



SMRT® Sequencing for Complete Genomes

Monday, January 16

12:50 - 3:00 p.m., San Diego Ballroom

Hosted by Jonas Korlach, CSO, PacBio

Presenting the 2017 roadmap for Sequel™ System enhancements

Speakers:

Introducing 5 New High-quality PacBio Genome Assemblies for Rice to Help Solve the 10-Billion People Question

Rod Wing, Arizona Genomics Institute

Comparative Analyses of Next Generation Technologies for Generating Chromosome-level Reference Genome Assemblies

Erich Jarvis, Rockefeller University

Using Iso-Seq to Fill in Your A_no_tion

Richard Kuo, Roslin Institute, University of Edinburgh

De Novo Sequencing of the Koala Genome

Rebecca Johnson, Australian Museum Research Institute

Genome Assembly and Molecular Genetics of the Dengue, Yellow Fever, and Zika Vector *Aedes aegypti*

Ben Matthews, HHMI/Rockefeller University



PLANT AND ANIMAL SCIENCES

PACBIO WORKSHOP

Expert Hours

Presentation and Discussion
Lexington Room; Space Limited

Iso-Seq™ Method
Jan 16, 4:00 - 5:00 p.m.

Ultra-long Libraries
Jan 17, 10:00 - 11:00 a.m.

SMRT Analysis
Jan 17, 3:00 - 4:00 p.m.

Plant and Animal SMRT Grant is here!

Win free SMRT Sequencing of your favorite genome
Stop by our booth to learn how to submit your proposal
www.pacb.com/smrtgrant



SMRT Informatics Developers Conference

Half-day session focused *de novo* assembly and analysis tools for Iso-Seq full-length transcript sequencing data.

Keynote Speaker: Sergey Koren, National Institutes of Health
January 18, 12:00 - 4:30 p.m. – Sheffield/Hampton Ballroom

Lunch will be served.

OTHER PROGRAMS

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Program Presentations

	Date	Time	Location	Author	Title
Plant	Sat, Jan 14	8:00 a.m.	Pacific Salon 3	Dario Grattapaglia Embrapa Recursos Genéticos e Biotecnologia	A Chromosome-Scale Assembly of the Cashew Tree Genome: Leveraging the Combined Power of PacBio, DNA-Chromatin Proximity Ligation and SNP Linkage Maps
		9:20 a.m.	Pacific Salon 2	Song Li Virginia Tech	Integrated Transcriptome and Proteome Analyses Reveal Cell Type-Specific Regulation of Alternative Splicing in Arabidopsis
		4:00 p.m.	Town & Country Ballroom	Matthew J. Moscou The Sainsbury Laboratory	Genomics of the Barley Immune System
		4:20 p.m.	California	Richard J. Harrison NIAB EMR	Use of Strawberry Genomic Resources in GDR
	Sun, Jan 15	8:10 a.m.	Royal Palm Salon 1-2	Olivier Garsmeur CIRAD, UMR AGAP	A Reference Sequence of the Monoploid Genome of Sugarcane
		9:00 a.m.	Golden West Ballroom	Hong-Qing Ling Chinese Academy of Sciences	Comparative Analysis of <i>Triticum urartu</i> Genome with Other Grass Genomes
		9:00 a.m.	Pacific Salon 1	Prashant S Hosmani Boyce Thompson Institute	Improvements in the Tomato Reference Genome (SL3.0) and Annotation (ITAG3.0)
		10:30 a.m.	Esquire, Meeting House	Peter J. Maughan Brigham Young University	A PacBio and Hi-C based proximity-guided assembly of Amaranth pseudo chromosomes
		10:30 a.m.	Royal Salon 3-4	Xavier Argout CIRAD, UMR AGAP	The Cacao Criollo Genome v2.0 : An Improved Version of the Genome for Genetic and Functional Genomic Studies
		10:50 a.m.	Royal Palm Salon 1-2	Robert J. Henry University of Queensland	The Long and Short of the Sugarcane Transcriptome
		1:50 p.m.	Sunset, Meeting House	Alex Harkess Donald Danforth Plant Science Center	Divergence of X and Y Chromosomes in Asparagus
		1:50 p.m.	Pacific Salon 6-7 (2nd Floor)	Dario Cantu University of California, Davis	Beyond the Grape Genome: Construction of a Vineyard Metagenome Reference
		2:00 p.m.	Sunrise, Meeting House	C. Donovan Bailey New Mexico State University	<i>Leucaena</i> (Leguminosae: Mimosoideae) Genomic Resources and a Novel Means of Recovering Hybrid Parentage from a Combination of Data Sources
		2:10 p.m.	Royal Palm Salon 1-2	Jeremy Shearman National Center for Genetic Engineering and Biotechnology	The <i>Saccharum</i> Mitochondrial Genome
		2:40 p.m.	Sunrise, Meeting House	Daniela Puiu Johns Hopkins University	Preliminary Studies of a Genome Assembly of the California Endemic Oak, <i>Quercus lobata</i> Née (Fagaceae) using Pacific Biosciences and Illumina Sequencing Data
		2:50 p.m.	Royal Palm Salon 1-2	Jisen Zhang Fujian Agriculture and Forestry University	Ultra High Density Mapping of the <i>Saccharum spontaneum</i> Genome
		4:00 p.m.	Golden Ballroom	Yinping Jiao Cold Spring Harbor Laboratory	The Complex Sequence Landscape of Maize Revealed by Single Molecule Technologies
		4:00 p.m.	Pacific Salon 3	Carlos Ernesto Maldonado Centro Nacional de Investigaciones de Café	Using PacBio Long-Reads to Generate High Quality References for the Allotetraploid <i>Coffea arabica</i> and its Diploid Maternal Ancestor <i>C. eugenioides</i> : Characterization of Genomic Regions Containing QTLs for Yield, Plant Height, and Bean Size
		4:20 p.m.	Golden Ballroom	Jianwei Zhang Arizona Genomics Institute	A Case Study from Reseq to Refseq-Two High-Quality Reference Genome Sequences for <i>indica</i> Rice
		4:40 p.m.	Golden Ballroom	Adam Healey University of Queensland	Sequencing the Branches of the Eucalypt Tree: Comparison Between <i>Eucalyptus</i> and <i>Corymbia</i> Genomes
		5:00 p.m.	Golden Ballroom	Susan R. Strickler Boyce Thompson Institute	The Genome of the Tetraploid Arabica Coffee and its Diploid Ancestors
5:00 p.m.	Royal Palm Salon 5-6	William Wadlington University of Illinois at Urbana-Champaign	Genomic Analysis of the Sex Determining Region of the Sex Chromosomes in Spinach		
5:40 p.m.	Golden Ballroom	Karen S. Aitken CSIRO Agriculture and Food	Update on the Sugarcane Genome Sequence		
Mon, Jan 16	1:10 p.m.	Pacific Salon 6-7	Detlef Weigel Max Planck Institute for Developmental Biology	1001 Genomes Plus (1001G+)	
	6:10 p.m.	Royal Palm Salon 1-2	Detlef Weigel Max Planck Institute for Developmental Biology	Genomics of <i>A. thaliana</i> : Beyond Resequencing	
	6:30 p.m.	Towne, Meeting House	Nagendra K. Singh ICAR-National Research Centre on Plant Biotechnology	A Reference Genome of Mango (<i>Mangifera indica</i> L. cv Amrapali)	

	Date	Time	Location	Author	Title
Plant, Continued	Mon, Jan 16	6:35 p.m.	Pacific Salon 3	Florian Jupe Salk Institute for Biological Studies & Howard Hughes Medical Institute	Next Generation <i>Arabidopsis</i> Genomics
		6:50 p.m.	Golden Ballroom	R. Kelly Dawe University of Georgia	Validation of PacBio and NRGene Maize Genome Assemblies by BioNano Genome Mapping
		7:05 p.m.	Pacific Salon 3	Alex Harkess Donald Danforth Plant Science Center	Optical Maps Finish Homologous X and Y Sex Determination Regions in Asparagus
	Tue, Jan 17	11:10 a.m.	Towne, Meeting House	Prashant S. Hosmani Boyce Thompson Institute	ITAG3.0 Annotation for the New Tomato Reference Genome SL3.0
		2:20 p.m.	Royal Palm Salon 1-2	Michael Giolai Earlham Institute	Improved Methodology for Large Fragment Plant Resistance-Gene Capture
		5:30 p.m.	Royal Palm Salon 1-2	Bo Wang Cold Spring Harbor Laboratory	Unveiling the Complexity of Maize Transcriptome Using Single-Molecule Long-Read Sequencing
Wed, Jan 18	11:10 a.m.	Royal Palm Salon 5-6	Dario Copetti Arizona Genomics Institute	Development of Gap-Free Genome Assemblies to Capture and Exploit Rice Genetic Variation	
	11:30 a.m.	Sunset, Meeting House	Sachiko Isobe Kazusa DNA Research Institute	Status of Sweetpotato Genome Sequencing Under TRAS Collaboration: TRAS Sweetpotato Genome Sequencing Consortium	
Animal	Sat, Jan 14	8:05 a.m.	Royal Palm Salon 1-2	Heather M. Holl University of Florida	De novo Assembly of a Dromedary Camel
		8:05 a.m.	Esquire, Meeting House	Surya Saha Boyce Thompson Institute	Using Long Reads, Optical Maps and Long-Range Scaffolding to Improve the <i>Diaphorina citri</i> Genome
		8:45 a.m.	Royal Palm Salon 3-4	Tom Goldammer Leibniz Institute for Farm Animal Biology	Genome Biology of Maraena Whitefish (<i>Coregonus maraena</i>) for Preservation of Baltic Fish Biodiversity
		9:05 a.m.	Royal Palm Salon 1-2	Mark F. Richardson Deakin University	Vicpac 3.0: A New and Improved Alpaca Reference Genome
		10:15 a.m.	San Diego	Benjamin D. Rosen USDA ARS	Updating the Bovine Reference Genome Assembly
		11:10 a.m.	San Diego Ballroom	Alan L. Archibald University of Edinburgh	Exploiting Long Read Sequencing Technologies to Establish High Quality Highly Contiguous Pig Reference Genome Assemblies
		1:30 p.m.	San Diego	Kim C. Worley Baylor College of Medicine	Rambouillet Sheep Genomic Resources
		4:05 p.m.	Royal Palm Salon 3-4	Matthew A. Conte University of Maryland	A High Quality Assembly of the Nile Tilapia (<i>Oreochromis niloticus</i>) Genome Provides Insights into the Structure of Two Sex Determination Regions
	Sun, Jan 15	4:45 p.m.	San Diego	Christine G. Elsik University of Missouri	Annotating the New Bovine Reference Genome Assembly S
		8:00 a.m.	Sunset, Meeting House	Wesley Warren Washington University School of Medicine-McDonnell Genome Institute	An Improved Chicken Genome Reference: Recovery of Missing Autosomes and Addition of a New W Chromosome
8:20 a.m.		Sunset, Meeting House	Thibaut Hourlier European Molecular Biology Laboratory	Genome Annotation of the New Chicken Assembly Gallus_Gallus-5.0	
Mon, Jan 16	9:00 a.m.	Sunset, Meeting House	Richard Kuo University of Edinburgh	Iso-Seq Sequencing and the Chicken Genome Annotation	
	11:30 a.m.	Towne, Meeting House	Kim C. Worley Baylor College of Medicine	Update on Rambouillet Assembly, the v5.0 Reference, and Plans for FAANG RNA Sequencing	
Tue, Jan 17	7:00 p.m.	Sunrise, Meeting House	Thibaut Hourlier European Molecular Biology Laboratory	Goat Genome Assembly Annotation	
	5:00 p.m.	Towne, Meeting House	Matthias H. Weissensteiner Uppsala University	Going the Long (Molecule) Way: Detecting Structural Features Influencing Recombination Rate via SMRT-Seq and Optical Mapping in the Crow Genome	
Methods	Sun, Jan 15	2:30 p.m.	Royal Palm Salon 3-4	Adam Frankish Wellcome Trust Sanger Institute	Annotating Non-Coding Loci in Ensembl and Ensembl Genomes
	Mon, Jan 16	6:10 p.m.	Pacific Salon 1	Wenkai Jiang Novogene	De Novo Assembly of Plant and Animal Genomes: From Next Generation to Next-Next Generation
	Tue, Jan 17	11:10 a.m.	Golden West	Maria Nattestad Cold Spring Harbor Laboratory	Visualization and Analysis Tools for Comparing Genomes and Assemblies

Poster Presentations

	Author	Title
P0005	Yinping Jiao Cold Spring Harbor Laboratory	The Complex Sequence Landscape of Maize Revealed By Single Molecule Technologies
P0009	Etienne Bucher Institut de Recherche en Horticulture et Semences	The Complete Apple Genome: Evolutionary Events Revealed
P0011	Mathieu Fouché INRA	The Sweet Cherry Genome: A New Sequencing Project
P0013	Sachiko Isobe Kazusa DNA Research Institute	Status of Sweetpotato Genome Sequencing Under TRAS Collaboration
P0014	Thiruvarangan Ramaraj National Center for Genome Resources	Draft Assembly of Diploid A1-genome, <i>Gossypium herbaceum</i> cv. Wagad
P0019	Alyssa Burkhardt USDA	Improving Genomic Resources for the Detection of <i>Macrophomina phaseolina</i> Infection of Strawberry
P0020	Won Cheol Yim University of Nevada, Reno	Genome Sequencing of Common Ice Plant (<i>Mesembryanthemum crystallinum</i> L.)
P0039	Darlon V. Lantican University of the Philippines Los Baños	Genome-Guided EcoTILLING Approach Towards Improved Fatty Acid Biosynthesis in Coconut
P0041	Celine Chantry Darmon INRA	Toward a Better Understanding of Plant Genomes Structure: Combining NGS and Optical Mapping Technology to Improve the Sunflower Assembly
P0041	Hayde F. Galvez University of the Philippines Los Baños	A Hybrid Approach for Improved Genome Assembly of Coconut (<i>Cocos nucifera</i> L.) to Aid Development of Breeding Tools
P0063	Samathmika Ravi Institute of Bioinformatics and Applied Biotechnology	Efforts Towards Building a Reference Genome from Draft Assemblies of <i>Amaranthus hypochondriacus</i>
P0072	Sara Goodwin Cold Spring Harbor Laboratory	<i>De novo</i> Sequencing of the <i>Vitis vinifera</i> cv. Flame Seedless Genome using Single Pass Library Preparation from Swift Biosciences
P0406	Le Wang University of California, Davis	The Comparison of <i>Aegilops tauschii</i> Sequence Assembled By NRGene's DeNovoMAGIC and PacBio-Illumina Hybrid Assembly with the MaSuRCA Mega-Reads Algorithm
P0524	Robert King Rothamsted Research	The Complete Genome Sequence of a UK Strain (UK99) of <i>Fusarium culmorum</i>
P0529	Kyoung Su Kim Kangwon National University	<i>De Novo</i> Genome Sequencing and Analysis of Genome and Transcriptome of the Anthracnose Pathogen <i>Colletotrichum acutatum</i>
P0540	Jeong-Hwan Mun Myongji University	Toward the Rs2.0: Upgrade of the Radish Genome Based on Long-Read Sequencing and Optical Genome Mapping
P0557	Song Li Virginia Tech	Integrated Transcriptome and Proteome Analyses Reveal Cell Type-Specific Regulation of Alternative Splicing in <i>Arabidopsis</i>
P0607	Travis R. Wrightsman University of California, Riverside	Exploration of Transposable Element Families in the Novel Citrus Genome Fairchild
P0614	Sara Montanari University of California, Davis	New Genomic Tools for Pear: High Quality Genome Assembly and High Density SNP Array
P0624	Yilong Yang University of New Hampshire	<i>De novo</i> Assembly of the Diploid Strawberry <i>Fragaria linumae</i> Genome
P0635	Nagendra K. Singh ICAR-National Research Centre on Plant Biotechnology	A Reference Genome of Mango (<i>Mangifera indica</i> L. cv Amrapali)
P0645	Rick Masonbrink Iowa State University	Scnbase: A Community Resource for Soybean Cyst Nematode (<i>Heterodera glycines</i>) Genomics
P0688	Stefano Lonardi University of California	Assembly of Eleven Pseudomolecules Representing the Cowpea Genome Sequence
P0704	Christopher Cullis Case Western Reserve University	A Novel Inversion in the Chloroplast Genome of Marama (<i>Tylosema esculentum</i>)
P0720	Jinghua Shi BioNano Genomics	Accessing the Genetic Dark Matter: Using BioNano Technology to Identify Large-Scale Repeat Structures in Maize
P0747	Melina C. Mancini University of Campinas	Recovering a Region in Sugarcane through of the Sorghum Synteny
P0749	Claudio B. C. Silva University of Campinas	BAC Sequencing Revealing Complex Genomic Organization in Sugarcane and Synteny with Sorghum Genome in a QTL Region
P0751	Jisen Zhang Fujian Agriculture and Forestry University	Ultra High Density Mapping of the <i>Saccharum spontaneum</i> Genome
P0797	Prashant S. Hosmani Boyce Thompson Institute	ITAG3.0 Annotation for the New Tomato Reference Genome SL3.0
P0811	Elena Lopez Girona The James Hutton Institute	Use of a Self-compatible Diploid Potato Genome Assembly and a Mutant Collection for Forward Genetic Studies

	Author	Title
P0928	Jesse A. Mayer University of Nevada, Reno	Generating a Robust Genome and Transcriptome for Prickly Pear Cactus
P0939	Eibertus N. van Loo Wageningen University	The Chromosome Scaffold Based Quinoa Genome: Its Building and Its Use to Find the Non-Bitter Mutations in Quinoa
P0941	Peter J. Maughan Brigham Young University	PacBio and Hi-C Based Proximity-Guided Assembly of Amaranth Pseudo Chromosomes
P0944	Woojong Jang Seoul National University	Ten Bacterial Artificial Chromosome Sequences Reveal the Genome Characteristic and Structure of <i>Panax ginseng</i>
P0945	Joel Kuon Institute of Plant Sciences, ETH Zurich	Chromosome-Level Assembly of Farmer Preferred Cassava Varieties Using Single - Molecule Sequencing (SMRT) Technology and Chromosome-Conformation Capture
P0958	William J. Palmer University of California, Davis	Developing Foundational Genomic Resources For High Throughput Phenotyping Of Pistachio
P0961	Peng Jiang Duke University	<i>De novo</i> Assembly of an Ornamental Plant Genome - <i>Penstemon barbatus</i>
TBD	Christine G. Elsik University of Missouri	Annotating the New Bovine Reference Genome
P0975	Bradley W. Langhorst New England Biolabs	White Tailed Deer Genome Assembly Improvement: Moving Toward Named Chromosomes
P0976	Tsunemi Yamashita Arkansas Tech University	Characterization of Toxin Genes from a Scorpion with Mild Venom
P1012	Sylvie M.A. Quiniou USDA	Third Generation Sequencing: Unraveling the Genome and the Immunoglobulin Superfamily Genes in Catfish (<i>Ictalurus punctatus</i>)
P1016	Tom Goldammer Leibniz Institute for Farm Animal Biology	Genome Biology of Maraena Whitefish (<i>Coregonus maraena</i> , BLOCH, 1779) for Preservation of Baltic Fish Biodiversity
P1019	Matthew A. Conte University of Maryland	A High Quality Assembly of the Nile Tilapia (<i>Oreochromis niloticus</i>) Genome Provides Insights into the Structure of Two Sex Determination Regions
P1024	Samathmika Ravi Institute of Bioinformatics and Applied Biotechnology	Comparative Assembly of Mammalian Genomes: Water Buffalo
P1103	Wesley Warren Washington University School of Medicine	A Improved Chicken Genome Reference: Recovery of Missing Autosomes and Addition of a New W Chromosome
P1109	Deborah A. Triant University of Florida	Genome Assembly and Annotation of the Io Moth, <i>Automeris io</i> (Lepidoptera: Saturniidae)
P1113	Sarah B. Kingan PacBio	A High-Quality Genome Assembly of SMRT Sequences Reveals Long-Range Haplotype Structure in the Diploid Mosquito <i>Aedes aegypti</i>
P1114	Wesley Warren Washington University School of Medicine	Given the Continued Intense Interest in and Need for Improvement of the Chicken Genome Reference (<i>Gallus_gallus</i> -5.0) We Have Built a New Preliminary Version of the Chicken Genome (Temporarily Termed <i>Gallus_gallus</i> -6.0) Using Single Molecule Real-Time Tech
P1117	Thibaut Hourlier European Molecular Biology Laboratory	Chicken Annotation in Ensembl
P1142	Kim C. Worley Baylor College of Medicine	Rambouillet Sheep Genomic Resources
P1146	Kim C. Worley Baylor College of Medicine	The Rambouillet Sheep Reference Genome Project
P1161	Amanda Warr University of Edinburgh	High-Quality, Highly Contiguous Re-Assembly of the Pig Genome
P1162	Haibo Liu Iowa State University	Swine Transcriptome Characterization By Combined Iso-Seq and RNA-Seq for Annotating the Emerging Long Read-Based Reference Genome
P1181	Mark F. Richardson Deakin University	VicPac3.0: A New and Improved Alpaca Reference Genome
P0031	Nick Sisneros PacBio	Best Practices for Whole Genome Sequencing Using the Sequel System
P0082	Tyson A. Clark PacBio	Full-Length cDNA Sequencing on the PacBio Sequel Platform
P0457	Shengqiang Shu DOE Joint Genome Institute	Plant Genome Reannotation Using Nextgen Sequences
P0501	Gregory T. Concepcion PacBio	Phased Diploid Genome Assembly with Single Molecule, Real-Time Sequencing
P0513	Cheryl Heiner PacBio	Profiling Populations and Diversity of Gene Pools with Highly Accurate Single Molecule Reads
P0961	Alex R. Hastie BioNano Genomics	Genome-Wide, Highly Accurate and Sensitive Structural Variation Detection in Plants and Animals by Next-Generation Mapping

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