Attend our Workshop:

**SMRT® Sequencing: Delivering a More Complete View of Genetic Diversity**

SMRT Sequencing in 2016: Technology Updates & Developments
Marty Badgett, PacBio

Oliver Ryder, San Diego Zoo Institute for Conservation Research

**The Genome Galaxy Initiative - Expedited Open-Access Genomic Investigations**
Jenny Gu, PacBio and Christina Tran, Experiment

Single-Molecule Sequencing of the Maize Genome and Transcriptome
Doreen Ware, USDA-ARS, Cold Spring Harbor Laboratory

An Improved Reference Pig Genome Sequence to Enable Research and Prediction
Alan L. Archibald, The Roslin Institute and R(D)SVS, University of Edinburgh

Empowering Genetics Research in *Chenopodium quinoa* with Single Molecule Genomics
Yung Shwen Ho, King Abdullah University of Science and Technology, Saudi Arabia

**Tuesday, January 12, 1:30 – 3:40 p.m., San Diego Room**

---

**Plant Presentations**

**Saturday, January 9**

**Genome Sequence of *T. urartu***
Hong-Qing Ling, Institute of genetics and developmental biology, CAS
8:40-9:00 a.m., Town and Country

**Assembly of the 4.5Gb Ancestral Wheat D-Genome from Hybrid PacBio and Illumina Data**
Alekssey Zimin, University of Maryland
9:00-9:20 a.m., Town and Country

**Sugar Beet BeetMap-3, and Steps to Improve the Genome Assembly and Genome Sequence Annotation**
Bernd Weisshaar, Bielefeld University, Department of Biology & CeBiTec
1:30-1:50 p.m., Towne-Meeting House

**Assembly of the pea genome by integration of high throughput sequencing (PacBio and Illumina) and Whole Genome Profiling (WGPTM) data**
Mohammed-Amin Madoui, CEA, Genoscope
2:30-2:50 p.m., Pacific Salon 1

**The Genome of *Chenopodium quinoa***
David E Jarvis, King Abdullah University of Science and Technology
3:05-3:25 p.m., Towne-Meeting House

**New Insights on Genome Size Reduction in the High-Polyploid Carnivorous Plant *Utricularia gibba* from a Long-Read, Third Generation Assembly**
Victor A. Albert, University at Buffalo, Dept. of Biological Sciences
3:10-3:30 p.m., Golden Ballroom

**The Azolla Genome Project**
Andrea Braeutigam, Leibniz-Institute of Plant Genetics and Crop Plant Research (IPK)
5:20-5:40 p.m., Towne-Meeting House

**Sunday, January 10**

**S. verrucosum, a Wild Mexican Potato As a Model Species for a Plant Genome Assembly Project**
Pirita M Paajanen, The Genome Analysis Centre, Norwich
8:00-8:20 a.m., Pacific Salon 1

**A Comprehensive Study of the Sugar Pine (*Pinus lambertiana*) Transcriptome Implemented through Diverse Next-Generation Sequencing Approaches**
Pedro J Martinez-Garcia, Dept. Plant Sciences University of California Davis
9:10-9:30 a.m., Sunrise-Meeting House
A Comprehensive lincRNA Analysis: From Conifers to Trees (Norway spruce)
Nicolas Delhomme, Umeå Plant Science Centre, Umeå University
9:50-9:54 a.m., Sunrise-Meeting House

Genome Sequencing, Comparative Genomics and Population Analyses of Aspen Species
Yao-Cheng Lin, VIB, Ghent University
2:10-2:30 p.m., Sunrise-Meeting House

Long Read Sequencing Technology to Solve Complex Genomic Regions Assembly in Plants
Helene Berges, Plant Genomic Center - INRA Toulouse
2:30-2:50 p.m., Royal Palm Salon 1-2

An update on sequencing the Cabernet Sauvignon genome
Grant Cramer, University of Nevada, Reno
3:10-3:30 p.m., Royal Palm Salon 5-6

Building High Quality Reference Genome Assemblies using PacBio long reads for the Allotetraploid Coffea arabica and its Diploid Ancestral Maternal Species Coffea eugenioides
Marcela Yepes, Cornell University
4:00-4:40 p.m., Pacific Salon 3

High Quality Draft Genomes of Medicago truncatula & Gossypium herbaceum using NGS, Dovetial & BioNano technologies
Thiruvarangan Ramaraj, National Center for Genome Resources (NCGR)
4:20-4:40 p.m., Golden Ballroom

Spotting the difference: comparing the genome of Corymbia with its larger cousin Eucalyptus grandis
Graham J. King, Southern Cross University
4:40-5:00 p.m., Golden Ballroom

Whole Genome Sequencing and High Density Genetic Maps in Pistachio Reveal a Large Non-Recombining Region of Sex Chromosomes
Salih Kafkas, University of Cukurova
5:20-5:40 p.m., Royal Palm Salon 5-6

High-quality draft genome of Gossypium herbaceum cv. Wagad
Thiruvarangan Ramaraj, National Center for Genome Resources (NCGR)
5:30-5:50 p.m., Sunset-Meeting House

Monday, January 11

Assembly of highly heterozygous mango (Mangifera indica cv. Amrapali) genome using PacBio long sequence reads
Nagendra K. Singh, ICAR-National Research Centre on Plant Biotechnology, Pusa Campus
7:50-8:10 p.m., Towne-Meeting House

Tuesday, January 12

Improving Reference Genome Resources Using Long-Read Sequencing Technology (Zea mays)
Bo Wang, Cold Spring Harbor Laboratory
3:10-3:30 p.m., California

Result of the de novo sequencing of the complex sunflower genome using PacBio technology (100X)
Nicolas Langlade, Laboratoire des Interactions Plantes Micro-organismes (LIPM), INRA/CNRS
3:30-3:50 p.m., Pacific Salon 4-5

Application of Single Molecule Sequencing to Facilitate de novo Sequencing of Wheat Chromosome Arm 7DL
Song Weining, Northwest A&F University
3:15-3:35 p.m., Pacific Salon 3

Construction of pseudomolecules for the Aegilops tauschii genome, the wheat D genome progenitor
Ming-Cheng Luo, University of California
3:55-4:15 p.m., Pacific Salon 3

Insights from genome sequencing of cassava and other Manihot
Jessica B. Lyons, University of California, Berkeley
4:00-4:20 p.m., Sunrise-Meeting House

Using PacBio Long Reads to Generate a High Quality Reference for the Allotetraploid Coffea arabica and its Maternal Diploid Ancestor Coffea eugenioides
Marcela Yepes, Cornell University/School of Integrative Plant Science
5:00-5:20 p.m., Pacific Salon 1

Wednesday, January 13

Genome Sequencing and Annotation of Sweetpotato Wild Progenitors
Zhangjun Fei, Cornell University
11:00-11:15 a.m., Sunset-Meeting House

Sequencing and Assembly of the Rice Variety N22 (Aus Group): a New Reference Genome to Study Comparative, Evolutionary and Functional Genomics of Rice
David Kudrna, Arizona Genomics Institute, University of Arizona
11:30-11:50 a.m., Pacific Salon 2

Animal Presentations

Saturday, January 9

Progress Toward a Low Budget Reference Grade Genome Assembly (Goat)
Benjamin Rosen, ARS, USDA
1:50-2:10 p.m., San Diego

Progress of the Shrimp Genomic Sequencing Project
Jianhai Xiang, Institute of Oceanology, Chinese Academy of Sciences
2:00-2:20 p.m., Royal Palm Salon 3-4

Quality Assessment of the Current Pig Genome for Variant Discovery; and High Quality Re-assembly Using 3rd Generation Sequencing
Amanda Warr, The Roslin Institute and R(D)SVS, University of Edinburgh
2:45-3:00 p.m., Royal Palm Salon 1-2

Annotating the Bovine Genome with Single-Molecule Transcript Sequencing
Christine G. Elsik, University of Missouri
4:00-4:20 p.m., San Diego

Sunday, January 10

Update on progress toward EquCab3 (Equine)
Theodore S. Kalbfleisch, University of Louisville
8:50-9:05 a.m., Royal Palm Salon 5-6

Approaches Taken, Progress Made, and Enhanced Utility of Long Read-based Goat, Swine, Cattle and Sheep Reference Genomes
Timothy P.L. Smith, USDA, ARS, USMARC
1:30-2:15 p.m., Golden West

Identifying and Cataloguing LncRNAs in Human and Mouse
Jennifer Harrow, Wellcome Trust Sanger Institute
4:00-4:20 p.m., Royal Palm Salon 3-4

Monday, January 11

Assembly of highly heterozygous mango (Mangifera indica cv. Amrapali) genome using PacBio long sequence reads
Nagendra K. Singh, ICAR-National Research Centre on Plant Biotechnology, Pusa Campus
7:50-8:10 p.m., Towne-Meeting House

Tuesday, January 12

Improving Reference Genome Resources Using Long-Read Sequencing Technology (Zea mays)
Bo Wang, Cold Spring Harbor Laboratory
3:10-3:30 p.m., California

Result of the de novo sequencing of the complex sunflower genome using PacBio technology (100X)
Nicolas Langlade, Laboratoire des Interactions Plantes Micro-organismes (LIPM), INRA/CNRS
3:30-3:50 p.m., Pacific Salon 4-5

Application of Single Molecule Sequencing to Facilitate de novo Sequencing of Wheat Chromosome Arm 7DL
Song Weining, Northwest A&F University
3:15-3:35 p.m., Pacific Salon 3

Construction of pseudomolecules for the Aegilops tauschii genome, the wheat D genome progenitor
Ming-Cheng Luo, University of California
3:55-4:15 p.m., Pacific Salon 3

Insights from genome sequencing of cassava and other Manihot
Jessica B. Lyons, University of California, Berkeley
4:00-4:20 p.m., Sunrise-Meeting House

Using PacBio Long Reads to Generate a High Quality Reference for the Allotetraploid Coffea arabica and its Maternal Diploid Ancestor Coffea eugenioides
Marcela Yepes, Cornell University/School of Integrative Plant Science
5:00-5:20 p.m., Pacific Salon 1

Wednesday, January 13

Genome Sequencing and Annotation of Sweetpotato Wild Progenitors
Zhangjun Fei, Cornell University
11:00-11:15 a.m., Sunset-Meeting House

Sequencing and Assembly of the Rice Variety N22 (Aus Group): a New Reference Genome to Study Comparative, Evolutionary and Functional Genomics of Rice
David Kudrna, Arizona Genomics Institute, University of Arizona
11:30-11:50 a.m., Pacific Salon 2

Animal Presentations

Saturday, January 9

Progress Toward a Low Budget Reference Grade Genome Assembly (Goat)
Benjamin Rosen, ARS, USDA
1:50-2:10 p.m., San Diego

Progress of the Shrimp Genomic Sequencing Project
Jianhai Xiang, Institute of Oceanology, Chinese Academy of Sciences
2:00-2:20 p.m., Royal Palm Salon 3-4

Quality Assessment of the Current Pig Genome for Variant Discovery; and High Quality Re-assembly Using 3rd Generation Sequencing
Amanda Warr, The Roslin Institute and R(D)SVS, University of Edinburgh
2:45-3:00 p.m., Royal Palm Salon 1-2

Annotating the Bovine Genome with Single-Molecule Transcript Sequencing
Christine G. Elsik, University of Missouri
4:00-4:20 p.m., San Diego

Sunday, January 10

Update on progress toward EquCab3 (Equine)
Theodore S. Kalbfleisch, University of Louisville
8:50-9:05 a.m., Royal Palm Salon 5-6

Approaches Taken, Progress Made, and Enhanced Utility of Long Read-based Goat, Swine, Cattle and Sheep Reference Genomes
Timothy P.L. Smith, USDA, ARS, USMARC
1:30-2:15 p.m., Golden West

Identifying and Cataloguing LncRNAs in Human and Mouse
Jennifer Harrow, Wellcome Trust Sanger Institute
4:00-4:20 p.m., Royal Palm Salon 3-4
Monday, January 11

From sequencing to chromosomes: new *de novo* assembly and scaffolding methods improve the goat reference genome
Sergey Koren, National Human Genome Research Institute, National Institutes of Health
5:05-5:20 p.m., Sunrise-Meeting House

An Update on Goat Genomics
Alessandra Stella, PTP Science Park
6:55-7:05 p.m., Sunrise-Meeting House

Tuesday, January 12

An Extreme Metabolism: Iso-Seq analysis of the Ruby-Throated Hummingbird Transcriptome
Winston Timp, Johns Hopkins University
5:50-6:10 p.m., Royal Palm Salon 1-2

Other Organism Presentations
Sunday, January 10

Genomics of anaerobic cellulose-degrading fungal symbionts of the herbivore gut
Alan Kuo, US Department of Energy Joint Genome Institute
2:55-3:15 p.m., Royal Palm Salon 3-4

Plant Posters

P0197 Improving Reference Genome Resources Using Long-Read Sequencing Technology (Maize)
Bo Wang, Cold Spring Harbor Laboratory

P0241 Telomere-to-Telomere Chromosome Assemblies and Identification of Structural Variations in *Arabidopsis thaliana* Ecotypes
Florian Jupe, Salk Institute for Biological Studies & Howard Hughes Medical Institute

P0388 *Arabidopsis thaliana* Iso-Seq and Gene Annotation
Shengqiang Shu, DOE Joint Genome Institute

P0448 PacBio *de novo* Assembly of the *Homalanthus nutans* Genome Provides Insight into Prostratin Biosynthesis
Jeff Wong, University of California

P0721 Building a Reference Genome for Indica Rice
Chengzhi Liang, Institute of Genetics and Developmental Biology, CAS

P0811 Sequencing the Genome of the Hexaploid Oat
Rachel N. Walstead, University of North Carolina at Charlotte

P0991 Sequencing and Genome Assembly of Cultivated Alfalfa at the Diploid Level (CADL) *Medicago sativa*
Diego A. Fajardo, National Center for Genome Resources (NCGR)

P0992 Scaffolding 3rd Generation Sequence Contigs using Dovetail and BioNano technologies (*Medicago truncatula*)
Karen M. Moll, National Center for Genome Resources (NCGR)

P1021 Assembly of the Pea Genome By Integration of High Throughput Sequencing (PacBio and Illumina) and Whole Genome Profiling (*WGP™* Data
Mohammed-Amin Madoui; CEA, Genoscope

P1041 A Draft Mitochondrial Genome for *Leucaena trichandra* (Mimosoidae: Leguminosae)
Sealtiel Ortega-Rodriguez, New Mexico State University

P1097 Fine-Mapping and Identification of Candidate Genes for *Rvi12* Based Apple Scab Resistance from *Malus baccata* ‘Hansen’s Baccata 2’
Sudharsan Padmarasu, Center for Research and Innovation, Fondazione Edmund Mach

P1136 A Draft Genome Sequence for the Cashew Tree (*Anacardium occidentale*) Based on High Coverage Pacbio Sequencing
Orzenil B. da Silva Junior, EMBRAPA Genetic Resources and Biotechnology

P1140 Whole Genome Sequencing and High Density Genetic Mapping in Pistachio Reveal a Large Non-Recombining Region of Sex Chromosomes
Salih Kafkas, University of Cukurova

P1147 Assembly of highly heterozygous mango (*Mangifera indica* cv. Amrapali) genome using PacBio long sequence reads
Nagendra K. Singh, ICAR-National Research Centre on Plant Biotechnology, Pusa Campus

P1191 A Comprehensive lincRNA Analysis: From Conifers to Trees (Norway spruce)
Nicolas Delhomme, Umeå Plant Science Centre, Umeå University

P1233 Leveraging Long Sequencing Reads to Investigate R-Gene Clustering and Variation in Sugar Beet
Andrew J. Funk, Michigan State University

P1244 The Genome of *Sesamum indicum* L
Hongmei Miao, Henan Sesame Reserach Center, Henan Academy of Agricultural Sciences

P1248 High Quality *De Novo* Genome Assemblies of the Common Ice Plant (*Mesembryanthemum crystallinum* L.) - a Functional Genomics Resource for Crassulacean Acid Metabolism (CAM) and Halophytism
Won Cheol Yim, University of Nevada, Reno

Informatics Presentations

Sunday, January 10

Deploying simple-to-use scalable workflows using the Agave API
Matthew Vaughn, Texas Advanced Computing Center
4:30-5:00 p.m., Stratford

Monday, January 11

Integrated approach towards sequencing a large and complex genome - iPlant Portal facilitates management of big data (*Aegilops tauschii*)
Ming-Cheng Luo, Department of Plant Sciences, University of California
6:30-6:50 p.m., California

Tuesday, January 12

Structural Variation Analysis with Long Single Molecule Reads
Michael Schatz, Cold Spring Harbor Laboratory
10:30-10:50 a.m., Golden West

MaSuRCA mega-reads assembly technique for haplotype resolved genome assembly of hybrid Pacbio and Illumina data
Aleksey Zimin, University of Maryland
5:20-5:40 p.m., Pacific Salon 1

Plant Posters

P0197 Improving Reference Genome Resources Using Long-Read Sequencing Technology (Maize)
Bo Wang, Cold Spring Harbor Laboratory

P0241 Telomere-to-Telomere Chromosome Assemblies and Identification of Structural Variations in *Arabidopsis thaliana* Ecotypes
Florian Jupe, Salk Institute for Biological Studies & Howard Hughes Medical Institute

P0388 *Arabidopsis thaliana* Iso-Seq and Gene Annotation
Shengqiang Shu, DOE Joint Genome Institute

P0448 PacBio *de novo* Assembly of the *Homalanthus nutans* Genome Provides Insight into Prostratin Biosynthesis
Jeff Wong, University of California

P0721 Building a Reference Genome for Indica Rice
Chengzhi Liang, Institute of Genetics and Developmental Biology, CAS

P0811 Sequencing the Genome of the Hexaploid Oat
Rachel N. Walstead, University of North Carolina at Charlotte

P0991 Sequencing and Genome Assembly of Cultivated Alfalfa at the Diploid Level (CADL) *Medicago sativa*
Diego A. Fajardo, National Center for Genome Resources (NCGR)

P0992 Scaffolding 3rd Generation Sequence Contigs using Dovetail and BioNano technologies (*Medicago truncatula*)
Karen M. Moll, National Center for Genome Resources (NCGR)

P1021 Assembly of the Pea Genome By Integration of High Throughput Sequencing (PacBio and Illumina) and Whole Genome Profiling (*WGP™* Data
Mohammed-Amin Madoui; CEA, Genoscope

P1041 A Draft Mitochondrial Genome for *Leucaena trichandra* (Mimosoidae: Leguminosae)
Sealtiel Ortega-Rodriguez, New Mexico State University

P1097 Fine-Mapping and Identification of Candidate Genes for *Rvi12* Based Apple Scab Resistance from *Malus baccata* ‘Hansen’s Baccata 2’
Sudharsan Padmarasu, Center for Research and Innovation, Fondazione Edmund Mach

P1136 A Draft Genome Sequence for the Cashew Tree (*Anacardium occidentale*) Based on High Coverage Pacbio Sequencing
Orzenil B. da Silva Junior, EMBRAPA Genetic Resources and Biotechnology

P1140 Whole Genome Sequencing and High Density Genetic Mapping in Pistachio Reveal a Large Non-Recombining Region of Sex Chromosomes
Salih Kafkas, University of Cukurova

P1147 Assembly of highly heterozygous mango (*Mangifera indica* cv. Amrapali) genome using PacBio long sequence reads
Nagendra K. Singh, ICAR-National Research Centre on Plant Biotechnology, Pusa Campus

P1191 A Comprehensive lincRNA Analysis: From Conifers to Trees (Norway spruce)
Nicolas Delhomme, Umeå Plant Science Centre, Umeå University

P1233 Leveraging Long Sequencing Reads to Investigate R-Gene Clustering and Variation in Sugar Beet
Andrew J. Funk, Michigan State University

P1244 The Genome of *Sesamum indicum* L
Hongmei Miao, Henan Sesame Reserach Center, Henan Academy of Agricultural Sciences

P1248 High Quality *De Novo* Genome Assemblies of the Common Ice Plant (*Mesembryanthemum crystallinum* L.) - a Functional Genomics Resource for Crassulacean Acid Metabolism (CAM) and Halophytism
Won Cheol Yim, University of Nevada, Reno
VISIT US AT BOOTH #421

Stop by to see our newest product, the Sequel™ System, and to discuss your research. We will have experts in the following areas at the booth during these times to ensure your specific questions are answered:

Monday 9:30-11:30 a.m. — Sample prep for SMRT Sequencing
Monday 3:00-5:00 p.m. — Informatics tools for assembly and analysis
Tuesday 9:30-11:30 a.m. — Iso-Seq™ transcriptome sequencing

www.pacb/agbio

For Research Use Only. Not for use in diagnostic procedures. © Copyright 2015, Pacific Biosciences of California, Inc. All rights reserved. Information in this document is subject to change without notice. Pacific Biosciences assumes no responsibility for any errors or omissions in this document. Certain notices, terms, conditions and/or use restrictions may pertain to your use of Pacific Biosciences products and/or third-party products. Please refer to the applicable Pacific Biosciences Terms and Conditions of Sale and to the applicable license terms at http://www.pacificbiosciences.com/licences.html.

Pacific Biosciences, the Pacific Biosciences logo, PacBio, SMRT, SMRTbell, Iso-Seq, and Sequel are trademarks of Pacific Biosciences. BluePippin and SageELF are trademarks of Sage Science. NGS-go and NGSengine are trademarks of GenDx. All other trademarks are the sole property of their respective owners.