Submitted Abstracts for Botany 2024

**A-1 Introduction to Phylogenetic Comparative Methods in R**

**Author:** John Schenk (Ohio University)

**Keywords:**

Advances in phylogenetic comparative methods have allowed biologists to robustly and objectively test macroevolutionary hypotheses, leading to a greater understanding of the processes of species diversification. Although the potential to answer numerous hypotheses across clades has invigorated macroevolutionary studies, learning how to apply phylogenetic comparative methodology remains a significant impediment. The workshop will provide foundational knowledge of phylogenetic comparative methods and how to apply them using the statistical program R. Attendees will gain hands-on experience applying methods, such as phylogenetic independent contrasts; phylogenetic generalized least squares; ancestral character estimations; constructing, fitting, and testing evolutionary models; fitting Brownian motion and Ornstein–Uhlenbeck models of evolution; lineage through time plots; and estimating phylogenetic signal in trait data. Participants will gain a theoretical understanding of phylogenetic comparative methodology and be able to apply even the most rigorous analyses to their own study systems. Prior experience applying phylogenetic comparative methods or using R is not expected or required. Early career scientists are especially encouraged to attend.

**A-2 SNPs, genes, genomes: using assembled genomes for answering evolutionary questions**

**Author:** Jacob Landis (Cornell University)

**Keywords:**

The costs of generating a draft genome assembly for a study organism of choice are declining each year and more tools are becoming available to help in the endeavor. Recent advances in long-read sequencing technology (Nanopore Q20+ kits and the PacBio Revi) make generating the necessary read coverage feasible for most plant groups. However, generating the appropriate sequence data for assembly and phylogenomic/comparative analyses is not a trivial matter and the magnitude of tools available for analysis can be bewildering. The focus of this workshop is to go through the necessary steps for genome assembly and annotation, while also focusing on comparative analyses when a closely related reference genome is not available for the species of interest. The workshop will give an in-depth overview of assembling genomes using PacBio HiFi data and scaffolding assemblies with HiC data. Additionally, we will touch on other approaches and discuss scenarios where different methods may be more appropriate. Methods for extracting high-quality DNA suitable for sequencing and library preparation will be discussed, as many plant species possess secondary compounds which can be problematic for sequencing. Downstream evolutionary analyses that can be performed after assembly will be covered while highlighting that a perfect assembly is not necessary to answer many questions. These will include genome annotation, SNP identification, gene family evolution, and using single copy genes in phylogenomic analyses. Participants will get hands-on practice with all the necessary steps using either the supplied test data or their own data if previously generated.

**A-3 Biodiversity data wrangling: Linking large phylogenies with species traits and ecologies**

**Author:** Ryan Folk (Mississippi State University)

**Keywords:**

Botany has seen a massive growth in "big data" resources ranging from DNA to plant distributions and morphological traits. Databases like GenBank and GBIF have accordingly become household words among meeting attendees, reflecting the impact data resources have had on today’s research landscape. BSA has seen productive workshop series focused on each of these data streams in isolation, such as the popular iDigBio and phylogenomics workshops. Based on sheer data scale, we are at the threshold of using these data as platforms for assessing species traits and ecologies at the kinds of truly continental and global levels needed to test fundamental theories and to produce the applied outcomes needed for environmental action. Yet biodiversity researchers are only beginning to tap the potential that these datasets have when employed in synergy. Needed is a relatively new set of skills to perform analytical integration: bringing distributions and phylogenetic trees together, bringing traits and distributions together, and other typical yet challenging tasks. We propose a crash course in performing an essential component of integrative science—Data Wrangling—that meets the increasing needs of students and academics.

The purpose of this workshop is to showcase novel methods and applications of biodiversity data in a phylogenetic and spatial context, exposing attendees to several typical workflows and hopefully inspiring them with new ideas for their own scientific systems and datasets. We will cover diverse research topics representing the future of the field, and instructors will include early-career individuals. We will offer hands-on instruction in each analysis topic, including ancestral niche reconstruction, trait-associated diversification, spatial phylogenetics, measurements of phenology, and other popular topics. We will focus our coverage on strategies to test popular hypotheses using publicly available data. Advanced and novice users are both encouraged to attend and will be divided into separate working groups. We aim particularly for those who have or are in the process of acquiring datasets and looking for ideas for analytical applications, and we refer to other BSA workshops those who are preparing datasets that will be used in the workshop experience. Users should plan to bring a computer that is set up with an R environment. For previous attendees: this year we will present new tools in the afternoon session focused on ecological modeling accounting for phylogeny.

**A-4 Common methods in leaf gas-exchange research: an introduction to measurements, theory, and data analysis**

**Author:** Christopher Muir (University of Wisconsin)

**Keywords:**

Plant ecophysiological methods are becoming increasingly popular because of their ability to inform ecological and evolutionary processes across scales, e.g., at larger ecosystem-level and smaller genetics-level scales. One of the primary aspects of plant function is leaf gas-exchange (CO2 and water vapor) which can be used to understand plant water-use, productivity, stress tolerance, trait screening and phenotyping, adaptation, trait-genotype associations, and more. We propose a workshop focused on current and commonly requested techniques in leaf gas-exchange, led by experienced ecophysiologists from academia and industry. The major components of the workshop will include measurement theory, equipment operation, data analysis, and modeling. We propose a full-day workshop which will divide into two half-day sessions. Part 1 will provide an introduction to measurement theory (e.g., responses to CO2) and focus on the basic operation of popular gas-exchange equipment. Part 2 will cover data analysis and modeling gas exchange using recently developed R packages. Participants can join either one or both sessions. This is similar to a workshop held at Botany 2022 but will be updated with new equipment and software advances.

**A-5 How to Tackle Teaching Plant Life Cycles**

**Author:** Emily Sessa (New York Botanical Garden)

**Keywords:**

Life cycles are a fundamental aspect of organismal biology, and a
cornerstone of most introductory biology and botany courses. Despite the importance of this topic and its ubiquity in the lab and lecture hall, plant life cycles can be a challenging subject to teach and students are often bewildered by the extensive terminology and unfamiliarity of the alternation of generations life cycle that plants undergo. During this workshop, the organizers and participants will share and discuss teaching methods for this topic, with the goal of providing everyone with a range of tools and approaches for tackling plant life cycles in their classes. We will discuss learning objectives, critical concepts, and assessment methods, and participants will be invited (if they wish) to share their own slides and/or other materials related to teaching plant life cycles, so that we can benefit from each other’s experiences. We will focus primarily on sexual reproduction and alternation of generations in land plants, but as time and participant interest permit, we may also discuss more advanced topics (e.g., selving, apomixis) and/or additional life cycles (e.g., fungi). Students are very welcome to attend, and prior teaching experience is not necessary.

**Topic: Workshop**

**A-6 Winter twig and fruit identification**

**Author:** Suneeti Jog (University of Illinois Urbana-Champaign)

Keywords:

The workshop will teach participants to identify common species of trees and woody shrubs of the midwestern and eastern United States, with a special emphasis on distinguishing species of oaks in the winter. Participants will learn to use basic botanical features used for identification such as buds, twig characteristics, bark, and fruits. This will be a hands-on workshop where participants will be able to discern morphological characters, distinguish odors unique to certain taxa, and experience pertinent textures that will aid in species identification. In an increasingly ever-changing digital world, this back to basics, old-school and resilient approach using only winter attributes will be a refresh for plant identification of woody species. Fresh as well as herbarium specimens of leafed out material will also be on display to compare with winter twigs, so that participants can associate dormant stages with active growth forms. The workshop will culminate with a keying exercise of unknown specimens of winter twigs. This workshop will be most beneficial to those who need field botany skills as well as international field botanists wishing to delve into winter botany. Identifying tree species accurately is very important for ecological monitoring and for protecting and managing natural areas, in an ever changing, anthropogenically altering world.

**Topic: Workshop**

**A-7 Conservation through Ethnobotanical Relationships: A case study in Generational Remembrance of Plants through Culturally Significant Foods in Metro-Detroit’s Ukrainian Diaspora**

**Author:** Nina Lawrin

Keywords:

I propose a conversation around how ecological knowledge is preserved after immigration. It can include a portion where participants participate in the creation of a food culturally significant plant relationship to take home with them as well as a conversation around how all we can reconnect to ourselves through the land and preserve ecological knowledge while sharing in unity during these times of change. In this pilot study I argue against the negative connotations of acculturation and acknowledge the fluidity, creativity, and adaptability of Ukrainian-American immigrants and their foodways. Ukrainian immigrants were able to assimilate to life within metro-Detroit while simultaneously preserving traditional foodways through celebratory foods. Through annual, familial holiday meals at Christmas, Easter and the occasional wedding, the matrachiral lineage has effectively preserved cultural keystone foods through language, use, and preparation. Community and schools also played a vital role in traditions and food preservation. First generation immigrants embraced transnational migrant identities which is reflective in their foodways. Second and third generations varied in frequency and seasonality as compared to first generation immigrants, although those who partook in annual Ukrainian celebratory foods were able to preserve key ecological food plant knowledge, usage, and language.

**Topic: Workshop**

**A-8 SISRIS: Supporting Inclusive and Sustainable (collections-based) Research Infrastructure for Systematics**

**Author:** Andrea Weeks (George Mason University), Shawn Krosnick (Tennessee Tech University)

Keywords:

Scientific discoveries derived from biological collections depend on the people who create the infrastructure of preserved specimens. However, currently accepted metrics of professional success for taxonomists ignore the essential functions of collection, identification, and annotation of research specimens that support published research. This results in an incomplete picture of the contributions of those working in biological collections. Recently, web-based informatics tools have been developed to improve the attribution of specimens, so that collectors and determiners can track their contributions to subsequent research discoveries made using their work and receive greater professional recognition. In this workshop, participants will learn how to create an inclusive and sustainable research ecosystem for collections-based research by increasing the attribution of the people. This half-day workshop will comprise four hours of instruction about the structure and use of the web-based informatics tool Bionomia and the other software services that interact with this platform, including ORCID, GBIF, Wikidata, and Zenodo. The workshop will emphasize (1) how participants can use these tools as part of their collections-based research activities and (2) how increased attribution can be used as a means to effect community-level change in how taxonomic expertise is acknowledged. Participants will practice attributing specimens to historical collectors from underrepresented groups, which will directly increase the visibility of hidden figures in natural history collections. To defray the costs associated with workshop participation and to encourage participation from underrepresented groups, 20 stipends of $350 each will be available to workshop attendees. Please visit [https://github.com/aweeks3/SISRIS](https://github.com/aweeks3/SISRIS) for more information on applying for participant support.

**Topic: Workshop**

**A-9 3D Printing for Science: From Design to Optimize**

**Author:** Mason McNair (Michigan State University)

Keywords:

The methods used to collect data vary greatly between different research programs. Standardized equipment rarely accounts for nuances relating to study system or resource limitations, creating a need for inexpensive, custom solutions. Bespoke equipment has historically been limited to well-funded research programs, but advances in 3D printing are making it possible for nearly all labs to design and manufacture their own research tools using the current generation of inexpensive and reliable printers. The goal of this workshop is to demonstrate the problem-solving potential of open-source hardware and 3D printing for scientists. 3D printing facilitates the adoption of custom equipment that can increase the rate and quality of data collection. 3D printing in most scientific fields is relatively new, but it is rapidly growing. Multiple peer-reviewed articles outlining potential uses of 3D printing in the sciences exist but adoption of this technology has been slow. For example, these are all areas that have successfully demonstrated the potential impact of 3D printing. Microfluidics ([https://doi.org/10.1016/j.addma.2018.10.028](https://doi.org/10.1016/j.addma.2018.10.028)) Microscopy ([https://www.preprints.org/manuscript/202105.0352v1](https://www.preprints.org/manuscript/202105.0352v1)) Phenomics ([https://doi.org/10.34133/2020/8640215](https://doi.org/10.34133/2020/8640215)) Education and outreach ([https://doi.org/10.1016/j.revpalbo.2023.104860](https://doi.org/10.1016/j.revpalbo.2023.104860)) To introduce and promote 3D printing in the sciences, this workshop is part of a series of in-person and online workshops that guide researchers through the process of designing custom tools for their research questions, setting up and using 3D printers, and performing maintenance on their machines. While the organizers will not receive any financial benefits from 3D printing companies or suppliers through this workshop, we will be contacting 3D printing companies and suppliers to request discount codes, supplies, and assistance in creating workshop teaching materials to give to participants and offset workshop costs. 3D printing can positively impact scientific research and is worth adopting as part of your research methods. This workshop aims to provide participants with the knowledge needed to successfully incorporate 3D printing into their research.

**Topic: Workshop**

**A-10 Seeing Seeds: An Artistic Investigation**

**Author:** Sharon Bladholm

Keywords:

In this interactive workshop that merges art and science, we will begin with a short PowerPoint presentation about Seed Rain: Seed Bank, a large ceramic installation I created and other seed inspired art. Participants will gain
inspiration, working from a large collection of actual seeds ceramic seeds, and my enlarged seed sculptures, both from the Midwest and tropical regions. We will then move into a multifaceted afternoon (or day) of art making where we can slow down and appreciate the forms, colors and textures of these small packages that are imbued with so much potential. Power to the plants. Plants power the planet! Participants will begin drawing with pencil to experientially understand these forms, simple and complex, add color with watercolors. The following investigation involves carving into small clay slabs, using brayer’s to roll nontoxic ink on them and lastly burning rice paper over the slabs, creating a print. There is something exciting and transformative about this process where the unexpected can happen. The clay slabs used for printing are beautiful as well and can be taken home. The final option is to use the self hardening clay to create small seed inspired sculptures, adding color with paint. Sharon is an artist inspired by the botanical realm in all its aspects, who loves to share her dual enthusiasm for seeds/plants and art making. She has participated as artist on plant hunting expeditions with the Field Museum, Conservation International, and the Botanical Research Institute of Texas’s, Andes to Amazon Biodiversity Program. She has completed artistic residencies in other remote areas of the Peruvian and Ecuadorian Amazon with Project Amazonas and the Tiputini Biodiversity Station. Her traveling exhibition Soils, Seeds and Sprouts: Tropical and Temperate explores botany and soil microorganisms, using art as a conduit to inform the public on important issues regarding nature, science, conservation, and biodiversity. She often teaches workshops for a diverse audience.

**Topic: Workshop**

**A-11 Planting Inquiry in Biology Classrooms**

**Author:** Muriel Poston (Pitzer College), Gordon Uno (University of Oklahoma), Anna Montfils (Central Michigan University)

**Keywords:** Science process and critical thinking skills play prominent roles in the revised Advanced Placement (AP) Biology curriculum, Vision and Change (AAAS, 2009, 2012, 2020) for undergraduate biology education, and other undergraduate teaching reform efforts e.g. Gordon Conference, Undergraduate Biological Education. In this interactive workshop, participants will engage in simple, yet effective, methods for instructors to help students develop their scientific literacy and science practice skills ranging from generating questions based on observations of the usual and unusual to exploring alternative explanations. Each person will leave the workshop with tested examples, ideas for using and adapting them in any science classroom, and increased confidence to promote student-centered learning and to introduce inquiry into an existing curriculum. The workshop has several major goals: 1) to demonstrate how to introduce inquiry instruction in a science classroom, to engage workshop participants in inquiry activities, and to work with participants to develop their own inquiry-based lessons; 2) to demonstrate the breadth of botanical examples that can be used to teach major biological concepts while using active learning; 3) to outline the key barriers to equity instruction in a science classroom and help workshop participants create activities that focus on scaffolded skills and concepts based on their own interests; 4) to illustrate the benefits and use of effective formative assessments in a science classroom and how instructors can create their own concept inventory questions; and 5) to identify methods for engaging a diversity of students in the study of science through an exchange of best practices and ideas among the entire workshop group.

**Topic: Workshop**

**A-12 Genome Skimming: A Bioinformatics Approach to Assembly-Free Analysis of Genomic Information**

**Author:** Eduardo Charve (UC San Diego)

**Keywords:** Genome skimming (low-coverage shotgun-sequencing) approaches to evolution and population genetics offer flexible alternatives to traditional methods left to DNA (meta)barcoding, bypassing the need for PCR amplification of marker regions or by avoiding computationally expensive processes of assembly alignment (Bohmann et al 2020). As the cost of shotgun-sequencing keeps decreasing, the potential use for these skimming methods in the study of geographic ecology is higher than ever. In this workshop, we will be looking at a low-coverage sequencing analysis pipeline with a variety of functions, including decontamination, genomic distance inference, phylogenetic placement, and estimation genome repetitiveness. The pipeline consists of a set of user-friendly command-line tools dedicated to analyzing low-coverage genome skims (https://github.com/smirarab/skimming_scripts). Firstly we will be talking about CONSULT-II: a taxonomic identification tool that extracts k-mers from a query read and classifies them against k-mers in a reference database. In the context of the pipeline, we will be using it to remove reads that classify as bacterial contaminants, keeping reads that are specific to our organism of interest (Şapçı et al 2022). We will also be discussing Skmer, an alignment-free tool that estimates distances between genomes by looking at how many shared k-mers are found between sequences and outputs a distance matrix which you can use to create a phylogenetic tree (Sarmashghi et al 2019). With a reference tree constructed by distance matrix generated from Skmer, we then use another tool APPLES for fast, alignment-free phylogenetic placement (Balaban et al 2020).

Finally, we will talk about RESPECT, a tool to accurately estimate properties like repetitiveness, genome length, sequencing coverage and error (Sarmashghi et al 2021).

This workshop will cover installation instructions, an overview discussion of how the methods function, and applying the suite of tools in your local computer and/or cluster. The workshop will work through a tutorial analyzing a small plant genome dataset.

**Topic: Workshop**

**A-13 Traditional Cyanotype Printing with Jessie Swimeley**

**Author:** Jessie Swimeley (Jessie Swimeley Fine Art)

**Keywords:** Create Traditional Cyanotype prints with artist, Jessie Swimeley. Learn the history, chemistry, and artistry of this historic photographic contact printing process. Traditional Cyanotype printing and botany have a long history of making beautiful blue works of art together! Bring fresh or pressed samples of your favorite botanicals to use to create your artwork. Plants with strong silhouettes work the best, but we can definitely try anything!

**Topic: Workshop**

**A-14 Ethnobotany, natural products, and microbiomes through a One Health collaboration**

**Author:** Matthew Kolp (Lincoln Memorial University)

**Keywords:** Join us to draw your focus back to the fundamentals of collaboration across disciplines, a core concept of One Health research. In this 2-hour workshop, we will discuss and invite discussion from participants on productive, collaborative behavior in their fields. Then we will present our research in ethnobotany: how do native plants of Appalachia and their derived natural products compare for the purported medicinal, immunological, and phytopathogenic effects? How do plant endophytes and microbiome members contribute to these traits? We present our methods including but not limited to the application of HPTLC, mass spectrometry, and microbiome analyses; we also share our preliminary findings. We end our workshop with an outline of a review paper on Plant Microbiomes and Appalachian Folk Medicine and invite workshop participants to join as authors. This workshop is for folks that attend our workshop will:

- Researchers and students at any stage of their career with no, some, or lots of expertise in topic areas (ethnobotany, plant endophytes, natural products, HPTLC and mass spec)
- Those interested in discussing the fundamentals of successful, productive, and collaborative behavior.
- Those interested in ethnobotany, phytopharmacology, plant chemistry, and/or endophytes.
- Those interested in collaborating with us to produce a One Health review paper on the intersection of ethnobotany, natural products, and microbiomes. 

Folks that attend our workshop will:

- Create a list of productive, collaborative behavior to use in their research.
- Discuss their experiences of successful collaborative behavior.
- Gain knowledge of ethnobotany of Appalachia, the significance of natural products research, and plant endophytes as an abundant source of bioactive compounds.
- Consider committing to a collaboration with our group to produce a review paper and conduct empirical research on plant endophytes of ethnobotanically important natural products.

**Topic: Floristics & Taxonomy**

**A-15 The “full species list” fallacy in floristic quality**
assess

Author: Suneei Jog (University of Illinois Urbana-Champaign), Jason Bried (University of Illinois Urbana-Champaign)

Keywords: coefficient of conservatism; floristic quality; survey

Biological assessments typically involve field surveys that are time consuming and require taxonomic expertise. We explored a long-held belief that Floristic Quality Assessment requires a comprehensive species list for accurate assessment of biological integrity. We used two approaches to explore the need for a full species list in floristic quality assessments. Our first approach used simulations of reduced effort in an intensive floristic survey. We found that estimator precision was maintained down to around 50% species loss. The second approach involved species lists from hundreds of one-time surveys and the use of dominant species as surrogates for entire local assemblages. Here we found that dominant species were mainly reliable when communities were relatively small such that dominants comprised a large fraction (>40%) of richness. Together these results indicate that a full species list is not necessary for a reliable Floristic Quality Assessment, and that users may aim for a representative rather than comprehensive floristic inventory.

Author: Alex McAlvay (New York Botanical Garden), Morgan Ruelle (Clark University), Emma Burnett (The Oxford Artisan Distillery), Seid Hassen (Wollo University), Asmara Demeke (Wollo University), Zemed Asfaw (Addis Ababa University), Marine Mosulishvili (Bia State University), Anna DiPaola (Cornell University), Endale Amare (Ethiopian Public Health Institute), Muhammad Al’ Zein, John Letts

Keywords: agriculture.ethnobotany; Poaceae; evolution; ecology

Food security depends on the ability of staple crops to tolerate new environmental stresses. Wheat, barley, and other small grains face substantial yield losses under all climate change scenarios. In the past, the diversity of grain fields in parts of Africa, Europe, and Asia was colder to grow wild grasslands, with mixtures of different species and varieties of wheat, barley, rye, and/or other crops. This practice of growing mixed grains, also called “maslins,” persists, and represents a risk-management strategy for coping with climate variability. This practice has been replaced by monocropping in most areas, due to an emphasis on uniform breeder’s varieties. We share findings from our farmer interviews, agronomic, agroecological, and nutritional analyses as part of The International Traditional Grain Project. This initiative partners with dozens of organizations in Ethiopia, Georgia, Lebanon, Morocco, the U.K., and U.S. to investigate and revitalize this practice and its potential as a climate-smart farming strategy. Farmers express benefits to fungal resistance, drought tolerance, and increased stability in general. Climate change and use of modern horticultural varieties are affecting the agricultural and culinary performance and appearance. The cultivated varieties (i.e. cultivars) of natives, also termed ‘nativars’, are now common in nurseries and the garden section of home improvement stores as they are being used broadly in horticulture and sometimes in restoration. As a result, vast numbers of nativars are spreading across many ecosystem types and may outnumber their wild relatives. This is particularly true in urban areas where they are more common than native varieties. In selecting for horticulturally desirable traits (e.g. novel floral form, color, phenology), the floral attractants and rewards may have been altered or diminished. It is important to examine the relative attractiveness to pollinators of these nativars as compared to their wild relatives. During two field seasons in 2019 and 2020, wild forms of Penstemon digitalis, Rudbeckia fulgida, Symphyotrichum novae-angliae, Sympyothrichum oblongifolium and a selection of their nativars were studied. The floral trait variation and pollinator visitation was compared and preferences of different groups of floral visitors was determined through monitoring of phenology, pollinator observations, and floral trait measurements. While our results suggest that there is no universal message regarding pollinator attraction between native plants and their cultivated varieties, we found that pollinator visitation varied on a per flower and seasonal basis for all taxa except Symphyotrichum novae-angliae in which the wild type was preferred. In general, however, pollinator preference seemed to be reliant on a combination of floral traits, rather than any one specific trait.

Author: Hit Kishore Goswami (Society of Botanists)

Keywords: rare species

Hit Kishore Goswami Isotes L. (the quillwort) is a cosmopolitan genus of mainly aquatic species, belonging to the group of heterosporous lycopsids and comprises of more than 250 species. Among these species, Isotes pantii Goswami & Arya, (diagnosis confirmed by phylogenetic studies based on rbcl genes, SEM studies of spores etc.) is the only species which exhibits several features not found in any other

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**Topic: Workshop**

**A-17 Data Analysis and Visualization In R**

**Author:** Eli Hartung (Kansas State University)

**Keywords:**

R (www.r-project.org) is a free software environment for statistical computing and graphics. This workshop introduces basic concepts, syntax, and usage in R programming, statistical analysis, and visualization techniques for botanical data. This workshop is intended for anyone who is working to analyze their research data (including graduate students, early career faculty and researchers, undergraduate researchers) and would like to learn how to automate data processing and presentation using the R programming language. This workshop stands as the final installments of the Early Career and Development Committee Intro to R and Data Analysis workshop series and will combine and review the topics covered in previous workshops to produce highly communicative figures. Bring your own dataset and we will work through the complete process of data familiarization, cleaning, analysis, and visualization. In the first half of this workshop, we will provide an overview of R and its basic usage. We will cover basic information about R syntax, the RStudio interface, and move through how to import CSV files, the structure of data frames, how to manipulate data frames, how to calculate summary statistics from a data frame, and a brief introduction to plotting. In the second half of this workshop, we will discuss and perform statistical analyses and visualizations best suited to your dataset. We will also discuss different data visualizations to illustrate both good and bad applications of design and visualization principles. By the end of the course, you will have the essential skills of processing, manipulating and analyzing data of various types, creating advanced visualizations, generating reports, and documenting your code. Attendees are asked to bring a computer with R and RStudio installed and their own data in order to participate in this coding-based workshop. In this workshop you will:
1. Become familiar with R and its applications
2. Perform a variety of statistical analyses for your dataset
3. Create publication ready figures
4. Be able to take these skills and apply them to your other projects

**Topic: Education and Outreach**

**A-20 Revisiting the term ‘Plant Blindness’ with Community Inclusion and Ground-Sourced Alternatives**

**Author:** Melanie Link-Perez (University of Tampa)

**Keywords:**

In 1998, the term ‘Plant Blindness’ was introduced and spotlighted public disregard for plants, with the term gaining global traction over two decades. Recent research has proposed the term ‘Plant Awareness Disparity’ to foster inclusive dialogue and avoid ableist language. While endorsing the shift, we argue for a community-driven renaming process. Our ongoing research seeks a ground-sourced alternative, inviting diverse perspectives for a more inclusive nomenclature.

**Topic: Ethnobotany**

**A-21 Remembering resilience: Revitalizing traditional grain mixtures to climate-proof our crops**

**Author:** Anna DiPaola (Cornell University), Endale Amare (Ethiopian Public Health Institute), Muhammad Al’ Zein, John Letts

**Keywords:** agriculture.ethnobotany; Poaceae; evolution; ecology

Rudbeckia fulgida, Symphyotrichum novae-angliae, Sympyothrichum oblongifolium and a selection of their nativars were studied. The floral trait variation and pollinator visitation was compared and preferences of different groups of floral visitors was determined through monitoring of phenology, pollinator observations, and floral trait measurements. While our results suggest that there is no universal message regarding pollinator attraction between native plants and their cultivated varieties, we found that pollinator visitation varied on a per flower and seasonal basis for all taxa except Symphyotrichum novae-angliae in which the wild type was preferred. In general, however, pollinator preference seemed to be reliant on a combination of floral traits, rather than any one specific trait.
species described so far. For example, Isoetes pantii plant species possess 2n=36 and or 2n = 48 chromosomes (n=12; not n=11 as is the basic number among the world flora of the genus); very distinct X and Y chromosomes (no other species possesses sex chromosomal mechanism) which have been proved by their movements during mitotic and meiotic divisions; C banding and Feulgen-staining and Southern blot studies by hybriding experiments on probing with human Y Py6 probe. Additionally, blasting DNA studies have confirmed that the pantii genome has lot many sequences akin to some human genome sequences. Comparative studies using many morphological traits among growing intermixed populations of Isoetes coromandelina, I. sampathkumaranii as well as other species, following unusual, totally unknown for the genus have been published during past 60 years: (i) Plants collected from original locality since 1966, also collected in recent years from far off places also possess heterosporous sporangia (now called as heterosporangium); (ii) both megaspores and microspores germinate within the heterosporangium and the embryonic stages are exoscopic. (iv) some of the megaspores from heterosporangia closely resemble Palaeeozorcyclops and (V) such megaspores released from the heterosporangia germinate on original soil medium and developmental stages of embryos have been observed. Furthermore that I. pantii is a natural hybrid product by the hybridization of I. coromandelina x I. sampathkumaranii has been proved not only by morphological features of spores and simple disc-gel electrophoresis on enzymes but also by the above mentioned drastic departures of evolutionary path and demonstrations of totally unknown traits for the genus.

**Topic: Ethnobotany**

**A-24 Exploring the Significance of Plants in Religious and Cultural Traditions Among Yoruba Tribe of Southwest Nigeria.**

**Author:** Olubunmi Sharaibi

**Lagos State University, Lagos, Nigeria**

**Keywords:** ethnobotany;Medicinal Plants

The Southwest region of Nigeria holds a rich and diverse cultural tapestry deeply intertwined with spiritual and religious practices, of the people in Southwest, Nigeria. The study delved into the historical, cultural, and ecological dimensions of this relationship, shedding light on the significance of plants in rituals, ceremonies, healing practices, and the overall spiritual worldview. By examining the varied ways in which plants are revered, utilized, and provide a deeper understanding of the intimate interplay between plants and spirituality in the Southwest, Nigeria. Ethno-botanical surveys were carried out to identify plants used in religious and cultural practices in Southwest Nigeria States of Lagos, Ogun, Ondo, Oyo, and Ekiti States. Oral interview method was used to obtain information from 100 respondents including traditional healers, religious leaders (Pastors and Alfas), herbalists and elderly people. Seventy plant species representing 33 families were identified during the ethno-botanical surveys... The family with the highest number of species was Fabaceae while the families with the least number of species were Lamiaceae, Sapotaceae, Tiliaceae etc. The habits of most of the plants used in these ceremonies are trees. Garcina cola, Cola nitida, Milicia excelsa, Dioscorea alata were frequently mentioned plants that are offered to appease deities or ancestors, acting as a conduit for spiritual communion and guidance. Traditional healers and spiritual leaders utilize these plants in rituals to promote physical, emotional, and spiritual well-being. Leaves and roots of particular plants are interpreted as part of divination rituals, helping individuals navigate life’s uncertainties while staying connected to the spiritual realm. Plants are deeply embedded in the cultural identity and belief systems of the Yoruba people, contributing to the continuity and richness of their spiritual heritage. **Keywords:** Plants, Cultural, Religious, Spiritual, Coronation, Tradition, Ritual practices.

**Topic: Ethnobotany**

**A-25 Traditional Uses and Conservation Strategies of Medicinal Plants by Indigenous People of Alimosho Communities in Lagos State, Nigeria.**

**Author:** Olubunmi Sharaibi

**Lagos State University, Lagos, Nigeria**

**Keywords:** ethnobotany;Indigenous Peoples;Medicinal Plants

Ethnobotanical studies of medicinal plants used by the Alimosho Local Government Area in Lagos State, Nigeria was carried out. The aim of the study was to identify and document medicinal plants used by the inhabitants in the study area for the treatment and management of various diseases and ailments. Information was collected via oral interviews using their local language (Yoruba) with traditional healers, herbal sellers and people of the study area. A total of seventy (70) species belonging to forty-one (41) families were identified. The family with the highest number of species was Apocynaceae (7) followed by Euphorbiaceae (6), Fabaceae (5), Anacardiaceae (3), Malvaceae (3), Cucurbitaceae (3), Rubiaceae (3), Phylanthaceae (2), Asteraceae (2), Annonaceae (2), Bignoniaceae (2) and the rest of the families had just one (1) species each. The most frequently mentioned plants were Carica papaya, Mangifera indica, Azadirachta indica, Morinda lucida, Cymbopogon citratus, Gossypium herbaceum, Vernonia amygdalina, Enantia chlorantha, Alstonia boonei and Bridelia ferruginea. According to the survey, the plants mostly utilized were leaves, barks, roots, and fruits. Flowers and bulbs were rarely used. The most popular mode of preparations were decoctions, and infusions. The most common method of administration is oral followed by liniment method. The conservation strategies used in conserving the medicinal plants include domestication, establishment of protected areas and sustainable harvesting of the medicinal plants to prevent extinction.

**Topic: Ethnobotany**

**A-26 Biocentrism in the Anthropocene: Co-Creating Ethnobotanical, Climate-Smart Agroforestry Systems**

**Author:** Abby Snyder

**Yale School of the Environment**

**Keywords:**

The Ewe proverb “Gbedokpo we nô wá nu” highlights the significance of embracing diverse ideas and fostering collaboration to achieve goals. In the context of Togo, the adverse impacts of climate change pose a substantial threat to natural systems, exacerbating food security issues and endangering ethnobotanical traditions due to declining biodiversity. Current climate predictions from the Intergovernmental Panel on Climate Change (IPCC) predict that the mean annual temperature in West Africa will increase between 3 °C – 6 °C by 2050. As temperature increases and precipitation patterns increasingly vary, crop yields drop, and preexisting food security issues are exacerbated. Simultaneously, Togo is facing a biodiversity crisis. Between 2000 – 2015, Togo had one of the highest deforestation rates in the world, and today only 8.5% of the country’s land area is demarcated as tree cover. What habitat remains is threatened by climate change and agricultural expansion. Biodiversity loss poses a significant threat to Togo’s biocultural diversity as the species they have coevolved with for centuries are increasingly strained. Scientists predict that many of Togo’s plants, and their interwoven traditional knowledge systems, may be displaced or lost forever in the Anthropocene. As plant and animal species diminish, so does Togo’s biocultural identity. To tackle these challenges, this proposed poster will discuss a decade-long project that aims to leverage participatory research strategies to integrate ethnobotanical knowledge and community-identified plant species into an existing agroforestry system. This holistic approach strives to safeguard Togo’s biocultural diversity while mitigating the detrimental effects of climate change on the country’s natural systems.

The poster will focus on the opportunities for climate adaptation that rest on the inclusion of ethnobotanical sciences; a multi-faceted approach to preserving cultural and environmental ecosystems. By recognizing the value of cultural ecosystem services alongside provisioning and regulating ecosystem services, there are opportunities to establish a sustainable system that can bolster climate adaptation and safeguard the knowledge systems of local communities. Through the strategic integration of agroforestry, ethnobotanical knowledge, and community engagement, this discussion will investigate models for sustainable development and cultural preservation not only in Togo but also for similar contexts globally.

**Topic: Ethnobotany**

**A-27 Effects of Salvia limbata C. A. Mey. Extracts on Sedative-Hypnotic, Anxiolytic Responses, Potential Adverse Effects, and Variation in Rosmarinic Acid Content Due to Phenological Stage and Altitude**

**Author:** Maryam Saffarlah

**University of California, Davis**

**Keywords:** Salvia limbata C. A. Mey. has been traditionally utilized in traditional...
medicine for alleviating central nervous system disorders such as insomnia, anxiety, and depression. Its pharmacological properties are attributed, at least partially, to the presence of rosmarinic acid (RA). However, investigations into the sedative-hypnotic effect, anxiolytic activity, potential side effects, and the mechanism of action of *S. limbata* extract are lacking. This study aimed to assess the sedative-hypnotic effect, anxiolytic activity, potential side effects, and mechanism of action of *S. limbata* extracts. Additionally, the influence of altitude and phenological stage on the RA content of *S. limbata* was explored. Sedative-hypnotic and anxiolytic effects were evaluated using the pentobarbital-induced loss of righting reflex test and open field test, respectively. Flumazenil was employed to elucidate the mechanism of action, while possible side effects were examined through passive avoidance and grip strength tests. Altitude and phenological stage effects on RA content were determined using reversed-phase high-performance liquid chromatography (RP-HPLC). Results revealed sedative-hypnotic and anxiolytic effects following behavioral tests. Flumazenil reversed these effects, suggesting modulation of GABA-A receptors as a potential mechanism. RP-HPLC analysis indicated that harvesting *S. limbata* in the vegetative stage at an altitude of 2500 m yielded the highest RA content (8.67 ± 0.13 mg/g dry matter), with the hydroalcoholic extract showing the highest RA content among different plant samples collected at this altitude and phenological stage. In conclusion, these findings provide insights into optimizing RA content and pharmacological activity, which may have significant economic implications for the pharmaceutical industry.

**Topic: Systematics**

**A-28 Genetic Diversity and Phylogenetic Relationships of Pediomelum tenuiflorum**

**Author:** Cynthia Anukege (University of Nebraska at Omaha), Pamela Kellar (University of Nebraska at Omaha)

**Keywords:** common garden; Fabaceae; Genetic diversity; herbarium specimens; molecular phylogenetics; next generation sequencing

Understanding the evolutionary histories of and genetic diversity within plant species is fundamental for effective conservation and management. *Pediomelum tenuiflorum* is broadly distributed across the Great Plains of North America and has at least two distinctive morphotypes. Challenges, including historical taxonomic shifts between genera and ongoing debates regarding species boundaries, reveal the need for a comprehensive investigation into its evolutionary history, population genetic structure, and morphology. This study aims to unravel the taxonomic puzzle surrounding *P. tenuiflorum* by integrating morphological analyses, next-generation sequencing, and Inter-Simple Sequence Repeat (ISSR) marker studies. Specifically, the research seeks to explain the potential divergence between the two morphotypes, which may represent distinct species or subspecies. The research methods involve a multi-step approach. First, a detailed morphological assessment is being conducted on 97 *P. tenuiflorum* specimens from a common garden. Measured traits include stem diameter, leaflet and flower dimensions, and aboveground biomass, complemented by image analysis using specialized software to quantify specific leaf area (SLA). Second, DNA has been extracted from over 100 common garden and herbarium specimens of *P. tenuiflorum* from across the distribution and has been sequenced on an Illumina NextSeq 550. Nuclear and plastid sequences obtained from genome skimming were used to estimate phylogeny. Third, ISSR using 50 markers is being analyzed to assess genetic diversity and population structure within *P. tenuiflorum*. The outcomes of this research are expected to provide valuable insights into the evolutionary dynamics and genetic differentiation within *P. tenuiflorum* populations. By elucidating the potential divergence between morphotypes, this study will provide evidence to resolve taxonomic debates surrounding *P. tenuiflorum*. Moreover, the findings will inform conservation efforts and management strategies aimed at preserving the genetic diversity and ecological integrity of *P. tenuiflorum* populations across its range.

**Topic: Ecology**

**A-29 Prediction of Tree Failure in Harvested Forests during Windstorms in Changing Climate**

**Author:** Ali Jahani (UC Davis), Maryam Saffarhia (University of California, Davis)

**Keywords:** forests; climate resilient

In managed forests, windstorm disturbances can significantly impact timber yield, necessitating unscheduled clear-cutting or thinning operations. Hyrcanian forests, characterized by strong permanent winds exceeding 100 km/h in changing climate, experience frequent damage to forest trees, leading to numerous tree failure incidents following tree harvesting and gap creation in forest stands. This study employs machine learning approaches to compare the effectiveness of multi-layer perceptron (MLP) neural network, radial basis function neural network (RBFNN), and support vector machine (SVM) models in identifying susceptible trees during windstorm disturbances. Fifteen variables were recorded across 600 sample plots, categorized into stand and tree variables. Artificial intelligence techniques, including MLP, RBFNN, and SVM, were utilized to develop a tree failure model. The MLP model demonstrated the highest accuracy in classifying target trees in training (100%), test (93.3%), and all data sets (97.7%). Key inputs influencing tree susceptibility in windstorm disturbances were identified as mean tree height, tree crown diameter, and target tree height. The MLP-based model emerged as an effective model for assessing tree susceptibility in Hyrcanian forests, particularly following wood harvesting. This model holds potential for integration into forest management planning to mitigate tree failure risks post-harvesting, allowing for modifications to tree cutting plans based on environmental decision support system tools aimed at reducing the risk of tree failures during wind events in changing climate.

**Topic: Phytochemical**

**A-30 Phytochemicals and bioactivity of two medicinally rich members of Gentianaceae collected from Spiti valley of northwest Himalayas**

**Author:** Kamaljit Singh (Panjab University, Chandigarh, India)

**Keywords:** ethnobotany; high altitude plant; traditional knowledge; herbal

The present study was based upon traditional knowledge of two medicinally relevant species of Gentianaceae namely Gentianella moorcroftiana (Wall. ex G. Don.) and Gentiana kirlowi Turcz. (Wall. ex G. Don.) for antioxidant and antimicrobial activity. Plants collected from the Spiti valley of cold desert region of Himachal Pradesh, India in the Northwestern Himalayas commonly grow in the grassy and moist meadows across the valley. The Amchies system of medicine traditionally use them for jaundice and headache purportedly strengthening the liver and improved digestion albeit without scientific validation. Their medicinal efficacy has been attributed to the presence of bitter glycosides. Total phenolics and flavonoids in the flowers and shoots were much higher in comparison to leaves in *G. moorcroftiana* than in *G. kirlowi*. DPPH assay revealed much stronger antioxidant activity of flowers of both the species than that of leaves and shoots. GC-MS analysis showed the varied number of antimicrobial compounds in each species e.g., *G. paludosa*: 4-leaves, 3-each in flowers and shoots; and *G. moorcroftiana*: 8-leaves, 5-shoots, 4-flowers. The common antimicrobial compound dibutyl phthalate present in both plants was active against bacterial spp., *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Staphylococcus aureus*. Notably, the antibacterial efficacy of *G. kirlowi* was much higher across all strains than of *G. moorcroftiana*. Leaf methanolic extracts were more effective. The study provides an insight into antioxidant and antimicrobial efficacy of phytochemicals of Gentianaceae members supporting their medicinal relevance.

**Topic: Fire’s role in plant conservation and restoration**

**A-31 Prescribed fire timing drives differing emergence phenology in a restored tallgrass prairie**

**Author:** Michelle Homann (University of Wisconsin Madison), Ellen Damshen (University of Wisconsin-Madison)

**Keywords:** phenology; tallgrass prairie; fire regimes

Disturbance by fire plays an important role in temperate grassland restoration by removing buildup of senesced plant material, stimulating grass and forb productivity, and promoting native species diversity. During tallgrass prairie restoration and maintenance, fire is typically prescribed on the shoulders of the growing season in either early spring or late fall. Yet, the timing of fire, even when prescribed during the “dormant” season, can alter prairie plant community composition. Spring emergence timing is an understudied aspect of plant community responses to fire, and may be an important driver behind long-term change in plant community composition depending on the timing of prescribed burns. To better understand how fire seasonality effects change in grassland plant community composition, we examined emergence timing, growth rate, and flowering effort for ten common tallgrass prairie plant species throughout the 2023 growing season. We hypothesized that spring prescribed burns would damage emerging plants, leading to delays in growth when compared to fall-burned conspecifics. To test our hypothesis, we collected weekly data on emergence timing and growth rate for species in plots that have been burned annually in April or November since 2016. Additionally, we estimated percent cover of flowers
weekly during the growing season. We found that plants in fall prescribed burn plots emerged up to two weeks early when compared to spring-burned or unburned conspecifics. Some species emerged prior to, and were damaged by, the spring prescribed burn. Percent cover of plants in the spring prescribed burn treatment was significantly lower than in fall burn plots for five weeks following the spring burn. Growth rate and flowering effort responded to fire timing in different ways depending on the species. Our findings suggest that plant emergence timing may be a mechanism that drives plant community responses to prescribed burn timing and can inform management decisions surrounding prescribed fire.

Topic: Ecology
A-32 Eco-Evolutionary Insights in the Function and Diversification of Complex Trichomes in Loasaceae
Author: Rosemary Glos (University of Michigan), Marjorie Weber (University of Michigan)
Keywords: Epidermal morphology; herbarium specimens; Loasaceae; Mentzelia; Phylogenetic comparative methods; plant-insect ecology; trichomes; plant defense
Trichomes are widespread, hyper-diverse, and ecologically important structures. As modified epidermal cells, they serve as an interface between plant surfaces and the environment, impacting defense, dispersal, pollination, nutrient acquisition, stress responses, and more. Nonetheless, despite the incredible variation present in this trait, we lack experimental tests of trichome function in many plant groups and know even less about the factors shaping trichome diversity on a macroevolutionary scale. Moreover, published studies typically limit their analyses to overall (buck) trichome density, which may obscure ecologically relevant patterns in species that produce multiple trichome types and limit our ability to detect the macroevolutionary drivers of trichome diversity. Our work integrates experimental and comparative methods to examine the function and evolution of trichomes in the Loasaceae, a family known for its extraordinary hairs. We will share patterns and potential drivers of fine scale trichome investment across the genus Mentzelia and preliminary experimental data detailing the impact of complex barbed and needlelike trichomes on a generalist herbivore. Our results shed light on longstanding questions about trichome diversity and emphasize the importance of considering the functional implications of micromorphological variation when measuring plant traits.

Topic: Ecophysiology
A-33 Unraveling the Physiological Function of Leaf Anatomical Traits in Cycads
Author: LENA BERRY (University of Wisconsin - Madison)
Keywords: Anatomical; Cycadales; Cycads; ecophysiology; gas exchange
Cycads are an ancient lineage of neotropical seed plants, and most are critically endangered today due to changing climates, environmental degradation, and overexploitation. Despite being an ancient group, cycads are largely underrepresented in physiological literature. Until recently, cycads were thought of as "living fossils", and while their gross morphology is similar to their ancient ancestors', recent evidence suggests that most extant species have rapidly diversified during a relatively recent aridification event in Earth's history (~20 mya). Cycads exhibit several leaf anatomical traits that may have permitted them to expand into drier habitats, but whose function is not well understood in any plant group. I am investigating the physiological role of one of these leaf structures, bundle sheath extensions (BSE) in the cycad genera Ceratozamia. It has been proposed that BSE may 1) act as "windows" channeling lights deeper into a leaf, directly illuminating a greater proportion of the mesophyll and thus increasing photosynthetic efficiency, or 2) directly link the vascular bundle and the epidermis, increasing the hydraulic conductance, or water movement, between these structures. Within Ceratozamia, some species have BSE and others do not, and within those with BSE the size and shape of the BSE varies. This makes it an excellent group to test the function of BSE due to the variation in their anatomical structure. Field measurements were completed at Montgomery Botanical Center (MBC) in Coral Gables, Florida. Using a LiCor-6800, on 11 species, I collected light response curves to test whether the presence of BSE increased photosynthetic light use efficiency and/or maximum rates. I also measured leaf level reflectance using a UniSpec spectral analysis system. These data will be paired with cross-sectional anatomical measurements, like cross sectional area occupied by BSE or mesophyll, and leaf chlorophyll content on collected leaf tissue to control for differences that could impact photosynthetic rate across species. Understanding the ecophysiological role that BSE played for cycads in the past will be broadly applicable to plant groups with BSE which are now facing analogous environmental changes towards drier and hotter environments.

Topic: Biogeography
A-35 Drivers of Alpine Plant Community Turnover in Western North America
Author: Joseph Kleinkopf (University of New Mexico)
Keywords: alpine; community assembly; Phylogenetic beta-diversity; turnover
Alpine habitats are among the most extreme on earth, experiencing freezing cold and persistent snow during the winter months, and intense ultraviolet radiation during the summer months. And yet, despite this environment of extremes, alpine plant species are incredibly biodiverse. The global alpine flora is made up of around 10,000 species from nearly 100 plant families, many of which are locally endemic or rare. However, despite their importance to global biodiversity, many questions regarding the processes underlying alpine plant community assembly remain. Because alpine habitats are amongst those most threatened by climate change, with many regions already seeing compositional and phenological changes in their alpine floras, a better understanding of the processes underlying alpine plant community assembly is imperative for predicting how these irreplaceable habitats will respond as our climate continues to warm. One approach to exploring the relative importance of current or historical factors in driving patterns of biodiversity is through beta-diversity, or turnover. Here, I explore possible abiotic drivers of turnover between alpine plant communities across western North America. Over 40 alpine plant communities were characterized from 2021-2023 across Washington State, Idaho, Colorado, and British Columbia. Taxonomic and phylogenetic turnover were quantified for every pair of communities. Preliminary results suggest that temperature and precipitation–two common drivers of turnover across many taxonomic groups–explain little to no turnover between alpine plant communities. However, geology appears to be a possible driver of turnover between alpine plant communities. These results provide insights into how alpine floras are structured over space and may allow us to identify areas of conservation interest as our planet continues to warm.

Topic: Phytochemical
A-36 Phytochemical Analysis of Bamboos And Its Utilization By Indigenous People of Himachal
A-38 Ex vivo and in vitro antiplasmodial activity and toxicity of Caesalpinia decapetala (Roth) Alston (Fabaceae)

Author: DOUGLAS OCHORA (North-West University), Caroline Murithi (University of Nairobi), RAEL MASAI (Kisii University), Godwin Anywar (Makerere University), Hoseah Akala (Kenya Medical Research Institute (KEMRI)), Abiy Yenesew (University of Nairobi), Edwin Kamau (Tripler Army Medical Center, Honolulu, Hawaii (HI, USA))

Keywords:
Background: Malaria remains to be among the most prevalent parasitic diseases globally with about 95% of the cases reported in Sub-Saharan Africa. The high malaria prevalence is mainly due to the ever-increasing emergence of resistant strains of malaria-causing parasites to the current antimalarial drugs. This, therefore, calls for the search for novel antimalarial compounds. Plants used in traditional medicine for the treatment of malaria offer possible sources of such compounds. Caesalpinia decapetala has been used traditionally for the treatment of malaria. However, the antiplasmodial activity of the plant has never been reported. Aim: To determine the ex vivo and in vitro antiplasmodial activities of the extracts of the roots, stem bark and leaves of Caesalpinia decapetala.

Methodology: The roots, stem bark and leaves of Caesalpinia decapetala (Roth) Alston (Caesalpiniaceae) were collected and air-dried under a shade then extracted consecutively with dichloromethane and methanol (1:1 (v/v) (4 × 0.8 L). The extracts were tested for antimalarial activities against four strains of Plasmodium falciparum (W2, DD2, 3D7, and D6) and fresh P. falciparum field isolates using the SYBR green I assay. The mean fifty percent inhibition concentration (IC50) was determined for each assay. An acute oral toxicity test was done based on the Organization for Economic Cooperation and Development (OECD 425) guidelines using Swiss albino mice.

Results: The leaves and stem bark extracts showed good antimalarial activities with IC50 values of 4.54 ± 0.86 μg/mL, respectively, when tested against the fresh field isolates ex vivo. Similarly, the roots extract showed an IC50 value of 6.49 μg/mL when tested against field isolates ex vivo. The roots extract showed the highest antimalarial activities among the samples when tested against W2 (IC50 = 6.12 μg/mL), DD2 (IC50 = 8.17 μg/mL), and D6 (IC50 = 16.02 μg/mL) strains of P. falciparum whereas the leaves showed the highest activity (IC50 = 9.3 μg/mL) when tested against the 3D7 strain of P. falciparum. No mortality was observed for the mice treated with 2,000 mg/kg of the leaves and stem bark extracts. The mouse treated with 2,000 mg/kg of the roots extracts regained weight by day 12 of the observation period.

Conclusion: Caesalpinia decapetala has the potential to suppress the growth of P. falciparum thereby contributing to combating the recurrent emergence of antimalarial drug resistance.

A-39 How does Penstemon cobeae style length variation develop and affect mating systems?

Author: Taylor Michael (University of Kansas), Lena Hileman (University of Kansas), Carolyn Wessinger (University of South Carolina)

Keywords: Penstemon;Development;Heterostyly;mating systems

Penstemon cobeae is a wildflower that has been documented as exhibiting striking variation in style length. Heterostyly, a genetic polymorphism is thought to increase the rates of outcrossing in plants that have this characteristic. The goals of my research are to 1) determine the developmental basis of distinct P. cobeae style length variation, and 2) test whether style length variation influences the P. cobeae mating systems. Field studies and greenhouse experiments, along with developmental and genomic approaches will be used to determine how heterostyly potentially shapes the P. cobeae mating systems. Results from this study will provide insight into how floral variation can affect critical life history traits, such as mating systems, which in turn affect genetic diversity in populations – the fuel of evolution
the role of structural heterogeneity? We aimed to improve ecological understanding by investigating how neighbouring trees interact in terms of epiphyte species overlap. Also, we aimed to identify the key drivers of stand variables on epiphyte diversity at tree level. We studied 24 plots, in the Black Forest, Germany, varying in recent and historical management impact. We analysed 96 tree/tree pairs of Fagus sylvatica, Abies alba and Picea abies and found that species diversity and interactions of proximate and distant tree pairs of different categories of diameter at breast height (DBH). Our findings reveal interaction patterns between co-occurring tree species, highlighting the importance of spatial proximity and tree species identity—particularly noting a stronger influence on lichens by species identity and on bryophytes by proximity. Light heterogeneity emerged as a critical determinant for species richness for both taxbi, with DBH heterogeneity significantly affecting lichens and tree species composition influencing bryophyte diversity. We confirmed the influential role of tree size on these dynamics and therefore underscore the importance of old-growth trees in (managed) forest stands. In conclusion, we propose promoting structural heterogeneity, including the practice of retention forestry, as a vital strategy for conserving epiphytic lichen and bryophyte diversity. Besides tree species composition and size, our study highlights the impact of spatial arrangement of co-occurring tree species in forest stands by impacting epiphyte diversity.

Topic: Development and Structure

A-43 Parallel evolution of corolla tube width shifts in Penstemon

Author: Haylee Nedblake (University of Kansas), Carolyn Wessinger (University of South Carolina), Lena Hileman (University of Kansas)

Keywords: morphology; Penstemon; convergence; flower; parallel evolution; Pollination syndrome; QTL mapping

Floral diversity is largely shaped by flower-pollinator interactions. This leads to suites of traits, pollination syndromes, that facilitate pollen movement by specific pollinators. Pollination syndromes are excellent for testing whether genetic and developmental parallelism complement the evolution of striking phenotypic parallelism in flowering plants. Flower corolla width is a particular pollination syndrome trait that plays a role in determining which pollinators are able to "fit" the flower from a pollinator’s perspective and to efficiently move pollen between conspecifics. Narrow corolla tubes, which are specialized to transfer pollen from and to a hummingbird's forehead as its bill reaches into the flower for nectar, can exclude bees through discouraging and preventing them to enter the flower. In Penstemon, shifts from bee pollination syndrome to hummingbird pollination syndrome often lead to a significant narrowing of the corolla tube. Penstemon is an ideal system to study genetic and developmental parallelism in convergent evolution because within this ancestorly bee-pollinated genus of approximately 300 species, hummingbird pollination has evolved 11-20 times. Through quantitative trait loci (QTL) mapping, I have identified the genomic locations underlying the parallel floral corolla width differences in two independent origins of Penstemon hummingbird pollination: between bee-adapted P. amphoreaeae and its close hummingbird-adapted relative P. kunthii, and between bee-adapted P. neomexicanus and its close hummingbird-adapted relative P. barbatus. After identifying genomic regions responsible for the genetic basis for the independent origins of this parallel hummingbird pollination trait, I will look for common genomic bases exists through assessment of QTL correspondence. Testing for QTL correspondence between the two distinct Penstemon mapping populations reveals whether parallel genetic changes are likely responsible for the striking corolla width parallelism in Penstemon.

Topic: Paleobotany

A-44 New paleobotanical and geological contributions from two stratigraphic sections of the Matzitzi Formation, Puebla, Mexico.

Author: Ivonne Vega-Valdez (Instituto Politécnico Nacional), Emilio Estrada-Ruiz (Instituto Politécnico Nacional), Michelangelo Martini (Universidad Autónoma de México), Mildred Zepeda-Martinez (Universidad Autónoma de México)

Keywords: extinction; Ferns; Geology; México; Paleozoic; Plant fossil; Triassic

In Mexico, there are four recognized stratigraphic units containing Permian fossil plants, the Matzitzi Formation being the most extensively studied and forming the focus of this research. Since 1986, various authors have proposed different ages for the formation. Based on the fossil flora, some authors have suggested a depositional age for the unit that span between Pennsylvanian and Permian time. The recent U-Pb dating of zircon grains from volcanic deposits interbedded with the fluvial deposits of the Matzitzi Formation and a hypabyssal body with peperite emplaced within it indicate
that the unit’s deposition occurred at least between latest Guadalupian and Middle Triassic time. The two sections studied in this work contain the dated volcanic rocks, giving an absolute temporal framework to our work. The Coatepec section is bracketed to late Permian time, whereas the Atotlottitan section to Middle Triassic time. These two sections span a time interval marked by the most severe mass extinction event in Earth’s history, The Great Dying. This catastrophic event witnessed the disappearance of up to 96% of marine species and 70% of terrestrial species, attributed to a combination of factors such as volcanic activity, climate change, and oceanic anoxia. The primary objective of this work is to elucidate the paleoflora and depositional environment of the Matzitzi Formation exposed at the Atotlottitan and Coatepec sections, aiming to deduce the impact of The Great Dying on regional plant diversity. The research was conducted in two stages. Firstly, we measured representative stratigraphic columns at each section and collected fossil plant samples from various stratigraphic levels. Then, we described and identified fossil samples. We collected total of 221 fossil samples, 135 from Atotlottitan and 86 from Coatepec. Based on the lithofacies across the sections, we infer the Matzitzi Formation is the stratigraphic record of an anastomosing river, with dominantly sandy channels bounded by extensive floodplains. All fossils plants were found in the floodplains suggesting they are authochthonous. Seven different genera of fossil plants have been identified, each exhibiting distinct characteristics that contribute to their classification. Among these, Asterocopa stands out, marked by its prevalence, and characterized by pinnules attached to the rachis, along with a distinctive mid vein and secondary veins. Odontopteris, another noteworthy genus, is identified by its indistinct midrib of leaves that do not bifurcate into sterile pinnules, on the other hand, is recognized by pinnules with a crenate margin and secondary veins that bifurcate. Neopteris sets itself apart with pinnules attached to the rachis through a petiole. The presence of Calamites is discerned by a regular pattern of nodes separated by inter-nodal spaces, contributing to its unique classification. Interestingly, Filotheca, initially reported for the Lower Permian in Argentina, has been discovered in the Middle Triassic within the Matzitzi Formation. The unexpected occurrence of Stigmia in the Middle Triassic challenges previous reports locating it in the late Permian. This discrepancy prompts a reevaluation of the temporal range of Stigmia and add a layer of complexity to our understanding of the paleobotanical landscape during the Middle Triassic period.

**Topic: Ecology**

**A-45 Mean Plant Toxicity Modulates the Effects of Defense Variability**

**Author:** Vincent Pan (Michigan State University), Kadem Gibert (Michigan State University), Will Wetzel (Montana State University)

**Keywords:**
Emerging evidence suggests plant trait variation suppresses herbivore performance, but these results are usually contingent upon a single mean. We manipulated the mean and variation of glucosinolate toxin concentration on Arabidopsis thaliana leaves and fed them to Trichoplusia ni in three field and greenhouse experiments. Plants painted with a greater mean glucosinolate concentration had higher fitness and herbivore resistance; however, at higher mean concentrations, variation reduced the defensive effect, while at lower mean concentrations, variation enhanced it. This reversal is consistent with recent models of plant defense that include herbivore food selectivity, but simulations revealed that the benefit of food selectivity to herbivores was minuscule. Instead, nonlinear averaging and physiological tracking effects likely drove patterns in plant fitness and herbivore resistance. We suggest that high defense variation in plants may be a widespread convergent defensive phenotype, but for well defended plants, variation may inadvertently lead to herbivore niche expansion.

**Topic: Ethnobotany**

**A-46 Balancing Flames: Traditional Fire Practices and Wild Edible Plants in South India’s Dry Forests**

**Author:** Smrity Ramavarapu (University of Hawaii at Manoa)

**Keywords:**
In the verdant expanse of the Malai Mahadeshwara Hills Wildlife Sanctuary, nestled between the Eastern and Western Ghats of South India, our research explores the critical interplay between traditional (low-intensity) fire regimes and their ecological and socio-cultural ramifications. This paper delves into the nuanced role of fire in dry forest ecosystems, historically utilized by the Soliga and Bedagampana communities for various ecological purposes, including vegetation management, biodiversity conservation, and cultural practices. The study investigates the consequences of altered fire regimes, primarily due to regulatory changes and the invasion of non-native species, examining their ecological and social impacts. Specifically, the study aims to understand the impact of changing fire regimes on the diversity and abundance of WEP, and its thereby impact on the social fabric of the community. Our empirical investigation employs a comprehensive approach, combining Normalized Burn Ratio to identify areas affected by varying fire intensities, and detailed field surveys to assess the abundance and diversity of wild edible plants (WEPs) across plots subject to different fire intensities (high, low, and control/no fire). Parallel to the ecological assessment, our study engages with the indigenous Soliga and Bedagampana communities through focused group discussions to uncover the socio-cultural implications of changing fire practices. Our findings reveal significant reductions in WEP density and richness in high-intensity plots, as well as increased variability in WEP richness. This is consistent with local perceptions of the effects of changing fire regimes. Focus group participants emphasized the role that WEP plays in building and maintaining familial and social networks, a driving force for social gatherings among women, and their value in festivals and other cultural events.

Overall, our findings suggest that low-intensity fires play a pivotal role in supporting local dietary and medicinal needs. The narratives gathered illustrate a deep-rooted connection between traditional fire regimes and the maintenance of cultural heritage, food security, and communal bonds. Our findings indicate that changing fire regimes threaten the cultural identity and livelihoods of these communities, severing ties with ancestral knowledge and altering the socio-economic fabric. This paper posits that the conservation of biodiversity, particularly WEPs, cannot be decoupled from the preservation of cultural practices and traditions that do. Through this research, we contribute to the ongoing discourse on fire ecology, indigenous rights, and conservation policy, highlighting the indelible link between fire, flora, and the human spirit.

**Topic: Development and Structure**

**A-48 Leaf architectural diversity of Annonaceae Juss. in Nigeria and the Cameroon**

**Author:** Benjamin Ajayi (University of Lagos)

**Keywords:** Annonaceae; leaf architecture; venation

This research article presents a comprehensive comparative analysis of leaf architecture, specifically on venation and cuticle characteristics, in forty species of Annonaceae collected from Nigeria and the Cameroon. Various leaf architectural characters such as areola formation and shape, vein category and course, angle of divergence, nerve endings, venation pattern, and veinlet structure were examined and graded across all studied species. The results revealed distinctive diagnostic values associated with the characters. Notably, areola formation was found to be well developed in most species, except Annona squamosa, I. congolana, I. dewevrei, I. zenkeri, Monanthotaxis schweinfthkii, Uvaria angolensis, and Dendettia

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tripetala, which displayed moderate development. Poor areola development was observed in Monodora tanalofila and Uvularia chamae. The predominant shape of the areola was four-shaped, although I. conglonata, I. campanulata, Monodora angolensis, Monantha taxis bicornis, M. barteri, and Uvularia chamae exhibited five-shaped figures or higher. The angle of divergence on tertiary veins ranged from 59° to 173°, with the lowest degree observed in I. zenkeri and the highest in X. acutiflora. The number of nerve endings in the studied species varied from 1 to 6, with M. myristica displaying no visible nerve endings. Venation patterns in the forty Annonaceae species analyzed were primarily brachidromous or eucamptodromous, but Annona muricata, Xylopia ethiopica, X. acutiflora, and Dennettia tripetala, which exhibited craspedodromous patterns. Other characters with diagnostic features were vein category, vein course, and veinlet patterns. Conclusively, the result of this study provides insights into the vascular system of the family Annonaceae in Nigeria and Cameroons and contributes to our understanding of their taxonomic relationships and ecological adaptations.

**Topic: Ecophysiology**

**A-49 Effect of electro priming on seed germination of plants: A case study in Pakistan**

**Author:** Pooja Oad (University of Karachi), Muhammad Adnan (University of Karachi)

**Keywords:** Salinity Tolerance; Seed germination; priming

Electroculture has been previously reported to enhance seed germination by hastening the processes of water absorption and respiration in seeds. This study aimed to investigate the effect of electric priming on the germination of Solanum lycopersicum (tomato), Brassica rapa (turnip), and Brassica napus (mustard) seeds. To accomplish this, 3-volt and 9-volt electric voltages were administered to the seeds before their germination was monitored for 7 days, and fresh weight, root length, and shoot length were measured. The impact of electric pre-treatment on several germination parameters, including germination percentage, germination rate, germination index, velocity, mean germination rate, and Timsin germination index, was analyzed. Distinct outcomes were observed, with voltage pre-treatment shown to expedite germination in some cases and exhibit no effect in yet others. The objective of the study also included assessing the effect of an electric pulse on seed germination in saline conditions. Although some improvement in germination was observed, it was not significant. Despite various electrical schemes enhancing germination in all types of seeds, no definitive treatment-response relationship could be established for either the interval time or the applied voltage.

**Topic: Development and Structure**

**A-50 SLY1-mediated gibberellin signaling is positively regulated by retromer subunit AtVPS29 in Arabidopsis**

**Author:** Wang Ki Min, Jun Soo Kwak, Hak Soo Seo (Seoul National University)

**Keywords:** arabidopsis; Growth; Meristem development; roots

In plants, the large retromer complex is known to play roles in multiple development processes, including cell polarity, programmed cell death, and root hair growth in Arabidopsis. However, many of its roles in plant development remain unknown. Here, we show that Arabidopsis trimeric retromer protein AtVPS29 (vacuolar protein sorting 29) modulates gibberellin signaling. The SLEEPY1 (SLY1) protein, known as a positive regulator of gibberellic acid (GA) signaling, exhibited lower abundance in vps29-3 mutants compared to wild-type (WT) plants. Conversely, the DELLA repressor protein, targeted by the E3 ubiquitin ligase SCLF (Skl, Cullin, F-box) complex and acting as a negative regulator of GA signaling, showed increased abundance in vps29-3 mutants compared to WT. The vps29-3 mutants exhibited decreased sensitivity to exogenous GA supply in contrast to WT, despite an upregulation in the expression of GA receptor genes within the vps29-3 mutants. In addition, the expression of the GA synthase in I. czekanewski was down-regulated in vps29-3 mutants, implying that the loss of AtVPS29 causes the down-regulation of GA synthesis and signaling. Furthermore, vps29-3 mutants exhibited a reduced meristematic zone accompanied by a decreased cell number. Together, these data indicate that AtVPS29 positively regulates SLY1-mediated GA signaling and plant growth.

**Topic: Education and Outreach**

**A-51 Data, Science, and Community: Research Project Building from Botanical Garden Database**

**Author:** ray volkin (Norfolk Botanical Garden), Lisa Wallace (Old Dominion University)

**Keywords:** community engagement; Data analysis; database; Education

What do public gardens and scientists have in common? They have a symbiotic relationship with the community, and they use databases to bridge that relationship. Databases are a powerful tool used by scientists of all disciplines and public gardens. Botanical Gardens offer a unique position to engage the community through public databases and educate in environmental action. Databases like IrisBG, BG base, and others are a powerful tool for horticulturists to not only manage basic collection information, but also to investigate and manage more complex questions. With the help of university and K-12 student groups and volunteers, gardens can collect and analyze data to interpret threatened plant status, tree risk assessment, disease control, canopy succession, and much more. The harmony of citizen-science based research and the access to the environment and education that public gardens offer makes for a unique opportunity and perspective for public gardens to expand botanical education. In this presentation, I demonstrate how the Norfolk Botanical Garden database is a rich source of information that can be analyzed to answer complex scientific questions. Our database has been used to evaluate tree risks, monitor a virulent plant disease over time, and evaluate vegetation patterns across our campus. These efforts have engaged high school and college students in active research and contributed to a better understanding of the Garden’s collection and plant science. As we continue to build upon these efforts, we strive to inspire other volunteer or student geared projects in the Garden to showcase the educational value of our collection to the local community and contribute to the scientific record.

**Topic: Biodiversity Informatics & Herbarium Digitization**

**A-53 The NPSdataverse: tools for authoring metadata, publishing, and accessing Open, FAIR data packages**

**Author:** Robert Baker (National Park Service), Joe DeVivo (National Park Service), Judd Patterson (National Park Service), Issac Quevedo (National Park Service), Kristin Vanderbil (National Park Service), Sarah Wright (National Park Service)

**Keywords:** FAIR; Open Access; open source; R; Open data sharing

The National Park Service (NPS), along with other federal agencies, is tasked with making data public, Open, and machine-readable. To this end, NPS has developed an ecosystem of tools (“NPSdataverse”) in the R statistical language to help author and publish Open, Findable, Accessible, Interoperable, and Reusable (FAIR) data and metadata. These tools and the suggested workflows will be most useful to scientists conducting research within National Parks, but useful to all researchers who need to make data and metadata available for publication, wish to publish data in data driven journals such as Data, Scientific Data, or Biodiversity Data Journal, or want to access NPS data from the NPS digital repository (DataStore). The R packages within the NPSdataverse include: 1) QCokl, a package for data quality control and data munging including detecting endangered species, converting UTMs to decimal degrees, finding elevation based on GPS coordinates, and facilitating use of DarwinCore naming schemes for enhanced interoperability. 2) The EML, EMLassembyline (from the Environmental Data Initiative) and EMLeditor packages containing tools for authoring, editing, and validating machine-readable metadata in the Ecological Metadata Language format. 3) The Dpchecker package to check metadata format and contents as well as verify that metadata correctly corresponds to the data it describes. 4) The NSutils package which offers an avenue for researchers to access data from the National Park Service’s digital repository (DataStore) and directly import into R, Power BI, or other analysis and visualization programs. Anyone can incorporate the NPSdataverse into their data management plans and everyone proposing research in the National Parks is encouraged to include the NPSdataverse and DataStore as part of their data management plans.

**Topic: Herbaria for the future: Early Career Researchers and Their Uses of Herbarium Specimens**

**A-55 Synthesizing digitized historical plant collections information with open-access spatial data to identify priorities for future collection efforts & increased research applications**

**Author:** Elizabeth Lombardi (University of New Mexico), Harpo Faust (University of New Mexico, Museum of Southwestern Biology), Hannah Marx (University of New Mexico)

**Keywords:** Synthesizing digitized historical plant collections information with open-access spatial data to identify priorities for future collection efforts & increased research applications
Biodiversity; Collections; digitization; herbaria; Herbarium

to understand how and where biodiversity is threatened, it is imperative to build historical baselines that accurately characterize the present and past state of biodiversity across environments. Botanical collections provide important ecological, evolutionary, and biogeographic information on the diversity and distributions of plant taxa, yet biases in collection efforts across spatial, temporal, and taxonomic scales are well-known. Here, we characterize and quantify trends in botanical collections made from across different abiotic, biotic, and sociopolitical boundaries within the present-day state of New Mexico. Using a biodiversity informatics approach applied towards a regional case study, we identify opportunities for efficiently improving natural history collection coverage and analyses of botanical diversity. Accurate representation of botanical biodiversity, preserved for future generations through vouched plant specimens deposited in herbaria, depends on collection decisions made now. This work aims to provide a useful workflow for synthesizing digitized regional botanical collections as researchers prioritize current and future resources in the face of global change.

Topic: Systematics
A-56 Understanding the Evolutionary History of the North American Desert genus Fouqueria through Phylogenomics and Niche Modeling
Author: Emeline Pano (University of Florida), Nico Cellinese (University of Florida)
Keywords: Deserts, Ericales, Mexico, Southwest USA, phylogenetic

The desert genus Fouqueria (Fouquieriaceae, Ericales) is native to North American deserts and is diversified in the bajada local, about 7 Ma. Past phylogenetic studies have supported the group as monophyletic using a few ribosomal, plastid, and nuclear markers. However, discordance at both deep and shallow nodes still challenge our current understanding of the evolution and biogeography of this group. Here, I propose a deep genome skimming approach to obtain low-copy nuclear and plastidome data to reconstruct the evolutionary history and test putative hybrids and current biogeographic hypotheses.

Furthermore, I aim to explore the genetic diversity and phylogeographic dynamics of two polyploid endemic species in Baja California, F. digueti and F. burragei, taking into consideration the region’s complex geological history and its impact on genetic patterns. Ecological niche modeling will help elucidate the processes that have caused the current species distribution and predict their response to climate change. This comprehensive approach not only contributes to our understanding of desert endemics but also sheds light on the potential significance of polyploidy in arid ecosystems.

Topic: Floristics & Taxonomy
A-57 Trajectory for Decolonial Methods in Grand Gulch Floristics within Bears Ears National Monument
Author: Amaya-Jean Roberts (Utah Valley University), Erin Riggs (Utah Valley University), Max Taylor (Self employed), Curtis Yanito
Keywords: Decolonizing

In southeastern Utah, the floristics of Grand Gulch within the Bear’s Ears National Monument have been understudied and require further investigation. This land has been occupied approximately 10,000-8,000 years by indigenous peoples and remains to be locally inhabited by Native American tribal members. Other researchers, such as geologists, historians, and archeologists, have studied Grand Gulch, but botanical sciences, including plant virology, have yet to report the vast diversity and richness of Grand Gulch flora, along with its accompanying branching canyons. Our research occurs on historically tribal land, thus the UVSC Herbarium at Utah Valley University, (Utah Valley State College, UVSC, museum acronym) aims to conduct floristics in collaboration with local Native American tribes by using decolonization methods. Decolonizing research methodology prioritizes creating meaningful, long-lasting relationships with indigenous people by including them in our field work, objectives, and findings, as collaborators they contribute significant cultural knowledge about the land, flora, and fauna. Tribes in this region have witnessed “parashoot researchers,” that drop in, collect data, and leave without communicating or learning from indigenous scientists and elders. This project is laying a foundation for collaboration with Bears Ears Inter-Tribal Coalition in a positive, cooperative, responsible, and considerate fashion. By building a respectful and courteous relationship with local tribes, we are learning important floristics pertaining to their cultures, conducting true knowledge sharing between UVU and indigenous scientists, and repatriate our floristic findings to the indigenous people of Bears Ears in a manner informed by their needs. As of 2024, we have covered approximately less than half of the 52 miles of Grand Gulch canyons, hanging gardens, and riparian area, resulting in quality museum and teaching collections. We will continue our work in Grand Gulch until we have a strong representation of the floristics in our collection.

Topic: Biogeography
A-58 The roles of phylogenetic niche conservatism and climatic niche divergence in structuring the distribution of ecologically diverse Andean Miconia (Melastomataceae)
Author: Juan Angulo (New York Botanical Garden), Fabian Michelangeli (The New Your Botanical Garden), Lucas Majure (University of Florida, Florida Museum of Natural History), Leo-Paul Dagallier (The New York Botanical Garden)
Keywords: Anedes

The tropical Andes is a biodiversity hotspot, harboring a diverse flora along steep elevational and ecological gradients. Species are not distributed evenly within these mountains and are ecologically constrained by the environmental conditions in which a species can persist, or its climatic niche. As a lineage diversifies species can continue to retain their ancestral climatic niche through phylogenetic niche conservatism (PNC) or diverge from it, particularly when presented with ecological opportunity. Both PNC and niche divergence have played roles in Andean species assembly, either through migration from temperate lineages into high elevation habitats (PNC) or colonization of lineages with Amazonian origins by way of niche divergence. However, we still lack insight into what role these processes play in structuring the distribution of lineages that have successfully diversified across the Andean ecological gradient, from warm lowlands to cold sub-alpine ecosystems. The genus Miconia (Melastomataceae) contains a clade (~500 sp) in which species are narrowly endemic to elevational bands, but as a whole the group can be found from sea level to 3500m. Most species are found in the tropical Andes, but there were two separate dispersal to the Caribbean and to Mesoamerica. We generate a new phylogeny of the group and use distribution and environmental data to reconstruct the dynamics of niche evolution as the lineage diversified within the Andes and dispersed out of it. We hypothesize that PNC has constrained diversification largely within climatic regimes, but that niche shifts have allowed for successful tracking of neighboring climatic regimes in Andean mountain slopes. We predict that dispersal out of the Andes, on the other hand, is characterized by the retention of ancestral niche. We predict that some aspects of the niche, such as precipitation related variables, are conserved, while others have shifted with more frequency, such as temperature. Our study contributes to the understanding of the biogeographical patterns of Andean plant diversity and the processes that generate it.

Topic: Reproductive Processes
A-59 ECOLOGY OF POLLINATION AND REPRODUCTION IN TAMARIND GENETIC RESOURCE: A WAY FORWARD IN FOREST GENETIC RESOURCES (FGR) MANAGEMENT
Author: Bagathsingh C (ICFRE-Institute of Forest Genetics and Tree Breeding), Chitra P. Easikammal S (2Tamil Nadu Pollution Control Board), Utchimahli M (Center for International Forestry Research and World Agroforestry (CIFOR-ICRAF)), Amaravel M (ICFRE-Institute of Forest Genetics and Tree Breeding), Mayavel A (ICFRE-Institute of Forest Genetics and Tree Breeding), Nagarajan B (ICFRE-Institute of Forest Genetics and Tree Breeding)
Keywords: reproductive biology

Tamarind is a highly prized genetic resource, cultivated across diverse regions supporting livelihoods among global rural communities. This study provides insight on the reproductive biology of Tamarindus indica L., emphasizing on its floral morphology, pollination science, and breeding biology. Studies indicate annual flowering rhythmic with duration variability among trees. Anthesis starts at 23:00 hrs and is completed by 04:00 hrs. Anther dehiscence is 3–4 hours after anthesis. Pollen grain exhibit
dimorphism with sizes ranging from 25–40 μm, with high pollen fertility (87.62%±3.20%). In-vitro germination rate of pollen varies in different sucrose concentrations (10.2±2.5 to 50.8±1.9). Stigma is papillate, wet and is receptive before anthesis, that peaks by 12:00 noon. Flowers typically offer pollen and nectar to visitors. The flowers possess a typical insect pollination syndrome, and eight group of visitors are observed during the study period. Bees, particularly those of the Apis genus, are identified as primary pollinators, exhibiting distinct foraging behaviors throughout the day. The study observes significant variation in natural reproduction rates among tamarind clones, ranging from 3.06% to 6.94%. Xenogamy (cross-pollination) resulted in higher fruit set rates (75.31% to 88.03%) compared to natural pollination.

**Topic: Phylogenomics**

**A-60 Ecological Release and Climatic Niche Evolution in the Aquatic Neptunia (Fabaceae: Mimosoid Clade)**

**Author:** Ellie Becklund (Ohio University), John Schenk (Ohio University)

**Keywords:** Angiosperms; Climatic niche; Fabaceae; Leguminosae; phylogenetics; phylogeny; polyploid; systematics; Mimosoid clade

Ecological release is the relaxation of selective pressures, allowing a population to occupy a different or broader niche, and is promulgated to be a driver of speciation. Ecological release has been studied at the population level, but the consequences of ecological release after speciation are difficult to determine and require the study of closely related species with divergent habitats. *Neptunia* Lourn. (Fabaceae) is comprised of 22 species that occur worldwide in the tropics and subtropics and is the sole mimosoid genus with fully aquatic species, *N. oleracea* and *N. plena*. The aquatic species are pantropically distributed whereas the terrestrial species are confined to continental barriers. Four *Neptunia* species are polyplody (two aquatic species, two terrestrial species). *Neptunia* species relationships are unresolved from previous studies of chloroplast and ITS markers, and it remains uncertain if the widespread aquatic species are valid species or a result of cryptic speciation. Evolutionary relationships are necessary for sister group comparisons to determine if ecological release occurred in *Neptunia* species and if aquatic habitat or ploidy have influenced species to occupy broader climatic niche spaces and distributions. We applied a target-capture approach with the Angiosperms353 bait set to sequence 353 nuclear genes and the chloroplast genome to infer species relationships of the 22 *Neptunia* species. For the 94 ingroup and 11 outgroup samples, exon + intron loci were reassembled with HybPiper, gene trees were reconstructed with maximum likelihood, and the nuclear species tree was visualized with principal component analyses to determine if aquatic and tetraploid species occupied similar, broader, or divergent niche space compared to their terrestrial or diploid sister groups. The two aquatic species are closely related, indicating a single transition into an aquatic habitat. A plectonic and terrestrial sister groups overlap in multidimensional niche space, while the aquatics occupied a broader niche space. The tetraploids also occupied a broader niche space compared to sister diploid species. The broadening of niche space in *Neptunia* species suggests ecological release had a role in speciation in *Neptunia* and could explain the pantropical distributions of the aquatic species.

**Topic: Floristics & Taxonomy**

**A-61 Anarchy to Harmony: Redbud (Cercis spp.) as a case for integrative taxonomy**

**Author:** Mason McNair (Michigan State University), Jim Leebens-Mack (University of Georgia)

**Keywords:** The genus Cercis, like many genera, is fraught with taxonomic controversy. Circumscriptions of species, subspecies, varieties, and forms of North American taxa are hotly debated in taxonomic and horticultural literature. Common garden assessment of phenotypic variation and documentation of the genetic basis of phenotypic variation can inform taxonomic circumscription. We investigated published delimitations for North American *Cercis* taxa through analysis of phenotypic variation among specimens growing in a common garden (JC Raulston Arboretum, North Carolina State University). In addition, we leveraged an available breeding population for genomic estimation via GWAS and for phenotypic traits that have been used to distinguish *Cercis canadensis* var. *canadensis* and *Cercis canadensis* var. *texasensis*. By combining phenotypic information with an understanding of the genetic basis of key taxonomic traits, we illustrate how a pluralistic and integrative approach to taxon delimitation can yield rigorous and reproducible species and intranspecific taxonomic concepts.


**A-62 Evaluating species viability under the Endangered Species Act using the Species Status Assessment Framework**

**Author:** Judy Che-Castaldo (USFWS)

**Keywords:** rare species; species conservation; population viability

Since 2016, the U.S. Fish and Wildlife Service has adopted the Species Status Assessment (SSA) Framework for informing decision-making under the Endangered Species Act. The SSA serves as a compilation of the best available science on a species and provides decision makers with a rigorous characterization of the species’ biological status. The SSA process consists of three components describing the species’ ecological needs, current condition, and future condition; and summarizes species viability using the “3Rs” principles of resiliency, redundancy, and representation. The SSA is intended to be a living analysis that can be updated over time as new informative becomes available. The stand-alone scientific assessment also allows for broader engagement of States and other government agencies, partner organizations, and external researchers in the science used to inform ESA decisions. This presentation will describe the SSA Framework and provide an overview of the regulatory steps involved in ESA implementation, from listing to recovery planning to delisting. It will also include example analyses and applications, as well as suggestions on how scientists and partners can get involved with SSAs.

**Topic: Ecology**

**A-63 Submerged aquatic plant diversity and growth form distribution in north temperate lakes**

**Author:** Linden Taylor (University of Wisconsin-Madison)

**Keywords:** Aquatic plants; Biodiversity; community ecology; Great Lakes region; growth form; distribution

Water chemistry is known to be an important driver of submerged aquatic plant community composition in lakes. However, our understanding of the extent that water chemistry and biotic interactions influence the submerged aquatic plant growth form—eclodes, taller statured plants with stems, and isoelids, shorter statured plants with basal rosettes—is still developing. This research assesses submerged aquatic plant growth form frequency and species richness along an alkalinity gradient—a proxy for bicarbonate availability—in lakes in Vilas County, Wisconsin selected for the North Temperate Lakes LTER Regional Lakes Survey. We additionally assess frequency of the regionally warmer isoeld growth form as a function of local plant coverad and compare growth form frequency in 2015 and 2022. Twenty-eight lakes were surveyed with the Point-intercept (PI) aquatic plant survey method along a spaced grid of points in the littoral zone. We found an increase in elodid frequency and species richness and decrease in isoeld frequency and species richness along a bicarbonate availability gradient, demonstrating the importance of modes of carbon uptake for submerged aquatic plant growth form distribution. We also found a discernable decline in isoeld frequency and increase in elodid frequency in oligotrophic, low development lakes from 2015 to 2022, suggesting abrupt ecological change with increasing competitive vegetation.

**Topic: Botanical History**

**A-64 Human Dependency on Plants for Survival and the Compelling Power of Okoubaka obrevillei growing in specific region of the world**

**Author:** Adjut Funke Ogundola (Ladoke Akintola University of Technology)

**Keywords:** Scientifically, in the study of Biology, plants are regarded as the pioneer and energy producers, on which every other life forms depend. All these huge belongings to plants also emanate from the autotrophic ability of plants (photosynthesis) and chemical synthesis through which they supply energy needed by and influence the growth of their dependence. The utilitarian purposes of plants covers a major part of human fulfillments in terms of food, shelter, medicine, source of income, environmental remediation purposes, instruments of protection from predators, climatic hazards, and as a means of globalization through exploitation of plant products. However, among big trees such as *Ceiba petandra*, *Milicia excelsa*, the honor accredited to *Okoubaka obrevillei* (Asorrin, *lgi-nla*) is distinguished for its strong power of allelopathy and its peculiarly. However, this allelopathic property of the plant went beyond ordinary, as no living organisms can come near it beyond certain distance and still remain alive.
Moreover, if need be, to contact the plant for collection of its parts for medicinal purposes, a life rooster pays for it after series of incantations. The query of such information is believed to be countered as the word in the beginning says, ‘All things are created for human pleasures.

Scientifically, in the study of Biology, plants are regarded as the pioneer and energy producers, on which every other life forms depend. All these huge accumulations to plants also emanate from the autotrophic ability of plants (photosynthesis and chemosynthesis) through which they supply energy needed by and influence the growth of their dependence. The utilitarian purposes of plants covers a major part of human fulfillments in terms of food, shelter, medicine, source of income, environmental remediation purposes, protection from predators, climatic hazards, and as a means of globalization through exportation of plant products.

However, among big trees such as Ceiba petandra, Milicia excelsa, the honor accredited to Okoubaka obrevillei (Asotnin, Igi-nla) is distinguished for its strong power of allelopathy and its peculiarity. However, this allelopathic property of the plant went beyond ordinary, as no living organisms can come near it beyond certain distance and still remain alive. Moreover, if need be, to contact the plant for collection of its parts for medicinal purposes, a life rooster pays for it after series of incantations. Conclusively, it is very glaring that man would not have survived without the help of self-sap on hybridization. Has most species in this family possess on Okoubaka obrevillei is believed to have been countered the word in the beginning says, ‘All things are created for human pleasures.

### Topic: Hybrids and Hybridization

**A-65 Testing hybridization potential for three novel crosses of papaya wild relatives**

**Author:** Deannah Neupert (Miami University), McKenna Oyer (Miami University), Ethan Grant (Miami University), Evan Gallagher (Miami University), Richard Moore (Miami University)

Interspecific hybridization is a potent evolutionary mechanism that may result in transgressive phenotypes and/or novel traits in hybrid offspring. In plants, interspecific hybridization can lead to the emergence of new species, as well as it is a tool by which plant breeders may introduce alleles from wild crop relatives to agronomically valuable species. Interspecific hybridization, however, may be compromised in dioecious taxa in which sex expression is regulated by sex chromosomes. This is due to potential incompatibilities in the sex chromosome systems that arise due to genetic divergence between related dioecious taxa, especially in more divergent taxa. The papaya family (Caricaceae) is an excellent model to study the impacts of sex polymorphism and hybridization potential on the evolutionary divergence and the efficacy of cross-species hybridization, including measures of reproductive success such as flower mass, seed number, seed mass, and seed viability. This work can provide the foundation to future investigations into the role that sex chromosome divergence plays in establishing species boundaries as well as the potential for Vasconcellea species to serve as wild germ plasm for papaya crop development.

### Topic: Crops and Wild Relatives

**A-66 Assessment of pollen viability and size of wild diploid potato species (Solanum sect. Petota) under heat stress condition from Embrapa Potato Genebank**

**Author:** Rodrigo Nicolao (Universidade Federal de Pelotas), Kram Bashir, Caroline Castro (Embrapa), Gustavo Heiden (Embrapa)

Pollen viability is the subject of interest among the breeders as the increased interest in F1-diploid potato (Solanum tuberosum) breeding. To develop heat-tolerant potato cultivars, it is essential to investigate the reproductive dynamics, such as pollen viability and 2n pollen production. To accomplish this goal, it requires exploring its wild genetic resources that are conserved in the genebanks. The objective of this study was to assess the pollen viability and size of the diploid potato wild relatives under heat stress condition. We assessed the pollen viability and size of nine potato accessions conserved at the Embrapa Potato Gene Bank, including Solanum chacoense Bitter (BRA 00167447-2, BRA 00167017-3, BRA 00167023-1, BRA 00167028-0), Solanum commersonii Dunal (BRA00167007-4, BRA00167420-9, BRA00183760-8), and Solanum malmeanae Bitter (BRA 00183755-8). All the accessions did not exhibit a significant reduction in pollen viability as the temperature increased. At the heat stress conditions, the accessions BRA 00167023-1 did not produce pollen and BRA 00167251-8 did not bloom. Estimated GCV was lower than PCV for pollen viability. Our results highlight the presence of considerable genetic variability within wild potato germplasm concerning pollen viability under heat stress conditions. Furthermore, these first insights serve as valuable guidance for ongoing and future endeavors in diploid potato breeding.

### Topic: Ecology

**A-67 The Effects of Drought on Competitive Interactions Between Barley and Corn**

**Author:** Jeneva Tomaszewski (Saginaw Valley State University), Brian Maricle (Saginaw Valley State University)

It is crucial to recognize effects of drought on plant interactions in agricultural and ecological contexts due to recent increases in drought severity. Crowding is an important agricultural phenomenon; studies that pair crowding with drought can help us better understand and project what may be needed in the future for the greatest crop success. In this study, chlorophyll and plant growth were measured in drought and well-watered treatments in a replacement series to assess inter- and intraspecific competition between corn and barley in a greenhouse experiment. Leaf chlorophyll concentration was not influenced by crowding or presence of the competitor but was affected by drought treatment. In the conditions of this study, height and biomass measures in barley were more influenced by competition and in corn were more influenced by drought. Drought reduced height in both species. In well-watered conditions, barley appeared to be more sensitive to interspecific competition, whereas corn was not affected by the presence of barley. Under droughted conditions, barley height seemed to be more sensitive to intraspecific competition, whereas corn seemed to be more limited by drought than competition. Biomass data from the replacement series indicated limited competition in well-watered conditions. Under drought conditions, intraspecific competition had more of an effect on barley, whereas corn appeared to be more impacted by water availability than either inter or intraspecific competition. Understanding the ecological processes behind this could give insight into understanding plant production in increasingly dry soils.

**A-68 Plant diet of fruit-eating birds reflects low resource availability and forest-edge foraging in early successional Atlantic forests**

**Author:** Carina Motta (UNESP)

**Keywords:** ecological restoration; Metabarcoding; plant-animal interaction; seed dispersal

Fruit-eating birds drive seed dispersal in naturally recovering areas, ultimately shaping the trajectory of forest regeneration. Understanding plant diet of fruit-eating birds allows us to predict seed dispersal as well as gain insights to the quality of resources available and foraging habits of bird species. In order to investigate overall plant diet of principal seed dispersers, we worked in ten plots of early successional forest throughout the Corumbataí river basin in São Paulo, Brasil. Bird droppings were collected by mist-netting over the course of a year and key seed dispersers were classified based on the frequency seeds were found in droppings. We use metabarcoding of a universal rbcL mini-barcode extracted and amplified from 31 droppings of ten captured bird species to analyze plant diet. Diet content and richness was classified for each bird species and we evaluated the frequency of consumption of plants according to origin (exotic or native), fruit-type (fleshy or dry), and plant habitat across all bird species. A total of 50 OTUs from 23 plant families were obtained, with an average of 1.70 ± 1.81 detections per OTU. We assigned 48 of the 50 OTUs to the genus level, while the remaining 2 OTUs were classified as being one of two genera. Plant diet content varied among individuals and species, with Miconia (Melastomataceae) being
consumed most frequently. Average richness of plant diet per species ranged from 1 - 3 plant genera. We identified four plant genera as exotic and determined that only ~70% of all genera possess fleshy-fruits, as well as classified genera as one of four principal plant growth forms: tree, shrub, climbing, and herbaceous. The presence of exotic, dry fruit producing, and herbaceous genera in fruit-eating bird diet indicates low resource availability for forest-edge foraging, allowing us to better understand seed dispersal dynamics in these early successional areas.

**Topic: Phylogenomics**

**A-69 EXPLORING EVOLUTIONARY RELATIONSHIPS OF NEW WORLD ASTRAGALUS THROUGH PHYLOGENOMIC ANALYSIS**

**Author:** Victoria Martinez (Loyola University Chicago)

The legume Astragalus is the single most diverse genus of plants encompassing nearly 3,000 species. Not only is Astragalus remarkably diverse, but many species have considerable economic importance. For example, toxic Astragalus species also known as "locoweed" contain the chemical swainsonine which affects the reproductive and developmental traits of livestock and causes $100 million in annual losses in the United States alone. The genus is primarily distributed in temperate regions and is particularly diverse in southwest Asia (ca. 2,000 spp.), the Sino-Himalayas (ca. 400 spp.), western North America (ca. 400 spp.), and the Andes (ca.100 spp.; Wojciechowski, 2005; Podlech & Zanne 2013). The taxonomy and systematics of both Old World and New World Astragalus have been determined primarily through morphological analyses (Barney 1964). Over the past 30 years, Astragalus has received considerable phylogenetics interest, which has yielded important results identifying the major groups, mainly in the Old World. However, due to the incredible species diversity and rapid diversification, previous efforts have been limited in their ability to resolve evolutionary relationships in this very large and complex clade. Previous studies have examined the relationships within Old World Astragalus but little is known about the major groups within the New World and the number of introductions from Asia. In this study, we sampled approximately 100 species from the extensive United States National Herbarium collection covering all sections of the New World to establish a phylogenetic framework for this poorly studied group. Using a novel technique called Hyb-Seq which combined hybrid enrichment with genome skimming, we were successful in obtaining both nuclear and chloroplast data to investigate the interesting relationships within Astragalus. We uncovered new migration events previously unknown, and elucidated on the complex relationships of this New World group.

**Topic: Ecology**

**A-70 Phylogenomics, pollination biology, floral chemical ecology, and historical biogeography of Western Australian Darwinia (Myrtaceae)**

**Author:** Patricia Chan (University of Wisconsin-Madison), Ashley Hamersma (University of Florida), Matthew Barrett (James Cook University), Thomas Givnish (University of Wisconsin-Madison)

**Keywords:** Myrtaceae;phylogenomics;Plant-pollinator;systematics;chemical ecology

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 are developing a Myrtaceae bait kit for phylogenomic studies of Darwinia, and have already sequenced 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 now to construct and date nuclear and plastid 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: Ecophylogeny**

**A-71 Drought response across developmental transitions: insights into the role of vegetative phase change**

**Author:** Erica Lawrence-Paul (Pennsylvania State University), Jesse Lasky (Pennsylvania State University)

**Keywords:** adaptation; Arabidopsis thaliana; drought tolerance; Ontogeny

Developmental transitions impact ecology and evolution by altering the way plants interact with their environment. Studies of germination and flowering show that developmental timing has significant impacts on plant fitness and performance, but very little attention has been given to the juvenile-to-adult transition: vegetative phase change (VPC). In this study we used 160 diverse genotypes of Arabidopsis thaliana to investigate how plants differentially respond to drought across vegetative development from both physiological and genetic perspectives. We found that the timing of vegetative phase change has significant impacts on plant performance in response to drought stress and that the developmental phase of a plant (i.e., juvenile or adult) alters the impacts of drought on plant growth and fitness. We found significant relationships between the timing of VPC and climate-of-origin, indicating that the timing of this transition may contribute to both adaptation and acclimation in plants. Finally, we conducted a genome-wide association study and identified genetic loci associated with differential response to drought stress, and natural variation in the timing of VPC. Our study provides further evidence that vegetative phase change results in important physiological shifts in plants that contribute to their success and should not be overlooked.

**Topic: Ecology**

**A-72 An Endangered Grass “Falls” for a Complex Hydrologic Regime in Everglades National Park**

**Author:** Raelene Crandall (University of Florida), Jimi Sadle (National Park Service), Ben Baiser (University of Florida), Owen Schneider (University of Florida)

**Keywords:** asexual reproduction; endangered species; flooding; integral projection model

Hydrologic regimes strongly influence plant population dynamics over time in seasonally flooded environments. Aspects of the hydrologic regime, such as the seasonal timing, magnitude, and frequency of flooding, should be considered when managing populations of endangered plant species in seasonally wet places. We tested the response of Digitaria pauciflora, a federally endangered grass, to different flooding regimes of Everglades National Park, where the extent and duration of flooding is generally greater during the wet season but varies spatially along topographic gradients. We established demography plots at both ends of D. pauciflora’s elevation range. We measured vital rates, including growth, survival, and reproduction, annually for four years (2020-2023). Results showed that D. pauciflora has a patchy distribution across the landscape, likely because it reproduces seasonally through vegetative reproduction via plantlets. Mature plants produce plantlets that remain on the plant until they become heavy and fall, allowing plantlets in direct contact with the ground. The plantlets can then begin rooting, providing they land in suitable microsites that are not flooded. We found that D. pauciflora had increasing population growth in lower elevation areas, but only when seasonal flooding ended before plantlets fell to the ground. In these instances, D. pauciflora had both higher establishment and survival of plantlets following events, the establishment of new plants was rare, causing a net decrease in population size (i.e., greater mortality than establishment). We suggest that D. pauciflora has a “boom or bust” population demography. Over the long term, this cycle should maintain populations of D. pauciflora provided bust years do not outnumber boom years during which the population can recover. Digitaria pauciflora and other plant species might be considered indicator species and should be recurrently monitored to guide the restoration of hydrologic regimes in Everglades National Park and elsewhere.

**Topic: Ecology**

**A-73 Pine trees structure plant biodiversity patterns in savannas of the southeastern U.S.A.**
A 74 Bunchgrasses are stable in frequently burned old-growth savannas

Author: Raeiene Crandall (University of Florida), Jennifer Fill (University of Florida), Edwin Bridges (Botanical and Ecological Consultant), Steve Orzell (Avon Park Air Force Range)

Keywords: fire; grasses; pine savannas

Old-growth grasslands are disturbance-dependent, biodiverse ecosystems dominated by grasses and herbaceous species. Long-lived perennial grasses are considered a defining feature of these ecosystems because they confer substantial resilience to disturbance and resistance to change. However, much of the support for their role in ancient grasslands is inferential. Although a large body of evidence supports the stability of ancient grasslands, data-based research is still lacking. We conducted two studies to provide data-driven support for this assertion. Our studies focused on the dominant, endemic bunchgrass Aristida beyrichiana (white grass) and its congeners A. stricta and A. striata, both considered key species or even foundational species across much of the southeastern United States. First, we developed demographic models of A. beyrichiana in wet and dry pine savannas that were burned at different frequencies and in different seasons for at least several decades. We monitored nine populations over 2-4 demographic transitions and developed integral projection models. Second, we used long-term community composition data from fire-frequented pine savannas along a moisture gradient in the same region to examine patterns of stability and abundance of A. beyrichiana over time. Our studies indicate extremely numerically stable populations of A. beyrichiana despite experiencing very different fire regimes (i.e., lambdas did not differ from one). Survival of populations was 100% in most years, and we conservatively estimate there was minimal contribution of recruitment to population growth or stability. Across a range of soil moistures, A. beyrichiana was the most abundant plant species in the long-term community data, remaining consistently over 50% dominant for over 20 years. In fact, changes in average relative percent cover between any two sampling years were less than 0.5%. The consistency of results between populations lends data-driven support to bunchgrass resilience to different fire regimes, inferred from studies in the literature. Furthermore, our study bolsters support for old-growth savannas in the southeastern U.S., which has, until recently, been very understudied and suffered from a lack of recognition by the global community.

A 75 Unraveling the systematics and biogeographical history of the eastern Asian-North American disjunct genus Physocarpus (Rosaceae)

Author: Audrey Spencer (Denver Botanic Gardens, University of Colorado Denver), Jennifer Ackerfield (Denver Botanic Gardens), Leo Bruederle (University of Colorado Denver)

Keywords: biodiversity; fire; pine savannas

Overstory trees serve multiple functions in pine savannas. Past research has shown that large canopies are associated with greater plant species richness and different species composition than beneath canopies. However, these studies did not examine such patterns at the scale of individual trees. The objective of this study was to determine the relationship between understory plant communities and proximity to individual pine trees in dry and mesic soils in the southeastern U.S. In six frequently burned sites (1–3 year intervals), we haphazardly selected trees and arranged sampling plots to examine whether canopy cover and plant communities differed between plots under tree driplines (i.e., open areas where pine needles increase fuel loads) as compared to plots adjacent to tree boles (basal), where duff often accumulates. We recorded the presence and abundance of plant species in all plots. Within each soil type, raw species richness was significantly greater in open locations, where light transmittance was higher. In contrast, rarefied species richness did not differ between open and basal locations. Community composition differed significantly between basal and open locations, driven primarily by patterns in a few common species. For instance, one native, woody species in each soil type was more abundant in basal plots. In wet and dry soils, eight and four understory forbs, respectively, were more abundant in open locations. We conclude that individual pines in pine savannas are associated with significant understory variation in plant communities. Because patterns and processes are scale-dependent, individual trees could influence patterns at scales that are not necessarily evident at landscape scales and vice versa. The environmental variation they create at small scales likely increases overall plant biodiversity.

A 76 Remote sensing as a method for enhancing sugar pine survival in California

Author: Wesley Radford (SUNY ESF), Shannon Lynch (SUNY ESF), Patricia Maloney (UC Davis), Susan Ustín (UC Davis)

Keywords: ecological restoration; pathogen; remote sensing

Present-day sugar pine (Pinus lambertiana, Doug.) populations in the Sierra Nevada clearly demonstrate the impacts of intense climate-driven selection pressures in California’s wildlands. These populations have been affected range wide for more than a century by Cronartium ribicola, the causal agent of white pine blister rust (WPBR), but intense drought followed by mountain pine beetle (Dendroctonus ponderosae) attack have recently amplified population loss in greater Tahoe area in California. Trees surviving these recent stressors have been identified as locally adapted, drought resilient seed sources for restoring diminished populations. WPBR resistance testing has been conducted on seeds sourced from these locally adapted trees, determining which individuals possess the major gene for resistance (MGR: Cr1 gene in sugar pine). Use of locally adapted seed stock with WPBR resistance can ensure climate and pathogen resilient trees are being restored around the Lake Tahoe Basin. One challenge of reforestation is high mortality rates of planted seedlings, causing wasted seedstock, growth resources, and time. Remote sensing, which detects and monitors physical land characteristics by measuring reflective surfaces from an aerial perspective, shows great promise as a useful tool to optimize selection of planting sites, effectively and efficiently reducing mortality rates of vulnerable seedlings. Here, I evaluate the efficacy of remote sensing in selecting planting sites to enhance seedling survival. My objectives are 1) to determine the factors involved with optimal site conditions, and 2) compare seedling mortality between designated optimal and suboptimal sites. Microtopographic maps were developed using remote sensing imagery and other geospatial datasets to develop GIS algorithms that identify site conditions to select appropriate microsites for planting locally sourced and diverse seed material resilient to anthropogenic and natural stressors. 1000 locally adapted sugar pine seedlings were planted within these test sites in November 2024. Mortality assessments will be conducted during summer 2025 and 2026. Results from this study will inform stakeholders and restoration scientists on the capabilities of remote sensing in reference to microsite selection, and the importance of local seed sources for restoring tree populations.

A 77 Investigating the genetic basis of transgressive floral delphinidin pigment production in Nicotiana section Repandae alloploids

Author: Elizabeth McCarthy (SUNY Cortland), Jacob Landis (Cornell University), Talleh Ostovar (SUNY ESF), Amy Litt (University of California, Riverside)

Keywords: Nicotiana; Solanaceae; alloploidy; Anthocyanins; Evolution; Flower color

Alloploidy involves both whole genome duplication and interspecific
hybridization and is a common phenomenon in angiosperm evolution. The merger of divergent genomes can result in the development of transgressive characters that fall outside the range observed across both progenitor species. Many studies have reported observation of transgressive characters in allopolyploids, but fewer have explored the genetic basis underlying these phenotypes. We investigate the genetic basis of the transgressive floral delphinidin pigmentation present in some species of Nicotiana section Repandae, which originated ~4 million years ago from N. sylvestris and N. obtusifolia progenitors, which do not produce floral anthocyanins. We analyzed corolla tissue transcriptomes from different floral development stages (buds of 60%, 85%, and 95% of anthesis length) from three species of allopolyploid Nicotiana section Repandae and their diploid progenitors to examine both expression patterns and sequence evolution in genes of the flavonoid biosynthetic pathway (FBP). This branched pathway produces both colorful anthocyanin (including pelargonidin, cyanidin, and delphinidin) and colorless (to humans) flavonoid pigments. Our questions are as follows. 1) Is transgressive delphinidin driven by sequence evolution or by differential expression of FBP genes or do both play a role? 2) If sequence evolution is an important factor in producing delphinidin in allopolyploid Nicotiana section Repandae species, is complementation of progenitor sequences observed (i.e., diploid progenitors have nonfunctional mutations in different FBP genes that can be complemented when allopolyploids are formed) or is there evidence of resurrection of previously nonfunctional genes during evolution of allopolyploid species?

**Topic: Mycology & Phycology**

**A-79 Antagonistic activity of Endophytic fungi against Sclerotinia sclerotiorum causal pathogen of leaf spot on African Yam Bean (Sphenostylis stenocarpa)**

**Author:** Iyabode Kehinde (Federal University of Agriculture, Abeokuta), Olajumoke Abiola-Kuforoji (Federal University of Agriculture, Abeokuta)

**Keywords:** Fungal endophytes, Pathogen, legumes, antagonist, biocontrol

African yam bean (AYB) is the most important cultivated species in the genus Sphenostylis and it is indigenous to tropical Africa. The nutritious pulse is popular in West Africa while its edible tubers are very common in the country have been illegally extracted from the Jaragua National Park, where the leaves of AYB are traditionally used to make local medicinal remedies to treat flu and other ailments. Other local uses include flavoring rum and other liqueurs, as well as milk and desserts. Given the unique flavors obtained from the leaves of *P. haiteiensis* and the multiple uses in local medicine, the species is heavily trafficked throughout the Dominican Republic given the wide demand for its leaves. All the products currently being sold across the country have been extracted from the Jaragua National Park, where wild plants have a very limited distribution. When illegal harvesters gather the leaves, trees are often severely mutilated and they cannot reproduce for years, or they even die. Therefore, understanding the phenology and pollination ecology of *P. haiteiensis* is important to design conservation strategies. In this study, we characterized the flowering and fruiting phenology of *P. haiteiensis* in the southwestern portion of the Dominican Republic. This species occurs naturally only in the province of Pedernales located in the southwestern portion of the Dominican Republic. The tree has aromatic leaves that are traditionally used to make local medicinal remedies to treat flu and other ailments. Other local uses include flavoring rum and other liqueurs, as well as milk and desserts. Given the unique flavors obtained from the leaves of *P. haiteiensis* and the multiple uses in local medicine, the species is heavily trafficked throughout the Dominican Republic given the wide demand for its leaves. All the products currently being sold across the country have been extracted from the Jaragua National Park, where wild plants have a very limited distribution. When illegal harvesters gather the leaves, trees are often severely mutilated and they cannot reproduce for years, or they even die. Therefore, understanding the phenology and pollination ecology of *P. haiteiensis* is important to design conservation strategies. In this study, we characterized the flowering and fruiting phenology of *P. haiteiensis* in the southwestern portion of the Dominican Republic. Over three years, we made monthly phenological observations on 31 healthy adult individuals and 15 of these trees were selected to observe floral visitors. Flowering occurs once a year, mainly from April to August, with its peak in May and June. The flowers are hermaphrodite and white. Floral visitors and potential pollinators were observed and captured and comprised insects from the orders Coleoptera, Diptera, Hemiptera and Hymenoptera. One of the main floral visitors and putative pollinators recorded was the introduced honeybee, *Apis mellifera*. The fruiting period ranges from June to July. In years of heavy rainfall, the fruiting season was absent or reduced, and the plants were not able to reproduce. **A-80 Phenology and pollination biology of Pimenta haiteiensis (Urb.) Landrum (Myrtaceae), an endangered tree of the Dominican Republic, Hispaniola Island**

**Author:** Jackie Salazar (Grupo Jaragua), Yolanda Leon (Grupo Jaragua), Judá Martínez (Universidad Autónoma de Santo Domingo), Marcos Caraballo-Ortiz (National Museum of Natural History)

**Keywords:** endangered species, Myrtaceae, phenology, endemc, animal pollination

*Pimenta haiteiensis* (Urb.) Landrum (Myrtaceae), commonly known as Jaragua canellilla, is an endemic tree threatened with extinction according to the IUCN Red List and the Red List of the Dominican Republic. This species occurs naturally only in the province of Pedernales located in the southwestern portion of the Dominican Republic. The tree has aromatic leaves that are traditionally used to make local medicinal remedies to treat flu and other ailments. Other local uses include flavoring rum and other liqueurs, as well as milk and desserts. Given the unique flavors obtained from the leaves of *P. haiteiensis* and the multiple uses in local medicine, the species is heavily trafficked throughout the Dominican Republic given the wide demand for its leaves. All the products currently being sold across the country have been extracted from the Jaragua National Park, where wild plants have a very limited distribution. When illegal harvesters gather the leaves, trees are often severely mutilated and they cannot reproduce for years, or they even die. Therefore, understanding the phenology and pollination ecology of *P. haiteiensis* is important to design conservation strategies. In this study, we characterized the flowering and fruiting phenology of *P. haiteiensis* in the southwestern portion of the Dominican Republic. Over three years, we made monthly phenological observations on 31 healthy adult individuals and 15 of these trees were selected to observe floral visitors. Flowering occurs once a year, mainly from April to August, with its peak in May and June. The flowers are hermaphrodite and white. Floral visitors and potential pollinators were observed and captured and comprised insects from the orders Coleoptera, Diptera, H...
biology of *P. haetensis* provides baseline data to inform strategies such as propagation, habitat restoration, and managed pollination to help recover populations of this species. More research is needed on population genetics, threats to recruitment, and the viability of small, fragmented populations. Conservation actions are necessary to increase population size and prevent overexploitation. Financial support: Franklinia Foundation.

**Topic: Biogeography**

**A-81** Historical biogeography and niche evolution of Lecythidaceae in the American tropics

**Author:** Diana Medellin (University of Michigan)

**Keywords:** Lecythidaceae (Ericales) is a pantropical family of woody plants of ca. 278 tree species with three subfamilies: Foetidioideae (Madagascar), Planchnioideae (Asia and Africa), and Lecythidoideae (ca. 232 species) restricted to the Neotropics. This family is within the 20 most-species rich families of trees in the lowland Amazon forests, providing important ecological services such as carbon sequestration and food resources for pollinators and seed dispersers. The global center of species richness and ecological importance is in the Amazon basin and Guiana Shield, where most Lecythidaceae research has been focused. However, there are genera occurring in the Andean and Chocó Biogeographic Regions where several knowledge gaps lie. Despite multiple studies having been performed for Lecythidaceae, there are still incongruences among hypotheses about the evolution of this family. To infer the geographic history of Lecythidaceae in the Neotropics, and identify areas of importance for its diversification, we performed a Maximum Likelihood analysis in IQ-TREE, based on nuclear markers targeted by the Angio353 probes in 94 species, and an ancestral range reconstruction, using a dispersal-extinction cladogenesis model (DEC) in BioGeoBEARS. According to our results, there is a high uncertainty about the ancestral area for the Neotropical clade. However, the Southern Andes was reconstructed as the most probable ancestral area for the zygomorphic-flowering clade, originated in the Paleogene (~34 Ma), while Central America and the Chocó were recovered as the most plausible ancestral area for the actinomorphic-flowering clade (originated ~37 Ma). Since most of the species included in this reconstruction occur in the Amazon region, and given the complexity of wetland habitats and their association with the Andean uplist that most likely had an important role in the evolution of Amazonian Lecythidaceae, increasing sampling from the InterAndean Valleys and Chocó will allow us to better understand the niche evolution and diversification history of this family.

**A-82** Sapotaceae across time and space: a taxonomic and historical biogeographic perspective

**Author:** Raquel Pizzardo (University of Michigan)

**Keywords:** Angio353 phylogenomics; long-distance dispersal; nuclear target sequence capture

Sapotaceae is one of the most important plant families in the world. With around 1,250 species and 62 genera, Sapotaceae is a pantropical family, and is usually restricted to lowland tropical rainforests. However, the taxonomy of the family is unstable and lacks in information on this ecologically important groups of angiosperms in the tropics. Many incongruences between phylogeny and classification in Sapotaceae have been noted, as well as alternative topologies for species-level phylogenies. Here, we generate a higher sampled Sapotaceae phylogeny and, for the first time, we aimed to determine the geographical origin of the pantropical family and the roles climate and dispersal have played in shaping its modern distribution. We used target sequence capture data from the Angio353 probe for 199 taxa. The concatenated maximum likelihood molecular phylogeny was constructed using IQ-TREE (v. 1.6) considering GTR+G and partition models, and 1000 bootstrap replicates. Dates of diversification events were estimated using two fossils and the penalized likelihood approach (treePL). The subsequent dated phylogenies were compared and analyzed for biogeographical patterns using BioGeoBEARS. The phylogeny moderately recovered the three subfamilies of Sapotaceae, showing relatively high support for Sapodiletidae but not for Chrysophyliidae. The phylogeny shows inconsistencies with the current morphological classification. Our results indicate that the ancestral range of the family was in East Asia c. 84 - 80 Ma, with dispersal to South America and Africa. Chrysophyliidae had an early diversification in Africa c. 71 - 57 Ma, with subsequent dispersal to the Neotropics (two events) and Australasia (singles event) during the Paleocene and Eocene. Sapodiletidae had an early diversification in Africa c. 71 - 50 Ma, with migration to Australasia and North America during the Eocene. Those results are somewhat congruent with previous studies. Long-distance dispersal has been an important mechanism for range expansion in Sapotaceae.

**Topic: Development and Structure**

**A-83** Understanding novelty through intraspecific and intragenic transcriptomic comparisons within *Mimulus*

**Author:** William Payton (Miami University), Deannah Neupert (Miami University), Robert Baker (National Park Service), Richard Moore (Miami University)

**Keywords:** *Mimulus*; differential gene expression; EvoDevo; novelty; RNAseq

The development of structural novelty is difficult to study, as most novelty is ancient and arose thousands of years ago. Within *Mimulus*, supernumerary axillary meristems are deposited in the axil of the nodes. For *Mimulus guttatus* (*Erythranthe guttata*), *M. floribundus* (*E. floribunda*), and *Mimulus gemmiparus* (*E. gemmipara*), the primary axillary meristem usually varies between becoming a branch or a flower. In *M. guttatus* and *M. floribundus*, the secondary axillary meristem may branch or flower while in *M. gemmiparus*, the secondary axillary meristem expands into a vegetative propagule, which then arrests and is ensheathed by the subtending leaf petiole resulting in a novel aerial bulb that shares homology with branches and leaves. To determine the genes responsible for the co-option of petioles and axillary meristems to form bulbs, we sampled homologous nodes in all three species and two nodes of *M. gemmiparus* with different fates for a differential gene expression analysis. We used Trinity to de novo assemble a transcriptome for *M. gemmiparus*. Next we used Trinotate to identify differentially expressed transcripts and conducted a GO term enrichment analysis. Through the analysis, we found an upregulation of transcripts associated with axillary meristem outgrowth and a downregulation of transcripts associated with photosynthetic processes. These results support the shift to asexual reproduction through the use of the novel aerial bulb by prioritizing vegetative growth.

**Topic: Physiology**

**A-84** Step one: Breaking dormancy of the novel aerial bulb in *Mimulus gemmiparus*

**Author:** Shannen McIntyre-Quinn (Miami University), Deannah Neupert (Miami University), Evan Gallagher (Miami University), David Klump (Miami University), Richard Moore (Miami University)

**Keywords:** *Mimulus*, Dormancy

The germination of seeds is the start of most botanical research. However, getting seeds to germinate may require the addition of plant hormones and other compounds. Gibberellic acid and potassium nitrate have successfully been used to increase the germination of seeds in diverse plant species. While these compounds have been used to break seed dormancy, they have not been used extensively to break dormancy of propagules. *Mimulus gemmiparus* (syn: *Erythranthe gemmipara*) is a critically imperiled Colorado endemic and found in only a handful of small populations around the Rocky Mountains growing under rocky overhangs. *Mimulus gemmiparus* reproduces primarily with the novel aerial bulb formed through the co-option of two structures, an axillary meristem and a petiole. While there is evidence of some sexual reproduction, clonal reproduction through the bulb is the predominant reproductive method. Preservation of this species is critical due to its small effective population size. However, the decreased outgrowth of the bulbs in common gardens is causing concern. To address these concerns, we applied different concentrations of gibberellic acid (GA3) and potassium nitrate prior to planting to determine if these compounds will break propagule dormancy. We will present our findings comparing this treatment in its efficacy to induce germination in seeds (using *Carica papaya*, *Mimulus guttatus*, and *M. floribundus* as a model) and its ability to increase the activity rate of the bulbs. We analyze the effect of applying KN03 and GA3 directly to the bulb by measuring the length of the main stem as well as internode length during development. This is an incredibly important study for maintaining bulb viability for planting. Having had previous trouble growing this plant in a laboratory environment, studying the plant has proven to be difficult. Maintaining a viable stock of bulbs from *M. gemmiparus* will continue to be important for the continued research on the novel reproductive method. Additionally, keeping a viable stock of bulbs could aid in the conservation of this species.

**Topic: Molecular Ecology**

Last Updated: Friday, March 8, 2024
A-85  Climatic and genetic determinants of biomass production and yield in the model grass for temperate cereals, *Brachypodium distachyon*

**Author:** Masoumeh Khodaverdi (University of Vermont)

**Keywords:**

Population growth and climate change are threatening the sustainability of our planet’s natural resources. Plants are sources of clean and renewable energy that can be used as an alternative to fossil fuels. Among the flowering plants, grasses comprise the fourth largest family that not only provide food crops, but also produce biomass that can be harnessed for biofuel production. Most plant biomass is produced before flowering, which makes flowering time a major determinant of biomass yield. In order to examine the effect of thermal irregularities due to global warming on plant fitness measured using biomass and grain yield, we used 24 *Brachypodium distachyon* populations from a variety of geographical locations and exposed them to a gradient of temperatures (5°C to 40°C) both spanning and going beyond current upper temperatures in the wild. We recorded several fitness outputs such as seed number, size, and weight from the treatment groups. Our preliminary results showed considerable variation among the populations’ flowering time and yield production in response to different thermal treatments. Of particular interest are populations that flower early regardless of temperature (phenotypically non-plastic) versus those that show thermal sensitivity and earlier flowering at elevated temperatures (phenotypically plastic). Furthermore, we conduct comparative transcriptomic analysis and compare differentially expressed genes across populations and temperatures to identify expressed genes associated with flowering time plasticity. The results of this study will be useful in designing optimal setups for growing plants with maximal biomass yield, which in turn, can lead to the increased and sustainable production of renewable biofuels.

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**Topic:** Systematics

**A-86 Phylogeny and Taxonomy of the *Eriogonum* deflexum Complex (Polygonaceae)**

**Author:** Mahima Dixit (Claremont Graduate University)

**Keywords:** Eriogonum; Great Basin; Mojave Desert; molecular phylogenetics; plant taxonomy

Effective conservation of biodiversity largely depends on accurate classifications which are based on multiple lines of evidence, including morphology, phylogeny, and ecology. With 252 currently recognized species and 445 species plus varieties, *Eriogonum* is the fourth-largest flowering plant genus in the United States. Despite this, knowledge of the phylogeny of *Eriogonum* is largely incomplete. An analysis by Kempton (2012) and other studies have shown that *Eriogonum* is not monophyletic and neither are most of its subgenera. More studies are needed to expand sampling to all species, study morphology in context of the phylogeny, and improve classification. This project represents a contribution to our understanding of *Eriogonum* by focusing on a group of species whose flowers are oriented upside-down, referred to as the *E*. deflexum complex (Polygonaceae; wild buckweeds). Species with this trait include a mix of annuals and perennials in subgenus Ganysma. The species are primarily distributed in the Mojave Desert and Great Basin, with some species having very limited ranges, and others being widespread across the western United States. This study group includes a possible species new to science that is found only on limestone outcrops in the Bristol Mountains area in San Bernardino County, California. The primary goals of this project are to study the evolutionary history of downward-pointing flowers, shed light on the relationships among these species, and make improvements on their classification based on new data and analyses. Thus far, fieldwork was conducted to sample from a number of the study species and others in subgenus Ganysma. From those samples, DNA was extracted using a modified CTAB method to prepare and sequence a library, and a preliminary phylogenetic estimate was generated. The data suggest that the complex is not monophyletic as taxa with deflexed involucres resolve in separate clades. An ancestral state reconstruction comparing taxa with deflexed versus not deflexed involucres suggests that deflexed involucres are a derived trait that evolved at least once with multiple reversal events. Additionally, based on an ancestral state reconstruction for the presence/absence of glands, glands are inferred to have evolved multiple times. More sampling is needed to further elucidate the relationship among these taxa. Furthermore, it is crucial to sample additional members of subgenus Ganysma for a broader context of species relationships. Fieldwork and labwork is currently being planned to further improve our understanding of the group.

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**Topic:** Ecology

**A-87 Floral scent and intersexual mimicry in dioecious highland papaya *Vasconcellea parviflora***

**Author:** Ethan Grant (Miami University), Richard Moore (Miami University)

**Keywords:** gas chromatography-mass spectrometry; Floral Scent

Floral traits, including color, morphology, and scent, play a crucial role in attracting specific pollinators, with floral scent being a significant component for both short- and long-range pollinator attraction. In dioecious systems, where male and female flowers are present on separate plants, sexual dimorphism often extends to floral displays driven by differing selective pressures on male and female reproductive success. In some dioecious species, females engage in Bakerian mimicry—offering no nectar rewards yet mimicking male pollination syndromes to deceive pollinators. Research has observed Bakerian mimicry in several species, but its evolutionary conservation within the largely dioecious Caricaceae family remains underexplored. This research utilizes *Vasconcellea parviflora* as a model to examine the characteristics of Bakerian mimicry within the Caricaceae. To do this, we analyzed floral volatiles collected over 2-hour windows from male and female inflorescences using gas chromatography and mass spectrometry. Preliminary results suggest low rates of volatile emission from both male and female flowers. Fieldwork was conducted to sample from a number of the study species, and make improvements on their classification based on new data and analyses.

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**Topic:** Phytochemical

**A-88 Fall colors in summer?: Red leaves in senescing Trillium**

**Author:** Megan Gauger (University of Pittsburgh), Jason Heberling (Carnegie Museum of Natural History), Brandon Brewster (University of Pittsburgh), Edith Fields (University of Pittsburgh)

**Keywords:** Trillium; anthocyanins; forest wildflowers; phenology

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Leaf color change in autumn has long captured public attention, yet with over a dozen hypotheses proposed, the function of fall colors remains surprisingly poorly understood and an active topic of debate. Further, research on leaf color change has been overwhelmingly focused on trees. However, many herbaceous species in temperate forests, even those that senesce earlier in the year, can have leaves that turn red. This observation became apparent during regular phenological monitoring during a different study, and more intriguing, not all individuals turn red. Inspired by this observation, we asked how common the phenomenon of red leaf coloration in summer-senescing forest wildflowers could be and if the red coloration is related to individual or site-wide conditions. We surveyed four spatially separated populations each of two species of Trillium at a site in southwestern Pennsylvania. In addition to site-level surveys, we monitored tagged individuals throughout the year, recording leaf traits, reproductive status, and reproductive phenology. We also measured site-level abiotic conditions (soil chemistry, soil moisture, light availability). We found red leaf color change in *Trillium recurvatum* to be uncommon (1% of individuals overall), but much more common in *T. grandiflorum* (12% of individuals). Within *T. grandiflorum*, red leaf color change was more common in species with smaller leaves (P<0.001) and those that were non-reproductive (P<0.001). There appears to be little correlation with red leaf coloration and site-level environmental variables (soil moisture, light availability), though additional analyses are underway. Overall, though we do not yet understand the function, we report an intriguing natural history observation that summer-senescing herbs in temperate forest understories can turn red. Currently overlooked, species in temperate forest understories deserve further attention alongside woody species in autumn leaf coloration research.

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**Topic:** Ecology

**A-89 Functional characterization of Geraniol**

**Author:** D. Sun (University of Pittsburgh), Heberling, Fields, Gauger

**Keywords:** Plant chemistry; floral scent; genetic determinants of biomass production; yield.

We found red leaf color change in *Trillium recurvatum* to be uncommon (1% of individuals overall), but much more common in *T. grandiflorum* (12% of individuals). Within *T. grandiflorum*, red leaf color change was more common in species with smaller leaves (P<0.001) and those that were non-reproductive (P<0.001). There appears to be little correlation with red leaf coloration and site-level environmental variables (soil moisture, light availability), though additional analyses are underway. Overall, though we do not yet understand the function, we report an intriguing natural history observation that summer-senescing herbs in temperate forest understories can turn red. Currently overlooked, species in temperate forest understories deserve further attention alongside woody species in autumn leaf coloration research.

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**Last Updated:** Friday, March 8, 2024
Synthase involved in monotropein biosynthesis in blueberry using computational and molecular based approaches  

Author: Ishveen Kaur (Virginia tech), Courtney Leisner  
Keywords:  
Blueberry is the second most important fruit crop in the US, owing to increased awareness of its health benefits due to the presence of several bioactive compounds. One such plant bioactive compound is monotropein. It has been reported that monotropein is found in only three plant species, namely Monotropa Uniflora, Morinda officinalis (Vaccinium spp.). Most work on monotropein has been done in Morinda officinalis where it has been shown to impart several human health benefits. Recent work has also identified monotropein in both wild and cultivated blueberries. However, how monotropein is produced and the type of candidate genes involved in the biosynthesis of monotropein in blueberries has yet to be elucidated.

Our research group has used bioinformatics, comparative genomics and protein engineering techniques to functionally characterize the iridoid synthase (ISY) gene which encodes for an enzyme involved in an important cyclization step in monotropein biosynthesis. This further gave u understanding of the key candidate genes involved in the monotropein biosynthesis pathway. Currently, we are focusing on functionally characterizing geraniol synthase (GES) gene, as recent work has found the expression of GES is significantly associated with the production of iridoids in other plant families using both long-reads and short reads. Our overarching goal is to elucidate the biosynthetic pathway of production of monotropein in blueberry to potentially breed blueberries with higher production of monotropein.

Keywords: bacteria; Chloroplast genome; genome assembly; heteroplasmic; mitochondrial genome

A-90 Plant-plant interactions in sorghum plants through chemical and physical communication belowground  

Author: Shiran Ben-Zeev (Pennsylvania State University), Amanda Penn (Penn State), Carolyn Lowry (Penn State), Jesse Lasky (Pennsylvania State University)  
Keywords:  
Plant-plant interactions have long been considered an important factor affecting stand-level productivity in ecology as well as crop science. Many studies have focused on how plants sense and respond to their neighbors, these primarily focused on shading and other above-ground cues and responses. We studied the response of sorghum plants to the below-ground presence of neighboring plants or the presence of their exudates. We studied 10 Sorghum genotypes in different experimental systems in which plants interacted with plants of another genotype, plants of a common competitor genotype (while preventing shading), or by exposure to leachates from pots of competitor plants. Our results indicate that, with ample fertilizer and water, the response of sorghum plants to actual neighbors had an opposite effect on the productivity and growth rate compared to the effect of leachates. The response of plants to the presence of plants growing in the same pots, with no limitation of fertilizer and water, resulted in a decrease in growth rate, stomatal conductance, height, and biomass, similar to the reduction caused by drought. Interestingly, the lactate transfer from competitor plants’ pots to focal plants resulted in increased leaf area, shoot and root biomass, and growth rate. Our findings suggest that plant-plant interactions in the rhizosphere could be divided into different channels, which may be targeted to increase stand-level productivity by improving individual productivity and harnessing the growth rate increase, especially at the earlier part of the growth season.

Keywords: From Listing to Recovery: The Science, Processes, and Challenges of the U.S. Endangered Species Act

A-91 Conserving petitioned pitcher Sarracenia rubra ssp. gulfensis: why genetics matter  

Author: Madeline Bednar (Miami University), Richard Moore (Miami University), Vivian Negron-Ortiz (US Fish and Wildlife Services)  
Keywords:  
Sarracenia rubra ssp. gulfensis is an imperiled carnivorous endemich pitcher plant to Florida’s western Panhandle. Most populations are located on two main managed lands, Eglin Air Force Base (EAFB) and Blackwater River State Forest (BRSF), in herbaceous bogs, creek edges, open wet grasslands, and pine flatwood savannahs. Threats to ssp. gulfensis include habitat loss and degradation due to development, and changes in soil hydrology and fire regimes. Currently, the U.S. Fish and Wildlife Service is in the process to initiate a status review to determine if listing of this species is warranted. To help inform the listing process, we performed a genetic analysis using SNP data generated by nextRAD sequencing. Approximately 342 samples were collected from 25 different populations in EAFB and BRSF. Preliminary sequenced data from six populations representing the geographic range of ssp. gulfensis as well as samples of co-occurring Sarracenia species and potential hybrids suggest that the observed heterozygosity is lower than the expected heterozygosity (SRR6: He= 0.1446, Ho= 0.1107; Sr26: He= 0.1564, Ho= 0.1304; Sr19: He= 0.1733, Ho= 0.1253) in ssp. gulfensis. These preliminary results indicate there is little gene flow between populations and lower heterozygosity. Populations displayed moderate divergence from one another (FST = 0.07-0.13). We detected the possibility of hybridization between ssp. gulfensis and two other co-occurring Sarracenia species, suggesting interspecific gene flow which could hinder the conservation of high value genetic diversity populations. The preliminary information identified five populations with low genetic diversity that require continued monitoring to guarantee survival. It also identified one population with most of the genetic diversity, which should be protected in situ and considered as the highest conservation priority. Additional data will be analyzed to provide a better understanding of the genetic diversity of ssp. gulfensis to help determine whether listing of this species under the Endangered Species act is warranted.

Keywords: bacteria; Chloroplast genome; genome assembly; heteroplasmic; mitochondrial genome

A-92 Traversome: a graph-based likelihood model for pangenome assembly and variant relative frequency estimation from mosaic samples  

Author: JianJun Jin (Columbia University), Deren Eaton (Columbia University)  
Keywords:  
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 probabilities 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 bacteria and organelles of plants. Traversome exhibits similar accuracy to other assemblers in the absence of mosaicism, but much 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.

Keywords: From Listing to Recovery: The Science, Processes, and Challenges of the U.S. Endangered Species Act

A-93 Phylogenetic partitioning of biomes is determined by ecological harshness, connectivity, and climatic stability  

Author: Cecile Renfro (Texas A&M University), Lydia Morley (Texas A&M), Daniel Spalink (Texas A&M University)  
Keywords: beta diversity; biogeography; ecoregion; Vegetational Patterns of Global patterns of community assembly are shaped by interacting ecological, biogeographical, and evolutionary processes. The relative
importance of these processes depends in part on climatic and geologic factors, which vary in space and through time. Biomes, climatically and geologically distinct regions often with unique floral communities, represent an ideal discretization of geographic space for examining these interacting processes, particularly as they relate to the impacts of evolutionary diversification and ecological filtering of plant diversity. Examining biomes through a beta diversity framework can help us to understand how this diversity has assembled across ecologically and geologically distinct regions through time. Here we use a global dataset of vascular plant occurrences coupled with a phylogenetic tree to quantify taxonomic and phylogenetic beta diversity across biomes. We then pair these indices with historical climate data using a general dissimilarity modeling framework to determine how the predictors of vascular plant community assembly differ within and among biomes. We test the hypotheses that: 1) overall beta diversity across ecoregions belonging to the same biome types should depend on the overall connectivity of the ecoregions and the harshness of the biome (e.g., extreme temperatures and precipitation, seasonality, stability through time); 2) taxonomic beta diversity should increase rapidly with geographic distance, whereas overall phylogenetic beta diversity should depend more so on bioclimatic distance; 3) specific bioclimatic predictors of phylogenetic turnover among ecoregions within biomes will vary by biome type, with geographical distance exhibiting more importance in ecologically harsh biomes like deserts, reflecting the ecological filtering of regional species pools coupled with local in situ diversification. Our findings largely support these hypotheses, which has implications for assessing the risk facing vascular plant communities in the Anthropocene.

Topic: Development and Structure
A-94 Investigating the Role of G-Fibers in Twining Bean Plants through Exogenous Brassinosteroid Manipulation
Author: Lena Hunt (New York University)
Keywords: growth form
The common bean (Phaseolus vulgaris) has emerged as a model system for exploring the role of G-fibers in twining vines. Twining bean plants undergo a transition from herbaceous shrubs to a developmental stage marked by rapid internode elongation and exaggerated circumnutation in search of a host for coiling. The twining growth habit is hypothesized to be governed by the emergence of G-fibers, cells with specialized tertiary wall layers providing contractile support to curved stems. Brassinosteroids, implicated in G-fiber development in other species, play a key role in this study. We investigated the interplay between brassinosteroids, G-fiber development, plant morphology, and differential gene expression. Bean plants were exogenously dosed with either 24-epibrassinolide or a brassinosteroid inhibitor (propiconazole) dissolved in lanolin. Dosing on the first climbing internode resulted in enhanced and delayed internode elongation, influencing overall plant morphology. Anatomical and morphological evidence, along with RNAseq analysis of the treated internode, elucidates the intricate mechanisms underlying twining stems. This investigation provides valuable insights into the interplay of G-fibers and climbing behavior in bean plants, contributing to our understanding of plant growth and development.

Topic: Ecology
A-95 Assessing Data Gaps in Regional Flora Representation of the Sagebrush Steppe and High Desert Ecosystems
Author: Elizabeth Mandala (Idaho State University)
Keywords: The sagebrush steppe and high desert ecosystems possess rich biodiversity crucial for ecosystem stability and resilience. However, accurate representation of flora within these regions is hindered by data gaps. This study aims to assess and identify these gaps to inform conservation and management strategies. We employed a review of existing literature combined with data analysis to evaluate the current state of flora representation. Our findings highlight significant deficiencies in species distribution data, taxonomic knowledge, and habitat characterization. Addressing these gaps is imperative for effective conservation planning and sustainable land management practices in the sagebrush steppe and high desert regions.

A-96 Seeing the forest for the trees: a comparison of taxonomic surrogates for floristic quality
Author: Matthew Finzel (University of Illinois)
Keywords: bioassessment, biogeography, floristic quality
Florescence Assessment (FOA) is a popular bioassessment tool nationally, with especially extensive use in the state of Illinois. FOA generally assumes that entire plant assemblages have been representedly sampled and identified to the species level. We tested three rapid taxonomic surrogate measures for floristic quality: indicator species, dominant species, and a rapid Floristic Quality Index (FQI). These methods were tested using two large Illinois wetland datasets stratified by latitude (northern vs. southern halves of Illinois) and community type (forest vs. non-forested). Each method attempts to simplify conventional FOA by easing the botanical expertise prerequisite. Candidate indicator species for high floristic quality were identified using an intensive iterative approach to Indicator Value analysis, and then evaluated based on the indicators’ sensitivity, fidelity, and false positive error. Dominant species were evaluated relative to the total species FOA output at each site. Unsurprisingly, the method that used the most species (rapid FQI) performed best, correctly classifying high floristic quality sites with 88–95% accuracy. Candidate indicator species outperformed dominant species in accurately predicting high floristic quality sites. Managers need be wary of the error that reductionist or simplistic FOA methods will generate compared to conventional FOA.

A-97 Phylogenomics of the North American Desert Radiation Linanthus (Polemoniaceae)
Author: Ioana Anghel (University of Illinois)
Keywords: aridity, California desert annuals, Diversification, flower color polymorphisms, molecular phylogenetics, Polemoniaceae, RADseq, target-capture
Understanding how arid-adapted plants have diversified in harsh environments is a central question in evolutionary biology. Linanthus (Polemoniaceae) occurs in biodiverse dry areas of Western North America and exhibits extensive floral trait variation, multiple color polymorphisms, differences in blooming time, and variation in life history strategies. Here, we reconstruct the evolutionary history of this group. We generated restriction-site associated (ddRAD) sequences for 180 individuals and target capture (TC) sequences for 63 individuals, with complete species sampling. Using maximum likelihood and pseudo-coalescent approaches, we inferred phylogenies of Linanthus and used these phylogenies to model the evolution of phenotypic traits and investigate the geographic speciation history of this genus. Shallow relationships are consistent and well supported with both ddRAD and TC data. Most species are monophyletic despite rampant local sympathy and range overlap, suggesting strong isolating barriers. The non-monophyly of some species is possibly due to rapid speciation or issues with current species delimitation. Perennials likely evolved from annuality, a rare shift in angiosperms. Night blooming evolved three times independently. Flower color polymorphism is an evolutionarily labile trait and is likely ancestral. No single geographic mode of speciation characterizes the radiation but most species overlap in range, suggesting they evolved in parapatry. Our results illustrate the complexity of phylogenetic inference for recent radiations, even with multiple sources of genomic data and extensive sampling. This analysis provides a foundation to understand aridity adaptations, such as evolution of flower color polymorphisms, night blooming, and perenniability, as well as speciation mechanisms.

A-98 RELIX: a dataset of vascular plant species presence for 350 prairie remnants in the Midwestern United States and associated prairie remnant metadata
Author: Jack Zinnen (University of Illinois Urbana-Champaign)
Keywords: Prairies, tallgrass prairie, prairies conservation
Tallgrass prairies have experienced severe declines since European settlement due to agricultural land production. After widespread land conversion, few prairie communities persisted, called prairie remnants—which were comparatively small and isolated compared to the past.
Remnants host a diverse pool of vascular plant species, making the communities important resources for floristic surveys and ecological science. Despite their widespread study and their conservation value, prairie remnant plant species data are widely scattered across a variety of different resources and often inaccessible without asking habitat managers. This makes simple questions about the plant species in prairie remnants difficult to address. To improve data accessibility for prairie remnants, and collate basic information about them, I detail the creation of the “RELIX.” RELIX is compiled data for over 350 prairie remnant species lists in eight states throughout the Midwest, using the USDA PLANTS database as its taxonomic backbone. Over 36,000 species records are included, overlapping with the core range of the historical extent of the tallgrass prairie. Remnant species lists are complemented by metadata associated with the utilized species lists, and basic characteristics of the sites, including soil types, hydrology, relative habitat heterogeneity, size, and location. Preliminary data analyses from RELIX are shown as demonstrations of the datasets, including species richness and characteristic species. RELIX is pending public release for use by botanists, ecologists, and managers to better-understand and protect these rare ecological communities.

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**Topic:** Conservation Biology

**A-99 Modeling Subnational Conservation Status Ranks for Tennessee Vascular Plants**

**Author:** Julia Prins (University of Tennessee at Chattanooga)

**Keywords:** NatureServe, plant conservation

Plants are crucial components of our earth’s ecosystems and understanding their risk of extinction is important for ensuring effective and efficient conservation. Conservation status ranks measure this potential risk for species taking into account rarity, threats, and species population trends. These ranks impact development initiatives, guide land management practices, and help establish conservation priorities, it is therefore important to have an up-to-date and completed list of conservation status ranks. The need for plant species to be ranked is especially important considering the high number of at-risk plant species and the minimal funding plant conservation receives. When ranking species it is crucial that a standardized system is used to reduce bias and misranking. The NatureServe ranking system has been in use for 45 years and has a network of natural heritage programs throughout North America. They have generated over 100,000 conservation status ranks from critically imperiled to secure at the global, national, and subnational levels. They are the leading source of biological information for conservation workers and have been a large contributor to understanding the threat status of the United States flora. NatureServe uses a standardized rank calculator based solely on scientific data with ten criteria each weighted a unique amount. There are currently 1,792 vascular plants in the state of Tennessee that are unranked under the NatureServe ranking system. The goal of this project is to generate subnational conservation status ranks for all Tennessee vascular plants using two analyses to get an estimate of rank, which will then be compared against ranks generated by three tools based on NatureServe’s rank calculator. The first analysis looks at s-ranks assigned in the states surrounding Tennessee and the second is based on the percentage of counties the species is present in. The three systematic tools being used are a Feature Manipulation Engine workflow, a series of expressions written in Arcade on ArcGIS Pro, and a Shiny app called RareCat. Each tool uses occurrence data from SERNEC and GBIF to calculate rank extent, area of occupancy, and number of occurrences from which an s-rank is determined. Using these various tools, we will progress towards a complete list of s-ranks for Tennessee plants, tremendously assisting conservation efforts.

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**Topic:** Comparative Genomics/Transcriptomics

**A-100 Identification of the sex determination regions and their evolution in Populus mexicana**

**Author:** Diksha Gambhir (Texas Tech University)

**Keywords:** Populus, sex determination

Only 5%-6% percent of angiosperms are dioecious, having male and female flowers on distinct individuals, whereas the bulk of angiosperms (90 percent) are hermaphrodites, with bisexual flowers bearing both male and female reproductive parts. Although dioecy is rare in angiosperms, it has been documented in around 160 flowering plant families, with at least 100 instances of independent genesis. Dioecy has a patchy phylogenetic distribution in angiosperms, indicating that sex chromosomes have developed numerous times independently in plants. The genus *Populus*, in plant family Salicaceae, is dioecious and has homomorphic sex chromosomes. The phylogenetic relationship of *Populus* also exhibit sex chromosome movements and sex turnover events, that provides an opportunity to study sex chromosomes and their evolution in this genus. *Populus mexicana* is located at the base of the *Populus* phylogeny and identifying the sex determination region in this species would help to understand the evolution of sex chromosomes and sex turnover events in this genus. We identified the sex determination region of *P. mexicana* on chromosome 19 with an XY system using association mapping. We mapped sequenced captured data of 24 males and 24 females on *P. trichocarpa* reference genome assembly and identified sex-linked region using GWAS. 44 SNPs were associated with sex on chromosome 19. We propose chromosome 19 as the ancestral sex determining region with XY sex determining system. Finally, mapping the sex determination system opens the opportunity to compare and contrast the sex-linked genes and evolution of sex chromosomes in this genus.

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**Topic:** Ethnobotany

**A-102 Ethnobotany of Bundelkhand, India: Socio-economic implications**

**Author:** Ashok Awasthi (BND College, CSJM University, Kanpur, India)

**Keywords:** ethnobotany

Ethnobotany in developing regions of South and East Asia especially, the problems of socio-economic development of the tribals vis-a-vis local resource and knowledge seems a meaningful discourse of local, regional
and global dimension. Bundelkhand region, India situates itself in an area rich plant diversity, vast array of local races and their wild relatives of medicinal and crop plants. The region is also a home of varied ethnic groups striving to carve their place in the developing societies. Despite this interesting socio-economic construct studies on the region have remained casual and patchy, providing no answers to tribals developments on the strength of local resource knowledge that are untapped. The present paper deals with socio-economic significance of the local independent tribal knowledge with regional and global implications vis-a-vis ethnobotanical significance of forests of Bundelkhand region, India.

**Topic:** Digital ethnobotany: exploring the digisphere in search of traditional and Indigenous knowledge and practices

**A-103 To pick or not to pick: Photographic voucher specimens as an alternative method to botanical collecting in ethnobotany**

**Author:** Alex Greene (CNRS), Irene Teixidor-Toneu, Guillaume Odonne (CNRS)

**Keywords:** ethnobotany; herbarium specimens; methods

The identification of plants according to the Linnaean system of taxonomy is a cornerstone of ethnobotany, allowing the discipline to be a comparative science. To accomplish plant identification, ethnobotanists have long relied on the collection of voucher specimens and their deposition in herbaria. Here we critically analyze the role of botanical collecting in ethnobotany and bring attention to a range of issues that can complicate, and sometimes hamper, the practice. In lieu of traditional herbarium specimens, the collection of photographic vouchers and their deposition in digital repositories is proposed as an alternative method for ethnobotanical research. The ever-improving quality and ubiquity of smartphone cameras, photographic citizen science applications like Plantnet and iNaturalist, and deep learning techniques of automated photo identification are discussed as elements that are contributing to a slow revolution in the role of digital data in the field sciences. Guidelines for when plant herbarium specimens versus photographic vouchers should be considered required are laid out. Although botanical collecting will doubtless and with good reason remain a foundational practice in ethnobotany, the use of photographic vouchers as a valid, scientifically rigorous and, in some situations, preferred method of identification.

**Topic:** Molecular Ecology

**A-104 The genetic, developmental, and physiological mechanisms of local adaption to oceanic salt spray in the yellow monkeyflower, Mimulus guttatus**

**Author:** David Lowry (Michigan State University)

**Keywords:** Abiotic stress; Development; Evolution; Local adaptation; monkeyflower; physiology

Understanding how multiple complex traits of an organism evolve in tandem to produce adaptations to environmental stress is a fundamental goal of evolutionary plant biology. Coastal perennial plants have had to adapt to toxic oceanic salt spray. Unlike stress caused by soil salinity, salt spray primarily damages plants by landing directly on aboveground tissues. To understand how plants evolve adaptations to salt spray, we are conducting research on three key mechanisms of adaptation to abiotic stress: (1) resistance to herbivory, (2) avoidance of toxic oceanic salt spray, and (3) tolerance to it. We have found evidence that transporter genes have evolved to increase tolerance of leaf tissues by pumping salt out of leaf cells into the apoplast and vacuole. We are currently testing hypotheses of functional evolutionary changes at the gene level through a newly developed and highly efficient plant transformation methodology, where Agrobacterium is injected directly into the ovary of *Mimulus* flowers. Ultimately, this research should result in an understanding of how the evolution of gene networks is responsible for local adaptation.

**Topic:** Ecophysiology

**A-105 An elevational cline in leaf variegation is best explained by abiotic heterogeneity and not shifts in herbivore pressure**

**Author:** Cierra Sullivan (Clemson University), Matthew Koski (Clemson University)

**Keywords:** adaptive traits; polymorphism; leaf morphological traits; elevational gradient; abiotic environmental variables

Plant species with multicolored leaves, termed leaf variegation, are prominent in tropical, subtropical, and certain temperate forest understories. While there are mixed findings on whether leaf variegation corresponds to less efficient photosynthetic yield, much of the literature attributes the maintenance of variegated species in natural populations in an adaptation that deters herbivores. Yet, more attention must be given to testing the hypothesis that abiotic heterogeneity maintains leaf variegation. We used field surveys, image analysis, and climate databases to explore both the anti-herbivory and abiotic heterogeneity hypotheses in maintaining a leaf variegation polymorphism in *Hexastylis heterophylla* and *H. shuttleworthii*. Specifically, across 21 populations, we recorded the frequency of variegated and non-variegated (uniformly green) individuals, measured the degree of herbivory experienced by each morph, assessed contemporary and long-term abiotic correlates, and measured photosynthetic efficiency metrics for both morphs. Because variegated individuals have variable ratios of pale to dark green leaf area (variegation intensity), we also investigated whether variegation intensity covaries with herbivore pressure and the abiotic environment. We found a significant decrease in the number of variegated individuals and variegation intensity with increasing elevation. There was no significant herbivore preference for either color morph across elevation, no significant difference in damaged area from herbivory, and no correlation between herbivory and variegation intensity. Variegated morph frequency and variegation intensity were positively associated with warmer temperatures, greater UV-B exposure, drier, more basic soils, and lower light exposure under summer canopies. Despite significant differences in chlorophyll concentrations, we found no evidence of contrasting photosynthetic efficiency between color morphs across elevation. Our results advocate for the increased investigation of leaf variegation as an adaptation to abiotic heterogeneity. Additionally, our findings further suggest that leaf variegation is not a guaranteed hindrance to photosynthetic efficiency.

**Topic:** Education and Outreach

**A-106 Fulbright US Scholar Program: Insights from an Alumni Ambassador**

**Author:** Nishanta Rajakaruna (California Polytechnic University, San Luis Obispo)

**Keywords:** cross cultural education; International collaboration

In this presentation, Dr. Nish Rajakaruna (Fulbright US Scholar and Alumni Ambassador, and Professor of Botany at California Polytechnic State University, San Luis Obispo) will discuss the Fulbright US Scholar Program and the process of applying for Fulbright grants. Postdoctoral fellows, early career faculty from community colleges, liberal arts colleges and more research-focused universities, as well as botanists from state and federal agencies and the private sector (including retired and emeritus faculty and independent applicants with no US institutional affiliation), are all eligible for Fulbright US Scholar Awards and are encouraged to attend the session. Dr. Rajakaruna will give a short summary of his times as a Fulbright US Scholar, discuss opportunities for teaching and research in botany through the Fulbright US Scholar Program, and share his approach to the application process. Dr. Rajakaruna has taught botany for 20 years and received two Fulbright US Scholar Awards, to Sri Lanka and South Africa, as well as two Fulbright Regional Travel Program Grants, to India and Madagascar. During his Fulbright awards, he established long-term studies with his host country collaborators on the diversity and ecology of plants and lichens growing on understudied serpentinite rock outcrops and other ‘harsh’ soils, taught a course in Geobotany, and gave public lectures in botany and ecology courses. He also visited high schools and universities across his host countries to share his research on rock outcrop plants and to promote opportunities for higher education and research in the United States. Since his Fulbright experiences, he has focused his efforts on promoting opportunities for cultural and educational exchange among his students and colleagues and in his professional circles and is excited to share his experiences as a Fulbright US Scholar with members of the Botanical Society of America. More information on Fulbright US Scholar Awards can be found here: [https://www.fulbrightprogram.org](https://www.fulbrightprogram.org).

**Topic:** Ecology

**A-107 Ephemeral visitors or permanent residents?**
Decadal change in the ruderal vegetation from a periurban university campus

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Keywords: invasive species; Urban ecology

The increasing aggregation of humans in urban areas have created new environmental conditions that affect the biodiversity. These new environmental conditions impose filters to plant establishment and can lead to plant diversity decline. However, in periurban spaces, the confluence of natural, urban, and agricultural processes can also influence local biotas and reduce the trend of biotic homogenization and loss of biodiversity due urbanization. We surveyed the ruderal vegetation from a periurban university campus in west-central México during the rainy seasons of 2008 and 2016–2018, time during which the campus underwent intensive construction. We use the built area such as disturbance indicator, area that grew from 4 ha in 2009 to 12.6 ha in 2017. We identified 234 different Angiosperms belonging to 165 genera and 43 families and the community composition changed over time. Families Asteraceae, Poaceae, and Fabaceae had the most species, Poaceae replacing to Asteraceae as the richest family when the disturbance increased. One hundred species were common to all the sampling years, and the families whose species number increased during the study were Asteraceae, Cyperaceae, Euphorbiaceae, Fabaceae, Lamiaceae, and Poaceae. Sixteen native species found in 2008 disappeared from the study site in recent years, nine of which have been related with low disturbance, por example Gongylocarpus rubricaulis, Ipomoea cristulata, Mecardonia procumbens, Stevia viscida, and Valeriana urticifolia. On the contrary, 98 new species were observed in the latter years, some associated to high disturbance or common species of urban areas, such as Avena fatua, Cymbalaria muralis, Lactuca serriola. Overall, species richness increased with time, including that of exotic species that increased from 16% of the total species in 2008 to 24% in 2018. The majority of the exotic species identified (43 species) are native from the old world, while four are from South America. We identified 13 of exotic species that are invasive in Mexico, such as Digitaria velutina, Asphodelus fistulosus, Mercurialis annua, and Senecio inaequidens, for which this was their first record in the city of Morelia (population 849,053), where the study area is located. These results suggest that environmental conditions imposed by disturbance can favor the proliferation of various species, especially grasses and several exotic species of different families.