamics provide tree boles as sites for forest regeneration (*i.e.*, nurse logs). These nurse logs are often colonized by bryophytes and tree seedlings that vary depending on the decay stage of the log. Thus, interspecific interactions between bryophytes and seedlings could change with nurse log decay. We surveyed tree seedlings and bryophyte communities in 166 plots on nurse logs (n = 112, 1 m x diameter of nurse log) and the forest floor (n = 52, 1m^2) in the Hoh rainforest on the Olympic peninsula in Washington to determine how bryophyte communities and tree seedling density change with nurse log decay. We also conducted a shadehouse experiment where we grew *Tsuga heterophylla* tree seedlings with the 5 most abundant bryophyte species along with a soil and a litter control for 100 days. Tree seedling density was highest on young logs with early colonizing bryophyte species that create thin mats (< 4 cm), such as *Plagiothecium undulatum*, and lowest on old logs and the forest floor with bryophytes that create thick mats (>4 cm; *Hylocomium splendens*). These field patterns were supported by the shadehouse experiment where tree seedling growth was increased when grown with *Plagiothecium undulatum* but decreased when grown with *Hylocomium splendens*. These findings indicate that interspecific interactions between tree seedlings and bryophytes shift from facilitation to competition as the log decays, and that logs are essential for tree seedlings to escape competition with forest floor bryophytes. Thus, the smallest plants in the forest influence the dynamics of some of the largest trees on the planet.

Topic: *Bryology and Lichenology*

A-822

Evaluating the Species Accumulation Model in a temperate rainforest

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Epiphytic bryophytes are integral and conspicuous components of temperate rainforests, yet little is known about their assembly and dynamics. Host trees have microhabitats that are created by gradients in branch size, canopy humus, and light, which can influence the distribution patterns of epiphytes. These microhabitats change with tree size, which in theory should influence epiphytic bryophyte succession. According to the Species Accumulation Model (SAM), as the tree grows, epiphytic bryophyte species should accumulate (species richness increases) across the entire tree, while they should follow a replacement model of succession within a particular microhabitat (i.e. inner branch: 0-2 m from the trunk). Using a chronosequence approach with tree size as a proxy for age, epiphytic bryophyte communities were surveyed across 6 tree zones in each of 16 Acer macrophyllum trees of varying size (2-102 cm diameter at breast height) in a temperate rainforest in Olympic National Park, WA to explore how bryophyte communities form and change during succession. Bryophyte species richness

increased with tree size, following the predictions of SAM. Bryophyte communities became more similar to large tree communities as the trees increased in size, and the species found on small trees were found on the outer crown of the large trees, indicating a high degree of nestedness. On the scale of one microhabitat, mid- and late-colonizing species replaced and dominated early-colonizing species as tree size increased. Dominance of a singular species in a particular microhabitat was most common in the largest trees, suggesting specialization is most prominent at late-stages of succession. Therefore, bryophyte succession takes different forms depending on scale: across the entire tree, an accumulation model is followed; within one microhabitat a replacement model is followed.

Topic: *Plant genome skimming: special uses and future potential*

A-823

Skim-seq enables organellar genomics and molecular taxonomy in even recalcitrant taxa

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Cheaper sequencing and library preparation has made genomic sequence data widely available across diverse taxonomic groups, but challenges remain in identifying annotated, single-copy sequences usable for addressing evolutionary questions. Organellar genomes represent easily identifiable portions of the genome that are widely used and studied, recoverable with very low coverage skim-seq approaches, and easily annotated to identify genes and gene function. Combined with single cell WGS, this approach has unlocked molecular taxonomy for previously intractable taxa, such as protists that resist culturing. We discuss the applications of skim-seq-enabled organellar genomics in systems ranging from land plants, lichens, and diatoms.

Topic: *Paleobotany*

A-824

Expanding our knowledge of the Middle Jurassic fossil floras from the Botany Bay Group, Antarctic Peninsula

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Mesozoic Antarctic floras provide us with unique windows to study ecosystems that can't be found anywhere on Earth today. Because of its history and scientific importance, the Jurassic flora of Hope Bay (Mount Flora Formation, Botany Bay Group, Antarctic Peninsula) is one of the most iconic Gondwanan plant fossil assemblages. An additional floral assemblage from the Botany Bay Group, discovered later at the Camp Hill Formation (Botany Bay area of the Antarctic Peninsula), has a comparable composition. These two floras have been used as references to study other Jurassic floras from Gondwana, allowing the establishment of regional geologic frameworks. However, the age of these Antarctic floras remained contentious, with different estimations ranging from the Early Jurassic to the Early Cretaceous, the former being the most widely accepted due to their floral composition. In recent years, field trips to these two emblematic localities, carried out by the Argentine Antarctic Institute, yielded over 2000 fossil plant specimens, hitherto unknown palynological records, and rock samples for radiometric dating. These intensive collection efforts were coupled with detailed geologic mapping and stratigraphic characterization. Among the most notable floral finds are those of Bennettitalean reproductive organs assigned to the genera *Williamsonia* (cones) and *Cycadolepis* (bracts). Although there has been a single previous putative record of *Williamsonia* from the Mount Flora Formation, its fragmentary nature left doubts about its assignment. The new specimens confirm the presence of the lineage for the Jurassic of Antarctica and are directly comparable with Bennettitalean occurrences from other regions of Gondwana, being remarkably similar to taxa from the Lower Cretaceous of Santa Cruz, Argentina, Baqueró Group. Additionally, the assemblage contains new articulated reproductive organs of Caytoniales, including two morphologies of *Caytonanthus* and *Caytonia*. Moreover, ovuliferous remains from Cupressaceae (e.g., *Austrohamia*), Araucariaceae (e.g., *Araucarites*), and undetermined conifer families (e.g., *Sphenolepis* sp., *Conites* sp.), were also identified in the assemblage. These conifer and caytonialean remains are comparable to fossil taxa described from the Lower Jurassic of Chubut Province, Patagonia, Argentina. Additional vegetative remains are consistent with equisetaleans (i.e., *Equisetum*/*Equisetites*), ferns (i.e., *Cladophlebis*, *Todites*, *Goeppertella*, *Marattia*, *Coniopteris*, *Spesia*), Cycadales and Bennettitales (i.e., *Taeniopteris*, *Otozamites*, *Zamites*, *Ctenis*, *Pseudoctenis*, *Dyctiozamites*), conifers (i.e., *Brachypyllum*, *Elatocladus*, *Pagiophyllum*), and "seed ferns" (i.e. *Sagenopteris*, *Archangelskya*, *Sphenopteris*, *Pachypteris* and *Komlopteris*). Furthermore, successful palynological preparations yielded spores, pollen, and isolated cuticle fragments for the first time for the Botany Bay Group. Spores are more numerous and diverse than pollen and are assigned to at least four different families (Gleicheniaceae, Schizaceae, Osmundaceae, and a possible additional Gleichenialean). Pollen grains belong to Araucariaceae and Caytoniales. Our absolute U-Pb ages constrain the age of deposition of these paleofloras to the Middle Jurassic (≈ 163 Ma, Callovian), challenging the previously accepted Early Jurassic age for these floras. Overall, our findings show that (1) a re-evaluation of the current biogeographic and biostratigraphic framework is due for the Jurassic of Gondwana, and that (2) the Jurassic paleofloras from the Botany Bay Group of Antarctica are composed of a mosaic of typical elements from different times and locations.

Topic: *Development and Structure*

A-825

The genetic basis of temperature dependent fruit maturation delay in a Sierra Nevada endemic Monkeyflower

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Plants possess the remarkable ability to modify their growth in response to external environmental cues. Temperature, an important abiotic factor, can significantly influence vegetative growth, flowering timing, and various other developmental processes. Here, we report a novel cold-dependent developmental response observed in the Sierra Nevada endemic Mimulus lacinatus (syn. Erythranthe lacinata). Under growth chamber conditions simulating the cold temperatures experienced by natural populations, fruit maturation is synchronously delayed across the indeterminate inflorescence. This results in an emergent phenotype wherein seed set can be delayed by up to two weeks. This plastic response, absent in milder growth chamber conditions, is termed cold-dependent developmental delay (CDDD). We hypothesize that CDDD enables plants to tolerate late-season cold spells typical of high-elevation mountain habitats, suggesting this response may be adaptive. The goal of this study is to understand the evolutionary and genetic origin underlying this plastic response. To achieve this, we first take a comparative genomic approach, utilizing population-level genome resequencing data from M. lacinatus alongside reference genomes of the sister taxa M. nasutus (syn. E. nasuta) and the closely related annual ecomorph of M. guttatus (syn. E. microphylla); the latter of which does not exhibit CDDD. We conduct genome-wide scans to identify putatively adaptive loci through pairwise comparisons across M. lacinatus, M. nasutus, and M. guttatus. To specifically pinpoint candidate loci associated with CDDD, we performed a time-course RNA-seq experiment of fruit maturation in both M. lacinatus and M. guttatus grown in conditions that either induce or do not induce CDDD. Preliminary results highlight genes involved in the transition to flowering and zinc finger transcription factors as candidate regulators implicated in the CDDD response. This work provides mechanistic insights into the genetic and evolutionary pathways facilitating the development of CDDD, contributing to our broader understanding of how plants adapt to novel environmental conditions.

Topic: *Conservation Biology*

A-826

Collaborative plant conservation in a biodiversity hotspot: California Plant Rescue

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California Plant Rescue (CaPR) formed in 2014 as a collaborative initiative focused on *ex situ* conservation efforts in the state of California, a biodiversity hotspot. The variety of organizations involved in the network helped secure state financial support in 2019, resulting in CaPR now maintaining 94% of California's rare, threatened, or endangered native plant taxa (California Rare Plant Rank 1B) in *ex situ* collections, primarily seed collections in long term storage. Funding and collective efforts allowed conservation-focused organizations in the state to reduce some species and population-level biases in the prior presence of rare taxa in conservation collections. Among factors that influenced plant presence in collection prior to state funding are U.S. Endangered Species

Act listing status, proximity of the species range to a CaPR institution, elevation range of the taxon's populations, and the number of documented occurrences per taxon in the California Natural Diversity Database.

State funding immediately impacted collections, increasing CaPR members' rates of rare plant seed collection and allowing collectors to seek species further afield or otherwise difficult to collect, but early successes in the formation of CaPR allowed the group to scale even prior to funding. The annual rate of new California rare taxa secured in conservation seed collection quadrupled after CaPR's 2014 formation. In efforts to make collections, the group also regularly updates population information for target taxa, allowing for updated conservation assessments and statuses helping to inform ongoing and future conservation work. Support from the Center for Plant Conservation in building and hosting CaPR's shared database was a key feature for understanding the breadth, quality, and patterns within our collective seed bank accessions. We plan to draw on the database further as we look to make the *ex situ* conservation collections more robust – capturing more genetic diversity across populations and taking climate change, threats, and evolutionary distinctiveness into account in our prioritization.

Topic: Defining forces in fern evolution: Celebrating the contributions of Kathleen Pryer and Michael Windham

A-827

Spore analysis of herbarium specimens reveals patterns of cytotype and reproductive mode diversity in homosporous ferns: case studies from the Pteridaceae

Author: Kathryn Picard, Amanda Grusz, Eric Schuettpelz
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Analysis of spore size and spore number per sporangium have been used in systematic and evolutionary studies of ferns for the better part of a century, highlighting the incidence of both polyploidy and asexuality across fern taxa. Despite the outsized role whole-genome duplication and apomixis play in fern evolution and diversification, few standardized protocols for determining either ploidy level or reproductive mode are available. Only within the last decade have protocols for both high-throughput (e.g., flow cytometry) and low-throughput (e.g., microscopic analysis of affixed spores) methods been developed for spore-based estimations of genome size in ferns. These methods allow for the efficient determination of relative genome size and, in the case of flow cytometry, reproductive mode of ferns and lycophytes, providing critical life history data necessary for untangling the often-complex breeding dynamics at play in these groups. However, as developed, these methods require significant input material for analysis and are thus best suited for recently collected accessions, or pressed specimens with sufficient tissue for more destructive sampling. Additionally, these methods do not allow for the collection of important diagnostic characters for many apomictic and hybrid lineages, such as variation in spore number per sporangium and the production of irregular (but viable) spores. Here we present a standardized protocol for using spore analysis of herbarium specimens to investigate patterns of cytotype and reproductive mode diversity in homosporous ferns. This protocol is inexpensive, replicable, and can be used on even the most poorly preserved herbarium specimens. We also present individual case studies from the Pteridaceae, demonstrating the utility of this method in informing studies of fern breeding dynamics across space and time.

Topic: Conservation Biology

A-828

Diversity and Specificity of Orchid Mycorrhizal Fungi in Calopogon tuberosus (grasspink)

Author: Hannah Ryu, Sarah Wetterer, Louise Egerton-Warburton
Affiliation: Northwestern University, Chicago Botanic Garden

Orchid conservation continues to be a challenging issue as irreversible damage from climate change and anthropogenic activities becomes increasingly evident. This project aims to investigate the effects of contrastive climates and human activity levels on orchid mycorrhizal fungi (OMF) communities in North American *Calopogon tuberosus*, a broadly dispersed orchid species. By comparing sequenced root OMF communities, soil properties, and symbiotic seed germination in different environmental conditions (pristine, disturbed) and geographic locations (IL, FL), we can assess OMF selectivity in *C. tuberosus* roots. Studying what kinds of conditions affect OMF selection could provide us with key information about how we can more effectively implement orchid conservation and restoration efforts.

Topic: Biodiversity Informatics & Herbarium Digitization

A-829

Using an LLM-powered agent system for data-centric botanical research

Author: Michael Elliott, Pamela Soltis, Jose Fortes
Affiliation: University of Florida

iChatBio is a biodiversity research-focused chatbot that uses artificial intelligence to fulfill users' information requests. For example, iChatBio can assist with finding, retrieving, visualizing, and processing occurrence records served by iDigBio, GBIF, and iNaturalist, as well as find related research literature in BHL. The chatbot adapts the same large language model (LLM) technology used by state-of-the-art AI chat services like ChatGPT, with the addition of specialized AI workflows and constraints to improve the system's ability to correctly and transparently work with biodiversity data and knowledge bases. iChatBio makes use of a growing number of LLM-powered agents (i.e., computer programs that run autonomously) which are designed to provide independent but synergistic new capabilities to the system, such as comparing occurrence records from different sources and retrieving species-related information. Each new agent not only expands iChatBio's capabilities to interact with online biodiversity services, but also facilitates new types of interactions between services. Examples of how iChatBio can be used in the context of botanical research will be presented, in addition to a high-level introduction to iChatBio.

Topic: Overcoming the barriers to on-going Castilleja research: From botanical enigma toward an emerging model system

A-830

What does it mean to be a 'species' in Castilleja?

Author: Sarah Jacobs, David Tank
Affiliation: California Academy of Sciences, University of Wyoming

Taxonomy in Castilleja is notoriously difficult, and for good reason, since data driven approaches to delimiting species have yielded at least as many questions as insights. This talk will highlight some insights and name remaining challenges to summarize a suggested approach towards species delimitation in the paintbrushes that acknowledges our emerging understanding of both the complex evolution this genus has experienced and the limitations of any one line of evidence to determine species boundaries.

Topic: Floristics

A-831

Floristic Survey of Carnivorous Plants in New Jersey (USA)

Author: Jamie Lubov, Lena Struwe
Affiliation: Rutgers University

This study explores the taxonomic diversity of species and hybrids of the genera *Drosera* and *Sarracenia* in New Jersey based on new field collections, iNaturalist, and herbarium data to evaluate changes in distribution and the presence of potential hybrids. The genus *Sarracenia* (pitcher plants, Sarraceniaceae) has a single native species in New Jersey, *S. purpurea*, and two introduced species, *S. rubra and S. flava*. The sundews in the genus *Drosera* (represented by *D. rotundifolia*, *D. intermedia*, and *D. filiformis*; Droseraceae) also have two hybrids native to New Jersey. The hybrid *Drosera* × *hybrida* (*D. intermedia* × *D. filiformis*) is only found naturally in the Pine Barrens of New Jersey. To get an updated view of carnivorous plant biodiversity, we conducted field surveys with new collections made during summer of 2024 at multiple state parks, preserves, and wildlife management areas. Pressed herbarium and liquid-preserved specimens were made of all three genera. In total, 27 *Drosera* and 4 *Sarracenia* were collected. All three native *Drosera* species were found and collected, as well as the rare *Drosera* × *hybrida*. A recently introduced *S. flava* population in Toms River, New Jersey was documented using photographs and measurements, where we also found the suspected hybrid of the two species (*S.* × *catesbaei*). Plants were identified to species in the field using local floristic keys, and confirmed in the lab through dissection and compound scopes if needed. Next step was spatial mapping of all records and species through time. For contemporary observations we used research grade observations in New Jersey from the community science platform iNaturalist. For historic observation data we downloaded New Jersey herbarium records from the Mid-Atlantic Herbaria Consortium. Distribution maps were created using ArcGIS to analyze changes in geographic range over time. Our results show that carnivorous plant distributions in New Jersey occupy fewer municipalities as urbanization has increased, with the majority of populations now occurring in

municipalities within the Pine Barrens region. Mapping shows that the population of the hybrid *Sarracenia* × *catesbaei* occur in some locations where the native *S. purpurea* and introduced *S. flava* overlap. This could be a concern if the goal is to keep the introduced genotypes out of the native species' gene pool.

Topic: Systematics & Taxonomy

A-832

Morphological Clustering of the High-Andean Nototriche (Malvaceae) of Argentina and Bolivia

Author: Martín Batalla, Lisa Wallace
Affiliation: Old Dominion University

The high-Andes host a variety of plant species that have not only evolved novel traits adapted to the region's harsh environmental conditions but have done so rapidly, given the recency of the Andes' final uplift (2–10 Mya). *Nototriche* (Malvaceae) is an endemic and characteristic genus of the high-Andes, with over 100 species distributed along much of the mountain chain's latitudinal extent. However, the genus remains enigmatic due to the strong endemicity of many species and the inaccessibility of their native habitats. The only full revision of the genus, published in 1909 by Arthur Hill, proposed two broad morphological groups based on the main leaf shape (flabellate versus non-flabellate), though this hypothesis has never been tested using morphometric analysis. In this study, twenty-seven qualitative and six quantitative morphological leaf traits were measured across 37 species collected in the dry punas of Argentina and the humid punas of Bolivia. Partitioning Around Medoids (PAM) clustering was used to evaluate support for distinct morphological groups, and to test whether similar patterns of trait separation occurred in both regions, suggesting that convergent evolution may have occurred. Given the prevalence of polyploidy in *Nototriche*, ploidy was also examined for its influence on clustering. PAM analyses of all collected species and of each country's dataset consistently favored two clusters, albeit with weak cohesion. One cluster predominantly included species with flabellate leaves and shallow primary leaf divisions, while the other grouped species with either palmate leaves featuring an enlarged middle lobe or pinnate leaves, both characterized by deeper primary divisions. Bolivian clusters could be distinguished by species with flabellate leaves with five or fewer lobes versus non-flabellate leaves with more than 5 lobes. On the other hand, Argentine species were clustered by those showcasing leaves with a deep primary division and the presence of tertiary division versus those with shallow primary leaf divisions and no tertiary division. Nevertheless, depth of the primary leaf division and the main leaf shape were still good indicators of cluster identity in Bolivian and Argentine species respectively, though with lower accuracy. Ploidy had minimal impact on clustering, with only weak influence in the Bolivian dataset. The identification of two broad morphological types is consistent with Hill's early proposal. Moreover, species with non-flabellate leaves and deep primary divisions typically grow in protected microsites, while species with flabellate leaves and shallow divisions grow more exposed to the environment, possibly due to a greater ability to buffer against atmospheric stress through their leaf morphology. The recurrence of this pattern in both countries suggests convergent evolution has allowed for species to occupy the same two ecological niches in each region. However, slight differences in clustering between Argentine and Bolivian species may also indicate that selective pressures are acting somewhat differently in each region, while the presumed recent radiation of the genus may also prevent clusters from being fully distinct from each other. Molecular data and phylogenetic analyses are needed to further resolve evolutionary relationships and to place this understanding of morphological evolution within a biogeographical context.

Topic: Conservation Biology

A-836

Establishing the Global Conservation Consortium for Food Plants: Integrating Botanical and Agricultural Approaches to Safeguard the World's Edible Plant Diversity

Author: Mauricio Diazgranados, Alex McAlvay, Colin Khoury, Hannes Dempewolf
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More than 25,000 plant species are used as human food, yet only a small fraction are widely cultivated, while thousands remain neglected, underutilized, and increasingly threatened with extinction—alongside the erosion of traditional knowledge associated with them. While genebanks and the agricultural sector have largely concentrated on conserving major crops, their cultivars, and varieties, botanical gardens represent a vastly underutilized reservoir of food plant diversity. The Global Conservation Consortium for Food Plants (GCC-FP) is a newly established, multi-sectoral initiative designed to address the urgent need for integrated, efficient, and complementary conservation of food plant genetic resources. Anchored at The New York Botanical Garden (NYBG) for its initial five-year term and co-coordinated with Botanic Gardens Conservation International (BGCI), the Consortium unites botanical gardens, genebanks, agricultural research institutions, and policy organizations to safeguard edible plant species and their wild relatives. As one of twelve Global Conservation Consortia under BGCI's framework, the GCC-FP promotes conservation through improved documentation, enhanced in situ and ex situ strategies, increased access to plant genetic resources, and strengthened global knowledge-sharing and capacity-building. It leverages tools such as BGCI's *PlantSearch* and *ThreatSearch* databases and aligns with key international agreements, including the Global Strategy for Plant Conservation, the Kunming-Montreal Global Biodiversity Framework, and the International Treaty on Plant Genetic Resources for Food and Agriculture. This presentation will outline the motivations behind the GCC-FP, its governance structure, and its implementation roadmap. It will highlight the momentum generated during its inception at the 8th Global Botanic Gardens Congress and its formalization through multi-institutional collaboration. Ultimately, the presentation will underscore the Consortium's role in bridging the gap between the botanical and agricultural sectors to ensure long-term conservation of food plant diversity for global food security and resilience.

Topic: Molecular Ecology

A-837

Investigating the role of chromosomal inversions in local adaptation of valley oak

Author: Heidi Yang, Victoria Sork
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Chromosomal inversions are a form of genomic structural variation (SV) that can shape phenotypic variation in evolutionarily significant ways. They are sequences flipped in orientation when compared to a reference, or standard, arrangement. This change in sequence homology between the standard and inverted arrangements suppresses recombination in heterozygotes, which is thought to maintain high genetic divergence across individuals. Inversions have been shown to be involved in local adaptation of numerous plant species, including sunflower, ragweed, and monkeyflower, by producing large, non-recombining sequences containing sets of adaptive loci. Locally adaptive inversions also tend to be longer and evolutionarily old, since they capture and/or gain more adaptive loci that have been co-selected for over many generations. As environmental conditions continue to shift, identifying the various genomic bases of local adaptation can be integrated into genome-informed conservation strategies, such as climate-adapted seed sourcing and assisted gene flow.

This work investigates the role of inversions in local adaptation of valley oak (*Quercus lobata*), a California endemic and foundational species of oak woodlands and savannas throughout the state. Previous studies in valley oak have identified genomic signals of local adaptation – associations between genetic and environmental variation – using candidate genes, single nucleotide polymorphisms (SNPs), and DNA methylation. Using a data set of 80 whole genome resequenced valley oak individuals, we explore hypotheses that locally adaptive inversions (1) are large and evolutionary old and (2) contain or disrupt genes involved in environmental response. To identify putative inversions, we use SV-calling programs as well as indirect discovery using signatures of abnormally high genetic divergence and linkage disequilibrium compared to the rest of the genome. After filtering and merging outputs from the programs, we found 8333 putative inversions across all 12 chromosomes, although many overlap and require further manual filtering and collapsing of duplicate calls. Using the indirect discovery approach, we identified highly divergent regions along each chromosome, all of which are largely driven by a handful of individuals; while an unexpected signature, this result shows that different parts of the valley oak genome have vastly different divergence histories, motivating further investigation of more subtle patterns of divergence that may be consistent with inversions.

To identify inversions putatively involved in local adaptation, we will correlate inversion frequencies with climate gradients across the valley oak range. We will then build time-scaled phylogenies of putatively locally adaptive inversions to estimate their age and document genes that are within or near them. This work will further our understanding of long-standing questions in evolutionary biology by investigating an understudied form of genomic variation, which can assess the extent to which chromosomal inversions shape genotypes under selection, thus offering an additional mechanism of local adaptation over SNPs.

Topic: Comparative Genomics/Transcriptomics

A-838

Mimulus Keeps the Score: Investigating Transgenerational Plasticity in Response to Temperature Change in Mimulus laciniatus

Author: Charlie Kortleven, Jack Colicchio, Benjamin Blackman, Ren Hamm, Sean Adams, Ian Anderson, Cameron Yuki, Chyna Robeson, Aspen Smith
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Plants can respond to environments experienced by previous generations through a process called transgenerational plasticity (TGP). TGP is a process whereby parental environmental effects alter phenotypic and genotypic expression in progeny. Theory predicts that TGP can evolve when the environment is temporally autocorrelated, when there is genetic variation in the norm of reaction, and when the cost of responding to the environmental cue is low. While previous research provided some insight into how TGP is induced and persists, the distinct genetic components which mediate TGP and that contribute to its evolution are less well understood. *Mimulus laciniatus* offers a tractable study system for investigating TGP and its evolution across an elevational and geographic gradient. It is a self-fertilizing species with ample genetic resources and a short generation time, and it is endemic to parts of Sierra Nevada Range where year-to-year climate parameters are temporally autocorrelated. To characterize the genetic basis of natural variation for both within-generation plasticity (WGP) and TGP to temperature, we employed a Multiparent Advanced Generation Inter-Cross (MAGIC) scheme cross constructed from six parental inbred lines. For recombinant inbred line panels generated from three distinct 4-way crosses of these parents, we simulated diurnal temperature patterns from the warmest (H) and coldest (C) environments experienced by natural populations in a full factorial design to measure and map quantitative trait loci (QTLs) for offspring phenotypes across all parental x offspring combinations (C x C, H x C, H x H, and C x H). In addition, to identify candidate genes mediating TGP within these QTLs, we performed RNA-Seq of the parental lines to identify which genes within the QTL intervals are genes differentially expressed between C × C and H × C treatments. While our preliminary mapping results indicate an absence of QTL for TGP or WGP in constitutive traits, we did identify that floral tube length and anthocyanin response to cold temperature (C x C) are determined by a rather simple genetic basis. Additionally, our transcriptomic results suggest that transgenerational effects alter global gene expression in offspring, and this response is population-specific. Continued efforts to characterize the genetic basis of transgenerational plasticity would benefit from functional validation of candidate genes.

Topic: Ecophysiology

A-839

Eco-physiological difference between sexes and reproductive states in a sexually mobile plant species

Author: Samuel Hodgson, Janaa Ward, Jennifer Blake-Mahmud
Affiliation: Hope College

Climate change is predicted to more adversely impact dioecious plant species. Many dioecious plants are agriculturally important, including cannabis, spinach, ginkgo, and asparagus. Understanding differences in sex-based physiology will help us predict how climate change may impact dioecious species. To do this, we study a plant species known as striped maple. Striped Maples are mainly dioecious trees, native to the understories of hardwood forests in northern Michigan. This species exhibits environmental sex determination, a mechanism by which individuals may change sex from year to year based on these environmental cues. These attributes above make striped maples an appropriate study species to examine sex-based differences in physiology because their distribution is not confounded by spatial segregation issues. We traveled to five field sites in northern Michigan and took demographic information on more than five hundred trees. For over a hundred of the study trees, we measured photosynthetic rate, growth, stress levels, and light exposure to look for physiological differences between the sexes. Notably, this lab has found females have significantly lower growth rates and photosynthetic rates than male trees. Females were also found to have a differential response to season as they had a larger photosynthetic rate decrease during seed set. These data are consistent with the idea that there is a substantial cost to reproducing as a female, suggesting that females may be disproportionately affected by climatic stressors. As female is the preferred sex in many separate-sexed agricultural species (e.g. hops, holly, and kiwi, among many others), we might expect these crops to be negatively affected in the coming years.

Topic: Biogeography

A-840

"This refugium ain't big enough for the both of us": Desert plant interactions under climate change

Author: Nicolas Graver, Brooke Rose, Lynn Sweet, Janet Franklin, Melanie Davis, Helen Regan
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Species interactions are the fundamental building blocks of ecology; they shape every aspect of a species' ability to survive in its environment. Climate change has the potential to shift not only a species' habitat range, but also the suite of interacting species which form that species' ecological niche. In arid regions of southern California, both competitive and facilitative relationships shape plant species' relationships with their environment across aridity gradients. One strength of species distribution models (SDMs) is that, if constructed correctly, they account broadly for all aspects that might shape a species' environment. However, species interactions represent an unknown factor that may not be fully accounted for in SDMs. By using standard similarity metrics, such as Sørensen similarity and Schoener's D Statistic, we compare the amount of overlap between species' ranges of a broad suite of California desert shrub and tree species. We use these metrics to compare the degree of range overlap between pairs of species across southern California at present and under future climate scenarios. We find that almost all species are projected to experience declining range overlap with each other species, with some species' overlaps that will be preserved under climate change and others experiencing up to 100% declines. Species experiencing more range-wide vulnerability due to climate change are simultaneously experiencing larger declines in their overlaps with interacting species, decreasing the likelihood that facilitative relationships will be able to moderate the worst effects of climate change. Furthermore, range overlaps under a hot/dry climate scenario (HadGem) experience more divergent outcomes, including some gains in overlap area, than the warm/wet scenario (CNRM). This analysis of range overlaps—which has not been previously conducted in the context of climate change—presents a future of decreasing available space for species interactions to occur. Whether plant species relationships are competitive, facilitative, or even parasitic, climate change represents a potential for widespread loss of these interactions, with significant consequences for the flora of southern California deserts.

Topic: Conservation Biology

A-841

Natural Selection on Lake Superior's Arctic Relicts in the Face of Climate Change: Phenotypic Selection Analysis of Three Species Across Three Years

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The waters of Lake Superior, the coldest and deepest of the five North American Great Lakes, generates a subarctic-like climate along the length of its shoreline. After the last glacial maximum, some populations of arctic plants persisted in this microhabitat along the rocky shore of the lake as the rest of the tundra continued to move north, resulting in disjunct distributions. These rare 'arctic relicts' along Lake Superior exist at their warm range edge and are of conservation concern due to the threat of climate change. In Minnesota, USA, winters are rapidly growing warmer, leading to less lake ice and a deterioration of the subarctic-like conditions along the shore. During the summer, extreme weather such as drought and heavy rainfall are becoming more common. These changing conditions will put the arctic relicts under stress, resulting in stronger selection on individuals. In particular, there is on average a 2 °C difference in temperature between the southern and northern reaches of the lakeshore within Minnesota; southern sites along this latitudinal temperature gradient could already be suffering from the stress of climate change. For three growing seasons, we repeatedly monitored the same individuals within populations of three arctic relicts with different life history strategies (*Primula mistassinica*, *Pinguicula vulgaris*, and *Euphrasia hudsoniana*) to track relative fitness and study the effects of climate change on phenotypic trait selection. This large dataset spanning three species, four sites, and three years allowed us to analyze selection along the shore's latitudinal gradient, compare years with greatly different weather conditions, and evaluate the impact of life strategies such as annuals vs. perennials. We found that selection on traits varied significantly across both sites and years. Surprisingly, despite differences in selection among sites, there was no clear latitudinal trend as

we expected. Instead, specific microclimates likely play a larger role in fitness and trait selection, highlighting both these species' resilience and the importance of continued monitoring and protection.

Topic: Phylogenomics

A-842

Exploring phylogenomic discordance and reticulation using a lineage-specific bait set for targeted enrichment in Lonicera (Caprifoliaceae)

Author: Aaron Lee, Mansa Srivastav, Dianella Howarth, Michael Donoghue, Wendy Clement
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Honeysuckles (Lonicera) are a group of ~140 species of woody vines, shrubs, and subshrubs distributed worldwide. Many are known for horticultural value, and are frequently invasive in their nonnative ranges. Species complexes with broad distributions and widespread intraspecific hybridization suggest that ancient reticulation events may have contributed to lineage diversification in this genus. Furthermore, our previous RAD-seq phylogeny recovered strong support across the tree except for a key node along the backbone. Targeted enrichment combined with a novel assembly pipeline may provide insight into the causes and consequences of this phylogenomic uncertainty. Parallel to our RAD-seq efforts, we designed a lineage-specific bait set from transcriptome and whole genome shotgun sequencing data to target 649 exons in 215 loci. We successfully targeted and sequenced these loci from 96 taxa across the genus, as well as Symphoricarpos, Leycesteria, and Heptacodium species as outgroups. The Angiosperms353 universal bait kit was also sequenced through targeted enrichment. Here, we compare hyb-seq assemblies between two pipelines, HybPiper and Captus, and explore the extent to which target sequence selection and assembly errors affect locus recovery. Using these data, we explore areas of phylogenomic discordance along the backbone of the genus and identify reticulation events underlying lineage diversification.

Topic: Phylogenomics

A-843

Phylogenomics and Biogeography of Zinniinae (Asteraceae: Heliantheae) using plastome and nuclear datasets

Author: Samuel Skibicki, Craig Barrett
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Zinniinae is a subtribe with a dizzying array of chromosome numbers (*n* = 8, 10, 11, 12, 13, 14, 16, 21, 22, 24, 28, and ?), a center of diversity in Mexico, and taxa with broad ranges across the Americas including many disjunctions. Zinniinae includes 57-66 species in seven genera: *Echinacea, Heliopsis, Philactis, Sanvitalia, Tehuana, Trichocoryne,* and *Zinnia*. *Echinacea* is a popular dietary supplement and *Heliopsis* and *Zinnia* are prominent members of the horticultural trade. A taxonomic treatment and molecular phylogenetic analysis (ITS and three plastid loci) of *Sanvitalia* uncovered recent and ancient polyploidy events, cytonuclear discordance, and uncertain placement of *Trichocoryne* making the subtribe a candidate for a plastome and multi-locus nuclear approach. A phylogenetic analysis of Zinniinae, using both the plastome and target sequence capture of the nuclear genome, was undertaken to investigate the evolutionary and biogeographic history of this understudied and captivating clade. We hypothesize that polyploidy, dysploidy, and dispersal have played major roles in the diversity we see in Zinniinae today. The plastome analysis included non-coding regions and microstructural changes to the plastome (as gaps coded as presence/absence data points) and showed patterns of paraphyly in the genus *Heliopsis* and the subgeneric delimitations inside *Zinnia*. It also expanded the limits of Zinniinae to include the sister subtribe Spilanthinae and confirmed the placement of the enigmatic genus *Trichocoryne*. The study of the nuclear genome confirmed the expected presence of paralogy, detected 15 nodes of the phylogenetic tree that did not follow the patterns expected under Incomplete Lineage Sorting, revealed ancient hybridization between *Heliopsis* and *Zinnia*, and provided evidence for taxonomic changes to address patterns of paraphyly in the subgenera and sections inside *Zinnia*. We created a chronogram to reconstruct the evolutionary history of the subtribe through time, estimated date ranges for major splits in the clade, elucidated the center of origin for Zinniinae to be Mexico, and found that speciation events from dispersal far outweighed the species richness gained by vicariance. This study resulted in taxonomic changes informed by the topologies of the phylogenetic trees, advanced knowledge in the utility of gap coding and non-coding regions of the plastome at the subtribal level, and provided further insights into the biogeographic patterns that have underpinned the floristic diversity found in Mexico.

Topic: Conservation Biology

A-844

Population genomic insights into the imperiled threecorner milkvetch (Astragalus geyeri var. triquetrus, Fabaceae)

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Astragalus geyeri var. *triquetrus* (threecorner milkvetch; Fabaceae) is a rare annual herb native to the Mojave Desert of Nevada and Arizona. This variety is small in stature, with diminutive white flowers that are sometimes cleistogamous. Successful germination of threecorner milkvetch is closely tied to years of above-average precipitation. In 2019 this variety was petitioned for listing under the federal endangered species act and currently, it is listed as Critically Imperiled (S1) in Arizona and Imperiled (S2S3) in Nevada. Despite its conservation concern, no genetic studies have been published on *Astragalus geyeri*, and little is known about the demographics, breeding system, or population dynamics of var. *triquetrus*. Here, we present the results of a population genetics study using ddRADseq data from six populations in Clark and Lincoln counties, Nevada. Our analyses provide new insights into genetic diversity, population structure, and effective population size. In addition, we report findings from a phylogenetic study evaluating the taxonomic status of the two recognized varieties: *A. geyeri* var. *geyeri* and var. *triquetrus*. Results from this study have informed the Species Status Assessment which is currently under review and will contribute to conservation strategies for this imperiled desert annual.

Topic: Comparative Genomics/Transcriptomics

A-845

Genomic signature of CAM photosynthesis loss

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CAM photosynthesis has evolved multiple times across the plant kingdom. While it provides greater water-use efficiency under arid conditions, it's also a costly adaptation. The genomic processes accompanying the loss of CAM once it is no longer advantageous remain largely unexplored. Members of the Montiaceae family express variable amounts of CAM photosynthesis and are broadly described as C3+CAM plants, able to perform CAM in addition of the regular C3 pathway from which they source most of their carbon. In this study, we investigate a plant lineage within this family - the genus Montiopsis - which occupies Andean alpine habitats and has secondarily lost the capacity to perform CAM. This configuration offers a rare window into the evolutionary dynamics of metabolic pathway reversal. Using comparative genomics, we identify a suite of molecular changes in Montiopsis compared to its C3+CAM relatives, consistent with ongoing degeneration of the CAM pathway. Several key CAM genes have been lost or pseudogenized and we detected shifts in selective pressure on others. Together, these findings suggest a multi-phase process of functional decay, highlighting how metabolic flexibility in plants is underpinned by dynamic and reversible genomic architectures.

Topic: *Macroevolution*

A-846

Developing an evolutionary framework for the model clade, Lonicera (Caprifoliaceae, Dipsacales) to investigate organ fusion: insights from phylogenomic and morphological studies

Author: Wendy Clement, Aaron Lee, Kendall Villalobos, Mansa Srivastav, Dianella Howarth, Michael Donoghue
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Lonicera or honeysuckles (Caprifoliaceae, Dipsacales) are a clade of ca. 140 species of shrubs and vines largely distributed throughout the northern hemisphere. While well-known for sweet scents and bright tubular flowers, honeysuckles in fact exhibit much variation in floral form, scent, and fused organs involving leaves, bracteoles, ovaries and more. With an array of fused structures, *Lonicera* offers a natural laboratory to facilitate studies on the evolution and development of fusion, a hallmark of plant evolution. Here, we will share key outcomes from collaborative studies of *Lonicera* encompassing phylogenomic, morphological, and evo-devo approaches to understanding the evolution of organ fusion across the clade. First, we discuss reconstructing a comprehensive species tree for the clade, using RADseq, HybSeq (including both Angiosperms353 and custom baits), and plastome data, in which cyto-nuclear discordance events were identified. Such events likely impacted, for example, the early evolution of clades *Periclymenum* and *Nintooa* and the interpretation of shared traits including a vine habit and large brightly colored corolla tubes. Next, we will present current work on tracing the evolution of organ fusion and associated traits from quantitative studies of leaves, bracteoles, and ovaries. These outcomes will be complemented with a discussion of gene trees of transcription factors including CUP-SHAPED COTYLEDON (CUC) known to affect organ boundary formation. Finally, we will discuss the deep engagement of our undergraduate research collaborators throughout all of these studies and the long lasting impact of involving undergraduates in fieldwork, benchwork, herbarium work, computational work, and scientific communication to train and propel the next generation of botanists.

Topic: *Biology of mycoheterotrophic and parasitic plants*

A-847

Fungal Host Diversity Across the Range of the Phantom Orchid, Cephalanthera austiniae

Author: Fred Disbrow, Hana Thixton-Nolan, Craig Barrett
Affiliation: West Virginia University

Mycoheterotrophs, plants that parasitize fungi, are fascinating systems in which to explore the genetic, morphological, physiological, ecological consequences of parasitism. Mycoheterotrophs typically contain reduced morphological and genomic characteristics, making them valuable subjects of research into parasite genome evolution. Mycoheterotrophs parasitize large networks of mycorrhizal fungi, which form relationships with many autotrophic species and can span entire ecosystems. Mycoheterotrophs cheat this network by stealing resources in a manner known as 'epiparasitism.' In addition to being targets of conservation themselves, this connection to both autotrophs and mycorrhizae allows mycoheterotrophs to act as an indicator of ecosystem health by giving insight into local biodiversity and maturity of the ecosystem. Previously, fungal host associations of mycoheterotrophs were thought to predominantly be highly specific, typically to a single family of fungi, or even to a few genera. The phantom orchid, *Cephalanthera austiniae* (Epidendroideae, Neottieae) is a fully mycoheterotrophic species native to the northwestern USA and southwestern Canada. This species was previously shown to form associations with ectomycorrhizal fungi in the family Thelephoraceae (Basidiomycota), specifically *Thelephora* and *Tomentella*. However, more recent research on host specificity in mycoheterotrophic plants has found that some species target a broader range of fungal families, though specificity within targeted families may still be high. For example, *Aphyllorchis* (tribe Neottieae) and *Corallorhiza* (tribe Calypsoinae) have both been shown to associate with Thelephoraceae and Russulaceae, but these associations vary by orchid species, and sometimes among populations within species. Our data based on Sanger sequencing of gel-extracted fungal ITS regions amplified from the roots of *Cephalanthera austiniae* (60 individuals from 17 populations across the geographic range) show that the orchid predominantly associates with ectomycorrhizal members of Thelephoraceae, most notably, *Tomentella*. However, there are some individuals within populations that associate with fungi in Russulaceae and Hymenogastraceae, other families of ectomycorrhizal fungi. This evidence is being corroborated by Illumina metabarcoding of the ITS2 region, allowing genus- or species-level identification, elucidating a more specific understanding of the types of associations formed. This metabarcoding approach also quantifies fungal associations within the phantom orchid, determining the most important families with which it is associated, the frequency of these associations, and their geographic patterns. By analyzing these specific associations mycoheterotrophic plants form within their environment, we gain insight into the mechanics by which these plants need to germinate and survive, as well as allowing for more targeted methods of conservation for the plant and their ecosystems.

Topic: *Comparative Genomics/Transcriptomics*

A-849

Can DNA methylation help us understand climate-adaptation in trees?

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The idea that forests and climate are intrinsically linked is a long-held view, both in the traditional knowledge of indigenous communities, and by European colonists observing drier climates following widespread deforestation. Woody plants create the ecosystems they occupy and shape their biodiversity, be they forests, tree-savannahs, or chaparral. Today's rapidly warming climate threatens these long-lived species by creating new environments in which existing populations become maladapted. Plants show enormous phenotypic diversity in response to environmental change, which can be caused by genotype or epigenetic mechanisms that influence the expression of the underlying DNA sequence. The influence of epigenetics on ecologically important traits in trees is a controversial topic. Here, we address the central question of whether epigenetics, and particularly DNA methylation, affect climate-associated traits in trees. We use a novel experimental approach to show an effect of drought on methylation in eight seedlings, comprising half-siblings of two maternal genotypes from a natural population of an oak endemic to California, *Quercus lobata*. We monitored abiotic stress by recording ecophysiological measurements throughout the drought treatments. Seedlings were sampled at three timepoints and were subjected to drought- and well-watered treatments. We sequenced 24 Oxford Nanopore PromethION long-read genomes and methylomes, and chromatin landscape for two samples. Our data show that drought stress results in extensive remodelling of tree methylomes, with gene flanking and intergenic regions, and transposable elements (TEs) enriched for CHH hypermethylation. Interestingly, it was TEs within the downstream and intergenic regions that were enriched in CHH hypermethylation. This CHH hypermethylation specifically targeted entire superfamilies near drought-responsive genes. We conclude that drought stress changes patterns of DNA methylation with possible functional consequences. Such changes have the potential to affect phenotypic response of oaks to drought stress, and future work will need to assess whether these methylome changes have a functional role by modulating gene expression.

Topic: *Biology of mycoheterotrophic and parasitic plants*

A-850

Phylogenomics of mycoheterotrophs: A walk on the dark side of plant life

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Fully mycoheterotrophic (FM) plants obtain fixed carbon and other nutrients from symbiotic relationships with soil fungi. FM lineages evolved at least 50 times in angiosperms; each evolutionary transition represents an independent loss of photosynthesis, in effect providing replicated "experiments" that we can use to better understand how plants live heterotrophically—and the resulting (and sometimes extreme) effects on their genomes and biology. The morphology of FM plants is often substantially modified. Their plastid, mitochondrial and nuclear genomes can also evolve rapidly, often accompanied by substantial gene loss. It can therefore be challenging to study their evolutionary history. Here we report on two projects aimed at understanding the phylogenetics and molecular evolution of FM plants. In the first, we used a nuclear target enrichment approach (Angiosperms353) on Gentianaceae and Dioscoreales, combined with dense taxon sampling from herbarium and other material. These two clades have experienced multiple losses of photosynthesis (the most outside orchids). Despite lower gene recovery rates than photosynthetic relatives—reflecting gene loss

and/or failure to recover genes due to rapid evolution—our phylogenomic analyses still provide generally well resolved insights for both major clades, substantially clarifying their phylogenetic history. We also report on progress in integrating their often highly modified plastid genomes into phylogenomic analyses, and report on the molecular evolution of the recently described FM family, Afrothismiaceae. This taxon has an exceptionally reduced genome and unusual molecular evolution, including (for some species) multiple retained genes that are likely functional, despite the existence of abundant internal stop codons.

Topic: Conservation Biology

A-851

Botanical gardens, genetic research, and collaboration to meet global plant conservation targets

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The Kunming-Montreal Global Biodiversity Framework is a monumental international agreement that seeks to bring about a transformation in the relationship between societies and biodiversity. It sets out ambitious policies, goals, and targets to enable coordinated conservation actions, which can be implemented, monitored, and reported, to halt and reverse biodiversity loss. Target 5 aims to ensure sustainable, safe, and legal harvesting and trade of wild species. This target is especially relevant to members of the cactus family as over 30% of the almost 2,000 species in this family are threatened with extinction, primarily due to habitat destruction, climate change, and poaching. As a case study, geneticists and horticulturalists at a university and several botanical gardens, have begun a collaboration to restore 400 poached and seized plants in the genus *Ariocarpus* to Mexico, their country of origin. As a first step toward restoration, genetic diversity of the seized plants was evaluated using microsatellites developed for the genus. The microsatellite analysis revealed the extent of genetic diversity in the poached plants and suggested the severity of potential loss of genetic diversity from the wild. In addition, microsatellite analysis contributed to planning for conservation actions, such as seed and seedling production for potential reintroduction. The next step will be to compare the genetic diversity of poached plants to wild plants in order to determine the most likely provenance of the poached plants. This project will provide a methodological foundation for how botanical gardens and researchers can work together to address illegal plant trade and improve the conservation and sustainability of plant populations in the wild.

Topic: Conservation Biology

A-852

Isolation and divergence in the endangered edaphic endemic Penstemon haydenii

Author: Erin Bentley, David Tank, Sean Harrington
Affiliation: University of Wyoming

Penstemon haydenii, an edaphic endemic native to the Ferris Dunes in Wyoming and the Sandhills in Nebraska, is an organism of conservation concern and evolutionary interest. It is listed as endangered across its range and has been since 1987 (USDI Fish and Wildlife Service, 1987). This plant was first discovered in Nebraska around 1857 and was later described in 1891 (Sutherland, 1988). It was not discovered in Wyoming until much later in 1996 (Fertig, 2000). Since then, there have been a handful of populations discovered in Wyoming, and it has been theorized that the Wyoming populations may have descended from those in Nebraska. Notable morphological differences have been observed between the NE and WY populations. Due to the narrow habitat specificity of *P. haydenii* and its limited range, the species may be experiencing a lack of gene flow between populations, and the two state populations at large may be diverging from one another. We assessed the evolutionary trajectory of the WY and NE species through demographic modelling approaches. From preliminary analyses we have discovered that the different populations of *P. haydenii* have embarked upon their own independent evolutionary trajectories. Through modelling the time since divergence and whether gene flow is still occurring and in what direction, we can determine the extent to which NE and WY *P. haydenii* is are diverging.

Topic: Ecophysiology

A-853

The impact of wildfire on environmental stress in a California oak

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Across the western United States, the area of land burnt each year increases exponentially with aridity, threatening ecosystems as some trees die while others endure stress but survive. In 2020-21, over 15% of the world's giant sequoia trees died following wildfires, a significant loss for biodiversity and climate resilience. This incident is one of many fire and drought events: in July 2024, the Lake wildfire burned 16,000 hectares in the Santa Ynez Valley, California, including 40% of the University of California Sedgwick Reserve. How surviving trees respond to fire, heat, and smoke is unclear. Trees respond to environmental stress through changes in leaf traits including physiological (e.g., stomatal conductance) and morphological (e.g., lobedness) traits. Many plant traits are connected through complex interactions that are shaped by environmental conditions, and studying these networks, namely the covariance between multiple traits, can help elucidate plant adaptation. Typically, trait integration increases in stressful environments because organisms coordinate traits to best optimise limited resources. Here, I used the unique opportunity following the Lake fire to measure environmental stress in mature *Quercus lobata* trees, a California endemic oak. Samples were from five zones: fire zone (n=6); very close <250m (n=5), close <500m (n=6), far <1km (n=4), and very far <2km (n=7). We measured immediate (within one month), short- (within three months), and will measure medium-term (within nine months) responses at physiological and morphological scales. Additionally, we measured fecundity and phenological impacts. We found that the Lake fire induced significant physiological and morphological changes in new leaf growth in fire zone compared with far (<1km from the fire zone) trees. Significant positive correlations were found between leaf lobedness and temperature, and leaf area and stomatal conductance; and negative correlations between leaf lobedness and stomatal conductance, and leaf area and temperature. Such integration between morphological and physiological traits increases photosynthetic area and rate and suggests optimized resource use. We also observed that fire zone trees produced fewer, but more fecund acorns than unburned zones. This study provides preliminary evidence that trees can undergo rapid phenotypic plasticity in response to, and which may alleviate, serious stress. We also provide evidence that acorn germination improves following wildfire. However, further studies are needed to understand whether this rapid plastic response causes medium- or long-term damage, or can be mitigated with time. Such information will provide foundational knowledge for forest recovery from transient wildfire stress.

Topic: Conservation Biology

A-854

A common garden study of the endemic subspecies of Dudleya cymosa (Lem.) Britton & Rose (Crassulaceae) in the Santa Monica Mountains, California

Author: Annie Ayers, Kristen Hasenstab-Lehman, C. Matt Guilliams
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The Santa Monica Mountains, just north of Los Angeles, California, contain the global ranges of three endemic subspecies of *Dudleya cymosa* (Lem.) Britton & Rose (Crassulaceae) -- subsp. *agourensis* K.M. Nakai, subsp. *marcescens* Moran, and subsp. *ovatifolia* (Britton) Moran -- along with two unnamed morphological forms (*D. cymosa* "Slant Rock" and *D. cymosa* "Split Rock"). The three recognized subspp. are each federally listed as threatened, while the forms are known from single rock outcrops and are treated as rare. Here, we report on a greenhouse study of these three taxa and two forms. We gathered seed from 13 populations of these taxa or forms and grew the resulting plants in pollinator exclusion tents under similar conditions by population. We performed daily counts of germination, flowering, and fruiting. At anthesis, we gathered data on 24 morphological and color features for up to 10 individuals per population. The resulting data showed taxon/form-specific differences in the timing of germination and flowering. We found moderate morphological differentiation between populations of the three recognized subspecies, with subspp. *agourensis* and *ovatifolia* particularly well-marked. The "Slant Rock" and "Split Rock" forms were not morphologically differentiated in these analyses. Interestingly, plants grown from seed of putative subsp. *marcescens* were not found to be morphologically different from plants grown from seed of co-occurring subsp. *cymosa*, suggesting that fine-scale habitat differences may be responsible for the expression of the suites of morphological features commonly

associated with subsp. *marcescens* and *cymosa* in the Santa Monica Mountains. Collectively, this common garden project sheds light on a rare and taxonomically difficult group of Dudleya. Future work will include in situ studies to characterize the micro-habitat of subsp. *marcescens*.

Topic: Molecular Ecology

A-855

Recent demographic history and climate-driven adaptations in a desert plant, Encelia farinosa

Author: Victor Andreev, Adrian Munguia Vega, Greer Dolby, Melanie Culver
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Cl imatic oscillations in the middle to late Quaternary h ave caused major range shifts, contributed to the currently observed patterns of population structure, and facilitated local adaptations. However , details regarding the demographic processes, associated patterns of natural selection, and regional-specific environmental factors driving adaptations are lacking. W e utilized whole-genome sequencing, demographic modeling, ecological niche modeling, and genetic-environment association analyses to investigate patterns and drivers of differentiation within *Encelia farinosa* A.Gray ex Torr. from the Baja California peninsula.

Our analyses revealed three genetically distinct lineages of *E. farinosa* , which differentiation can be linked to the recent climatic history of the region . Demographic analyses indicat ed fluctuations in the effective population sizes and two lineage divergence events coincid ing with the onset of glacial cycles. The ecological niche modeling recovered concordant southward shifts and decrease s in the suitable habitat for all *E. farinosa* lineages during the Last Glacial period. Analyses of putative adaptive loci suggested that climate, and especially the regional differences in annual precipitation, has been an important driver of adaptive genetic variation in *E. farinosa* . We found that local adaptations in *E. farinosa* involve multiple genes associated with immune response, stress response, and response to environmental stimuli associated with arid climate, such as water availability and high levels of solar irradiation.

Our findings indicate that the current genetic makeup of *E. farinosa* from the Baja California peninsula can be explained by the glaciation-mediated demographic processes and climate-driven lineage-specific adaptations to local conditions.

Topic: Systematics & Taxonomy

A-856

Rediscovery of Gesneria lanceolata (Gesneriaceae): Expanding the geographic range of an elusive species in Hispaniola

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Erik Leonard Ekman (1883–1931), a Swedish botanist, made significant contributions to the study of Caribbean flora, particularly in Hispaniola, which includes present-day Haiti and the Dominican Republic. Among his many collections, he discovered and described Gesneria lanceolata (Gesneriaceae) from the Massif de la Selle in Haiti. However, the species description was based entirely on mature fruits and vegetative features, as flowers were not available for study. Until recently, the species was only known from Ekman's type collection in 1927.

Recent fieldwork across both Haiti and the Dominican Republic yielded several Gesneria specimens that were evaluated for resemblance to the type material of Gesneria lanceolata from Haiti. Molecular sequence data were generated from nuclear ribosomal DNA (nrDNA) Internal Transcribed Spacer (ITS) sequences. Using these molecular tools, specimens from Haiti were matched with a population from the Dominican Republic, significantly expanding the species' known geographic range.

These findings expand the distribution of Gesneria lanceolata beyond the type locality in Haiti and underscore the importance of fieldwork, herbarium research, and molecular tools in resolving long-standing taxonomic questions. The results highlight the value of continued botanical exploration in underexplored regions such as the Caribbean.

Topic: Molecular Ecology

A-857

A prickly problem for rare cacti: Is the diversity of S-alleles low across Cactaceae?

Author: Charles Carignan, Boris Igic, Karolis Ramanauskas
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Most flowering plants feature hermaphrodite flowers that potentially self- pollinate. Nevertheless, roughly one half of all angiosperm species possess a genetic mechanism that prevents self-fertilization, by rejecting all incoming pollen grains that match a specific genomic region of the pistil (S- locus). Many so-called "self-incompatibility" (SI) mechanisms exist, but one is widespread, ancestral and homologous across pentapetal eudicots. It uses members of style-expressed T2/S-RNase protein family to dramatically assassinate self-pollen, as well as pollen with matching S-locus content, following pollination. As a result of this rare-allele advantage, the S-loci exhibit extreme polymorphism.

Many species in the cactus family express SI, and we recently showed that RSI operates in *Schlumbergera truncata* (Cactaceae), a seasonal floriculture favorite (Ramanauskas and Igic 2021). We employed candidate-based transcriptome sequencing (RNA-seq), along with classic biosystematic and molecular evolutionary approaches, to rapidly uncover the molecular basis of SI.

Here, we show additional data, including putative S-allele sequences from several species, which also imply a low number of allelic lineages at the S- locus. Specifically, we interrogate new and previously published transcriptomes to detect S-alleles, and find unexpectedly low S-locus diversity. Awaiting results from a broader sample of species across the family, we speculate about the causes and consequences of the restricted allelic richness, particularly in relation to the demographic history and conservation practices of this charismatic family.

Topic: Ecology

A-858

Heavy metal accumulation and tolerance in soils and plants across an urban-rural mosaic

Author: Alex Arena, Janet Steven
Affiliation: Christopher Newport University

Urbanization is one of the most impactful catalysts for ecological change in the modern era., Urban areas across Virginia, including Newport News, are growing in population and expanding in area. Heavy metal pollution can be high in urbanized areas due to industry, construction, and high traffic presence. Newport News, Virginia, has a relatively high population density, but has also served as the primary port for coal shipped by rail from the coal fields of the Virginias since 1881. The transfer and storage of coal at what is now the Dominion Coal Terminal in an urban landscape may have harmful impacts on both the environment and its human inhabitants. Coal can carry a variety of heavy metals, depending on geographic region and coal seam of origin, and often includes lead, cadmium, manganese, and zinc. Metal pollution accumulates within the soils and eventually plants within the city, and the rate at which metals accumulate may change with both distance to the Dominion coal terminal and with human population density. This accumulation may lead to decreased ecological and human health through bioaccumulation in soils, plants, or through direct uptake (ex., inhalation, absorption). So far in this research, metal pollution has already been found to increase in areas of higher urban influence, especially in industrial zones. Aluminum was found to have the highest correlation of concentration to urban index for soils at -0.397, followed by lead at -0.295. In plants, this correlation is much lower at -0.124 for aluminum. This suggests that the form of metal distributed across sites is unable to be taken up efficiently by vegetation. However, this does not discount the potential harm that this spread of metal may have on a broader ecosystem level. Additionally, knowing of pollution hotspots caused by urbanization can indicate where plant communities may be most impacted within Newport News for carrying types such as nutrient or chemical pollution. By understanding how metal accumulates in the environment based on both levels of urbanization and distance from heavy industrial areas, cities can employ the use of green spaces to mitigate potential ecological harm.

Topic: Education and Outreach

A-859

Still Cultivating: Evolving insights from ungrading in a sophomore-level plant biology course

Author: Rebecca Penny
Affiliation: Aquinas College

Ungrading, a student-centered and growth-minded pedagogy, continues to interest educators as a way to support curiosity and intrinsic motivation and to question power hierarchies within the classroom. In spring 2024, I implemented contract grading—a form of ungrading—in a sophomore-level Plant Biology course. Student feedback indicated high engagement, strong intrinsic motivation to learn course material, and relatively low anxiety about grade outcomes. Over the semester, the average Plant-Awareness Disparity Index also improved significantly.

Returning to contract grading for a second year (spring 2025), I encountered familiar challenges. While some students thrived, others were intermittently disengaged or uncomfortable with the open-endedness of this nontraditional approach. The time and emotional investment required of the instructor did not diminish with experience as it might with other pedagogies, and significant effort was devoted to supporting student agency and collaborative goals.

This poster reflects on the experience of ungrading, sharing emerging patterns, persistent tensions, and considerations for future course design. I will report quantitative assessments of student learning outcomes and course perceptions, along with new analysis of qualitative student reflections gathered across two semesters.

Topic: Bryology and Lichenology

A-860

Metabarcoding Bulk Samples Reveals Greater Lichen Diversity and High Replicability

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Lichens are present in nearly all terrestrial ecosystems. They represent a substantial portion of biodiversity, play important ecological roles, and are commonly used to monitor ecological health. Consistently detecting and representing lichen diversity remains challenging, even when standardized surveys are conducted by experts. In fact, recent work suggests that lichen detectability is unexpectedly low, even some of the best-case scenarios, with striking differences among independent sampling efforts. DNA metabarcoding of bulk of environmental samples holds promise for improving detectability in lichen inventory surveys. Here, we investigate consistency in characterizing lichen communities between independent bulk sampling efforts of minimally trained student technicians and high-throughput sequencing. Students were instructed to collect small lichen fragments representing the range of observed lichen diversity in a narrow limestone canyon on the eastern edge of the Great Basin. One student opted for a detailed, time-intensive approach, spending an estimated 80 hours sampling throughout the site. The other, spent no more than six hours collecting bulk samples. Metagenomic DNA was extracted from the independent bulk samples, and lichen-forming fungal diversity was inferred using Illumina high-throughput sequencing of ITS2 amplicons. Illumina short reads were processed using FROGS, a pipeline for inferring operational taxonomic units, and taxonomic assignments were made with a customized pipeline. Results of the metagenomic sampling approach were compared to a traditional lichen inventory completed in the early 1990s. The bulk sampling-metagenomic inventory captured three times the diversity documented in the traditional, morphology-based survey (190 species vs. 63). We observed high overlap in capturing species-level diversity between the two bulk sampling efforts, with more than 70% similarity despite different sampling strategies. However, only limited overlap in species was observed between the composite bulk sampling lichen inventory and the decades-old, morphology-based inventory. Furthermore, ca. one third of the species-level lineages inferred from metagenomic reads could not be assigned to a known species with confidence. We discuss the implications of our results in consideration of using bulk sampling and metagenomic barcoding for lichen biodiversity research.

Topic: Population Genetics/Genomics

A-861

Genetic Diversity at the Northern Range Edge of U.S. Johnsongrass Populations

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Invasive species negatively affect both agricultural production and ecosystem health, costing millions of dollars in damage and hampering biological diversity. Johnsongrass (*Sorghum halepense* (L.) Pers.) is a polyploid grass known for its invasive nature. Reproducing via both copious amounts of seeds and through aggressively vigorous rhizomes have allowed Johnsongrass to invade and establish in disturbed areas around the world. Introduced into the United States in the early 1800s, Johnsongrass populations in the United States exhibit significant allelic variation, gene flow with crop species, and wide-reaching dispersal, contributing to their success in different climatically diverse regions. The species has expanded across much of the Southeast, the lower Great Plains, parts of the Midwest, Southwest, and California reaching up into Ontario. The northern edge of the range in the United States is likely a strong physiological barrier due to the absence of freezing tolerance in rhizomes, hindering the ability of the species to establish perennial stands. Here, we seek to characterize allelic variation within and among Johnsongrass populations that are found in different climatically diverse regions of the United States, highlighting the difference between the northern edge and the core of the species range. To do this, we sampled 525 individuals from 15 populations across the United States. Seven populations were collected from a latitudinal transect in the northern edge of the range (~40°N), while the remaining populations were collected from a latitudinal transect in center of the range (~34°N). Using low coverage (4x-6x) whole genome shotgun Illumina sequencing, we characterized the genotype likelihoods variation among Johnsongrass populations. Here, our findings demonstrate that Johnsongrass populations differ significantly not only between the two major transects but also within the same transect. Associations with diverse environmental factors (e.g. average annual temperature, precipitation, photoperiod and seasonality) appear linked to diverse populations. Populations at the 40°N transect are distinct from those found at the 34°N transect leading us to posit that this is a consequence of range expansion. Future work is required to characterize specific genes that contribute to the success of populations form the northern edge of the US range. Moreover, the contributions of the polyploid nature of the species and how variation in paralog retention contributes to invasion success will be a topic for future study.

Topic: Macroevolution

A-862

The desert in the rainforest: evolution of epiphytism and succulence traits in epidendroid orchids

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Of all the environments where plants face water scarcity, tropical rainforests may be the last to come to mind. Yet even in rainforests, epiphytic plants can experience intermittent desert-like conditions, due to high irradiance in the canopy, sporadic atmospheric water supply, and the absence of soil to retain the water around the roots, combined with a very low water potential of the bark, strong enough to drain water off the epiphyte's roots. The succulent forms that are widespread in epiphytes are surmised to have evolved as an adaptation to these highly desiccating conditions. However, succulent organs also exist in terrestrial plants, and the question of the concomitant evolution of epiphytism and succulence has received little attention, not even in epidendroid orchids, despite accounting alone for nearly 68% of the recorded 31,311 species of vascular epiphytes. We therefore inferred a new time-calibrated phylogenetic tree of 203 genera of epidendroids and used a Hidden Markov model, corHMM, to test for the correlated evolution of epiphytism with traits related to water scarcity (stem and leaf succulence, as well as the number of root velamen layers that enhance water uptake and prevent water loss) while estimating ancestral states. We identified three major independent evolution of epiphytism, 39.0 million years ago (Mya) in the common ancestor of the Malaxideae and Cymbidieae, 11.5 Mya in the Arethuseae, and 7.1 Mya in the Sobralieae. Stem succulence was inferred to have evolved once, in a terrestrial ancestor of the two oldest epiphytic lineages, thus preceding the emergence of epiphytism by at least 4 My. If lost, stem succulence was almost systematically replaced by leaf succulence in epiphytic

lineages. Epiphytes also tend to have more velamen layers than their terrestrial counterparts. Interestingly, we identified five major events of secondary terrestrialization in which species have mostly retained these ancestral epiphytic features. Our results suggest that the emergence of stem succulence in early terrestrial epidendroids was a key innovation in the evolution of epiphytism rather than an adaptation to epiphytism per se, fa cilitating the colonization of epiphytic environments that later led to the greatest diversification of epiphytic orchids.

Topic: Overcoming the barriers to on-going Castilleja research: From botanical enigma toward an emerging model system

A-863

Conservation genomics and host requirements for Castilleja coccinea, the scarlet paintbrush

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Scarlet paintbrush *(Castilleja coccinea, Orobanchaceae)* is the only widespread species of *Castilleja* in the eastern and midwestern United States. Formerly common, *C. coccinea* has rapidly declined in recent decades. Only two small populations with phenotypic signatures of inbreeding depression remain in Pennsylvania out of 100 historically documented populations. Habitat destruction, climate changes altering the phenology, invasive species, decline in pollinators, and inbreeding depression are among the possible causes of the rapid region-wide decline, even from locations that appear to remain well suited to *Castilleja* growth. Our research aims to address significant gaps in knowledge about habitat requirements, host preference, seed storage and germination best practices, the role of inbreeding/outbreeding, and genetic structure to build a foundation for an informed and comprehensive recovery plan for this species. We performed a population genomic analysis for *C. coccinea* using Genotyping by Sequencing (GBS/ddRADseq) to determine population structure, quantify genetic diversity and inbreeding, and estimate gene flow and effective population size. Sequence data comprised 576 plants representing 21 localities from 14 eastern and midwestern states, with a median of 25 plants per locality. Sampled localities include six sites containing few (< 100) individuals as well as 15 sites with medium to large populations. Reads were mapped to a newly constructed reference genome for *C. coccinea*. Data analyses are in progress, but preliminary results indicate that all samples are of high quality, and reads are mapping well (94-97%) to the *C. coccinea* reference genome. These studies should provide a scientific basis for efforts to enhance genetic diversity and fitness in existing populations and suggest optimum source material for establishing or re-establishing *C. coccinea* populations. Although *C. coccinea* is a generalist hemiparasite with a broad taxonomic range of host species, preliminary evidence suggests that different populations may exhibit specific host preferences, possibly reflecting geographically differentiated ecotypes. To test this, we evaluated the number of haustorial connections in individuals from eastern (Pennsylvania) and western (Missouri and Oklahoma) populations. Plants were grown with hosts from four phylogenetically disparate plant families: Fabaceae, Asteraceae, Poaceae, and Rosaceae, using transparent growth boxes (rhizotrons). Haustorial vascularization was further characterized via microscopy using ink-vinegar vital staining. Our results suggest that aligning host species with local ecotypes may be key for the successful recovery and conservation of *C. coccinea*.

Topic: Pteridology

A-864

Investigating the fossil root(let)s of Isoetes with phylogenetic methods

Author: Meg Nibbelink, Mark Holder
Affiliation: University of Kansas

To those unenlightened to the wonders of lycopods, the humble outward appearance of *Isoetes* may obscure its most captivating feature upon first glance: an enchanting evolutionary history complete with the dramatic collapse of a photosynthetic empire. This lineage, which arose from simple Devonian plants approximately 400 million years ago, eventually swathed the Earth's surface with the vast forests of 'scale trees' emblematic of the Carboniferous (~350MYA). A series of climate change events in the Permian (~280MYA) wreaked havoc on their swampy kingdom, and by the Triassic (~250MYA) the persistence of a lineage that commanded landscapes less than one hundred million years prior is evidenced only from a sparse fossil record for the lineage demonstrating dramatic declines in body size, diversity, and abundance. Further, critical periods in the evolutionary history which gave rise to *Isoetes* today remain obscured by a nonexistent-to-spotty fossil record since the Carboniferous. With this context an observer can now appreciate *Isoetes* as an unassuming living monument to this 400-million-year evolutionary odyssey, evidenced today only by the enigmatic morphology and anatomy of *Isoetes*.

To investigate these remaining questions, we analyzed an amended version of a previously published matrix of Carboniferous isoetalean taxa (Bateman, DiMichele, Phillips 1992), to which we added seven younger species from five genera of this lineage ranging in age from Mesozoic to extant (*Annalepis*, *Pleuromeia, Isoetites, Nathorstiana, Isoetes*) in Mesquite. This matrix was analysed using Bayesian (MrBayes, RevBayes) phylogenetic inference methods to lend probabilistic insight towards explaining *Isoetes'* Mesozoic origins. Similarly, statistical models were employed within this phylogenetic context (phylogenetic comparative methods, 'PCMs') to quantify the details of this timeline. While circumstantial, these methods do not only aim to illuminate our understanding of relationships in the Isoetales through time, but additionally intend to stand as an imperfect example of how the creative employment of modern techniques may provide new insight on historically challenging questions regarding the evolution of plants, and explore the possibilities of modern *Isoetes'* ancestry where the fossil record is unlikely to provide answers anytime soon.

Topic: Ecology

A-865

Macroecology of plant ploidy in the Anthropocene

Author: Connor Wilson, Gabriel Moulatlet, Brian Enquist, Michael Barker
Affiliation: University of Arizona

The effects of polyploidy on plant ecology and evolution have long been of keen interest to botanists. Ledyard Stebbins (1950) and others hypothesized that polyploidy may be a long term evolutionary 'dead end', but also provide a short-term advantage in stressful environments, such as those with extreme temperatures, water limitation, and high seasonality. Over the past few decades, across fields ranging from population genetics, physiology, and biogeography, evidence has been emerging to support this picture. However, few tests of this polyploidy-stress hypothesis have been conducted at the broadest geographical and taxonomic levels. With a novel integration of diverse biodiversity informatics databases, we examine the predictions of this hypothesis at macroecological scales. We show that plant communities tend towards higher proportions of polyploids at greater latitudes and elevations, and in postglacial regions, all of which tend to have more extreme and variable environments. Additionally, polyploids average larger geographic ranges and broader climatic niches than diploids. Finally, we analyze the proportion of polyploid and diploid species represented on the IUCN Red List, finding that polyploids are less likely to be threatened with extinction. Our synthesis is consistent with the polyploidy-stress hypothesis, and provides crucial context for understanding how ploidy will impact species responses to global change.

Topic: Plant phenology in an era of rapid global change: new perspectives and frontiers

A-866

Delayed flowering phenology of red-flowering plants in response to hummingbird migration

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Topic: Comparative Genomics/Transcriptomics

A-867

Plant Mitogenome Heteroplasmy and Assembly

Author: JianJun Jin, Deren Eaton
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Organelle genomes are essential sources of fundamental data for functional, phylogenetic, and evolutionary research. Thus, their accurate and complete assembly is of utmost importance. However, numerous organelle genomes, particularly most plant

mitochondrial genomes, still lack effective means for high-quality resolution. This is due to abundant repetitive sequences, isomers, and subgenomic structures (heteroplasmy). Here, we will discuss the challenges in plant mitogenome assembly, as well as the advantages and limitations of existing tools—including our own Traversome—in addressing these challenges.

Topic: Systematics & Taxonomy

A-868

Field, herbarium, and molecular data reveal Gesneria lanceolata (Gesneriaceae), once thought endemic to Haiti, also occurs in the Dominican Republic

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Affiliation: New College of Florida, Marie Selby Botanical Gardens

Erik Leonard Ekman (1883–1931), a Swedish botanist, made significant contributions to the study of Caribbean flora, particularly in Hispaniola, which includes present-day Haiti and the Dominican Republic. Among his many collections, he discovered and described Gesneria lanceolata (Gesneriaceae) from the Massif de la Selle in Haiti. However, the species description was based entirely on mature fruits and vegetative features, as flowers were not available for study. Until recently, the species was only known from Ekman's type collection in 1927.

Recent fieldwork across both Haiti and the Dominican Republic yielded several Gesneria specimens that were evaluated for resemblance to the type material of Gesneria lanceolata from Haiti. Molecular sequence data were generated from nuclear ribosomal DNA (nrDNA) Internal Transcribed Spacer (ITS) sequences. Using these molecular tools, specimens from Haiti were matched with a population from the Dominican Republic, significantly expanding the species' known geographic range.

These findings expand the distribution of Gesneria lanceolata beyond the type locality in Haiti and underscore the importance of fieldwork, herbarium research, and molecular tools in resolving long-standing taxonomic questions. The results highlight the value of continued botanical exploration in underexplored regions such as the Caribbean.

Topic: Paleobotany

A-869

New fossil wood samples contribute to understanding Late Cretaceous biodiversity and paleoclimate of the Antarctic Peninsula

Author: Abigail Kohn, Selena Smith, Brian Atkinson, Matthew Lamanna
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While there is robust evidence that there were Late Cretaceous forests on the Antarctic Peninsula, these ecosystems have no direct modern analogue. Antarctica was still proximal to South America and Australia, with a unique Gondwanan floral composition, and its high-latitude light regime would have limited photosynthesis for part of the year. Fossils can provide data to better understand the biodiversity, ecology, and evolutionary history of Gondwanan Cretaceous forests. Here, new wood samples collected from Late Cretaceous marine deposits exposed on Seymour Island (López de Bertodano Fm, Maastrichtian), Vega Island (Snow Hill Island Fm, Campanian–Maastrichtian), and James Ross Island (Santa Marta Fm, Campanian) were studied using the cellulose acetate peels and thin sections. Wood traits were recorded and compared with the literature and the InsideWood database. The woods examined range in quality of preservation, with some samples not preserving all features needed for identification, and others with abundant Teredo borings. Nothofagoxylon and Illicioxylon are among the angiosperms represented. Conifers from James Ross Island were examined for functional traits to be used as proxies for ecology (evergreen vs. deciduous) and paleoclimate, including tracheid diameter and Mean Sensitivity (MS) of growth ring width, a measure of a tree's ability to withstand annual variation in climate. Variation in growth ring width produced 2.8x higher MS values than previously observed in comparable taxa. These new values cross the threshold from uniform to fluctuating annual climate variation. This finding could suggest that the Late Cretaceous climate of the Antarctic Peninsula may have had more annual variation than previously thought. By tracing lineages through space and time and evaluating key functional traits, these fossil woods can inform us about the plant biodiversity of these extinct forests and how they responded to their unique environment.

Topic: Systematics & Taxonomy

A-870

"Digitizing Bangladeshi Herbaria: Enhancing Global Collaboration Through GBIF and OpenHerbarium

Author: Tabassum Tamima, Mary Barkworth
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Though Bangladesh is full of plant's biodiversity,the data of herbarium and digitalization of data are limited in global biodiversity databases. Our project finds the gap of not sharing data of Bangladesh on global biodiversity facilities(GBIF). This projects aims to present the importance of sharing data by using Open Harbarium (OH) and GBIF from Bangladesh herbaria. We got 19 image data of Sylhet division from Bangladesh National Herbarium (DACB) and updated information on OH. We created checklist of bryophyta and tracheophyta from online published work by Bangladeshi Botanist and, added over 35,000 occurrence records to OH from GBIF. Of the uploaded records, 47% included geographic coordinates but very few provided information for the uncertainty or datum. OH offeres different tools like lebel printing, checklist, map making.Herbarium digitization can greatly increase the use of herbarium collections, but it is difficult to document that use. The combination of OpenHerbarium, GBIF and Bionomia can help with this. By this project, the Bangladeshi botanist will going to notify and learn the inportance of data sharing and,also those people who are interested to work with biodiversity of Bangladesh.

Topic: Conservation Biology

A-871

Using botanic gardens to assess hybridization events in ex-situ collections of cycads

Author: Stephan Girard
Affiliation: Chicago Botanic Garden

The collections curated by botanic gardens play a pivotal role in safeguarding rare, endemic, and exceptional plant species from extinction. If these collections are to continue to play such a large role in future conservation and reintroduction efforts, they must be managed to maintain the genetic diversity of founding plants, minimize inbreeding, and avoid hybridization. Currently the risk of hybridization in ex-situ collections has not been heavily investigated, however, in bringing a large number of taxa into a small location where geographic and reproductive barriers are removed, it is likely to promote hybridization events. Cycads are one of the most threatened plant groups in the world and are difficult to conserve due to long life stages and being exceptional species whos seeds cannot be stored long term. Therefore, botanic gardens are increasingly bringing cycads into ex-situ conservatoin efforts along with increased protections against poaching. While the risk of interspecific hybridization in this group has historically been considered low due to haveing species specifc obligate pollinators, recent observations by curators suggest this may not be the case in some ex-situ collections. Understanding if interspecific hybridization is occuring in ex-situ collections is critical for conservation of rare species. In this study I investigated this laregly unexplored phenomena in ex-situ cycad collections with the hypothesis that cycad pollinators may be more opportunistic than specific, cross-pollination events between species is happening and creating viable hybrid seeds. I tested this by creating a genetic database of individuals from the two largest cycad collections in the U.S., gathering genetic material from leaves of putative parental species (52 Encephalartos, 18 Dioon, 25 Zamia) along with naturally pollinated seedling and volunteer seedlings (60 individuals). I generated genetic information using next-generation target enrichment HybSeq sequencing and used the flagellant plant specific GoFlag bait set. I used the HybPiper pipeline for de-novo sequence assembyl and HybPhaser to phase sequences to investigate potential hybridization events. These sequences were also used to create phylogeneies using Astral and IQtree to infer evolutionary distances between the putative parental species of potential hybrids. My results show a distinctive clade of offspring that show many signs of being hybrids created via natural pollination. The results from this study will provide essential information for ex-situ cycad collection management practices, and can possibly extend to any ex-situ conservation collection managing rare taxa that may be prone to hybridization.

Topic: *Development and Structure*

A-872

Floral color evolution in Penstemon

Author: Haylee Coffman
Affiliation: University of Kansas

Floral color is a hugely important determinant in pollination syndrome in angiosperms. Hue is widely known to play a major role in pollination syndrome; however, independent of hue, brightness, caused predominantly by flower pigment intensity, is another critical determinant in pollination syndrome. This is because brightness highly impact's a flower's conspicuousness against a foliage background, especially for pollinators who see in in the UV spectrum, such as bees. Flowers of hummingbird-adapted species can show brighter flowers with more pigment intensity than bee-adapted species, independent of hue and this trend holds especially true across independent evolutionary origins of hummingbird-adaptation in the genus *Penstemon*. Using a cross derived from bee-adapted *P. amphorellae* and hummingbird-adapted *P. kunthii,* I aim to explore the genetic basis of pigment intensity differences in these species by identifying how the anthocyanin pathway is different and where causal variants for pigment intensity differences may reside in the genome. This work is highly facilitated by a well-established set of specific candidate genes for regulation and production of anthocyanin pigments.

Topic: *Phytochemical*

A-873

Enzyme expression and metabolomics in the carnivorous plant Drosera capensis

Author: Zane Long, Gemma Takahashi, Carter Butts, Rachel Martin
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Drosera capensis L. is a carnivorous plant that traps its prey in sticky mucilage. Its feeding response is induced by the small molecule jasmonic acid, a plant defense hormone. Here, we use RNA-seq to measure differential expression of enzymes related to digestion and untargeted LC-MS metabolomics to identify molecular changes in D. capensis leaves in response to feeding and jasmonic acid treatment. We treated unfed D. capensis leaves with jasmonic acid to induce the feeding response, while monitoring the transcriptional regulation of proteins. Jasmonic acid treatment induces upregulation of proteases and other digestive enzymes, in addition to proteins associated with cell wall remodeling. At the same time, other cellular housekeeping proteins are downregulated. We also ran a comparative untargeted liquid chromatography//tandem mass spectrometry (LC-MS/MS) metabolomics experiment, measuring the relative abundances of observable small molecules in response to jasmonic acid treatment as well as feeding with insect prey. We find that the levels of some free amino acids increased during carnivory, whereas others are consumed immediately. Treatment with jasmonic acid and the introduction of prey also resulted in increased production of diverse lipids and other signaling molecules, along with potentially defensive compounds. These results will be discussed in terms of implications for understanding D. capensis metabolism and nutrient use from prey, as well as the potential for useful antimicrobial compounds and enzymes for use in chemical biology laboratories.

Topic: *Education and Outreach*

A-874

Tree of Heaven (Ailanthus altissima) range expansion and control

Author: Maegan Tikiryan, Heather Townsend
Affiliation: Community College of Rhode Island

Ailanthus altissima, commonly known as the Tree of Heaven, is an invasive species native to China and Taiwan that has spread rapidly across North America and other regions. This project investigated the ecological impact, spread patterns, and management strategies associated with *Ailanthus altissima*. This poster focuses on the tree's ability to outcompete native flora through its rapid growth, seed production, and tolerance to various environmental conditions. Data collected from field observations, research, and soil biodiversity assessments reveal the negative effects of *Ailanthus altissima* on our local ecosystems, including reduced plant diversity and soil degradation. Furthermore, this Course-based Undergraduate Research Experience (CURE) project explored various control methods, including chemical treatments, mechanical removal, and biological control, to assess their effectiveness and long-term viability. Our findings suggest that while complete eradication may be challenging and next to impossible, strategies such as a combination of the above methods, can help mitigate the tree's impact and promote the recovery of native plant species. This research contributes to the understanding of invasive plant management and provides valuable insights into maintaining ecological balance in affected areas.

This research was conducted as a CURE developed by the Biological Collections in Ecology and Evolution Network (BCEENET). BCEENET CUREs use digitized natural history collections data and free open source tools to increase accessibility to undergraduate research opportunities while also participating in innovative research.

Topic: *Phylogenomics*

A-875

Phylogenetic Network Analysis Comparing Evolution of Primary and Specialized Metabolism Across the Genus Botrytis

Author: Lori Pradhan, Jordan Dowell
Affiliation: Louisiana State University

The genus Botrytis consists of over 35 necrotrophic fungal plant pathogen species that cause great economic impact to both the agricultural and floricultural industries. Variations in host preference across these species are not well established in the literature beyond broad separations of species into a clade of eudicot generalists and another of monocot specialists. Using a comparative genomics approach, we found about 5000 orthologous single-copy protein-coding genes across the genus. Prior evidence for incomplete lineage sorting across the genus indicates the potential for gene tree discordance. Primary metabolic genes associated with growth and reproduction and specialized metabolic genes that mediate host-pathogen interactions can influence the spread and virulence, respectively, of a fungal pathogen. Comparing the evolutionary histories of primary and specialized metabolic genes will allow us to identify correlations between host range diversification and the evolution of specific metabolic pathways across the genus. Our results serve to assess the potential impact of incomplete lineage sorting on the divergence of primary and specialized metabolic diversity.

Topic: *Reproductive Processes*

A-876

Winter Drought Dynamics: Understanding the Reproductive System of Phlox divaricata

Author: Mohamed Abdulsattar, Franceska Isufaj, Kyra Krakos
Affiliation: Maryville University

Climate and environmental factors, like drought winters, can influence a plant's morphology, reproductive systems, and how it attracts pollinators. In this study, we examined the effects of drought winters on the morphology and pollination system of *Phlox divaricata*, a self-incompatible perennial wildflower found in the Missouri woodlands. Using data collected from 2014-2024 at Shaw Nature Reserve, we investigated: (1) the occurrence of drought winters, (2) the impact of drought on plant morphology, (3) changes in pollination systems during drought years, (4) the relationship between display size and pollinator visitation, and (5) the presence of pollen limitation during drought and non-drought years. Our data showed that Shaw Nature Reserve experienced drought winters in 2023 and 2024. There was no statistical difference in plant morphology, meaning a change in height, floral display, and corolla span between drought and non-drought years. Pollination systems on the other hand, did have a shift during drought years, with mid-sized pollinators such as *Apis mellifera* and *Lepidoptera* dominating, while during non-drought years, we saw a higher activity from smaller pollinators like syrphids and halictid bees. Even though we did see a change in some pollinators, there was no evidence of pollen limitation in either drought or non-drought years. There was also no correlation found between floral display size and pollinator visitation rates. Our findings suggest that *Phlox divaricata* is a robust native species with a flexible, generalist pollination system that ensures reproductive success under varying environmental conditions. This resilience highlights its potential to positively impact ecosystems that are experiencing climate change. Future research could explore how this wildflower can help sustain pollinator diversity in times of environmental stress.

Topic: *Ecology*

A-877

A comparative study of the reproductive biology of Asclepias syriaca in urban vs rural populations

Author: Ibrahim Ahmed, Franceska Isufaj, Rida Sait, Kyra Krakos
Affiliation: Maryville University

Habitat fragmentation as a consequence of urbanization has the potential to impact reproductive success of plant species. In this study, differences in plant reproductive success were compared between urban and rural populations of native plant species *Asclepias syriaca* for two years. Plant morphology, pollination systems, and soil pH were measured in order to determine any significant differences between the populations of *A. syriaca* located at Shaw Nature Reserve and Litzsinger ecology center We also conducted experiments to determine if there was pollen limitation. Our results show that Litzsinger is more acidic than soil at Shaw in both 2022 and 2023. In 2022, on average *A. syriaca* was taller at Litzsinger, but had fewer umbels and smaller corolla span compared to the population at Shaw, whereas in 2023 *A. syriaca* at Shaw had larger umbel and corolla spans. *Bombus* was the primary pollinator at both locations. There was no pollen limitation in either population in any year, which indicates this species is reproductively successful. *A. syriaca*'s robustness in reproductive success regardless of differences in urbanization indicates its potential as a resource for pollinator conservation efforts.

Topic: *Biodiversity Informatics & Herbarium Digitization*

A-878

A Novel Framework for Evolutionary Analysis of 3D Morphometrics: Insights into Convergent Floral Evolution in Pedicularis

Author: JianJun Jin, Yue Yang, Nina Kornfeld, Deren Eaton
Affiliation: New York Botanical Garden, Columbia University

Floral morphology holds significant importance across multiple disciplines, including taxonomy, evolution, and pollination ecology. However, traditional methods of measuring live, pressed, or digitally imaged specimens often fail to comprehensively capture floral morphology. When preparing specimens, flowers are prone to losing variations and covariances in complex traits, particularly those related to 3D structure.

To overcome these limitations, colored 3D morphometric modeling has emerged as a powerful technique for preserving and analyzing flower morphology. For the past three decades, Generalized Procrustes Analysis (GPA) has been the dominant approach in landmark - based geomorphometrics. Although GPA is statistically robust, it has a tendency to oversimplify the complexity of biological models. This oversimplification can result in misinterpretations of morphological variations at local scales.

In this study, we present a novel framework designed to address the limitations of GPA in the evolutionary analysis of 3D morphologies. Our method employs weighted relative vectors for geomorphometric analysis, offering a more biologically realistic view of shape variations. By generating a relative vector set for each point and assigning weights according to phylogenetic variances, our approach effectively captures local changes, circumventing the global adjustments characteristic of GPA.

We validate the effectiveness of this framework through both simulated experiments and empirical studies of Pedicularis flowers. The genus Pedicularis exhibits remarkable diversity in floral shape. Our results demonstrate that this vector - based method improves the accuracy of ancestral 3D reconstructions. It also shows the potential for interpretable results regarding morphological disparity and shape modularity. This research contributes a valuable tool to studying morphological trait evolution, especially in the context of complex 3D structures. Additionally, it offers new insights into the convergent floral evolution within the Pedicularis genus.

Topic: *Conservation Biology*

A-879

Genomic and morphological evidence clarifies species boundaries in Utah endemic Astragalus species

Author: Richie Hodel, Ava Brinkley
Affiliation: Northern Arizona University

The genus *Astragalus*, with over 3,000 accepted species, is the largest genus of flowering plants and a powerful model for investigating evolutionary dynamics in morphologically complex and rapidly radiating groups. In the Intermountain West of the United States, *Neo-Astragalus* lineages exhibit exceptional species diversity, frequent morphological convergence, and many species are of significant conservation concern.

Here, we examine two closely related and morphologically similar taxa—*Astragalus loanus* and *Astragalus welshii*—both endemic to volcanic substrates of central Utah. These species have historically posed challenges to taxonomic resolution due to overlapping morphological traits and a lack of molecular data. We integrate traditional morphological analyses with double-digest RADseq (ddRAD) data to address four key objectives: (1) characterize morphological variation, (2) generate the first intraspecific genomic-scale data for both species, (3) assess phylogenetic relationships within and between each taxon, and (4) inform conservation status and priorities.

Our results support the recognition of *A. loanus* and *A. welshii* as distinct evolutionary lineages. Despite morphological similarity and substantial geographic overlap, they follow independent evolutionary trajectories. Importantly, the clarified taxonomic boundaries reveal a narrower distribution for *A. loanus*, elevating its conservation urgency due to limited range and potential habitat threats.

This work demonstrates the value of integrative approaches—combining genomic and morphological data—to resolve species boundaries in challenging plant groups. Our findings also underscore the importance of accurate taxonomy in guiding conservation strategies for rare and endemic taxa in biodiversity hotspots like the Intermountain West.

Topic: *Reproductive Processes*

A-880

Does Drought Matter? A comparative study of the reproductive biology of Melanthium virginicum in rural vs. urban populations.

Author: Ahmad Kaziz, Franceska Isufaj, Kyra Krakos
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A rural or urban environment coupled with the effects of a drought-winter can negatively impact the reproductive success of a plant population. Abiotic differences such as soil pH can result in morphological differences. Plant morphology such as height and display size can impact pollinator visitation rates for the flower. Differences in habitat including drought winters can negatively impact the reproductive success of the plant. In this study we examined the effect of an urban or rural habitat and a drought-winter on the reproductive success of the native flower *Melanthium virginicum*. Our studies took place in two populations of *M. virginicum*; a rural population at Shaw Nature Reserve, in Gray Summit Missouri, and an urban population at Litzsinger Ecology Center, in Ladue, Missouri. We sampled the pH of the soil at both sites and morphological traits were measured alongside pollinator observations. Open and supplemental hand treatments were performed, and fluorescent microscopy was used to determine pollen limitation. Despite previous studies finding otherwise, our data found no pollen limitation across habitats or growing seasons. However, during 2023, a drought winter, there was a noticeable drop in the number of pollen tubes compared to previous years. Many factors could have caused this including a drop in soil pH or a shift in main pollinator from beetle to halictid seen in drought years. This robustness in a prairie native suggests it could be useful in conservation of pollinator resources. Further studies are needed to look at *M. virginicum's* role in a broader ecosystem.

Topic: *Phylogenomics*

A-881

Updates on a drought-driven hypothesis for the origin of obligate apomixis in ferns

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Just as tropical rainforests are a surprising environment in which to find a cactus, ferns thriving in deserts are unexpected because they usually depend on water for sexual reproduction. Consequently, many desert ferns reproduce asexually via obligate apomixis, which involves two distinct modifications to the typical, sexual life cycle: the production of unreduced diplospores via meiosis (diplospory), and the apogamous development of a new sporophyte from somatic gametophyte tissue. Apomixis is widespread in desert ferns, and water limitation has been proposed as a primary driver of the transition to apomixis. However, apomixis is not restricted to desert-adapted ferns. Is this syndrome most likely to evolve in xeric habitats, or is its distribution shaped by shared ancestry? Using the GoFlag nuclear target probe set and plastid genome skimming, coupled with cytogenetics and trait surveys, this study aims to infer the phylogenetic relationships of all taxa in the genus, including unique combinations of ploidy levels and reproductive modes within *Myriopteris* Fée (Pteridaceae). We also estimate the ancestral reproductive syndromes, the phylogenetic signal, and the correlated evolution of reproductive traits with abiotic environment (e.g., temperature, substrate composition, and water availability), and we implement hidden-state State Speciation and Extinction (SSE) models to assess the impact of life history traits on diversification rates.

Topic: *Ecology*

A-882

How does grazing management affect plant communities on North Texas Rangelands?

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Grasslands are being degraded by threats such as urbanization, climate change, and overgrazing. These anthropogenic factors have caused the loss of 99% of tallgrass prairies, leaving less than one percent intact. Among the remaining grasslands, rangelands are managed through livestock grazing and have the potential to provide habitat to diverse plants. Grazing disturbances can alter plant communities because of different plant species' tolerances to environmental conditions. In addition, different species of grazers (e.g., cows and sheep) preferentially remove certain plants. These plant community changes may be partly due to trait differences among plant species. Plant communities are made up of species that consist of different life history and morphological traits. These trait differences contribute to species' ability to persist in disturbed communities. To understand how plant communities are shifting in response to grazers we asked how traits mediate plant community responses to grazing.

We investigated how different grazing management strategies affect plant communities. Our focal grazing management strategies include continuous grazing (no rotation), low-intensity rotational grazing (livestock rotated among pastures every two or more weeks as vegetation depletes), and high-intensity rotational grazing (livestock moved every few days among smaller pastures). We asked two questions. (1) How does the plant community shift under different grazing management strategies? (2) Are specific plant traits mediating plant community shifts? We focused on plant life history and morphological traits obtained from the TRY database: plant life form, plant lifespan, plant reproductive phenology, leaf type, flower color, and inflorescence type. We measured plant species' presence and flower abundance at 19 rangeland sites with largely native vegetation across North Texas in the summers of 2023 and 2024. Our results will show how plant communities respond to grazing, and whether management can help prevent further grassland degradation. Analyses of community responses can help landowners understand how their land management affects which forb species are available to their livestock as forage.

Topic: *Comparative Genomics/Transcriptomics*

A-885

Traversome: a graph-based likelihood model for pangenome assembly and variant relative frequency estimation from mosaic samples

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Variation among multiple related genomes is commonly represented in the form of a pangenome graph, a data structure constructed from multiple genomes that are first assembled individually. A related but more challenging problem involves the inverse processing of multi-genome data: disentangling distinct genomes from a mosaic DNA sample. A bulk DNA sample can exhibit mosaicism for several reasons, ranging from mutational variation among cells within a single multicellular individual, to variation among multiple genomes pooled together from two or more multicellular, unicellular, or acellular individuals. An assembly graph constructed from bulk genome data, depicting the connections between contigs, often harbors ambiguity regarding the scaffolding of these contigs, stemming from both repetitive sequences within individual variants and mosaicism across variants. Consequently, disentangling the graph to isolate each genome individually emerges as the primary challenge in genome assembly. Current genome assemblers typically collapse mosaic variants into one or two best estimates, resulting in either chimeric assembly errors or the loss of low frequency variants. Here, we introduce an alternative approach that enables disentangling and assembling multiple genomes from a mosaic DNA sample separately and estimating their relative frequencies. We derive a new likelihood framework for comparing genome variant sets assembled from mosaic DNA samples based on the distribution of traversal paths of long reads mapped to an assembly graph, with mapping positions modeled as multiple multinomial probability densities. Our approach is implemented in the new pangenome assembly tool Traversome. We demonstrate Traversome using both simulated mosaic DNA samples as well as empirical datasets from organelles of plants. Traversome exhibits similar accuracy to other assemblers in the absence of mosaicism, but greater accuracy when genome variants are present. By treating DNA mosaicism as a default expectation, Traversome transforms genome assembly into a pangenome assembly process. Our tool and novel graph-based likelihood algorithm provide a major advance for identifying and analyzing chromosome-scale genome variants.

Topic: *Ecophysiology*

A-886

Leaf Functional Trait Variation in Arctostaphylos (Manzanita) Species: Does Habitat Diversity Lead to Greater Leaf Physiological Diversity?

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Manzanitas (Arctostaphylos species), with their twisting branches covered in reddish bark and clusters of urn-shaped flowers, are some of the most recognizable and enigmatic shrubs and trees of the chaparral habitats throughout the California Floristic Province. The majority of Arctostaphylos species are narrow endemics found in the coastal regions of central and northern California, and relatively few manzanitas are widespread. One of those few widespread manzanita species, Arctostaphylos glauc a (Big berry manzanita), occurs mainly in chaparral areas but also in other habitat types, including maritime coastal and montane environments. It also has a population in the Mojave Desert, which is an atypical environment for manzanita species and regularly experiences extreme drought and heat in the summer months. This desert population is at the eastern edge of the range of A. glauca, and as an edge-of-range population, may represent the adaptive limit of the species. Understanding such limitations is critical for predicting how populations and species will likely respond to changes in weather patterns, particularly increases in frequency and severity of drought and heat extremes. Adaptations to the local environment can be reflected in leaf functional traits (LFTs), several of which are associated with drought tolerance. We measured and compared several LFTs in the A. glauca desert population to those of a coastal population and multiple populations from its typical chaparral habitat to determine if there are significant differences that may indicate adaptation to local conditions. We also compared LFTs of A. glauca to 11 narrow endemic species across a latitudinal gradient in California to determine if there are differences in averages and variation in those traits between a widespread species with populations in various habitat types and species with a very

restricted range in a single habitat type. We hypothesize that 1. A. glauca overall will show greater variation in LFTs, reflecting response to local conditions, and 2. individual populations of A. glauca will show similar levels of variation in LFTs as narrow endemic species. These analyses offer insight into the potential limitations of drought adaptation within the genus and provide critical information for effective conservation strategies.

Topic: Biodiversity Informatics & Herbarium Digitization

A-887

iNaturalist-facilitated insights into Monarda (Lamiaceae): M. mexicana rediscovery and mapping floral color of M. fistulosa

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Monarda, a small genus in the mint family (Lamiaceae), is endemic to North America and culturally significant, yet its diversity remains relatively understudied. Recent taxonomic revisions, absence of a species-level phylogeny, and evidence of ongoing hybridization complicate our understanding of its evolutionary history and biology. Here, we present two vignettes demonstrating how community science data from iNaturalist can enrich our understanding of Monarda. First, we highlight the rediscovery of *Monarda mexicana*, a species initially described from a single historical specimen in the early 1900s but later synonymized under *M. citriodora* var. *austromontana*. A recent iNaturalist observation prompted further field investigations, leading to the discovery of two present-day populations. Second, we investigate geographic patterns in floral pigmentation within the widespread species *Monarda fistulosa*, finding that the western variety, *M. fistulosa* var. *menthifolia*, exhibits significantly deeper purple flowers than eastern varieties. To conduct this analysis, we developed a novel computational pipeline capable of filtering observations for flowers and extracting flower-specific pixel color data. Collectively, our findings underscore the value of broad community participation in advancing our knowledge of biodiversity and natural history.

Topic: Symbioses: Plant, Animal, and Microbe Interactions

A-888

Host and Hemiparasitic Plant Dynamics with Mycorrhizal Associations

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There are 4,000 species, 270 genera, and 20 families of parasitic plants found across most major biomes (Press and Phoenix, 2005). Parasitic plants support species diversity as keystone species and modulate resource availability in environments as ecosystem engineers (Press and Phoenix, 2005). Hemiparasitic plants, partially parasitic plants retaining the ability to photosynthesize, are not dependent upon a host plant for growth and survival (Hodzic et al., 2022). Hemiparasites have been observed as a keystone species by improving species populations across four trophic levels (Hartley et al., 2015). In North America, where hemiparasites are understudied, grassland ecosystems harboring parasitic species like Agalinis auriculata are conservation priorities due to historical land use and anthropogenic disturbances degrading these habitats (Alexander et al., 2018). Global climate change decreases ecosystem biodiversity yet the presence of Agalinis auriculata increases plant diversity and stabilizes grassland communities, thus it is now utilized in restoration practices (Alexander et al., 2018). Researching the positive effects of hemiparasites in grassland communities would grow our understanding of plant community ecology and conservation (Press and Phoenix, 2005., Hodzic et al., 2022).

Understanding the impacts of hemiparasitic plants is incomplete without studying belowground interactions (Brundrett, 2002). Herbaceous species in grassland ecosystems coevolved with arbuscular mycorrhizal fungi (AMF) (Brundrett, 2002). Researching the above and belowground interactions of hemiparasites, mycorrhizae, and their host plants is imperative for restoration and community ecology (Li and Guan, 2008). Despite its vital role in ecosystems, above and belowground interactions of Agalinis have not been studied to date. Our study will provide the first assessment of how hemiparasitic Agalinis influences the above and below ground dynamics of their hosts with and without mycorrhizal associations.

To assess these dynamics, seeds from Agalinis purpurea and Heterotheca subaxillaris (host plant) were collected from south Georgia in 2025. Agalinis purpurea will be grown with Heterotheca subaxillaris in pots for six weeks. The treatments are hemiparasite, hemiparasite-host, or host and live or sterilized soil inoculation with AMF, fully crossed, resulting in six treatment combinations. We will have 12 replicates of each treatment with a total of 72 pots. During the growth phase, height and number of leaves will be collected weekly. Following the growth phase of six weeks, the parasite-host complex will be dug up, cleaned, and cross sections of the roots will be taken. A subset of roots will be stained and mounted to observe the arbuscular mycorrhizal fungi presence on the roots of Heterotheca subaxillaris and Agalinis purpurea. Another subset of roots and soil samples will be taken for root nutrient analysis and soil chemistry tests. Above and below ground biomass will be weighed and proxy cross sections of roots will be taken to account for below ground biomass lost for the microscopy and the root nutrient analysis test.

Topic: Biogeography

A-889

Climatic rarity and parallel niche shifts underlie variable patterns of range size in Clarkia polyploids

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Polyploidy has been hypothesized to enhance the capacity for adaptation to novel environments and lead to larger geographic ranges than related diploids. However, evidence for these hypotheses is mixed. An alternative hypothesis suggests that polyploidy causes predictable niche shifts (due to the physiological consequences of a larger genome) but the consequences for range size depend upon how widespread the newly-invaded habitat is relative to that of the diploid progenitors. In this study, we use the genus *Clarkia* (Onagraceae), a putative example of polyploidy increasing range size, to test for evidence of consistent niche shifts and whether changes in range size are associated with changes in habitat rarity. In contrast to polyploidy increasing range size, we find that polyploids typically have smaller and more environmentally homogenous ranges than progenitors. For the few polyploids with large ranges, range size increase was associated with invading a geographically common environment. Whether polyploid range sizes were larger or smaller than progenitors, polyploids typically shifted their niche towards environments buffered from drought extremes. Our results highlight that while increased genome size may cause polyploids to shift their niche away from progenitors in similar ways, whether this shift is associated with range size increase or decrease is partly predicted by the rarity of suitable habitat.

Topic: Conservation Biology

A-890

Mining for the Renewable Energy Transition Threatens Endemic Plant Diversity: A Global Review and a Case Study in Western North America

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Transportation is the largest source of carbon emission in the United States, making this sector critical to decarbonization of our energy systems and reducing the impact of the climate crisis. As we work to achieve zero emissions, some amount of mining of so-called energy transition minerals (e.g. lithium, nickel and cobalt) will be needed to supply batteries, such as those found in electric vehicles. Yet mining poses a significant threat to biodiversity, including plant species endemic to soils rich in transition minerals. In D.R. Congo over 500 species of plants grow on soils rich in cobalt and copper, 70% of which are endemic and threatened by habitat destruction from mining. In New Caledonia, nickel mining threatens plant species that display the remarkable adaptation of hyperaccumulating the metal. This association has resulted in the exploitation of these plants as indicators for new mining territories. Lithium mining threatens plants endemic to salt flats of the Atacama Desert in Chile and their related counterparts in the Great Basin Desert in the U.S. A lithium mine affected plant species, *Eriogonum tiehmii* (Tiehm's buckwheat) is a low-growing, mat-forming perennial in the Polygonaceae (buckwheat family) whose global range is included with the approved Rhyolite Ridge Lithium-Boron Project boundary. The direct and indirect impacts of mining are of such magnitude, and taken in combination with other documented threats (e.g. competition with invasive species, dust deposition, impact to pollinator communities and co-occurring native plant species), that the Project leaves *Eriogonum tiehmii* in danger of extinction throughout all of its range. Despite being listed as an endangered species

under the U.S. Endangered Species Act, the project was approved by the Bureau of Land Management. In this presentation I will provide a review of global threats to plant diversity from the mining of transition minerals, including a case study to conserve and protect *Eriogonum tiehmii* in western North America.

Topic: Common gardens in the 21st Century: the intersection between evolution and ecology, science and management

A-891

Common garden studies of a California endemic oak, Quercus lobata, reveal genetic differences among populations in climate-associated traits and maladaptation to current and future climates

Author: Victoria Sork, Alexander Goetz
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Adaptation is a major evolutionary concept. An adaptation is a genetically-based phenotype that enhances survival, growth, and reproduction. Adaptation is also a process by which individuals become adapted to their local environment and is measured by how well individuals grow in their local environment versus a foreign environment. Common gardens have a long tradition in plant ecology, evolutionary biology, and forestry as a tool to test genetic differences in traits and to measure fitness differences among individuals sampled across a species' range. Both types of information can be useful in identifying which local populations possess traits or fitness characteristics that will allow them to persist under future climate conditions. In California, rapid climate warming combined with increased fire frequency create urgency to develop strategies for management and restorationof tree populations. The overarching goal of this talk is to use the findings of a long-term provenance study of valley oak (*Quercus lobata*), a foundational and iconic oak of California ecosystems, to demonstrate how climate-associated adaptive phenotypes and extent of adaptation as measured by fitness traits can inform restoration practices. In 2012, we sent field workers throughout the heterogeneous landscapes of California to collect over 11,000 acorns from 672 trees ('families') and 95 localities that were germinated and planted into two common gardens administered by the USDA Forest Service in Chico and Placerville, CA. Using a quantitative genetic design, we found significant genetic differences in several morphological and physiological leaf traits in progeny of families sourced from differing climates. In addition, using data from 5- and 12-year-old trees, we modeled growth rates and performance (measured as height * survival), and found that these trees perform best at temperatures significantly cooler than where they were sourced. In other words, current populations are maladapted to today's climate, raising concern about what will happen to populations as their environments further warm. We utilize information about adaptation and maladaptation to test three seed source strategies for planting oaks: local seed sources, seed sources from matching climates, and empirically derived climate-adapted seed sources. In one study, the use of genomic information associated with growth in warmer climates reveals that climate-adapted seed sources will produce better-growing trees under predicted warmer climates. In a second study, the use of climate-adapted phenotypes based on the provenance study findings will produce better-growing genotypes. Finally, we discuss how common gardens can be used to validate the use of landscape genomic tools as proxies for identifying regions of maladaptation and seed sources for restoration. We conclude that long-term, and even short-term common garden experiments, when possible, will provide valuable information to mitigate potential maladaptation to current and future climate, especially in a climatically heterogeneous region like California.

Topic: Macroevolution

A-892

An updated diversification history of Andean bellflowers (Campanulaceae)

Author: Laura Lagomarsino, Katherin Arango-Gómez, Rosana Zenil-Ferguson, Leilani Cielito
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Building on past research, we present an updated understanding of macroevolution of Andean bellflowers in relation to biogeography, pollinators, seed dispersers and habitat heterogeneity across the Neotropics. We highlight both development of new diversification models and training opportunities this research has presented.

Topic: Education and Outreach

A-893

Build A Plant: A free educational video series covering the basics of plant anatomy

Author: Joyce Onyenedum, Zachary Kozma, Molly Edwards
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Plant anatomy is a foundational discipline that provides the terminology and developmental framework to understand plant diversity. Yet in the age of "big data" and molecular biology, the field is in decline: research opportunities are shrinking, and few U.S. institutions still offer plant anatomy courses. As Dr. Katherine Esau (1991) once warned, "People who go through such a course eventually will not know what a plant is like, since they see so little of the plant… they don't even see what comes from the plant". Two central challenges hinder the training of new anatomists: (1) anatomical methods are time-intensive and yield small datasets relative to molecular biology, but the insights they provide are irreplaceable; and (2) plant anatomy is often taught through static, decontextualized images, making the subject appear abstract and disengaged from real plants. We present *Build A Plant*, a free, college-level educational video series designed to re-energize the teaching of plant anatomy by highlighting its relevance to development, evolution, and structure-function relationships. The first four episodes cover roots, primary growth, secondary growth, and leaves, using a mix of live plant footage, lab-based dissections, and microscopy to make plant anatomy tangible and dynamic. Modeled after cooking shows, *Build A Plant* doesn't just show the final product (e.g., roots)—it walks viewers through how it's developmentally constructed (e.g., meristems, tissues). By bridging traditional anatomical training with digital pedagogy, we aim to support students, educators, and researchers in reclaiming anatomy's central role in plant biology.

Topic: Biodiversity Informatics & Herbarium Digitization

A-894

Herbarium specimens as a tool to assess the genomic and environmental drivers of phenotype in the Prunus serotina (black cherry) species complex

Author: Richie Hodel
Affiliation: Northern Arizona University

The phenotypes of organisms have been used for centuries to quantify biodiversity in museum collections, and represent the primary tool early naturalists used to study evolution. Phenotypes are the targets of natural selection and directly influence an organism's survival and success in variable environments. To understand patterns of biodiversity, both genomic and phenotypic variation must be considered, as each contributes to species diversification. Yet, the interplay between genotype, environment, and phenotype is complex and often difficult to disentangle. In the era of genomics and big data, we can now readily generate genomic and environmental data from field-collected and herbarium specimens to study genetic variation across environmental gradients. However, scalable methods for capturing phenotypic data remain limited. Recent advances in computer vision and machine learning offer promising tools for extracting high-throughput phenotypic data from digitized biological images, including herbarium specimens.

The black cherry (*Prunus serotina*) tree species complex occupies a variety of environmental conditions across its wide native range in North and Central America. Within the species complex, there are five named subspecies that have distinct morphological features, such as leaf shape, size, margin, and texture. Previous genetic investigations indicate some differentiation among subspecies, but genome-scale data are needed to resolve genetic relationships within and among subspecies. Here, using herbarium specimens from the US collections, I aim to explicitly connect genotypic, phenotypic, and environmental big data sets to determine how the phenotypic characters observed on herbarium sheets may have arisen via ineteractions between the genome and environment.

Using nuclear loci and SNPs generated via Hyb-Seq, I assess genomic variation among herbarium specimens of Prunus serotina collected across the U.S., Mexico, and Central America. Environmental data are derived from bioclimatic variables linked to each specimen's georeferenced coordinates. To capture phenotypic variation, I extract leaf traits directly from digitized herbarium sheets using the machine learning tool LeafMachine2. This integrative approach has the potential to transform how phenotypic data are captured from herbarium specimens and to greatly expand the scale of trait data available for studies of morphological evolution and biodiversity.

Topic: *Ecology*

A-895

Pollinator Behavior of a Natural Highbush Blueberry Hybrid Zone

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With ~88% of flowering plants pollinated by animals, the interactions between plants and pollinators are intrinsically linked to the maintenance of biodiversity. Unfortunately, global pollinator populations continue to decline, especially for native bees, making research on factors that alter interactions important for future conservation efforts. Natural plant hybridization, or the cross between species, can produce plants with unique or variable traits due to an increase in genetic variation. These traits may differ from the parent species in terms of resource provision or attractiveness, potentially altering plant-pollinator interactions in ways that may benefit or compromise pollinator population health. Unfortunately, very little research attempts to understand the influence of natural hybrid plants on pollinator behavior and vice versa. This project investigates the pollinator behavior of a wild highbush blueberry hybrid, *Vaccinium* × *marianum*, in relation to its native parent species, *Vaccinium fuscatum* and *Vaccinium formosum*. We hypothesize that hybrids provide an additional resource to pollinators or that hybrids attract a diverse set of pollinators compared to the parents. The project was conducted at Grafton Ponds Natural Area Preserve, a vernal pool system in eastern Virginia. Highbush blueberry individuals (15 for each taxon) were monitored from February to May to document floral bud development and phenology. During flowering, 54 hours of pollinator interactions with hybrid and parental plants (18 hours per taxa) were filmed. From the videos, floral visitors were identified, and the number of visitations and length of time spent on a flower was determined. Additionally, floral traits (floral length, corolla opening diameter, floral shape, style protuberance, calyx color) and reproductive traits (berry number, berry mass and diameter, seed mass and number) of all reproducing plants (n=42) were collected. The flowering period of the parent species was slightly asynchronous, with the full bloom of V. fuscatum occurring before *V. formosum*. Although floral traits of all taxa varied, *V. fuscatum* and *V.* × *marianum* maintained smaller flowers than *V. formosum*. Highbush blueberry flowers were visited by a diversity of insects including numerous bees, flies, and butterflies. While there was a considerable overlap in pollinator diversity across taxa, *V. formosum* was more regularly visited by large visitors including bumblebees and butterflies. Vaccinium formosum produced more berries and *V. fuscatum* the least, however *V. fuscatum* produced more and heavier seeds. The hybrid, *V.* × *marianum*, exhibited reproductive output comparable to its parent species, suggesting that hybrid traits attract and support pollinators resulting in successful pollination. This indicates that hybrid highbush blueberries are not detrimental to pollinator population health and may continue to support native pollinators in the future. Additionally, due to the shared floral visitors between taxa, pollinator behavior could account for on-going hybridization between the parent species and may also support backcrossing between hybrids and parental plants. With changing climatic conditions and anthropogenic impacts shifting plant distributions and increasing hybridization rates, it is increasingly crucial to understand the role that natural plant hybridization will have in shaping the future of pollinator populations.

Topic: *Systematics & Taxonomy*

A-896

Describing the leaf shape variability across the Euphorbia fendleri complex (Euphorbia, Euphorbiaceae)

Author: Nathan Taylor, Mark Fishbein
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Taxonomists commonly use leaf shape to distinguish between species. However, leaf shape is subject to ontogenetic variation that can obscure differences. This is especially the case in situations where species are weakly differentiated. The *Euphorbia fendleri* complex exhibits considerable leaf variation with the narrowest forms classified as *E. chaetocalyx*. Here, we collected approximately 1000 leaves sampled from approximately 120 plants from 26 populations across the geographic range of *E. fendleri* and *E. chaetocalyx*. We measured 12 leaf characteristics representing basic dimensions and asymmetry. All leaves at each node were sampled to account for anisophylly. Results suggest that populations of *E. chaetocalyx* and *E. fendleri* differ in leaf aspect ratio (leaf narrowness) where they co-occur in western Texas and southern New Mexico. As is found in previous studies, *E. chaetocalyx* produces narrower, mostly lanceolate leaves while eastern populations of *E. fendleri* produce mostly ovate to orbicular leaves. However, we report morphological integration across the western range of the complex. Implications for species delimitation within the complex are discussed.

Topic: *Development and Structure*

A-897

A new mechanism for the evolution of tricellular pollen

Author: Tonika Birmley, Joe Williams
Affiliation: University of Tennessee

Polyploidy has played an important role in the diversification of flowering plants. There is wide debate on the effects that ploidy has on development across cellular and organismal levels. It is generally thought that initially polyploidy increases cell size and delays development, but subsequently rapid evolution of the rate and duration of the cell cycle can occur. Most flowering plants develop pollen that is dispersed in a sexually immature or bicellular state, but 30% of flowering plants have shifted to dispersing their pollen in a sexually mature or tricellular state (with sperm already formed). Little is known about how evolutionary transitions from bicellular to tricellular pollen occur, because species are rarely stably polymorphic for both types of pollen. Based on earlier observations on *Galax urceolata*, a mixed ploidy species 2n=2x=12 and 4x=24, we hypothesized that ploidy could be one such mechanism. Flowers were collected from an average of N= 22.7 plants from 2x populations and N=22 plants from 4x populations. Conventional methods of staining and microscopy were used to calculate the proportion of bicellular and tricellular pollen present in flowers of four different ages. The accumulation of temperature was calculated over 15 days prior to each collection using data from the nearest weather station. The results show that the diploid populations produced a mix of both bicellular and tricellular pollen in flowers of all ages, rising from 28% at the tricellular stage in pre-anthesis and 40% tricellular pollen in senescent flowers. In tetraploid populations, anthers contained nearly 100% tricellular pollen from before flower opening and at all later stages. Diploid and tetraploid populations had overlapping elevations and temperature had no significant effect (P = 0.81). In multicellular organisms polyploidy is thought to prolong or slow development, but polyploidy can also provide opportunities for cell cycle evolution. Our study suggests that polyploidy provides an opportunity for the rapid evolution of precocious sexual maturity of pollen, perhaps explaining the many shifts we see from bicellular to tricellular pollen in flowering plants.

Topic: *Pteridology*

A-898

Rhizome Vascular Anatomy and Growth Form Evolution in the Fern Genus Elaphoglossum (Dryopteridaceae)

Author: Ana Martinez, Alejandra Vasco, Weston Testo, Rosa Nejapa, Marcelo Pace, Eric Schuettpelz
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Understanding how ecological transitions drive morphological diversification is central to evolutionary biology. In vascular plants, shifts in growth form—particularly from terrestrial to epiphytic lifestyles—are often associated with major anatomical innovations. While extensively studied in angiosperms, the evolutionary consequences of such transitions in ferns remain largely understudied. *Elaphoglossum*, a species-rich fern genus (~600 spp.), exhibits remarkable ecological and morphological diversity, including terrestrial, climbing, hemiepiphytic, and holoepiphytic forms. Early anatomical studies by Bell and others described basic rhizome structure in *Elaphoglossum,* but these were limited in taxon sampling and lacked a phylogenetic framework. In this study, we build on that foundational work to investigate how transitions in growth forms have shaped rhizome vascular anatomy across the genus. Using a phylogenomic framework based on ~350 nuclear loci, we are examining rhizome anatomical characters in 37 species representing all major clades of *Elaphoglossum*, to understand both the evolution of these characters and the correlation between growth form and vascular anatomy. Our preliminary results suggest that holoepiphytic species are characterized by reduced vessel diameter, increased in vessel density, thicker cell walls, and more parenchymatous tissue compared to terrestrial and epipetric species. Based on studies in flowering plants, we hypothesize that the only known climbing species in the genus will have sclerenchymatous fibers, a character not present in species with other growth forms. Our findings will provide insights into how developmental changes in vascular anatomy have contributed to diversification in *Elaphoglossum* and, more broadly, highlight the role of internal structural evolution in plant adaptive radiations.

Topic: Systematics & Taxonomy

A-899

Phylogenomics of the western North American genus Oreocarya (Boraginaceae)

Author: Kristen Hasenstab-Lehman, C. Matt Guilliams, Ronald Kelley
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Oreocarya (Boraginaceae) is a species-rich genus of 70 currently recognized minimially ranked taxa, endemic to western North America. Its principal center of taxonomic diversity is the Colorado Plateau and Great Basin regions, primarily in Nevada, through Utah, to western Colorado. Taxa in the genus usually grow in xerophytic habitats, occur at a wide variety of elevational ranges, and are often poor competitors uncommonly found intermixed with shrubs or under tree canopies. All members of the genus require well-drained soils, are intolerant of winter season wetness, and many species flourish as the only dominant taxon on barren, loose slopes and outcrops, derived from various igneous and sedimentary, and to a lesser degree metamorphic, substrates. More than half of the taxa recognized here are geographically restricted endemics, with many also edaphic specialists. Seasonal phenological differences have likely contributed to isolation in sympatric taxa. In contrast to closely related genera, heterostyly is present in approximately one third of the recognized taxa, including some widespread species, whereas many of the narrow endemics are homostylous. In this study we sample 52 of the currently recognized taxa, and build a phylogenomic dataset using ddRADseq methods. We infer evolutionary relationships within the genus, and use the resulting phylogeny to examine character evolution and biogeographic history. We conclude with updates to taxonomy supported in this study, and recognized in the upcoming Flora of North America.

Topic: Comparative Genomics/Transcriptomics

A-900

Comparative Genomics Reveals Patterns of Whole Genome Duplication Resolution in US Johnsongrass

Author: Michael McKain, Fae Bramblepelt, Bishnu Adhikari, Nathaniel Hofford, Mkayla Motley, Bryan MacNeill, Andrew Busby, Caitlin McCann, Susie McLaughlin, Alaina Richardson
Affiliation: The University of Alabama, University of Alabama, Geological Survey of Alabama, Cornell University, Mississippi State University

Johnsongrass (*Sorghum halepense* (L.) Pers.) is an invasive, allopolyploid grass species found throughout the world in tropical, subtropical, and temperature regions. Likely originating in the Mediterranean region of western Asia, this species is a tetraploid hybrid of *Sorghum bicolor* (L.) Moench (2n = 20) and *Sorghum propinquum* (Kunth) Hitchc. (2n =40). The accepted hypothesis is that the genome of Johnsongrass comprises 20 chromosomes from each parent for a total of 2n = 40. Introduced in the early 1800s into the United States, Johnsongrass has spread from the Southeast across much of the US outside of the Rocky Mountains and south of ~40° N latitude. Multiple instances of Johnsongrass crossing with cultivated sorghum are well known, resulting in weedier hybrids and triploid individuals. Backcrossing of these hybrids to Johnsongrass has resulted in cultivated genes being present across multiple populations of US Johnsongrass, though the extent of this introgression is unknown. Depending on the extent of backcrossing and recombination of subgenomes, the composition of US Johnsongrass genomes varies in parental species total contributions. Additionally, typical aspects of polyploid genome evolution, such as fractionation and homoeologous exchange, likely contribute to a wide array of genomic variation in the species. In this study, we investigate the extent of that variation by sequencing five, high quality Johnsongrass genomes from across US. Origins of these accessions include Alabama (present since at least the 1840s), Arizona (a known second introduction site), Indiana (the northern edge of the US range), Nebraska (the northwestern edge of the Central Plains distribution), and Tennessee (a second representative from the Southeast). Using four pseudomolecule-scaffolded genomes and one high quality contig assembly, we demonstrate the extent to which rearrangement of the parental subgenomes have shaped the evolution of US Johnsongrass germplasm. Using synteny-aware phylogenomics, we establish likely instances of homoeologous exchange and identify potential regions of introgressed cultivated sorghum genomes in our sampled individuals. Finally, we explore the extent to which fractionation has occurred and identify genes of interest that may contribute to the expansion of Johnsongrass across the US. These data provide us with novel understanding of the subgenomic dynamics of Johnsongrass and will serve as a valuable resource for weed biologists.

Topic: Population Genetics/Genomics

A-901

Divergent lineages, reproductive isolation, and restoration seed source variation in landscape genomics of Elymus elymoides

Author: Seth Romero, Elizabeth Leger, Rob Massatti, Thomas Parchman
Affiliation: University of Nevada, Reno, USGS Southwest Biological Science Center, University of Nevada Reno

Landscape genomic analyses aid understandings of how genetic differences are partitioned across spatially-complex environmental gradients in widespread species. Furthermore, genetic data can be leveraged to detect reproductive isolation among sympatric populations that may be missed in phenotypic studies. These cryptic patterns of evolutionary divergence are essential context not only for interpreting phenotypic divergence, but also to inform management practices like restoration, assisted migration, and *ex situ* conservation. However, population genetic data is often lacking for widespread plants of ecological interest. *Elymus elymoides* (bottlebrush squirreltail), is one such species that lacks modern genetic perspective despite being widely used as a restoration "workhorse". Prior common garden studies have identified strong patterns of local adaptation, but uncertainty around subspecies and potential hybrids has been a confounding factor. To address these unknowns, we generated the first SNP dataset (ddRADseq) for this species that includes 695 individuals representing 60 *in situ* wild populations, 16 *ex situ* collections from the Germplasm Resources Information Network (GRIN), 3 populations of farm increased seed, and 2 commercial cultivars. Results identified a complex population structure comprised of multiple divergent lineages that exhibit both allopatric and sympatric distributions with notably minimal evidence for hybridization between groups. These results are consistent with subspecific taxonomy, and suggest some lineages exhibit reproductive isolation despite geographic overlap. While *ex-situ* collections reflected natural patterns of landscape genetic variation, the two commercial cultivars aligned with separate lineages and exhibited strong divergence from related wild populations, illustrating the potential for substantial genetic shifts in mass produced seed employed in restoration. These findings expand on and refine the phylogenetic complexity of this species identified in early genetic studies and highlight potential consequences of haphazard population movement and mixing via restoration practices.

Topic: Phytochemical

A-903

Narrowing the targets of selection: Characterization of the purple-white petal color polymorphism in Linanthus parryae (Polemoniaceae)

Author: Ioana Anghel, Melissa León-Osper, Eduardo Narbona, Victor Rossi, Katie Conrad, Amelia Fuller, Justen Whittall
Affiliation: University of California, Santa Cruz, Santa Clara University

Flower color polymorphisms can be maintained by direct selection on petals or indirect selection on a linked trait. The *Linanthus parryae* color polymorphism is thought to be maintained by selection, with pigmented morphs producing more seeds in dry years. Characterizing anthocyanins in petal and vegetative tissues in *L. parryae* can help us determine if petal color is maintained by pleiotropic effects or epistatic effects in a shared biosynthetic pathway. Using UV and visible digital images, UV-vis reflectance spectra, and the underlying biochemistry, we examine the conspicuousness of the petal color variation to bees, then compare anthocyanins and UV absorbing flavonoids across the range of petal color morphs and in vegetative tissues. Cyanidin 3-rutinoside confers color on a continuous gradient from dark purple to white in *L. parryae*. All petals are highly UV absorptive with no correlation between the visible and the UV wavelengths. Bees and other pollinators with similar visual systems do not distinguish between the color morphs. Petal anthocyanins vary independently from both vegetative anthocyanins and vegetative UV absorbing flavonoids. Indirect selection on petal UV protection is unlikely because petal morphs do not differ in their production of UV absorbing flavonoids. Pleiotropy is unlikely because visible pigment and UV absorbent flavonoid production is decoupled in petal and vegetative tissues. We found no support for pollinator mediated selection because color variation is indistinguishable to possible pollinators. The targets of selection are either direct on petal anthocyanins, or on a linked unsampled tissue or metabolite.

Topic: *Biodiversity Informatics & Herbarium Digitization*

A-904

Taking inspiration from iNaturalist, how can we facilitate online curation of biodiversity collections?

Author: Nathan Taylor
Affiliation: Oklahoma State University

Significant and important work is being done to create global biodiversity databases. However, these datasets are plagued by inaccurate data. Manual curation with the current infrastructure is difficult to nearly impossible. Additionally, the current methods for reviewing specimen records are tedious and require good organization skills on the part of the identifier. Further, communicating the information needed to correct errors or misidentifications requires contacting herbaria directly. Though far from perfect, the curation system used by iNaturalist has facilitated the efficient curation of millions of observations online. For specimens with correct determinations, agreeing annotations can be applied and recorded online by simply tapping a single key on your keyboard. Disagreeing annotations are added by simply typing in the name for the species. Reviewing the next observation is as simple as hitting the right arrow key on your keyboard. In all cases, these changes are immediately published online and, depending on the nature of the change, may be sent to GBIF. Incorporating ideas from iNaturalist might allow specialists to more efficiently find and curate herbarium records online. In this presentation, I note the need to develop new online based curatorial programs and practices by comparing iNaturalist with two existing biodiversity databases (GBIF and Symbiota). I discuss the limitations of iNaturalist's system of curation and how future resources could overcome those limitations.

Topic: *Molecular Ecology*

A-905

Population genetic structure mirrors community structure in Pedicularis across the Hengduan Mountains biodiversity hotspot

Author: Jared Meek, Patrick McKenzie, JianJun Jin, Richard Ree, Deren Eaton
Affiliation: Columbia University, Harvard University, New York Botanical Garden, Field Museum

The accumulation of diversity and endemism within biodiversity hotspots makes them well-suited for investigating the drivers of diversification and adaptation. The Hengduan Mountains Region (HMR) biodiversity hotspot, located along the eastern edge of the Qinghai-Tibetan Plateau in China, harbors an exceptional diversity of plant species richness distributed across a range of temperate montane habitats dissected by deep river valleys. The spatial distribution of biodiversity in this region is hypothesized to reflect divergence and speciation associated with dispersal over major geographic barriers during climatic fluctuations. It is commonly assumed that the same processes that generated diversity historically continue to generate divergence and speciation today. Here, we investigated this hypothesis by examining the impact of landscape barriers in driving diversification in the HMR across both population-genetic and phylogenetic timescales in the species rich genus Pedicularis, which has diversified in the HMR to comprise >300 endemic species.

To examine the spatial distribution of population genetic variation we generated a comparative phylogeographic dataset of genomic sequences from 12 widespread species sampled across hundreds of populations spanning the entire HMR. Stacked effective migration surfaces revealed both similarities and differences among species in the effect of major barriers on spatial patterns of genetic similarity. However, despite many similarities in effective migration, most species split over the same geographic barriers at different times, and in different orders. To examine the concordance of these incipient patterns of speciation with phylogenetic-scale patterns of biogeography and community assembly, we examined macroecological turnover of >130 species of Pedicularis across the landscape. Our results show that the geographic barriers structuring contemporary population genetic diversity within species are also associated with the turnover of communities and phylogenetic diversity in the HMR.

Topic: *Phylogenomics*

A-907

Automated creation of taxon-specific target datasets using Captus

Author: Edgardo Ortiz, Elizabeth White, Douglas Soltis, Pamela Soltis
Affiliation: University of Florida

Captus (available at github.com/edgardomortiz/Captus, described in detail at doi.org/10.1101/2023.10.27.564367) is a user-friendly bioinformatic tool aimed at processing genomic data, such as sequencing reads (target capture, genome skimming, whole genome sequencing, RNA-Seq) and/or assembled genomes and transcriptomes, into multiple sequence alignments ready for phylogenetic analysis. Besides consistently retrieving more and longer loci than similar tools it keeps comprehensive logs and produces HTML reports that show useful statistics that guide the selection of parameters for subsequent steps.

Here we describe a new feature of Captus, the ability to derive a new set of target sequences from the user's own assembled data in an automated fashion, and how we applied it to data captured using Angiosperms353 probes for *Xyris*. Loci recovery in this taxon, as in many other Monocots, is far from complete when using the original Angiosperms353 target file or even the taxonomically expanded version Mega353, with an average of ~290 (out of 353) loci and an inconsistent individual locus length recovery across samples. Thanks to this new algorithm in Captus, that clusters the aligned *Xyris* sequences and carefully selects new loci representatives as targets (according to several parameters that the user can control), we were able to increase recovery to ~315 loci while also increasing the consistency of the recovered lengths for individual loci.

Additionally, since the new target sequences represent the most common assembled proteins across one's own samples, they facilitate paralog-filtering as well as the detection and removal of alignment errors. More importantly, the feature offers new possibilities for target file creation. For example, we show how to create a new target file consisting of full-gene sequences (in contrast to the original target file that only includes CDS) and how the addition of introns in the target sequences affects recovery and ultimately the resolution of the estimated gene and species trees.

This new function 'new_targets from_alignments' is available in Captus since v1.3.9.

Topic: *Comparative Genomics/Transcriptomics*

A-908

Latitudinal effects on Vaccinium membranaceum flavonoid gene expression and production

Author: Chloe Drummond, Shuhan Yin, Charlotte Atherton, Solimar Guzman-Rubalcaba, Tanya Renner
Affiliation: Mount Holyoke College, The Pennsylvania State University

The biogeographic pattern of vascular plants that are disjunct between western North America and the Great Lakes region is an important system for investigating questions of species persistence in the face of climate change. Not only are the populations in the Great Lakes region isolated and sometimes threatened or endangered, but the populations that are more widespread in the West are ideal for studying trait variation and plasticity across a latitudinal gradient that can shed light on the potential tolerance for a future northward range shift. Here, we present updated results from our study that focuses on one of the disjunct species, *Vaccinium membranaceum* Douglas ex Torr., to investigate changes in flavonoid production across a latitudinal gradient. We hypothesize that plants would have an induced flavonoid photoprotective response when located at higher latitudes due to longer growing season daylight length and lower temperatures that reduce photosynthetic capacity. We reason that excess light, exceeding photosynthetic capacity, can induce photoprotective responses to avoid cell damage. To test our hypothesis, we analyzed RNA-Seq transcriptomic and LCMS untargeted metabolomic data from *V. membranaceum* leaves collected from seven populations along a latitudinal gradient, within a three-week period in August 2021. Genotyping-by-sequencing data were also analyzed to account for covarying effects of environment and genetic background. Because field transcriptomic studies can include environmental variation, we also analyzed gene expression data in individuals grown under three different shading treatments within a controlled greenhouse setting. Ultimately, this study may serve as a foundation for understanding how this species may respond to movement to higher latitudes in the future due to climate change.

Topic: *Ecology*

A-909

Flowering phenology across plant richness and insect presence in an experimental Texas Blackland Prairie grassland

Author: Liliana Benitez, Elena Adams, Sarah Ortiz, Damla Cinoglu, Amy Wolf, Shalene Jha
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Global changes have the potential to alter phenology, the seasonal timing of biological processes, via mechanisms such as changes in temperature and precipitation, life stage or emergence mismatches, and altered resource availability. The impacts of global change on plant phenology are largely understood through abiotic mechanisms such as climatic conditions and resource inputs. However, recent studies have shown that biotic factors like plant community composition and presence of mutualists may be important drivers or mediators of phenological change. Loss of biodiversity due to global change factors can have additional effects on the immediate microclimate, competitors, and mutualistic partners. While many studies have examined climate change impacts on phenology, there is emerging interest in understanding how plant richness impacts phenology through microclimate; few studies have explored these impacts in combination with insect loss. In this study we aimed to answer the following questions: a) how does loss in local plant species richness affect flowering timing and duration? b) how does the loss of insect abundance affect flowering timing and duration? We conducted this study within a biodiversity-ecosystem functioning experiment consisting of experimentally-seeded plant communities, where both plant species richness and insect presence were manipulated to evaluate the effects of biodiversity loss on ecosystem functioning. Plots were 2 m x 2 m and seeded from a pool of 12 common Blackland Prairie plant species. Each plot consisted of four 1 m x 1 m quadrants with different levels of netting to exclude insects: 1) full exclusion - one quadrant was fully covered with insect netting to reduce insect presence, 2) no exclusion - two quadrants remained fully open with no net. 3) exclusion control - one quadrant was partially covered by the net but allowed for insects to pass underneath. We collected flowering phenology data in the spring and summer of 2023 from 7 focal forbs from 72 plots varying in plant species richness. The insect exclusion treatment significantly delayed the overall peak flowering date (PFD) and lengthened flowering duration compared to the control when all species were considered together ($p < 0.01$). While reduction in plant species richness did not influence the PFD or flowering duration of the overall community, it was important for some species. For example, loss in plant richness significantly advanced PFD in Centaurea americana (0.5 days per species lost, $p < 0.05$) and marginally significantly advanced PFD for Lupinus texensis (0.45 days per species lost, $p = 0.09$). A decrease in species richness significantly lengthened duration only in Phacelia congesta, by about 2.04 days per species lost ($p < 0.01$). Our study adds to the building literature of shifting phenology in response to plant species richness loss and insect decline. We demonstrate that insect loss does have an impact on individual species as well as community-wide flowering phenology, and that different species respond differently to a loss in the surrounding plant species richness. As anthropogenic changes rapidly drive biodiversity loss, it is increasingly important to understand how phenological phenomena will respond to these biotic and abiotic shifts.

Topic: *Biodiversity Informatics & Herbarium Digitization*

A-911

Digitization and Enrichment of U.S. Herbarium Data from Tropical Africa to Enable Urgent Quantitative Conservation Assessments

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Affiliation: Missouri Botanical Garden, University of Ghana, Montana State University Bozeman, University of California Davis, Harvard University, Arizona State University, Fort Worth Botanic Garden, Carnegie Museum of Natural History, Bringham and Young University, Univeristy of Rwanda, Brown University, Field Museum of Natural History, University of California Berkeley, Louisiana State University, Drexel University, University of Arizona, Malawi University of Science and Technology, California Botanic Garden, National Herbarium of Gabon

Herbarium specimens make up the raw data upon which our knowledge of plant diversity is built on. However, many herbarium specimens remain inaccessible to the greater community of scientists, remaining only available to those able access physical herbaria. This project aims to make African herbarium specimens and their associated data more accessible by digitizing the rich data resources held in 21 U.S. herbaria. Imaging and data capture is being carried out at each of the herbaria, and data are then aggregated for efficient georeferencing. Currently, the project has imaged 558,577 specimens, of which 251,991 have data captured with georeferencing being conducted by plant scientists in Gabon, Ghana, Malawi, and Rwanda. Recent advances in Large Language Models (LLMs) have allowed more efficient data capture from images such that technicians now verify, and correct LLM derived data records read from images. Finally, project data is openly available to the scientific community via a dedicated "African Plants" portal on Symbiota (african-plants.org/portal/index.php), as well as integration into biodiversity data portals such as iDigBio and GBIF. The project has thus created a broad, international, intercontinental network of scientists and students interested in and experienced with management and analysis of data about African plant distributions. These rich data resources will be used to understand the conservation status of African plant species in much greater detail than has been possible to date.

Topic: *Hybrids and Hybridization*

A-912

Exploring subgenome evolution in allopolyploid and diploid hybrid species of Selaginella

Author: Alex Stewart, Michael Barker
Affiliation: University of Arizona

Hybridization and polyploidization are common processes in plants and often occur in tandem. As such, it is difficult to untangle the contributions of hybridization versus polyploidization to the evolution of allopolyploid species. This is due, in part, toa paucity of groups where a homoploid hybrid and an allotetraploid exist from the same parental cross. Here, we use a unique species complex in *Selaginella* to explore the impacts of hybridization and polyploidization on genome evolution. *Selaginella* is one of the largest genera of lycophytes, despite having one of the smallest nuclear genomes found in vascular plants. The southwestern US and mainland Mexico are a center of functional and taxonomic diversity in *Selaginella*. In the transition zone between the Lower Colorado River valley and Arizona Upland subdivisions, diploid hybrids and allopolyploids of *S. arizonica* × *S. eremophila* thrive. Both hybrid taxa have distinct levels of desiccation tolerance and occupy more extreme environments than either of the parents. Using a combination of transcriptome and genome data, we assembled and annotated five reference *Selaginella* genomes, including the two hybrid taxa: an outgroup (*S. bigelovii*), a putative homoploid hybrid (*S. 'organpipe'*), an allotetraploid (*S. 'phoenix'*), and the putative parent species for both hybrid taxa. Assemblies range in size from ~90MB to ~200MB and have high BUSCO completeness (>95%). We are classifying the parental subgenomes present in the hybrid species, examining the patterns of gene retention in each species, and testing for hybrid speciation events.

Topic: Ecology

A-914

Differences in mortality across the Mojave Desert reveal the effects of climate change on growth and survival of Joshua trees (Yucca spp.)

Author: Bjorn Domst, Christopher Smith
Affiliation: Willamette University

Joshua trees (Yucca brevifolia and Yucca jaegeriana) are woody monocots endemic to the Mojave Desert. They are species of conservation concern, threatened by climate change and habitat loss due to renewable energy development and urbanization. They are subject to special protection in the State of California and are the objects of significant popular interest. Previous work in Joshua Tree National Park has shown a strong association between age class distributions and long term climate variables, with low elevation sites showing few or no seedlings. To assess the long-term effects of climate change on growth and survival, we surveyed tree populations across the species' range at intervals over a 14-year period, measuring height and branch numbers for all trees found in a series of ~50m radius study plots arrayed in a linear transects at each site. In the summer of 2024, we revisited 14 of these sites to remeasure trees and determine rates of mortality at each site. We summarized long term climate data from the BioClim database using principal component analysis and compared these values against the growth and survival data. Whereas growth rates were largely similar across sites, with an average increase in height of 1-4 cm/year for most sites, mortality rates varied markedly between sites, with some sites having no observed mortalities and some sites seeing losses of up to 44% of the individuals censused in the original surveys. The results also revealed showed a significant association between climate principal component two and rates of mortality, with sites showing higher maximum summer temperatures and more intense dry periods having the highest annualized mortality rates. The findings indicate that, consistent with past modelling studies, climate is a predictor of Joshua tree mortality, corroborating previous predictions. Ongoing changes in the temperature and rainfall regimes across the Mojave due to anthropogenic climate change will likely exacerbate the effects seen in this study.

Topic: Biology of mycoheterotrophic and parasitic plants

A-916

Isotopic and root fungal community analyses of the mycoheterotrophic fern Botrychium

Author: Mari Wilson, Sean Graham
Affiliation: University of British Columbia, University of British Columbia (UBC)

Botrychium is a diminutive fern that alternates between a fully mycoheterotrophic subterranean gametophyte generation and a photosynthetic sporophyte generation. The sporophyte has characteristics suggestive of partial mycoheterotrophy. It produces one leaf annually, has a reduced root system, can remain dormant belowground for extended periods of time, and has documented albino occurrences in two species. My research aims to (1) explore the extent of mycoheterotrophy in the sporophyte generation by using stable isotopes and (2) identify the fungi associated with the sporophyte through root fungal community metabarcoding. I collected leaf and root samples from seven species of Botrychium from 16 sites across British Columbia, Washington, and California. Preliminary stable isotope results show variability in isotopic enrichment, an indicator of mycoheterotrophy. Within this variation, some sites and species have strong signals of mycoheterotrophy. Fungal metabarcoding of the roots is underway and will document the arbuscular mycorrhizal community associated with Botrychium using primers designed to amplify two clades of arbuscular fungi, Glomeromycotina and Mucoromycotina, the latter of which can be overlooked with non-inclusive primers.

Topic:

A-917

Belonging in Botany: The Immigrant Experience

Author: Karolina Heyduk
Affiliation: University of Connecticut

Join us for a live panel to discuss the lived experiences of immigrant scientists in our society. The panel discussion will be helpful to those seeking to build community, as well as mentors and others in leadership who are looking for guidance on best practices to support immigrant scientists. Our panel is composed of immigrant scientists from a diverse array of institutions and organizations. Due to the sensitive nature of this topic, names of panelists will not be shared in advance.

Topic: Ecology

A-918

Identifying Mycorrhizal Fungi in Joshua Tree Root Zone Soil with eDNA

Author: Ajia Buvit, Christopher Smith
Affiliation: Willamette University

Topic: Comparative Genomics/Transcriptomics

A-919

Investigating the breakdown of dioecy through comparative genomics: a study of the threatened Amaranthus pumilus, or seabeach amaranth, and its weedy relatives

Author: Jason Leung, Deren Eaton
Affiliation: Columbia University

Topic: Ethnobotany

A-920

A Look at CaliBaja Ethnobotany Through a Gastronomic Lens

Author: Giovanni Gil, Justin Shorty, Lluvia Flores-Rentería, Changqu Liu
Affiliation: San Diego State University

Indigenous knowledge is a cornerstone for many facets of our modern lives. From resource management to community development, native wisdom continues to provide western cultures with repositories to pull from. This is especially true for ethnobotanical uses across the North American landscape. We are choosing to focus on indigenous knowledge of resilient food systems by utilizing region-adapted, native edible plants as a method to address food insecurities in food deserts.

Our project is focusing on the documentation of native edible plants in the CaliBaja region such as *Salvia columbariae and Quercus agrifolia var. agrifolia & oxyadenia*. We aim to take first-hand accounts of indigenous uses and preparations for these native edible plants as well as quantify the nutritional profiles which are currently undocumented in scientific literature. Along with our findings we also plan to create a comprehensive database about the nutritional breakdowns and historical preparational strategies of native edible plants for indigenous communities to access as well as the public.

For nutritional analyses, we plan to use a total phenolics analysis to test for plants that contain high concentrations of tannic compounds and have been known to need preparation before consumption. We also plan to use proximate analysis to determine general percentages of fats, proteins, minerals, moisture, and carbs to begin giving nutrition facts about traditional dishes.

Our initial sampling consisted of collecting the fruits of *Quercus agrifolia* from Mission Trails Regional Park and using ArcGIS to record the geolocation of the individuals sampled. We are also including in our analysis previously collected *Salvia columbariae* seeds. After the samples were collected, they were stored in a -18° freezer for long term storage. The proximate analysis results of *Quercus agrifolia* showed the acorns contained: 45% carbohydrates, 20% lipids, 4% proteins, 30% moisture, and 1% ash by weight. For *Salvia columbariae,* a proximate analysis was performed and showed that these seeds contained: 40.2 ± 2.1% carbohydrates, 32.8 ± 2.0% lipids, 16.4 ± 0.8% proteins, 6.0 ± 0.0% moisture, and 5.0 ± 0.2% ash by weight. We have already begun literature reviews of nutritional breakdowns and traditional recipes and found consistent gaps in both aspects which we hope to fill.

We expect to have information that informs indigenous communities about the nutrition of the foods that they eat, and in addition to informing those communities, it is important to correspond and communicate as to what should be done with information gathered about these foods and their methods of preparation.

Topic: *Phylogenomics*

A-923

The origin, patterns of diversification, and ecology of an Iris clade endemic to the Sierra Nevada and transverse ranges of California.

Author: Carol Wilson
Affiliation: University of California, Berkeley

Iris series *Californicae* is a recently diverged clade (approximately 8.5 mya) that is distributed in foothill, mountain, and valley landscapes from western Washington to southern California, with *I. munzii* and the four infraspecific taxa of *I. hartwegii* endemic to foothill and mountain habitats in the Sierra Nevada, and San Gabriel and San Bernardino mountains. Previous studies have shown that *I. munzii* and *I. hartwegii* are sister species resolved in a distinct subclade in the series. Twenty-six populations and 97 nuclear genes were used to develop phylogenetic, coalescence, dating, and ancestral reconstruction hypotheses of these two species, while herbarium records were used to determine current distributions. Distribution records with downloaded bioclim data were analyzed to develop preliminary climate niche hypotheses for each subclade resolved. Results suggest that one taxon, *I. hartwegii* subsp. *pinetorum*, is not within the *I. hartwegii* species complex and may have a hybrid origin, *I. munzii* is the earliest diverging taxon in the clade, and *I. h.* subsp. *hartwegii* populations from the southern Sierra Nevada are most closely related to *I. h.* subsp. *australis* populations in the transverse ranges. The clade is hypothesized as originating in northern Sierra Nevada high and foothill regions, an area of plant paleo-endemism in California, about 5.6 mya with subsequent dispersal south. Results from PCA and boxplots indicate that both temperature and precipitation contribute to the distributional patterns of the six major subclades resolved. Analyses that include soil information together with niche modeling are underway to further explain habitats occupied by these taxa and to predict future shifts in distributions.

Topic: *Population Genetics/Genomics*

A-924

Unlocking the Polyploid Ks Histogram with Forward Time Simulations

Author: Tamsen Dunn, Arun Sethuraman
Affiliation: San Diego State University

Multiple rounds of whole-genome duplication (WGD) followed by diploidization have occurred throughout the evolutionary history of flowering plants (angiosperms). Much work has been done to model the genomic consequences and evolutionary significance of WGD. While researchers have historically modeled polyploids as either allopolyploids or autopolyploids, the variety of natural polyploids span a continuum of differentiation across multiple parameters, such as the extent of polysomic vs. disomic inheritance, and the degree of genetic differentiation between the ancestral lineages. Here we introduce the Ks histogram simulator DemographiKS, an individual-based forward simulation, which exposes both population, genome, and molecular evolutionary modeling parameters. We validate DemographiKS against theory and pre existing simulations. We use DemographiKS to explore the effects of recombination, migration, bottlenecks and expansions on the Ks distribution, for a generalized tetraploid model. While it is often naively assumed that the peak of the Ks histogram corresponds to the time of WGD, our research shows that the location of the Ks peak may instead correspond to the time of parental divergence (for allopolyploids), the mean time of coalescence of the diploid ancestor (for autopolyploids under a population expansion), or the time of most recent migration between the parental species. We demonstrate how the shape of the Ks distribution is influenced by recombination rate, as well as ancestral and polyploid population size. In summary, we demonstrate that the Ks distribution represents a novel and powerful test statistic sensitive to many aspects of ancient demography. Used with appropriate caution, the Ks histogram may serve as a companion to other methods such as the site frequency spectrum to corroborate demographic inference in polyploid species.

Topic: *Ecophysiology*

A-925

The Early Steps in C4 Plant Evolution

Author: Rowan Sage
Affiliation: University of Toronto, Annals of Botany

Rowan F. Sage, Arthur Leung, Tammy L. Sage. Department of Ecology and Evolutionary Biology, University of Toronto

C_4 photosynthesis is one of the most prolific complex traits in the biosphere, having independently evolved over 65 times in flowering plants. Understanding C_4 evolution will provide insights into how evolution builds complex life forms that transform the biosphere. From biogeographic inferences of where distinct C_4 clades evolved, we conclude C_4 lineages largely evolved in hot, dry or saline environments favoring extreme rates of photorespiration, which C_4 photosynthesis is recognized to overcome. However, C_4 evolution originates within the context of C_3 photosynthesis, and any initial trait arising to deal with high photorespiration must be considered in terms of improved fitness of C_3 plants. In this talk, we examine the initial developments that jumpstart C_4 evolution. We hypothesize that high photorespiration in the mesophyll tissue of ancestral C_3 plants overloads the mesophyll (M) tissue with excess photorespiratory glycine, which then spills over to the bundle sheath (BS) tissue to be metabolized to CO_2, ammonia and serine within BS mitochondria. Rapid recovery of the amino N in the ammonia pool within the BS is essential, and both the structural and biochemical elements of the C_4 pathway appear to be upregulated in C_3 ancestors to facilitate this recovery. In support of this hypothesis, we present data that BS cells of ancestral C_3 species of C_4 lineages exhibit enhanced numbers of mitochondria and chloroplasts, which provide capacity to metabolize glycine overflows from the M tissue. BS cells of ancestral C_3 species have reduced length to width ratios, which we hypothesize occurs to i) generate more organelles in the BS; ii) enhance the frequency of plasmodesmata in the BS-M interface, and iii) increase resistance to slow loss of ammonia produced in glycine decarboxylation. Consistently, plasmodesmatal frequencies at the BS-M interface are elevated in C_3 sister species of C_4. These changes lead to the establishment of a two-tissue, BS to M photorespiratory cycle that facilitates the evolution of Kranz-anatomy, rapid BS to M metabolite transport, and upregulation of elements of the C_4 biochemical cycle. In short, the recovery of photorespiratory N in the ammonia pool establishes a facilitation cascade that creates the bridge from C_3 to C_4 photosynthesis.

Topic: *Ecology*

A-927

Identification of Arbuscular Mycorrhizal Fungi in the Roots of Joshua Tree (Yucca spp)

Author: Sarah Jones, Christopher Smith
Affiliation: Willamette University

Joshua trees (Yucca brevifolia and Yucca jaegeriana) are the archetypical plants of the Mojave desert, but are threatened by increasing drought and temperature extremes driven by anthropogenic climate change. Arbuscular Mycorrhizal Fungi (AMF) form a mutualistic relationship with their host plant by colonizing their young roots and accessing nutrients that are less bioavailable to plants, such as phosphorus and water, in exchange for sugars provided by the plant. A number of studies have suggested that AMF may ameliorate the effects of drought stress in plants. Recent work in Joshua Tree National Park suggests that some mycorrhizae may aid in the establishment of Y. brevifolia seedlings and that the mycorrhizal community varies across an elevational gradient. However, the effects of plant genotype on the relationship and the extent of host specificity have not been explored. Here, we use environmental DNA to examine differences in mycorrhizal community between Y. brevifolia and Y. jaegeriana in a hybrid zone, where there is large genetic variation between plants and where the effects of soil type and can be assessed independently.

Topic: *Disabled in Botany: Breaking Barriers in Plant Science Research*

A-928

Locke's Demonstration garden as vehicle for cultural connection in transnational communities on the Sacramento Delta

Author: Mayra Concepcion
Affiliation: UC Davis

The Sacramento Delta has a profound historical and cultural significance, emphasized in its transformation from marshland to agricultural land through traditional ecological knowledge. I honor my cultural heritage in transnational communities, through a graphic narrative that integrates personal family history, autoethnography and my experience gardening heirloom vegetables along the Sacramento Delta, in Locke, California. I reflect on the challenges of recognizing personal limitations, cultural pluralism, and the ethnobotanical impact of colonization through Southeast Asian plant distribution. The project aims to explore the concept of heritage and what it means to be American, integrating personal and cultural connections with the land. In the process, I share my journey in gaining a better understanding of what it means to be a 'researcher'. How has engagement with the Locke Demonstration Garden helped me understand community, heritage, and belonging?

In my time at a tier 1 research university, my disability was often seen as a liability. However, as I confronted unsustainable work practices, loss of serveral community members, unethical research practices, and a culture of complicity I am learning what it takes to maintain integrity in academia. In a way, my disability is my saving grace, reminding me to hold my own boundaries and stay true to myself.

Topic: *Development and Structure*

A-932

Comparative Effects of Nitrogen Fertilization on Seedling Growth in Four Bromeliad Species

Author: Victoria Barrow, Rachel Jabaily
Affiliation: Colorado College

The Bromeliaceae, a predominantly neotropical family, is well known for its biodiversity and adaptive strategies. Bromeliads play essential roles in ecosystems and hold economic significance in the horticultural and agricultural industries. Bromeliad species span a gradient from fully terrestrial to epiphytic, and some bromeliads have evolved specialized leaf tanks and absorptive trichomes to aid in water and mineral uptake. Early seedlings lack many of these features and may be more reliant upon roots for mineral acquisition than they will as adult plants. Nitrogen is a key and often highly limiting nutrient in many bromeliad habitats. This study examines the early growth responses of seedlings from four bromeliad species spanning the terrestrial to epiphyte gradient (Puya mirabilis, Aechmea recurvata, Billbergia brasiliensis, & Vriesea rafaelii) to three concentrations of nitrogen (0 vs. low- 0.01mM Urea vs. high- 1.00mM urea). I hypothesized that nitrogen application would stunt root growth and promote shoot growth in all but the most epiphytic species (V. rafaelii), and that the fully terrestrial species (P. mirabilis) would have the most sensitivity to differing nitrogen treatments. I germinated over 550 seeds per species and tracked their earliest growth and development for three weeks. I took data on the root & shoot lengths of all seedlings at weekly intervals, which were analyzed with ImageJ pixel analysis.

A linear mixed-effect model revealed that high nitrogen application significantly inhibited root growth for three of the four species (A. recurvata, B. brasiliensis, P. mirabilis) at later developmental stages, supporting my hypothesis. Shoot growth increased but showed less consistent responses to nitrogen availability. This suggests either greater root system sensitivity to nitrogen or methodological limitations in shoot tissue measurement. Additionally, only P. mirabilis responded significantly to the low nitrogen treatment, supporting its greater hypothesized sensitivity to nitrogen as a terrestrial plant. Growth results for V. rafaelii under the different nitrogen treatments were not significant, potentially due to its slow life history strategy as a highly epiphytic bromeliad. Results also showed that high nitrogen treatment decreases the root to shoot ratio compared to other treatments, but remains consistent with species specific patterns of organ tissue investment over time. This study provides a foundation for understanding how bromeliad functional traits and life history strategies respond to nitrogen availability.

Topic: *Kaplan Memorial Lecture*

A-933

The secret life of buds

Author: Pamela Diggle
Affiliation: University of Connecticut

Topic: *Floristics*

A-935

Vascular Flora of the Clover Mountains, Nevada, U.S.A.

Author: Mathew Sharples
Affiliation: Arkansas Tech University

The Clover Mountains of Nevada comprise a large swath of ridgelines and canyons rising above the Mojave Desert near its intersection with the Great Basin and Colorado Plateau. Though relatively proximate to Las Vegas and St. George, the area has never been focus of deliberate floristic inventorying efforts, and in 2017, herbarium databases indicated the presence of only <300 species in the study region. In 2017, deliberate floristic inventorying efforts were begun, and have continued through 2024-2025. Based upon over 1,100 newly collected voucher specimens, the flora of the Clover Mountains is now known to comprise at least 664 species of vascular plants, the vast majority of which (almost 99%) are Angiosperms. Included in this count are hundreds of new mountain range records, and dozens of new county records--these latter of particular note, given the vast size of Lincoln County, NV. The Asteraceae contain a significant proportion of this flora with over 110 species, and other exceptionally diverse families include Poaceae, Polygonaceae, Brassicaceae, and Fabaceae, similarly with other regional floras. Although dominated by montane Mojavean and Great Basin-type pinyon-juniper woodland vegetation communities, the area yields to relatively mesic ponderosa forest at its highest elevations, and supports a number of presumed Pleistocene-refugial habitats. The area is also a notable local center of diversity for species of Cactaceae. Once the area is fully documented, it may be revealed as one of the most botanically diverse Mojavean mountain ranges, particularly as its elevational gradient is relatively narrow compared to more towering, nearby Mojavean ranges. I will also update the community on the first public Vascular Flora of Nevada (first mentioned at Botany 2023), which is likely to be under review for publication in book format by the onset of Botany 2025.

Topic: *Phylogenomics*

A-936

Systematics of Hebecarpa (Polygalaceae)

Author: Christopher Munoz, Michael Moody, Tom Wendt
Affiliation: The University of Texas at El Paso, University of Texas at El Paso, The University of Texas at Austin

This ongoing study aims to use phylogenetic analysis of the taxonomically unresolved plant genus *Hebecarpa* to delineate species limits and resolve genealogical relationships within the group. Several USA-endemic species have distributions mostly restricted to mountain-proximal habitats in the southwest deserts with substantial geographic disjunction between populations. Preliminary data show compelling evidence of cryptic diversity within the *H. barbeyana* & *H. obscura* species complexes. Abbott & Pastore (2015) listed 41 species of *Polygala* (recently circumscribed under *Senega* along with all other North American taxa formerly under *Polygala*) that are morphologically diagnosable to *Hebecarpa*; the totality of these taxa has yet to be phylogenetically assessed (Abbott & Pastore, 2015; Barea Pastore et al., 2023). The total number of species within the genus is still unknown, with Abbott (2009) having suggested the number of species sitting somewhere between 19 and 70—a range that highlights the uncertainty revolving around the systematics of the genus. The timing of diversification within *Hebecarpa* is still unclear. The analysis will comprehensively sample taxa otherwise presently difficult to obtain through fresh field collections due to safety concerns involving remote travel in parts of Mexico, the center of diversity for the group (Abbott & Pastore, 2015). To circumvent this, a rich collection of *Hebecarpa* and *Polygala* samples, largely collected in the 1970's, are housed at TEX and LL as well as UTEP and, with permission from curators, can be used in conjunction with target capture methods employing phylogenetically informative nuclear genes to resolve the genus wide phylogeny (Carter et al., 2019; Johnson et al., 2019; Andermann et al., 2020). These analytical approaches can then be integrated with morphological datasets, built using LeafMachine2 (Weaver & Smith, 2023) learning algorithms that can measure an array of morphological structures across a multitude of digitized herbarium specimens, in order to map traits thought to facilitate

propagule dispersal onto the phylogeny. Phylogenetic signal can then be used in order to evaluate the degree to which the elaiosome and samaroid fruit capsule's winglike visage is constrained by phylogenetic relatedness to allied lineages (Castor Package v1.6.6, Louca & Doebeli, 2018; ggtree v2.4.1, Yu et al., 2017; Beaulieu, 2022). The variability in these morphological traits in conjunction with the differing habitat extents/habitat connectivity of the species within *Hebecarpa* can then be tested for correlation where findings may either comply with the dispersal reduction hypothesis (Waters et al., 2020) or fail to corroborate the idea that more insular taxa will tend to undergo, through evolutionary change, a reduction in dispersal capability over time.

Topic: Molecular Ecology

A-937

The many ways of calculating phylogenetic diversity from eDNA metabarcoding data

Author: Rachel Meyer, Madeline Slimp, Natasha Stavros, Matthew Rossi, Meghan Hayden, Jacob Nesslage, Sean Johnson
Affiliation: University of California Santa Cruz, WKID Solutions, CU Boulder, University of California Merced

There are many ways to measure biodiversity--richness, evenness, and divergence--using genetic data. Taxonomic biodiversity is most often used, where genetic information is first converted to taxonomic lineages, and these units are then used to calculate the metrics. Genetic biodiversity can also be measured by counting unique variants without linking to the taxa they derive from at all (e.g. k-mer counts) or by examining allelic diversity within what has been assigned to a taxon (population-level or clade-level counts). Taxonomic and genetic diversity are often found to have no relationship or to even be inversely correlated. Phylogenetic diversity, in turn, offers a different perspective on how genetic variation maps over space and time. But how do we meausure it?

The million-dollar questions relate phylogeny to function, specifically to ecological niche partitioning: can we expect low taxonomic redundancy but high phylogenetic redundancy, where sister taxa are reliably found in different locations, suggesting related species play similar roles in the community and are important? Is the breakdown of phylogenetic diversity the most telling of ecological processes and health?

Great botanists have advanced theories of what different phylogenetic diversity metrics can reveal, and perhaps the botanical community has developed these theories further than others. Here, we capitalize on the algorithms and real-world ecological connections that botany theoreticians have forged, and we test how these metrics behave in DNA metabarcoding data from the BioSCape project surveying the Western Cape of South Africa. We compare several phylogenetic diversity metrics to taxonomic diversity and remotely sensed functional diversity to derive explanations of how ecological processes and metrics all relate. Further, we examine how these metrics hold up across spatial scales. We hope this work contributes to the theoretical frameworks for using eDNA metabarcoding for biomonitoring beyond standard taxonomic biodiversity, which alone is too limited to inform people about the ecological traits and processes needed to estimate ecosystem health, evaluate ecological state, and alert managers when intervention is needed to assist nature.

Topic: Bryology and Lichenology

A-938

Abraham Halsey: Forgotten botanical pioneer and father of North American lichenology

Author: James Lendemer
Affiliation: The New York State Museum

Abraham Halsey published the first checklist of New York City lichens in 1823. It was the first work on lichens in North America. Study of this baseline—among the oldest, most comprehensive outside of Europe—has been complicated because the supporting vouchers were believed destroyed in an 1866 fire. Halsey's collection has been rediscovered and is reported here. His checklist is updated to modern concepts, and the original baseline is compared to present day. Shifts in the lichen biota of New York City, occurring after near-complete extirpation in the 1960s, followed by subsequent recolonization, demonstrate modern trends toward lower foliose and fruticose lichen diversity, lower diversity of sexually reproducing taxa, and lower diversity of taxa that associate with ecologically restricted photobionts such as *Trentepohlia* and cyanobacteria. This talk will focus on the legacy of a pioneering naturalist whose work came to be reduced to a footnote and whose role in American botany has been forgotten. This study also highlights the value of herbaria and the urgent need to assure these are preserved, digitized, and most importantly, continuously restudied.

Topic: Bryology and Lichenology

A-939

Appalachian Lichens: Trends and patterns across a biodiversity hotspot

Author: James Lendemer, Jessica Allen, Eli Denzer, Stephen Sharrett, Jeremy Howland
Affiliation: New York State Museum, University of California - San Diego, Eastern Washington University, City University of New York

The Appalachian Mountains are a globally recognized biodiversity hotspot that hosts a large and significant diversity of lichens. This presentation will draw on two decades of biodiversity inventory and analysis carried out across this region to summarize diversities, distributions and conservation priorities. In particular it will emphasize the need for quantitative gap analyses and targeted studies to fill existing sampling gaps and establish robust, comprehensive datasets with wide utility both within, and beyond, the field of lichenology.

Topic: Comparative Genomics/Transcriptomics

A-940

svArcher: A Reproducible Structural Variant Calling Pipeline Module For Plant Genomes.

Author: Trevor Mugoya, Arun Sethuraman
Affiliation: San Diego State University

Structural variation refers to differences in genomic regions that are larger than 1 Kbps between individuals, and can arise as a result of errant DNA repair mechanisms, whole genome duplications and transposable element activity across the genome. Recent advances, optimizations and cost reductions in next generation sequencing technologies have facilitated the exponential increase in the amount of available short and long read genomic data. Subsequently, the number of plant species sequenced has grown over the past 20 years, paving the way for a better understanding of their genetic diversity. Plant genomes also vary widely in ploidy, size, and amount of repeat content. This presents challenges in detecting structural variation, especially with short read genomic sequence data. Numerous methods and bioinformatics tools have been developed to detect signatures of structural variation from short read sequence data. Here I present svArcher, a reproducible structural variant calling pipeline written in Snakemake. svArcher implements an ensemble suite of structural variant callers (l umpy-sv, delly and gridss) as a module within the snpArcher pipeline. I then apply svArcher to short read whole genome plant sequence data using Arabidopsis thaliana as a study species for benchmarking against a validated set of 155,440 structural variants. I utilize 4 HiSeq X Arabidopsis whole genome sequence samples from BioProject(PRJNA293798) as a prototype subset to validate pipeline workflow. Preliminary structural variants counts pre-genotyping differ slightly between lumpy and delly callers (SAMN08235956; delly-10713, lumpy-sv-9198, SAMN08235960; delly-9836,-lumpy-sv-8066, SAMN08235961; delly-11740,lumpy-sv-9531, SAMN08235962; delly-11159,lumpy-sv-9011). Further development is currently underway to incorporate the gridss structural variant caller and further filtering and variant call merge functionality in the "svArcher" branch on GitHub at github.com/ChabbyTMD/snpArcher/tree/svArcher.

Topic: Plant genome skimming: special uses and future potential

A-943

PhyloAlps & PhyloNorway, a snapshot of Arctic-Alpine plant diversity

Author: Eric Coissac, Inger Alsos, Sebastien Lavergne, PhyloAlps Consortium, PhyloNorway Consortium
Affiliation: Université Grenoble-Alpes, UiT - The Arctic University of Norway

PhyloAlps and its twin project PhyloNorway are a ten-year story. Their goal was to create a genetic reference library covering the entire Arctic-Alpine flora based on the genome skimming method. In total, they produced about 8000 genome skims covering 6105 species. The complete data set is now available in the Short Read Archive (PRJEB85061; PRJEB56160). The concept of genome skimming emerged in 2012 (Straub et al) as a

low coverage shotgun approach to whole genome sequencing. Together with Pete Hollingsworth, we proposed in 2016 to use these genome skims as an extension of the DNA barcode system to address the complexity of plant diversity where classical makers fail (Coissac et al 2016). But what can we actually do with a genome skim? Since the average coverage of the genome is less than 1X, we cannot expect to assemble any part of the genome. Genome skims have to be considered as a new genome reduction method that can be easily implemented on any sample without any species-to-species adaptation, unlike some other techniques like RAD-Seq. The easiest to skim are highly repetitive elements such as the chloroplast genome or the nuclear ribosomal cluster. These sequences allow large phylogenies to be calculated (Lavergne et al. 2025). From the nuclear part of the genome it's easy to extract some population makers like microsatellites (Cheddadi et al. 2022) or SNPs (Lammers et al. 2024). Reference libraries based on genome skimming have demonstrated their great advantage over any currently available alternative for the taxonomic annotation of ancient DNA metagenomes (Wang et al. 2021), and we have recently developed WholeSkim, a new tool dedicated to this task (Elliott et al. 2024). However, more is expected from the development of new metrics and methods based on KMER techniques to address the sparseness of the data produced and to provide information on genome structure and relationships.

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Lammers, *et al.* (2024). Multiplexing PCR allows the identification of within-species genetic diversity in ancient eDNA. *Molecular Ecology Resources*, *24*(3), e13926. doi.org/10.1111/1755-0998.13926

Lavergne, *et al.* (2025). Towards a comprehensive barcoding and phylogenomic reference for the European arctic-alpine flora. In *Research Square*. doi.org/10.21203/rs.3.rs-6136147/v1

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Topic: Crops and Wild Relatives

A-944

Starch deficiency may lead to absence of BER in tomato (Solanum lycopersicum) crops

Author: Evelyn Elkington
Affiliation: Boyce Thompson Institute

Blossom End Rot (BER) is a problem that has affected tomatoes (*Solanum lycopersicum*) as well as other vegetables in the Solanaceae and Curcurbitaceae families for over a century. This physiological disorder is characterized by severe decay at the blossom-end of the fruit, and has devastating effects on crop production across the globe. This disorder can occur under several abiotic plant stress conditions, including irregular watering conditions, and Calcium (Ca^{2+}) deficiencies or excesses. As climate change continues to increase the abiotic stress placed on crop plants, it is vital to find ways to combat this devastating disorder to keep up with the demand for food worldwide. Previous studies show that starch deficiency in tomato plants leads to an absence of BER, which shows promise for creating a crop tomato that is resistant to the disorder. However, this theory has not been tested in commercial tomato crop accessions, such as M82, and has only been observed in research varieties. To remedy this, CRISPR/Cas9 gene editing was used to knockout the gene responsible for starch production in M82 plants, and rates of BER, fruit production, and plant growth patterns were observed. To understand how the expression of the starch gene affects BER, a chimeric construct was also used to knockout a promoter that is expressed exclusively in the fruits, so that a plant with starch in the leaves but not in the fruit was created. This has led to the discovery that plants without starch still produce fruits with BER, but at a much lower rate than those with starch, suggesting that there are other factors that lead to the development of BER. In plants that express starch in the leaves but not fruit, no BER has been observed, although this has yet to be tested in commercial accessions. Further testing is required to confirm that plants without starch grow at similar rates to those with starch, and that other factors, such as yield and food quality is not affected by this genetic change. However, these results show promise for the future of tomato crops, as well as other crops in the Solanaceae and Curcurbitaceae families such as pepper (*Solanum capsicum*) or watermelon (*Citrullus lantanus*).

Topic: Plant phenology in an era of rapid global change: new perspectives and frontiers

A-945

Engaging undergraduate students in exploring volunteer-contributed phenology data bears much fruit

Author: Theresa Crimmins, Martha Whitaker
Affiliation: University of Arizona

Some of the most robust, consistently collected phenology observations contributed to *Nature's Notebook*, the USA National Phenology Network's platform, have been contributed by Local Phenology Programs (LPPs) -- groups of individuals that collectively document phenology on plants and animals at a site. Many such groups have contributed regular observations for ten years or more. However, many of these observers are limited in their abilities to access and analyze these observations, so are left wondering what contributions their efforts are making to a broader understanding of phenological change in the U.S. To address this need, as well as to offer undergraduate students with real-world, hands-on experience in research, we established a Vertically Integrated Project (VIP) focused on exploring relationships between environmental conditions and plant and animal phenology at the University of Arizona, where the USA-NPN is based, in 2021.

In the 2024-25 academic year, nine students worked with phenology datasets contributed by four LPPs, gaining and refining skills in cleaning, summarizing, analyzing, and visualizing data and presenting results in poster and oral presentation formats. The students' findings have yielded valuable findings, helping to answer questions the LPP members had articulated and summarizing results in formats that the LPPs can use in messaging with new and existing volunteers and host institutions. This model, of connecting volunteer data collectors with students seeking to grow research-ready skills, is readily replicable to other academic institutions.

Topic: Biology of mycoheterotrophic and parasitic plants

A-946

Evolutionary ecology of mycoheterotrophic and parasitic plants

Author: Thomas Givnish
Affiliation: University of Wisconsin-Madison

Fully or partly heterotrophic angiosperms constitute roughly 5000 species of parasites and 28,000 species of mycoheterotrophic plants (MHP); 10% and 2% of these gain all their energy, water, and nutrients from autotrophic plants or fungi. Hemiparasites tap into host stems or roots and obtain much/all their fixed carbon via photosynthesis; partial MHPs obtain carbon from both photosynthesis and the mycorrhizal mutualists of autotrophic neighbors. Different ecological conditions should favor parasites and MHPs. Deeply shaded understories should favor mycoheterotrophy, given the limited energy available via photosynthesis and the abundant, easily tapped energy in mycorrhizal networks fed by sunlit canopy trees. Although dense shade might appear to favor parasitic plants, constraints on access to host tissues and C sources should favor hemiparasitism in grasslands (due to the abundance of and easy attachment to shallow primary roots in grasses) and tree and shrub canopies by mistletoes (due to the thin bark of twigs and abundant local C flows in fully or partly sunlit twigs). Hemiparasitism should be especially common at intermediate levels of soil water and/or nutrients and abundant light, with little growth and competitive advantage obtained in moist, fertile sites or shady sites, or in dry and highly infertile sites. High transpiration in hemiparasitic mistletoes, and low ratios of photosynthesis to leaf N content, have been ascribed to nutrient piracy from host xylem. However, these patterns might also arise because hemiparasites do not pay for the roots needed to replace transpiration but obtain photosynthetic benefits via greater stomatal conductance. Data on mistletoe and host *Eucalyptus* leaves along an Australian rainfall gradient support this economic model. The occurrence of >90% of ca. 50 origins of mycoheterophy in angiosperms within the monocots may reflect the reliance of monocots only on primary roots with voluminous root parenchyma, easily infected by mycorrhizal fungi. Fully parasitic and mycoheterotrophic plants have highly reduced plastid genomes. Limited data suggests that many nuclear photosynthetic genes have also been lost, or are no longer expressed, in such heterotrophs. A recent study of nuclear genomes in *Platanthera* showed loss of most photoreceptor and auxin

transporter genes and transcription factors regulating root development in fully mycoheterophic species, and enhanced expression of trehalase genes (which might enhance uptake of the sugar trehalose from fungi). Parasites should be favored by low-diversity communities with high host densities, but hemiparasites themselves can – if they attack dominant autotrophic hosts – diversify plant communities around them, as has been observed in several grassland systems.

Topic: Bryology and Lichenology

A-948

Creating Engaging and Informative Educational Materials

Author: Eli Denzer, James Lendemer, Jessica Allen
Affiliation: New York State Museum, The New York State Museum, University of California - San Diego

Over the past six months we have been working on a series of pamphlets to educate the public on lichens. Through this we have come to realize the importance of being able to communicate complicated ideas and jargon in an effective way. These pamphlets are used as a case study on the importance of writing to your audience and highlighting quick and easy ways to spruce up educational materials to make them more engaging. Getting and holding an audience's attention is vital to helping them absorb the information you are trying to impart.

Topic: Biodiversity Informatics & Herbarium Digitization

A-949

How to Setup an Imaging Station from Scratch

Author: Eli Denzer, James Lendemer, Jessica Allen
Affiliation: New York State Museum, The New York State Museum, University of California - San Diego

A quick introduction to getting digitization efforts up and off the ground with information about how to set up an imaging station on a budget, including materials, arrangement options and expenses involved. Specifically focusing on camera and lighting setups and postprocessing software for vascular plants, cryptogams, and other difficult to image specimens.

Topic: Plant genome skimming: special uses and future potential

A-950

Genome Skimming and Phylogenomics Inform a Species Recovery Plan for a Threatened Allopolyploid Plant

Author: Sven Buerki, Mathew Geisler, Peggy Martinez, Jim Beck, Ian Robertson
Affiliation: Boise State University

In the United States, 944 plant taxa are listed as threatened or endangered under the Endangered Species Act. Brassicaceae is the fourth most threatened family with 41 listed species. This study focuses on slickspot peppergrass (*Lepidium papilliferum*), a threatened Brassicaceae endemic to southwestern Idaho which is experiencing significant population decline and reduced fecundity. Our goal is to support the establishment of a breeding and genetic rescue program to restore populations of this species by addressing the following objectives: () confirm its genomic origin and the role of segmental allopolyploidization in its evolution, () investigate the importance of ancestral hybridization on its origin, () propose a phylogeographic hypothesis to inform its restoration, and () offer conservation and restoration guidelines. We sampled 44 individuals from 27 element occurrences (~populations) across three landscape management regions, including 16 individuals from closely related species. Using a genome skimming approach, we assessed genome size and heterozygosity, and conducted phylogenetic analyses on *de novo* assembled nuclear rDNA and plastome sequences. Results showed that *L. papilliferum* has an allopolyploid origin, with genome size variation and genotype frequencies supporting segmental allopolyploidization. Genomic discordance suggested the occurrence of ancestral hybridization events. Phylogenetic analysis of nuclear rDNA confirmed the species' monophyly, possibly because of genetic isolation driven by ecological speciation. We used nuclear rDNA clades to redefine landscape management regions for the species, offering new boundaries for a forthcoming species recovery plan. This research provides essential genetic insights to inform the restoration of slickspot peppergrass populations and guide conservation efforts.

Topic: Cultivating Collaborative Futures: Botanical Research Across Borders

A-952

Equitable botanical collaboration USA-Mexico: principles and perceptions

Author: Julieta Rosell Garcia, Mark Olson
Affiliation: Universidad Nacional Autónoma de México

Home to around 10% of the world's plant species, and representing North Temperate, tropical, and even many Southern Hemisphere lineages, as well as the full spectrum of global plant form and growth habit diversity, Mexico stands alone as the country that most comprehensively reflects the world's botanical diversity. It is no surprise, then, that Mexico is a natural magnet for botanical research. This attention is particularly strong from the United States, which has a long history of botanists working in Mexico. Today, interest in Mexican plants among US researchers is greater than ever. With major US herbaria and botanical gardens housing key collections of Mexican flora, and with industries built around Mexican ornamentals (cycads, cacti, orchids, bromeliads, poinsettias), as well as crop plants like native corn and bean landraces, it is essential to examine US–Mexico botanical collaboration through the lens of equity and decolonization. We present results from a survey of US and Mexican botanists regarding their perceptions of fairness and reciprocity in collaborative work. We highlight areas of agreement as well as points of divergence, and draw on personal experiences to explore practical ways to foster equitable research partnerships. Given the inevitable constraints of time and funding, we ask: how can botanists avoid "helicopter science" (research conducted without meaningful local collaboration or investment) and instead contribute to building scientific capacity within Mexico in ways that strengthen scientific communities on both sides of the border?

Topic: BSA Incoming President's Address

A-953

Botanists and Botanical Allies: Stronger Together

Author: Ken Cameron
Affiliation: University of Wisconsin-Madison

These are unprecedented times to be a botanist. Federal funding for research and education is being slashed, programs and institutions are being shut down, academic freedoms in our universities are under attack, agencies within which many of us work have been weakened, and existential threats to life on Earth are accelerating at a rapid pace. Human population already has doubled in my short lifetime and now exceeds 8 billion, CO_2 levels have crossed critical thresholds, deforestation is on the rise, and global warming leading to catastrophic climate change shows no sign of slowing down. There are days when many of us feel helpless and without hope for the future, but now is precisely the moment for us to stand strong together. Over the last several months social media has been flooded with excerpts from what has been called an "Authoritarian Regime Survival Guide." One of the reminders in this essay that stands out to me says that *strength lies in unity*, and that we must *resist allowing others to divide us*. We depend on family, friends, and allies. This has me thinking a great deal about the theme of this year's conference ("Botany without Barriers") and my own personal journey as a gay scientist helped along the way by straight allies both inside and outside of academia. I also have been thinking about the people around me who give me strength as a botanist. Yes, these include my professional colleagues, collaborators, and students, but they also include allies from outside the academic tent. I am a strong advocate for sharing our passion for plants, fungi, and Nature with those who do not hold degrees in botany, biology, or other plant science fields, but who are equally passionate about these subjects – our botanical allies. For example, I serve as an officer within several local garden clubs, and I engage in meaningful conversation online with plant hobbyists around the world. I cherish my fellow botanists, but I have come to learn that I also depend on my botanical allies. The Botanical Society of America recognizes the need to expand our community and to break down barriers -- we are not a group of academic elites. Indeed, one of the explicit goals of our current Strategic Plan is to increase membership in the BSA by people outside of academia by at least 10% over five years. There is no better time than now to reach out to our botanical allies and to give back when they reach out to us. We have so much in common; together we are stronger.

Topic: *Regional Botany Special Lecture*

A-954

Stranger in a Strange Land: The California flora vs a northeasterner's idea of "normal

Author: Amy Litt
Affiliation: University of California, Riverside

Topic: *Trees, Traits, and Time*

A-956

Exploring the Push and Pull of Patterning: the Diversification of the Epidermal Patterning Factor (EPF) Gene Family and its Potential Implications for Stomatal Patterning

Author: John Hodge, Andrew Leakey
Affiliation: University of Illinois Urbana-Champaign

Epidermal Patterning Factors (EPFs) are key signaling ligands which are best known for their role in facilitating stomatagenesis through the regulation of epidermal cell proliferation. EPF1/2s in Arabidopsis act as cell division inhibitors, reducing the formation of stomatal precursors. EPF1/2s are in turn inhibited by their close relative, EPFL9 (STOMAGEN), which promotes cell proliferation and the formation of stomatal precursors. Despite being members of the same gene family and acting through the same signal transduction mechanism, efforts to reconcile how the relationships of EPF1/2s and EPFL9s to one another, as well as the other major clades of EPFs, have left knowledge gaps. We have generated a phylogeny of all extant EPFs representing over 40 tracheophyte genomes to identify how and when these genes diversified. Current evidence shows that the EPF1/2 and EPFL9 clades are sister to one another suggesting that the cell proliferation inhibitor (EPF1/2s) and its own interference inhibitor (EPFL9s) are the possible result of an ancient duplication of this gene family. Moreover, synteny analyses suggest that these core EPF clades generally maintain their genomic context through deep time although key cases can be found in which specific EPF1 or EPFL9 orthologs have been shuffled following key genomic rearrangements during angiosperm evolution. Taken together this work hopes to better resolve our understanding of how the modern EPF clades arose, how recent duplicates tend to diversify and acquire new functions, and ultimately resolve how these processes could drive variation in stomatal patterning, and the broader angiosperm body plan.

Topic: *Plant phenology in an era of rapid global change: new perspectives and frontiers*

A-958

Phenobase: An open-access, integrated database of global plant phenology

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Plant phenology—the timing of key life-cycle events such as leaf-out, flowering, and fruiting—plays a critical role in ecosystem function and has been tracked by humans for millennia. In the face of rapid global change, it is vital we understand historical phenology baselines and rates of change across diverse environments and taxa. Continued long-term concerted efforts to collect plant phenology information, recent rapid growth of contributory science platforms, and specimen digitization initiatives have produced massive quantities of phenologically-relevant data at unprecedented scales. However, data from these many sources are difficult to integrate, phenological information is challenging to extract from images, and large temporal, taxonomic, and spatial gaps remain. Here, we discuss Phenobase, an open-access database which includes integrated global plant phenology information from *in situ* monitoring programs, community-collected plant photographs, and digitized herbarium specimens. We specifically leverage machine learning approaches to extract phenological data from millions of iNaturalist and digitized specimen images, and integrate these data using the Plant Phenological Ontology (PPO). We cover challenges of working with phenology data at scale, and discuss key strategic choices made to ensure stakeholders can trust and utilize downstream data.

Topic: *Phylogenomics*

A-959

A New Torreya species and its cryptical hybrid Discovered in Japan Sheds Light on the reoccurring hybridization events in late Oligocene

Author: Wenbin Zhou
Affiliation: UNC-Chapel Hill

Natural hybridization plays a crucial role in conservation biology, yet its underlying evolutionary mechanisms remain unclear. In this study, we reranked a variety T. nucifera var. radicans Nakai as a new species T. fruticosa Nakai and identified a potential hybrid species based on the different morphological characteristics, environmental niches, and molecular evidence. To investigate their evolutionary history, we applied genome skimming to sequence six individuals of T. fruticosa from Inami, Mie and Furuya, Kutsuki -mura in Japan. By integrating previously generated Hyb -Seq and RAD-seq data, we constructed both plastome and nuclear gene phylogenies. Subsequently, we employed PhyloNet to detect hybridization events in Torreya and used the fossilized birth-death model to estimate the divergence times of Japanese Torreya species. Our whole-genome resequencing data combined with previous RAD-seq data indicate that T. fruticosa forms a monophyletic group sister to T. nucifera, while plastome evidence suggests that all T. fruticosa individuals, except one potential hybrid, are monophyletic, which is

Topic: *Comparative Genomics/Transcriptomics*

A-960

Looking for adaptation to shade: Genome comparison between two rush species from shade vs. open and wetland vs. dryland habitats

Author: Wenbin Zhou
Affiliation: UNC-Chapel Hill

Adaptation to contrasting light environments, such as sun vs. shade, wetland vs. dryland habitats, influences plant physiological and genomic traits.

We performed whole-genome sequencing and assembly for two closely related species, *Juncus roemerianus* and *J. validus*, inhabiting open-sun, coastal wetland and shade forest understory environments, respectively. Additionally, we compared stomatal characters, genome size variation, and centromere organization, integrating RNA-seq data to explore functional correlations.

Our findings reveal that the sun-adapted *J. roemeranus* exhibits higher stomatal density but a lower stomatal index compared to its shade-adapted counterpart *J. validus*. We attribute the increased stomatal density to enhanced photosynthesis and over expressed key genes related to the stomata development. Surprisingly, we found the species growing in wetland genes related to drought tolerance are higher than the forest understories species due to the high salinity of the wetland environment. In contrast, the lower stomatal index in the shade species is associated with genome expansion and increased cell size. We found a whole genome duplication event shared between Juncaceae and Cyperace. But the expansion of genome size in shade species (*J. validus* ~550M) is not driven by whole-genome duplication but by a recent proliferation of repetitive elements, with repeat content reaching ~75% in the shade species versus ~35% in the open-sun species. Furthermore, we observed distinct centromere organization patterns between the two species. Specifically, we found a holocentromere-like genome in *J. validus* and a monocentromeric genome in *J. roemerianus*, suggesting that this structural genomic divergence is associated with light and water adaptation.

Our study provides insights into how a genome trait affects cell size expansion, stomatal patterning, and centromere organization to drive plant adaptation to different light and water environments. These findings highlight the role of repetitive element accumulation in genome size variation and its potential impact on cellular and physiological traits in response to habitat differences.

Topic: *Trees, Traits, and Time*

A-961

Spur shape and the diversification of Impatiens

Author: Jeff Rose
Affiliation: The Ohio State University

The evolution of nectar spurs has been hypothesized to be a "key innovation" in spurring species diversification in angiosperms. Spurs have evolved in at least 15 families, sometimes multiple times within families. Co-evolution between spur morphology and pollinators should lead to a new adaptive zone, resulting in reproductive isolation among populations. The evolution of nectar spurs has been studied from the perspective of its total length. However, nectar spurs are more complex structures than a one-dimensional measurement, varying in aspects such as length, width, depth, attenuation, curvature, and color. Moreover, nectar spurs may show temporal variation in their interactions with pollinators and different shapes may lead to differences in male and female reproductive success. The mega-diverse genus *Impatiens* (Balsaminaceae), with ~1,000 species distributed mainly in Africa and Southeast Asia, shows a diversity of nectar spur shapes, including multiple losses of spurs. Using a broadly sampled dataset of spurs and a phylogeny for ~40% of the genus, I quantify several aspects of shape in nectar spurs and examine their correlation with diversification rates across Balsaminaceae. These results shed light onto the effects that complex traits may have on diversification processes within spur-bearing flowering plants.

Topic: *Dryland Floras*

A-964

The historical assembly of the Atacama Desert flora

Author: Federico Luebert, Tim Böhnert
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The Atacama Desert, located on the western side of the Andes in northern Chile,is one of the most arid places on Earth. Despite its extreme aridity, it harbors over 1,000 vascular plant species, around one third of which are endemic to this area, with a mix of paleo- and neoendemics. During the last three decades, several floristic, phylogenetic, biogeographical and population genetic studies, along with increasing availability of species distribution data, incl. their close relatives, have shed light on the biogeographical relationships of the Atacama Desert flora (ADF). We conducted a systematic review of these studies to understand the historical assembly of the ADF. Phylogenetic studies combined with distribution data from over 80 clades present in the ADF reveal that four major floristic elements can be recognized, which represent four major patterns of biogeographical relationships: (1) Tropical Andean, (2) Chilean Mediterranean, (3) Trans-Andean and (4) Antitropical elements. The first two represent floristic connections between the ADF and its neighbouring areas, which account for the great majority of the studied plant lineages. The third describes a disjunct pattern of occurrence of certain groups both in the Atacama Desert and in the drylands just east of the Andes, but not in between. The fourth one is a well-known disjunct distribution pattern in the drylands of both North and South America. Divergence time estimates for some of these lineages range from the early Miocene to late Pliocene/early Pleistocene and reflect the ages of the most recent common ancestors of Atacama Desert species. Tropical Andean and Chilean Mediterranean elements may have originated from relatively recent floristic exchanges through range expansion between the ADF and both neighbouring regions during the increasing aridification of the Atacama Desert, possibly along low-Andean corridors. Trans-Andean elements may have originated through Miocene vicariance as a result of the Andean uplift. Finally, the Antitropical element may be the result of several long-distance dispersal events throughout the Neogene and even the Quaternary. The current distribution and population structure of ancient lineages of the ADF (paleoendemics), which originated before the Neogene, appear to be the result of recent event during the Pliocene to Quaternary. There is increasing evidence that *in-situ* diversification of plant lineages in the ADF was strongly influenced by alternating pluvial and arid cycles, resulting in range contraction and expansion, leading to allopatric speciation followed by secondary contact. The latter by few studies of relatively diverse plant groups currently having over four closely related, sympatric species. However, the conclusions drawn here still await to be confirmed with more robust evidence derived from next-generation data and a larger number of plant groups that have not yet being investigated.

Topic: *Common gardens in the 21st Century: the intersection between evolution and ecology, science and management*

A-965

Adaptive significance of Quercus macrocarpa leaf morphology based on a reciprocal transplant experiment across a latitudinal gradient

Author: Laura Ostrowsky, Lucy Rea, Mariana Hernandez Leal, Andrew Hipp, Heather McCarthy, Rebekah Mohn, Mira Garner, Jeannine Cavender-Bares
Affiliation: Harvard University, University of Minnesota, Harvard, The Morton Arboretum, University of Oklahoma, University of Minnesota - Twin Cities

As the climate changes, manyNorth American trees are facing novel environmental stressors that threaten their survival. It is unclear whether ecologicallyimportant tree species have the genetic variation necessary to adapt in situ to these changes, or if the speed of adaptation can keep pace with the rate of climate change. Species with wide geographic ranges often exhibit local adaptation between populations that experience variable environmental conditions. Research into intraspecific local adaptation can provide insight into the capacity of trees to adapt to novel stressors. This study uses a reciprocal transplant experiment of bur oak (*Quercus macrocarpa*) across a climatic gradient to test for local adaptation and plasticity in leaf morphological traits that may confer fitness in varying environments. Northern populations had high mortality in the southern garden, demonstrating the risk to northern trees under future climate conditions. Southernpopulations had greater growth and fitness in all gardens, which may indicate that these populations could succeed in adaptive management and assisted migration programs for this species. The populations had distinct leaf morphologies and suites of covarying morphological traits, including a much greater degree of leaf lobing in the southern population. The suites of functional traits relate to fitness and demonstrate that leaf lobing may confer fitness in bur oak. While the most southern population had more lobed leaves, the most southern garden had the least lobed leaves, displaying counter-gradient variation in lobing as a functional trait. A comparison of FST to QST using SNP data provides evidence for diversifying selection on leaf lobing between populations. These results characterize the potential for adaptation and acclimation in morphological traits across the geographic range of bur oak and may have important implications for adaptive management of bur oak in a changing climate.

Topic: *Common gardens in the 21st Century: the intersection between evolution and ecology, science and management*

A-966

Genetic and genomic studies of local adaptation and genotype-by-environment interaction in switchgrass (Panicum virgatum) using common gardens

Author: Thomas Juenger
Affiliation: University of Texas at Austin

Plants live in an ever-changing and unpredictable environment. As sessile organisms, they must acclimate or adapt to complex environmental changes occurring across both space and time. Which environmental variables matter the most? What physiological or metabolic mechanisms buffer responses to the environment? How are these responses encoded in genomes and how do they evolve? Genome-enabled research is helping to address these longstanding questions by characterized a myriad of "-omic" responses to common abiotic and biotic stresses and environmental gradients. The challenge now is to disentangle evolved and adaptive responses of plants to stress from the deleterious results of stress. A promising avenue is the use of locally adapted natural variation and common garden studies to better understand genetic and environmental responses. Here, I report on progress in the development of genetic and genomic resources for switchgrass, as well as present results from common garden field experiments aimed at understanding the genetics of upland/lowland ecotype divergence, plasticity, and local adaptation.

Topic: Plant genome skimming: special uses and future potential

A-969

Updated Skmer Improves Reference- and Alignment-Free Population Genomics

Author: Eduardo Charvel, Vineet Bafna, Siavash Mirarab
Affiliation: UC San Diego, UCSD

Skmer (Sarmashghi et al, 2019) addresses the problem of obtaining nuclear genomic distances based on skimming data, which had previously largely been constrained to barcoding and organelle assembly. It does so by estimating coverage and error rates, which are then incorporated into a distance estimate derived from the observed *k*-mer set similarity (Jaccard index) as computed by Mash (Ondov et al., 2016). However, because of its assumptions of haploidy and non-repetitiveness, it remains largely naive to biological phenomena that may complicate genomic data. These effects are especially felt in population level applications, where samples are only separated by very small genomic distances. In this talk, we will address both of these issues by presenting new developments to the method and how they can lead to better alignment-free and reference-free population genetic analyses.

Repetitive Genomes: One way of measuring repetitiveness of a sequence is through its k- mer repeat spectrum, which can be obtained directly from a reference assembly or estimated through methods like RESPECT (Sarmashghi et al 2021). A new version of Skmer, called Skmer-Repeat, incorporates repetitiveness into its distance estimation by modeling how the repeat spectrum of organisms within a population can impact the observed number of shared k -mers.

Diploid Organisms: Because diploid organisms within a population have different combinations of heterozygous and homozygous alleles, a ploidy-agnostic approach cannot always lead to an accurate estimate of distance. With the introduction of Skmer-Diploid, we will explore how heterozygosity can impact the Jaccard index of diploid samples and discuss how simulating diploid evolution with the coalescent model can help generate more accurate estimates of distance.

We will also be discussing potential applications of Skmer in phylogenomics, estimating nucleotide diversity (π) and fixation index (Fst), as well as population clustering. Finally, we will present best practices for data preprocessing and postprocessing, along with pipelines that can be used to analyze your data quickly on HPC clusters and optimal parallelization for quick turn around of biological analyses.

Topic: Macroevolution

A-970

A climate-change-proof adaptation found along an Alaskan latitudinal cline

Author: Marcel Carita Vaz, Ned Fetcher
Affiliation: Natl Inst of Research for Amazon, Wilkes University

Arctic plants that make up the tundra and boreal forests have been subjected to drastic changes in climate for the past millennia. As ice sheets expanded and retracted several times, these species were repeatedly pushed out of their environmental optima, yet they managed to somehow quickly adapt to the new conditions. Although plants may have tracked their optimum climates through latitudinal migrations, they still had to traverse a very steep gradient of seasonal light regime, with summers getting shorter, but summer days getting longer as they moved Northwards. The current phenomenon of Arctic amplification is actually offering us a great opportunity to test how these plants have adapted to the decoupling of light and temperature regimes throughout their evolutionary histories. We focus on a 10-year long, reciprocal transplant experiment done in North Alaska with *Eriophorum vaginatum* (Cyperaceae), a crucial foundation species for the tundra. Because leaf senescence is an essential adaptation against frost damage, we looked at the environmental factors triggering this behavior for different ecotypes found between Coldfoot (67°15'5"N 150°10'34"W; taiga) and Sagwon (69°22'0"N 148°42'0"W; tundra). With the support of light and temperature manipulation experiments done in the field and in the lab (growth chambers), we found that seasonal changes in both light and temperature independently trigger leaf senescence. Moreover, light cues varied across ecotypes in a manner that makes adaptive sense, with Southern plants requiring longer nights to start senescing than Northern ones (the nights get darker in the South first). Although this might seem like a disadvantage for all migrating plants, Southern plants can actually remain active for most of the ever-expanding summer in the North, while Northern plants in the South will senesce way before the end of the summer. This clear advantage of Northward migrations, however, only exists because of global warming. By extension, one could assume that if climate was getting colder, then the late senescence of Southern ecotypes would be more severely punished by increasing frost damage, thus favoring Southwards migrations. Therefore, by coupling their leaf senescence response to the seasonal variation in photoperiod, *E. vaginatum* might have evolved a climate-change proof adaptation that allows them to outperform Northern ecotypes when the climate is warming and vice-versa, provided latitudinal migration is not blocked.

Topic: Systematics & Taxonomy

A-971

Revising the Tauschia of the Western United Sates - Old Names and New Combinations

Author: Mary Ann Feist, Phebian Odufuwa, Michael Krellwitz, James Smith, Amanda Shalit, Don Mansfield, Mark Darrach
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The genus *Tauschia* Schltdl. as currently delimited has 32 species found across the Americas. The majority of these species are endemic to Mexico, but seven are endemic to the western United States, one species is known from both from Mexico and the United States, two are endemic to Guatemala, one is known from Mexico and Ecuador, and one from Mexico, Guatemala, Colombia, and Venezuela. Typically, *Tauschia* species have the following combination of characters: acaulescent or low caulescent habit, lacking stylopodium, ribs filiform to prominent but not winged, fruit slightly laterally flattened, seed nearly terete in cross-section, seed face deeply concave or sulcate. However, many species of *Tauschia* deviate in one or more of these characters. This genus has always been problematic for taxonomists; the species currently in *Tauschia* have previously been assigned to 16 different genera. Recent molecular studies utilizing cpDNA and nrDNA revealed the genus Tauschia to be highly polyphyletic. Follow-up studies utilizing Agiosperm 353 data have allowed a better understanding of the species currently assigned to the genus Tauschia. Many of the species in this genus are being reassigned to new genera. In many cases old genera are being ressurected and new combinations are being made. The results of this work will be presented.

Topic: Ecophysiology

A-973

Physiological plasticity of temperate lianas in response to altered light environments

Author: Dianne Pater
Affiliation: Vassar College

Plants contend with a variety of environmental conditions that influence their growth and success, with light availability being one of the most limiting. As both the quality and quantity of light vary continuously both spatially and temporally in the forest understory, the ability to efficiently capture light is essential for the success of understory plants. As non-native invasive liana species have become increasingly common in North America, with extensive colonization in areas of landscape fragmentation and human disturbance, understanding their physiological characteristics can help inform control and conservation efforts. This research seeks to characterize the photosynthetic and water-use characteristics of the non-native liana species *Ampelopsis brevipedunculata* and *Celastrus orbiculata* under sun and shade conditions.

Topic: Cultivating Collaborative Futures: Botanical Research Across Borders

A-974

Roots and Responsibilities: Decolonizing Botanical Collaborations Across Borders

Author: Makenzie Mabry
Affiliation: University of Florida

As cross-border collaborations in botany continue to grow—particularly between the United States and Mexico—it is vital to ask: What does equity in scientific collaboration truly require? How can we move beyond extractive models to center justice, reciprocity, and shared authorship, especially when working with underrepresented and Indigenous communities? This presentation reflects on the colonial legacies embedded in botanical research and the ongoing need to reimagine collaboration through more equitable and inclusive practices. By revisiting the narratives of plants and the structures of our field,

we consider how historical exclusions continue to shape who conducts research, whose knowledge is recognized, and who benefits. Drawing from experiences in international and community-based research, I discuss the challenges and opportunities of building collaborations rooted in mutual respect, transparency, and long-term commitment. This talk aims to contribute to a broader dialogue about how we, as a botanical community, can acknowledge past harms and collectively define practices that promote fairness, accountability, and shared stewardship in our research partnerships.

Topic: Tropical Biology

A-975

Growth-reproduction trade-offs in trees: management applications for a taxonomically complex forest in the Central Amazon

Author: Marcel Carita Vaz, Nívia Lopes, José Luis Camargo
Affiliation: Natl Inst of Research for Amazon

Topic: Ecophysiology

A-976

The environmental factors driving tree phenology in one of the Southernmost Brazilian wooded savannas

Author: Marcel Carita Vaz, Matheus Victal Cerqueira, Jamil Ayach Anache
Affiliation: Natl Inst of Research for Amazon, Universidade de Sao Paulo

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Topic: Ecophysiology

A-977

Nature v.s. Nurture in the Alaskan Arctic: Are Photosynthetic Traits Genetically or Environmentally Determined in Tussock Sedges?

Author: Marcel Carita Vaz, Caleb Edwards, Ned Fetcher
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Topic: Biogeography

A-978

The lichen Scytinium plicatile, a member of family Collemataceae, documented in Humboldt County, California

Author: Leo Buoncristiani, Elizabeth Faidley
Affiliation: Cal Poly Humboldt

Scytinium plicatile (Ach.) Otálora, P.M. Jørg. & Wedin is a lichen within the family Collemataceae known from Europe, North America, and rarely, Australasia. In North America, the genus *Scytinium* has a cosmopolitan distribution, with S. plicatile found in California, Oregon, Washington, Nevada, Arizona, Utah, South Dakota, Idaho, Colorado, Iowa, and Massachusetts. *Scytinium plicatile* is an irregularly lobate, rosette forming, gelatinous cyanolichen with a photobiont in the genus *Nostoc*. North American material is frequently fertile, with globose isidia. It has a substrate preference of moist calcareous rocks and is often found in seeps or drainage sites. *Scytinium plicatile* was not known to be present in Humboldt County, California, until 2023, when we collected a specimen from concrete on a building on the Cal Poly Humboldt campus in Arcata. The species identification was done via macro- and micro-morphological analysis and DNA sequencing. The partial ITS 1, 5.8s ribosomal RNA gene, and partial ITS 2 regions from the primary fungal symbiont were compared to sequences of confirmed collections at Oregon State University. Since 2023 we have found two more populations of *S. plicatile* on concrete on the Cal Poly Humboldt campus, but the species has yet to be observed in the region in a non-anthropogenic habitat. This finding is important as a new geographic record for the species. The closest known *S. plicatile* population to this site is approximately 160 miles away, in Sonoma County, California. Additionally, we used scanning electron microscopy to observe various morphological features of the species for the first time, such as the cellular organization of the cortex and isidium development. The isidia of *Scytinium plicatile* are produced laminally, and in our material, remain spherical throughout their development. *Scytinium plicatile* has an unusual cortex organization, which in surface view looks like irregular, jigsaw puzzle pieces, a feature that it shares with a small group of closely related species within the genus. The cells that make up the cortex are long and interwoven, lending it the irregular appearance in surface view. This cortical structure, whose functional significance, if any, has yet to be determined, is also present in several other unrelated lichen genera, such as *Leptogidium contortum* (Pannariaceae), *Bryoria fremontii* (Parmeliaceae), and *Sinuicella denisonii* (Peltigeraceae).

Topic: Plant genome skimming: special uses and future potential

A-980

Eight years into the California Environmental DNA Program CALeDNA: lessons learned, and imagining the future

Author: Rachel Meyer
Affiliation: University of California Santa Cruz

CALeDNA started out as a community science program focused on using metabarcoding all kinds of organisms from all kinds of habitats to make a biodiversity baseline of California. Students from around the state led grassroots projects and explored machine learning techniques to predict biodiversity and hypothesize what the patterns were indicating about the state of nature. Seeing the value of data integration across projects, CALeDNA spun out the eDNA Explorer webtool to help people globally integrate data and learn from each other. We evolved the CALeDNA program and webtool together to bring in other kinds of metagenome skimming techniques such as capture hybridization for population, kinship, and density diagnostics, and more sensitive assays such as dPCR and qPCR to target species of special concern. In this presentation I will describe the latest CALeDNA case studies to measure nature (especially plant interactions and processes!) and will describe the opportunities to find nature based solutions from integrated eDNA data, remote sensing and other biodiversity data, and AI / Machine Learning tools combined with human local expertise. I'll also highlight the challenges and lessons learned along the way in hopes to help people who want to start their own eDNA research projects or coordinate programs. This talk has relevance to people interested in conservation, restoration, biodiversity health, and in enterprise that works in harmony with nature.

Topic: Bryology and Lichenology

A-981

A genomic reevaluation of the species delimitation based on chemistry in the Lecanora leprosa species complex using reference-based restriction-site-associated DNA sequencing data (RADseq)

Author: Alejandrina Barcenas-Peña
Affiliation: The Grainger Bioinformatics Center & Negaunee Integrative Research Center

Species delimitation is largely based on morphological, anatomical, or chemical characters. However, molecular studies have demonstrated the common occurrence of cryptic species, representing distinct lineages lacking prominent morphological or chemical characters. More recently, reduced genomic data sets, such as Restriction-site Associated DNA sequencing (RADseq), have significantly enhanced species delimitation and provided a robust framework for assessing gene flow among lineages during the speciation process.

This study investigates species delimitation within the *Lecanora leprosa* complex, which includes three pantropical species that are morphologically similar and primarily distinguished by their main secondary metabolites: 1) *L. achroa* with usnic acid and atranorin, 2) *L. helva* with 2'-O-methylperlatolic acid and atranorin, and 3) *L. leprosa* with gangaleoidin and atranorin. Although previous studies based on ITS sequences recovered the three species as distinct phylogenetic lineages, they did not fully resolve the relationships among them. We integrate morphological, anatomical, and chemical analyses with RADseq-based population genomic analyses to evaluate species delimitation in the species complex. Our phylogenomic data revealed four well-supported clades within the complex. Population genomic analyses indicated the absence of gene flow among these four clades. Two previously recognized species were strongly supported, whereas *L. achroa* included two distinct lineages, one of which will be described as a new taxon

Topic:

A-982

Management of Chilli Leaf Curl Virus (ChLCV) of Chilli using selected Agrobotanicals, Raw cow milk, Bioagent and Insecticide under field condition

Author: Tabassum Tamima
Affiliation: Sher-e-Bangla Agricultural University

Chilli (Capsicum annum), belonging to the Solanaceae family, is one of the world's most important horticultural crops and spices. It is also one of the oldest domesticated crops, originating in the Americas. In Asia, 65% of chilli is produced. For the past three decades, ChLCV has been one of the problematic diseases of chilli, spread by white fly(Bemisia tabaci). Management of ChLCV has been based primarily on insecticides against the whitefly vector. However, the use of insecticides is only partially effective, costly for producers, and represents a hazard to farmers, consumers, and the environment. In this research we found that the lowest disease incidence, the lowest per cent disease index were recorded in T5(Malathion) and T1 (Neem leaf extract) at 35,55,75 DAT, respectively. The highest yield and lowest yield reduction over control were in T4(Malathion) and then in T1(Neem leaf extract). It was recommended to use the readily available neem leaf extract to manage this disease for eco-friendly management as this is cost-effective and easy to get in Asia.

Topic: Cultivating Collaborative Futures: Botanical Research Across Borders

A-983

What is (de)coloniality? Anthropological and other interdisciplinary critiques of science and North-South collaborations in biological/ botanical research

Author: Francisco Vergara-Silva, Eduardo Restrepo
Affiliation: Universidad Nacional Autónoma de México, Universidad Católica de Temuco

The subject of 'decolonization of science' has been recently addressed by communities of biological researchers, not only in specific locations across a North-South geopolitical divide, but also 'globally'. For practicing biologists involved in this conversation, however, it might not be clear how 'coloniality' and 'decoloniality' were proposed and elaborated as analytical categories throughout the past few decades, among groups of politically-engaged anthropologists, philosophers, and other social scientists, several of them located in Latin American countries. Intended as a brief (conceptual, historical) introduction to the subject, the two participants in this recorded conversation will highlight the original contributions of Latin American critical anthropological theory to the 'rise of decolonial studies'. The potential relevance that the ethical, political dimensions of current academic and intellectual debates on '(de)coloniality' might have for ongoing dialogues on North-South collaborations in botanical (and other biological) scientific research will be discussed, highlighting the role of plants in the historical trajectory of the interactions between New Spain / Mexico and past and present 'colonial powers'.

Topic: Bryology and Lichenology

A-984

Assessing Bryophyte Communities of On-Trail versus Off-Trail Rockhouses in Pickett CCC Memorial State Park and Pogue Creek Canyon

Author: Aspen Mazzatta, Jessica Budke, Eric Shershen
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Located in the Cumberland Plateau, Pickett State Park and Pogue Creek Canyon contain many sandstone overhangs (rockhouses) that contain rare flowering plants. The mosses and liverworts (bryophytes) living in these cool, moist microhabitats have not been comprehensively surveyed. Thus we do not know if they contain rare species of conservation concern or how park visitors might impact these communities. This study assessed the bryophytes and evaluated species richness and abundance in the rockhouses of Pickett State Park and Pogue Creek Canyon. We carried out both community inventories and 30-meter transect coverage surveys for eight rockhouses. We analyzed these data in R using Welch's two sample t-tests. We found three bryophyte species that are designated as critically imperiled in Tennessee. Their locations will be shared with park managers, so steps can be taken to enhance their conservation. We also observed that on-trail sites tended to have lower bryophyte cover compared to off-trail sites. However, tests of these data were not statistically significant. This study expands our knowledge of bryophyte communities and helps to inform conservation efforts for these small and understudied plants.

Topic: Cultivating Collaborative Futures: Botanical Research Across Borders

A-985

Dilemmas and horizons in decolonizing ecology: implications for international research agendas

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Science has been marked by a colonial legacy that has favored both institutions and researchers from the Global North while marginalizing those from the Global South. This is particularly true in the biological disciplines, including botany and ecology more broadly. Such a colonial practice in biological research has been critically questioned only recently under the general motto of the "decolonization of science". Key proposed actions include: fostering equitable global research collaborations that move beyond parachute science; valuing local ecological knowledge; reforming undergraduate and graduate curricula; adopting inclusive, multilingual editorial policies; and addressing historical and taxonomic injustices within natural history museums and botanical gardens. While these proposals are both necessary and provocative, their implementation often reveals dilemmas and paradoxes. In this talk we will look at the dilemma that decolonizing ecology presents for young scientists in terms of building a solid academic career under current standards of excellence. We will also problematize how open access publishing policies paradoxically widen the publication gaps between ecologists from the Global North and South. Finally, we will explore the contributions that decades of Mexican ethnobiology can offer for the construction of a diverse and collaborative bi-national botanical agenda, based on a truly decolonial compass.

Topic: Cultivating Collaborative Futures: Botanical Research Across Borders

A-986

US-Mexico collaboration: a two-decade case study pursuing the live oaks (Quercus section Virentes) across the tropical temperate divide

Author: Jeannine Cavender-Bares, Antonio González-Rodríguez
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In 2003, a shared interest in the biogeography of live oaks (*Quercus* section *Virentes*) sparked a collaboration between Jeannine Cavender-Bares (then an assistant professor at the University of Minnesota, UMN) and Antonio González-Rodríguez (then a graduate student at Universidad Nacional Autónoma de México, UNAM). What began as an email exchange and a collecting trip across Mexico evolved into a long-standing partnership bridging institutions, countries, and generations. Motivated by the ecological and evolutionary significance of Mexico's oak diversity, our collaboration has integrated fieldwork, genomics, and functional ecology. Over time, our partnership has expanded through shared postdoctoral training, fieldwork in Baja California and Central America, and co-teaching a Distributed Graduate Seminar in Sustainability Science with colleagues from UMN, UNAM, Harvard University, Arizona State University and others. Despite challenges—particularly in sustaining funding for cross-border work and navigating institutional asymmetries—the collaboration thrived due to enduring friendship, mutual respect, and a network of supportive oak researchers, including the International Oak Society. Language dynamics, personal growth, family connections and a network of colleagues shaped the working relationship as much as scientific goals. Numerous joint publications emerged, enhancing understanding of oak diversification and introgression across the Americas. A key strength has been a focus on fairness, reciprocal mentorship, and openness to evolving needs, resulting in cross-institutional training and long-term scholarly exchange. This collaboration illustrates the value of investing in relationships that extend beyond research outputs. While logistical and financial obstacles persist, the benefits—for science, for students, and for institutional ties—are clear. Trust, patience, and the recognition that collaboration is both scientific and deeply human have sustained this partnership for over two decades. As students and postdocs now cross borders in both directions, the collaboration continues, reminding us that friendship can be as foundational as data in advancing science.

Topic: Cultivating Collaborative Futures: Botanical Research Across Borders

A-987

Offshoring and Nearshoring in Academia: Taboo or missing opportunity?

Author: Rodrigo Mendez Alonzo, Mark Olson
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Offshoring, the relocation of company activities such as production, services, or research and development to other countries to reduce operating costs, has been a widely adopted strategy throughout the 20th and 21st centuries. It has fueled globalization, driven market liberalization, and brought wide-ranging benefits to national economies. Despite its prominence in the corporate world, offshoring has been far less studied in the realm of science. Scientific institutions, from universities to research centers, rarely appear in discussions of offshoring, even though they increasingly operate in globalized contexts. In this presentation, I explore the parallels between corporate and scientific offshoring and argue that, when thoughtfully structured, scientific nearshoring and offshoring can spark meaningful collaborations, stimulate local, regional, and national development, and improve the quality of life for graduate students and postdoctoral researchers. By drawing on concrete examples, I will show how the redistribution of scientific resources can foster more equitable partnerships and deepen long-term ties between academic communities in the Global North and Global South.

Topic: Paleobotany

A-988

Osmoxylon-like fossils from early Eocene South America: West Gondwana–Malesia connections in Araliaceae

Author: Peter Wilf
Affiliation: Penn State University

Araliaceae comprise a moderately diverse, predominantly tropical angiosperm family with a limited fossil record. Gondwanan history of Araliaceae is hypothesized in the literature, but no fossils have previously been reported from the former supercontinent. I describe large (to macrophyll size), palmately compound-lobed leaf fossils and an isolated umbellate infructescence from the early Eocene (52 Ma), late-Gondwanan paleorainforest flora at Laguna del Hunco in Argentine Patagonia. Living species comparable to the *Caffapanax canessae* leaf fossils belong to five Araliaceae genera that are primarily distributed from Malesia to South China. The most similar genus is *Osmoxylon*, which is centered in east Malesia and includes numerous threatened species. The *Davidsaralia christophae* infructescence is also comparable to *Osmoxylon*. The *Caffapanax* leaves and *Davidsaralia* infructescence, potentially representing the same source taxon, are the oldest araliaceous macrofossils and provide direct evidence of Gondwanan history in the family. The new fossils and their large leaves enrich the well-established biogeographic and climatic affinities of the fossil assemblage with imperiled Indo-Pacific, everwet tropical rainforests. The fossils most likely represent shrubs or small trees, adding to the rich record of understory vegetation recovered from Laguna del Hunco.

Topic: ASPT Incoming President's Address

A-989

The Peculiar Advantages of Natural History

Author: Andrew Hipp
Affiliation: The Morton Arboretum

As systematists, we play a vital role in increasing people's appreciation of biodiversity. We collaborate with land managers and help shape conservation policy. We promote herbaria as archives, research platforms, and spaces for researchers to work shoulder-to-shoulder with amateurs. We build and translate humans' understanding of plant diversity. We mentor educators and students. In all of this, we play an often-understated role in helping people learn the vital skills of natural history: seeing, describing, and making sense of complex patterns in the natural world. The practices of systematics and natural history enable us to appreciate the complex networks of organisms that inhabit our neighborhoods, local parks, and natural areas. Our discipline thus builds foundational knowledge and skills that are useful to every member of society. As ASPT approaches its centennial, our continued success will depend on the strength of a diverse community of artists, educators, researchers, land practitioners, and enthusiasts. Supporting and continuing to build this extended plant systematics community is our best way to ensure its effectiveness and strength.

Topic: Common gardens in the 21st Century: the intersection between evolution and ecology, science and management

A-990

Leaf traits and whole-tree architecture detected by drone photogrammetry reveal adaptive genetic variation in a common garden study of Quercus lobata

Author: Alexander Goetz, Derek Young, Berenice Badillo, Kara Sanghera, Victoria Sork
Affiliation: UCLA, University of California, Davis, US Forest Service, US Department of Agriculture

Common garden provenance studies allow us to quantify adaptation of trees to past and current climates and can in turn improve management outcomes under future abiotic stress. Remote sensing techniques have been commonly used to collect detailed individual tree-level morphological and physiological data on coniferous trees, but relatively few studies have applied these techniques to non-timber broadleaf species, probably because their greater structural heterogeneity and lateral growth make them more difficult to measure. We quantified morphology (crown shape and width) and greenness (which broadly indicates plant health and photosynthetic rate) of 1,338 12-year-old valley oak (Quercus lobata) trees from 601 maternal lineages in a common garden using drone-mounted photogrammetry, supervised automated treetop detection, and multi-band spectroscopy. We then validated these measurements using hand-collected tree height data (all trees) and leaf trait data (subset; n = 161). Finally, we tested associations of tree morphology, greenness, and leaf traits with tree genetics and climates of maternal origin. Drone-estimated tree height scaled closely with field-collected tree height (R^2 = 0.81, slope = 0.999). Resource-conservative leaf traits (thickness, dry mass/area, and trichome density) were correlated with more compact whole-tree growth form per unit height, suggesting that the same selective pressures shape intraspecific variation in both leaf morphology and tree architecture. Greenness and three-dimensional structure were strongly differentiated by maternal lineage and significantly associated with climate of maternal origin. Trees from hotter, drier climates had higher greenness in the garden than trees from cooler, wetter climates despite tending to exhibit resource-conservative growth strategies, suggesting that stress tolerance is more advantageous than resource acquisition in the garden environment. The pattern of trees from hotter, drier origins outperforming those from cooler, wetter origins is consistent with past work in this common garden. In closing, we report that drone-based remote sensing provides a useful high-throughput means of quantifying growth and measuring genetically based leaf differences in broadleaf species.

Topic:

A-991

An Italian Herbarium Network: How a Digitization Project at the University of Florence Became a Pathway for Seven More Herbaria

Author: Victor Shields, Elena Canadelli
Affiliation: Picturae

Since the time of Luca Ghini in the 16th century, herbaria across the Italic Peninsula have collaborated to advance botanical knowledge. These networks of naturalists, both within and beyond Italy, left behind collections and research that remain valuable today. In 2023, the National Biodiversity Future Center was established with European Union funding and tasked with coordinating national efforts to preserve Italy's biodiversity. One pathway toward this complex goal is to make centuries of botanical data in Italian museum collections digitally accessible to researchers and the public.

By the beginning of 2024, a project coordinated by the University of Padua and jointly funded by the NextGenerationEU and PNRR programs began at the University of Florence to digitize the entire FI herbarium collection using technology from the digitization specialist, Picturae. As many herbaria that digitize their collections discover, pre-digitization specimen counts often differ from the actual counts at the end. In this case, the resulting discrepancy opened opportunities for new partnerships, allowing additional institutions to join and complete the digitization of their collections by the end of 2025.

This expanded effort will result in 4,250,000 specimens becoming digitally accessible, including significant collections from Padua (PAD) and Rome (RO) that were not originally part of the project. We are pleased to share this story at Botany 2025 and remain optimistic that the project's data will eventually be integrated into GBIF in support of biodiversity conservation, continuing Italy's long-standing tradition of networking within the botanical community.

Topic:

A-992

Two Mesozoic Paleoendemics With Contrasting Fire Adaptive Traits: Impact of Recent Megafires on Sequoia and Sequoiadendron

Author: Jon Keeley
Affiliation: US Geological Survey

Coast redwood (*Sequoia* sempervirens and giant sequoia (*Sequoiadendron* giganteum) are two iconic paleoendemic species with limited distributions, well known for their spectacular size. Recently, they have been exposed to high-severity crown fires, with starkly contrasting responses. We used all available published literature and field observations to understand the responses to fire in an evolutionary context. Coast redwoods, found in California's coastal rainforests, were highly resilient to high-severity fires, with most trees surviving due to their ability to resprout from the base and trunk, though seedling regeneration was largely lacking. In contrast, giant sequoias, native to the Sierra Nevada, do not resprout, leading to significant tree mortality after very high-severity fires; they released seeds only in patches of moderate-high severity fires where some trees survived. We conclude these high-severity fires were novel events for giant sequoias, but not for coast redwoods. Fire suppression has disrupted the natural fire regime in the giant sequoia ecosystem by preventing frequent lightning-caused surface fires, resulting in high severity fires that killed a substantial number of these giants. In coast redwood forests, infrequent but high severity crown fires were the norm prior to Native American burning. Frequent, low severity burning by Native Americans over the past few hundred years was localized and 20 th century fire suppression has returned the natural fire regime to these forests. The recent crown fires do not represent a threat to redwood conservation, however, other management goals may require emulating Native American burning practices, best termed cultural restoration.

Topic:

A-993

From Forests to Mountains: A vision for conservation, sustainable development and livelihood protection

Author: Uromi Goodale
Affiliation: Xi'an Jiaotong-Liverpool University

Professor Uromi Manage Goodale's scientific journey is deeply rooted in the mentorship of Professor Graeme P. Berlyn, whose pioneering work in plant physiology and ecological adaptations profoundly shaped her approach to conservation science. As a doctoral student under Berlyn and Professor Mark Ashton at Yale University, she developed a strong foundation in plant ecophysiology, with a particular emphasis on the response of tropical forest species to environmental stress. Her early work investigated the physiological resilience of flora in Sri Lanka with the objective of using them for reforestation, moving towards the coastal sage and Chapparal plants in California to design restoration systems that are resilient to climate change. Working then for 13 years in China, across diverse ecosystems—from the rainforests of Xishuangbanna and the biodiverse subtropical forested systems of subtropical Guangxi high-altitude biomes— Goodale applyed Berlyn's principles of leaf structure-function analysis and plant-environment interactions. Her research with her student's has tried to consistently bridge the gap between ecological theory and applied conservation, while being true to exploring plants from their botanical grounding. Her focus on Orchids, Ficus Species and the Regeneration Ecology, Seed Bio-physiology and Conservation of flora roots back to Berlyn's and Dr. Anitra Thorhaugh's introduction of Goodale to the Botanical Society of America. Culminating in her most recent work, Goodale is leading transformative initiatives focused on grassland rehabilitation and forest protection in the fragile mountain habitats of the Qinghai-Tibetan Plateau. In this high-elevation ecosystem, where climate change and overgrazing threaten ecological stability, her team is focused on developing innovative restoration protocols that combine remote sensing, local ecological knowledge, and physiological monitoring to promote resilience in native species. This final chapter of her research stands as a testament to Berlyn's enduring legacy: science grounded in curiosity, rigor, and a deep commitment to protecting the natural world, especially his vision for conservation, sustainable developmentent that does not compromise the livelihood protection of the mountain people.

Topic: Phytochemical

A-994

Biostimulants in Action: Evaluating Nutrient Uptake in Lettuce (Lactuca sativa)

Author: Maria Alvarez Zavala, Anahi Flores, Omar Holguin
Affiliation: New Mexico State University

The demand for efficacious organic soil amendments has increased as agriculture moves toward more sustainable and regenerative practices in the horticulture and agronomy industries. Amendments based on microalgae have attracted interest due to their promise to stimulate soil microbial activity, facilitate better nutrient availability, and support overall plant health. Microalgae-derived substances have shown promising effects on macronutrient absorption in lettuce (*Lactuca sativa*), a highly nutritional and economically valuable crop. Algae cultivated in aquaculture environments have also demonstrated potential in soil remediation and fertility enhancement. This research examines the effects of an aquaculture-based organic amendment derived from algae grown in nutrient-rich aquaponic systems, evaluating its potential to improve food production and support economic development in agricultural land.

The experiments consisted of two treatments: an organic amendment PhycoTerra®, a biostimulant derived from aquaculture production, and a control with no amendment addition. Lettuce seeds (*Lactuca sativa*) were grown in 50-cell seedling trays under an18 hour of light and 6 hours of dark photoperiod, while temperature (24˚C) and humidity (between 80-90%) were maintained constant. After 2–3 weeks of growth, the shoot tissue was harvested for macronutrient and micronutrient analysis. The extracted nutrients were nitrogen (N), phosphorus (P), potassium (K), boron, iron, manganese, magnesium, calcium, copper and zinc. All extracted according to Soil and Plant Analytical Methods P-3.10 Ver 4.10 from the Western States Laboratory Proficiency Testing Program. Briefly, dried tissue was extracted with 2% acetic acid, shaken, and analyzed via spectrophotometry (NO_3-N) and ICP-OES (PO_4-P, K, and micronutrients).

Results suggest that amendment grown lettuce has bigger biomass and has higher manganese concentrations when compared to the control. Thus, we anticipate that the lettuce cultivated using the organic amendment will have greater levels of macronutrients than the control group. Further replication can offer helpful information on the prospects of microalgae-based amendments as a green substitute for synthetic fertilizers. The inclusion of microalgae-based amendments could have the potential to significantly transform future farming practices and also contribute to healthier crops and increasing both yield and nutritional quality.

Topic:

A-995

Large to Very Large Fern Genomes provide new insights to the limits of genome size

Author: Harald Schneider, Liu Hongmei, Ilia Leitch
Affiliation: Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Royal Botanic Gardens, Kew

This presentation will honor the contribution of Kathleen Pryer and Michael Windham to our understanding of the evolution of ferns by demonstrating the importance to study ferns when aiming to test macroevolutionary hypotheses aiming to explain the evolution of the green branch of the Tree-of-Life. Large to very large genomes—genomes containing 50 or more pg of DNA per diploid nucleus—continue to attract interests despite their extreme rarity. Utilizing cytofluometric and related technologies, the genome size has been determined for more than 10,000 species including representatives of all major lineages of land plants,with about 93 accessions large to very large genomes were found in less than 1% of the studied taxa. Despite the extreme rarity, these genomes are not randomly distributed across the green tree-of-life but clustered in three lineages. While four of these genomes belonged to the parasitic Santanales lineage nested in the superasterids, with about 73 accesions the majority of large genomes were detected in two orders of monocots, namely the Asparagales (~10%) and Liliales (~70%). Recent research recovered an increasing amount of large to very large genomes including the largest genome known have been found to belong to ferns. While the majority of large to very large fern genomes belonged to the two orders of the ancient ophioglossoid lineage, several large genomes have been also detected in the

derived fern lineage, Polypodiineae. This study explores the impact of these findings on the proposed hypotheses on large to very large genomes such as the maximum genome size, ecological biases, and cellular biases.

Topic:

A-996

Evidence for adaptive variation in Quercus macrocarpa (L.) leaf morphology from a reciprocal transplant experiment across a latitudinal gradient

Author: Laura Ostrowsky, Lucy Rea, Mariana Hernandez Leal, Rebekah Mohn, Mira Garner, Lindsey Worcester, Cathleen Lapadat, Andrew Hipp, Heather McCarthy, Jeannine Cavender-Bares
Affiliation: Harvard University, University of Minnesota, The Morton Arboretum, University of Oklahoma

Many North American trees are facing novel environmental stressors that threaten their survival. Genetic variation is critical to the resilience of forest species in responding to change, yet it is unclear whether ecologically important tree species have the genetic variation necessary to adapt to these changes. Tests of intraspecific local adaptation using reciprocal transplant experiments can characterize the capacity of trees to adapt to novel stressors. This study uses a reciprocal transplant experiment of bur oak (*Quercus macrocarpa* L.) across a climatic gradient to test for genetic variation and plasticity in leaf morphological traits that may confer fitness in varying environments. We combine two quantitative genetics approaches (Aster fitness modeling and Q_{ST}-F_{ST} comparisons using genomic data and common garden traits) to test for evidence of adaptive variation in leaf traits between populations. We show that three populations of bur oak have distinct leaf morphologies and suites of covarying morphological traits, including far greater leaf lobing in the southern population across sites. We found evidence for adaptive variation in leaf lobing and a strong relationship between lobing and fitness, demonstrating that leaf morphological traits can confer fitness advantages in bur oak. While the southern population had the most lobed leaves, the southern garden had the least lobed leaves, displaying counter-gradient variation in leaf lobing as a functional trait. These results characterize the potential for both adaptation and acclimation in morphological traits across the geographic range of bur oak and provide a basis for assessing bur oak as a candidate for assisted migration.

Topic:

A-998

Physiology, spectroscopy, and phenology in a bur oak common garden inform assisted migration

Author: Lucy Rea
Affiliation: University of Minnesota

Climate change threatens trees because their migration rate often does not match the rate of warming. Assisted migration and assisted geneflow are proposed solutions for forest resilience by helping trees to migrate at the rate needed to keep pace with climate change and to maintain sufficient genetic diversity in populations for persistence in fluctuating environments. In species with broad latitudinal ranges, populations may have become locally adapted to climates across their range, making them vulnerable to climate change, but also providing opportunities for sourcing of seeds adapted to warmer climates to be moved into the historically cooler climates in the north. We use *Quercus macrocarpa* L. (bur oak), with a widely distributed latitudinal range from southern Canada to southern Texas as a model to examine the performance of populations from across the species' range in various climates. We established a reciprocal transplant experiment using populations of bur oak collected in maternal family groups from Minnesota, Illinois, and Oklahoma. These populations were planted out in common gardens in Minnesota, Illinois, and Oklahoma. The design of this experiment allows for tests of gene by environment interactions. We ask the following central questions: 1) Are populations of bur oak locally adapted to their home environment, and 2) Do populations of bur oak show potential to adapt to future climate change?

We collected growth, survival, physiological and spectral reflectance data in each of the gardens over three years to assess differences in the population's performance in each garden, and employed quantitative genetic methods to calculate fitness, genetic variance, selection, and adaptation potential. We found that the Illinois common garden resulted in the highest survival, growth, and photosynthetic rates among populations. We also found that growth and survival were correlated in the Illinois garden, but were decoupled in the northern and southern gardens, indicating that stressful conditions at either end of the latitudinal gradient shifted carbon allocation from growth to stress response. Our findings indicate that bur oak will maintain high physiological performance and fitness in response to warming in the expected range over the next 30-40 years. We found evidence for local adaptation for the Oklahoma population in its home garden, but low fitness for the Minnesota population in the Oklahoma garden, indicating that warming at high levels may have negative impacts on the northern populations. Quantitative genetic analyses using Aster models revealed high genetic variance in the Oklahoma population for traits under strong selection, indicating high adaptation potential for these traits in warmer climates in the southern population. Our results indicate that the Oklahoma population may be a good seed source for assisted geneflow to help northern forests adapt to climate change because 1) the Oklahoma population is well adapted to warmer climates and performs similarly to the northern populations in northern gardens and 2) has high adaptation potential for traits selected for in warmer climates. Consequently, findings from our study are informative for seed sourcing to promote climate-adapted bur oak populations in the Midwest.