

You are encouraged to check the PAG website for any presentation you are interested in attending as times and room locations are subject to change.

Workshop Presentations

Saturday, January 12th

Session	Time	Presentation Title
Fruits/Nuts	8:02 AM	Improvement of Genome Resources for Hazelnut
Camelids	8:05 AM	Improving the North African Dromedary Genome with Hi-C and PacBio Reads
Camelids	8:25 AM	Preliminary Sequence Assembly of the Alpaca (Vicugna pacos) Y Chromosome
Camelids	8:45 AM	Dromedary Camel Genome Sequence
Cattle/Swine	8:50 AM	Benefits from Adoption of a New Reference Genome Assembly and Use of a Larger SNP Set in Genomic Predictions for US Dairy Cattle
Arthropod Genomics and Genome Engineering	9:00 AM	Making It Better: Improvement of a Mature Genome Assembly with Long- Read and Long-Range Sequencing Data
Camelids	9:00 AM	Chromosome-Level Alpaca Reference Genome VicPac 3.1 Improves Genomic Insight into the Biology of New World Camelids
Buffalo Genomics	11:20 AM	Chromosome-Level Assembly of the Water Buffalo Genome Surpasses Human and Goat Genomes in Sequence Contiguity
Legumes	12:00 PM	PacBio Resequencing of Medicago truncatula A17 Genome and Discovery of Symbiotic Co-Regulated Genomic Islands
Cool Season Legumes	1:30 PM	Improved Lens culinaris Reference Assembly gives new Insight into Regions of Genomic Complexity
Non-Seed Plants	4:20 PM	De novo Genome Assembly and Annotation of Sanionia uncinata (Amblystegiaceae: Hypnales), a Pleurocarpous Moss Dominant in Antarctica

Sunday, January 13th

Session	Time	Presentation Title
Sugar Cane (ICSB)	8:05 AM	Allele Defined Genome of the Autopolyploid Saccharum spontaneum L.
Cacao Genomics Workshop	11:06 AM	Long-Read Sequencing Provides Insights into Large Scale Genomic Expansions in the Phytophthora palmivora and megakarya Genomes
Non-coding RNA	1:30 PM	Long Non-Coding RNA Annotation in Chickens using Novel Iso-Seq Methods
Ornamentals	1:30 PM	High-Quality Chromosome-Level Rose Genome Sequence provides insights on Domestication and Major Traits
Grape Genome Initiative	2:50 PM	Genomic Diversity Among Wine Grape Cultivars and Clones
Functional Genomics	3:01 PM	Single-Molecule Sequencing Reveals Increased Complexity of the Transcriptome Landscape in Maize and Sorghum
Coffee Genomics	4:20 PM	Coffea arabica variety Caturra and C. eugenioides Genome Assembly and Annotation
Sequencing Complex Genomes	4:20 PM	De novo Genome Sequencing and Hybrid Assembly of Punica granatum, a Complex Fruit Genome
Cucurbit Conomics	5:00 PM	Chromosome Evolution in Cucurbitaceae using a Reference-Quality Genome
		Assembly of Bitter Gourd (Momordica charantia)
Sequencing Complex Genomes	5:20 PM	Sequencing the Genome of the Mushroom Coral (Heliofungia actiniformis)
		with Multiple Long Read Technologies

Monday, January 14th

Session	Time	Presentation Title
PacBio: Sequence with Confidence - How SMRT Sequencing is Accelerating Plant and Animal Genomics	1:10 PM	The Bat1K Project: Bat Genomes, Biology, and Implications
PacBio: Sequence with Confidence - How SMRT Sequencing is Accelerating Plant and Animal Genomics	1:30 PM	Dawn of the Crop Pangenome Era
PacBio: Sequence with Confidence - How SMRT Sequencing is Accelerating Plant and Animal Genomics	1:50 PM	Reference-Quality Drosophila Genome Assemblies for Evolutionary Analysis of Previously Inaccessible Genomic Regions
PacBio: Sequence with Confidence - How SMRT Sequencing is Accelerating Plant and Animal Genomics	2:10 PM	Using Iso-Seq to Annotate, Evaluate, and Phase Plant and Animal Genomes
Phase Genomics: From Contigs to Chromosomes: How Hi-C is Transforming Genome and Metagenome Assembly	5:00 PM	PacBio Long Reads and HiC: Recipes for Generating High Quality de novo Genome Assemblies for Outbred Plants and Animals
Phase Genomics: From Contigs to Chromosomes: How Hi-C is Transforming Genome and Metagenome Assembly	5:20 PM	Hi-C Based Chromatin Interaction Maps Enabled Haplotype-Resolved Chromosome- Level Assemblies of the Brahman and the Angus Genomes
Phase Genomics: From Contigs to Chromosomes: How Hi-C is Transforming Genome and Metagenome Assembly	5:40 PM	Toward the Genome-Enabled Improvement of Shea Tree for Sub-Saharan Africa

Tuesday, January 15th

Session	Time	Presentation Title
Bioinformatics	10:50 AM	Falcon-Phase Integrates PacBio and HiC Data for de novo Assembly, Scaffolding and Phasing of Diploid Genomes
Banana Genomics	11:10 AM	Gene-Edited Cavendish utilizing the Draft Genomes of Wild and Domesticated Bananas
Cannabis Genomics and Breeding	11:30 AM	Using Cryptocurrencies and Blockchain Technologies to Fund the De Novo Sequencing, Assembly, and Open Access Publishing of the Cannabis sativa L. Genome
Crop Genomics for Global Food Security	2:10 PM	High Quality Genomic Resources to Understand Independent Domestication Processes and Genetic Diversity in Lima Bean
Bionano Genomics	2:40 PM	The Vertebrate Genomes Project: Building Accurate and Complete Reference Genomes for All Vertebrates
Lexogen: The Power of Transcriptome Analysis – Enabled by Lexogen Full-Length and Targeted RNA-Seq Tools	2:50 PM	Five-Prime Cap Selection and Normalization for Full Length High Efficiency Iso-Seq Sequencing
Crop Genomics for Global Food Security	3:10 PM	SMRT Renseq-Based Characterization of Nucleotide-Binding-Leucine-Rich Repeat Gene Family Resistance Genes in Arachis, Glycine and Musa Species
IWGSC – Wheat Genome Manual and Functional Annotation	3:50 PM	Wheat Prolamin Gene Regions in Chinese Spring using the Sequences Generated by PacBio Long Reads and Validated by Bionano Maps
Yam Genomics	4:00 PM	A Chromosome-Scale Genome Assembly for Dioscorea alata L.
Avian Genomics – Going Wild!	4:20 PM	Trio Parental-Child Approach Generates Nearly Complete Diploid Avian Genome Assembly and Reveals Large Differences between Haplotypes and Complete Sex Chromosomes
Root Genomics	5:20 PM	High Quality Assembly of White Lupin's Genome, a Model to Study Root Developmental Adaptations

Wednesday, January 16th

Session	Time	Presentation Title
Duckweed Research and Applications	2:00 PM	Cytogenomic Elucidation of the Spirodela Genomes
Sweetpotato Genomics	2:12 PM	Sweetpotato Genome Sequencing Efforts by the TRAS Community

Poster Presentations

Even Numbered Posters – Monday, January 14th, 10-11:30 AM

Poster	Poctor Titlo
Number	
24	Korea National Marine Organism Genome Project
E 2	NextCorrect: A Novel Method and Software Tool for Fast and Accurate Error Correction on Long-Read
52	Sequencing Data
66	SequelQC: Analyzing PacBio Sequel Raw Sequence Quality
104	Sweet Genomes: Sequencing, Assembling, and Annotating Two Maples
182	Genome Assembly Improvement with Long Reads and Long Jumps
188	SMRT Long-Reads and DLS Optical Maps Allow Whole-Genome Comparative Studies at the Chromosome Scale:
	The Case of the European Barn Swallow
214	Mitochondrial Genome of Phytophthora sansomeana, a Soybean Root Rot Pathogen
218	Comparative Genome Analyses of Four Geographically Distant, Rice-Infecting Isolates of Rhizoctonia solani
210	Anastomosis Group 1-IA (AG1-IA)
240	Diaphorina citri Resources for Exploring the Citrus Greening Disease Complex
284	The Sea Cucumber Genome Provides Insights into Morphological Evolution and Visceral Regeneration
394	Rambouillet Sheep Transcriptome Annotation Resources
466	An Annotated de novo Hybrid Assembly for the Dromedary Camel
650	De Novo Draft Genome Sequence of Japanese Pear (Pyrus pyrifolia Nakai)
702	De Novo Genome Sequencing and Hybrid Assembly of Punica granatum, a Complex Fruit Genome
824	Sequence, Assembly and Annotation of Maize Inbred Line B104: A Maize Transformation Resource
836	Structural Variants in Rio Sweet Sorghum Using PacBio Long-Read and Illumina Sequencing
946	Whole Genome Sequencing of Capsicum annuum 'Dempsey' Using Pacbio and Hi-C
1070	Database for the Chromosome-Level Assembly for a Liverwort Marchantia polymorpha
1118	The Genome of Murraya koenigii Provides Insight into the Evolution of Bioactive Compounds of Medicinal
1110	Importance

Odd Numbered Posters – Monday, January 14th, 3-4:30 PM

Poster Number	Poster Title
61	A Fast and Efficient Long-Read Genome Assembly Approach for Large and Complex Genomes
71	Corrected PacBio Iso-Seq CCS for Plant Genome Annotation
83	TAMA: Software for Iso-Seq Transcriptome Annotation
87	Isophase: Haplotyping Using Full-Length Transcript Sequencing in a F1 Maize Hybrid Reveals Allele-Specific
	Expression
101	Investigation of Strategies to Improve Annotation and Assembly of Conifer Genomes
125	Localization of DNA Sequences on the Chromosomes Derived From Bienertia sinuspersici Genome Sequencing
	Project
179	A Low DNA Input Protocol for High-Quality PacBio De Novo Genome Assemblies from Single Invertebrate
	Individuals
185	Library Prep and Bioinformatics Improvements for Full-Length Transcript Sequencing on the PacBio Sequel
	System

189	Benchmarking Ultra-High Molecular Weight DNA and Tissue Preservation Protocols for the Vertebrate Genomes Project
219	A Metagenomic Approach to Understanding Stand Failure in <i>Bromus tectorum</i>
225	The Genome of Fish Tapeworm Nippotaenia percotti as a Potential Bookmark for Gene Loci that Facilitates
225	Anthropogenic Infection
233	Draft Genome Assemblies of Two West African Cassava Bemisia tabaci Populations
245	Genome Sequencing of Divergent Streptophyte Algae
279	Genomic Resources for California Abalone Species
463	Ensembl Updates for Farm Animals
475	SMRT Sequencing of Gonad Full-Length Transcriptome of Bamboo Grasshopper Ceracris kiangsu
479	Identifying Genomic Underpinnings of Diversification Rate Shifts in Tapeworms using Phylogenetic Rate Tests
493	Why So Pale and Wan: Comparative Genomics of a New Cavefish in Europe
523	Developing Genomic Resources for Tripidium As a Novel Biomass Crop
529	Reconstruction of a Full-Length Transcriptome of Cryptomeria japonica
522	Full-Length cDNA Isoform Collection from Japanese Larch (Larix kaempferi) and Kurile Larch (Larix gmelinii var.
555	japonica) and the Interspecies Comparison
577	Highly Performed Genome Sequences of Brassica rapa Using BioNano's Third-Generation Optical Mapping and
5//	PacBio Sequences
627	High-Fidelity, Long Reads for Comprehensive Genomic Analysis of Cabernet Sauvignon Clones
691	Segregation of Aphid Resistance from 3 Wild Sources in Black Raspberry Cross Populations and Exploration of
	Genetic Basis of Aphid Resistance with IsoSeq Technology
719	Identification and Distribution of the Nucleotide-Binding Leucine-Rich Repeat Gene Family in Musa
763	The Genome of the Soybean Cyst Nematode (Heterodera glycines)
783	Genome Resources for Cowpea (<i>Vigna unguiculata</i> [L.] Walp)
793	Diversity, Heteroplasmy and Inheritance of Chloroplasts in Marama Bean (Tylosema esculentum)
817	Comparative Analyses of NAM Founder Lines Using Whole Genome Assemblies.
837	Gene Presence-Absence Variation in Sweet Sorghum Identified Using Both PacBio Long-Read and Illumina Short-
	Read Sequencing
883	Regulation of Recipient Parent's Genomic Structure Via Epigenetic Patterns from Donor Parent Lead to
	Transgressive Segregants in Rice
925	High-Quality <i>de novo</i> Reference Genome Assembly of Tomato Using Single-Molecule Technologies
929	Clarification of the Genome Structure of Micro-Tom, a Model Cultivar of Tomato (Solanum lycopersicum)
959	Understanding the Complexity of Wheat Prolamin Locus Regions using High-Quality Sequences generated by
	PacBio Long Reads and Bionano Maps
1089	Assessing Haplotype Variation and Visualizing Synteny in the Diploid Genome Assembly of Hop (<i>H. lupulus</i>)
1109	A High-Quality <i>de novo</i> Genome Assembly of the Resurrection Plant <i>Haberlea rhodopensis</i>
1121	Genome Sequences of the <i>Mimulus lewisii</i> Species Complex, a Model System for Plant Genetics, Development,
1127	Genomic Variability of <i>Phytophthora palmivora</i> Isolates from Different Oil Palm Cultivation Regions in Colombia