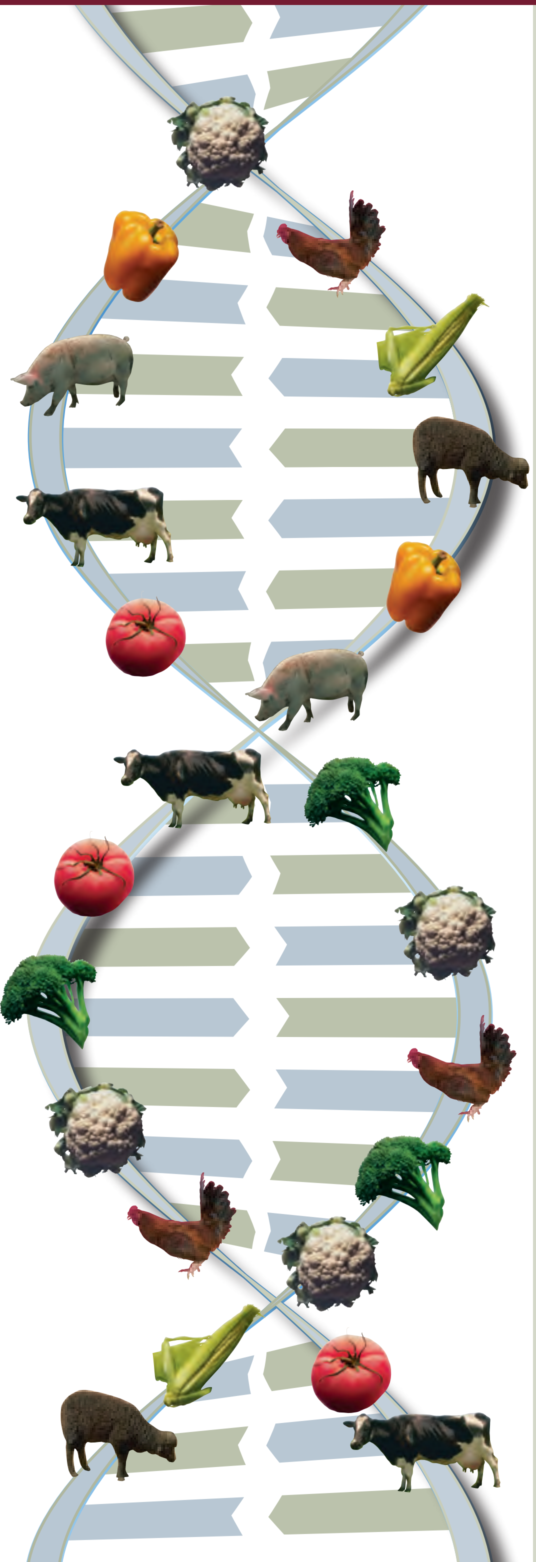
January 14-18, 2017
Town & Country Hotel
San Diego, CA

PLANT & ANIMAL GENOME XXV

THE INTERNATIONAL CONFERENCE ON THE STATUS OF PLANT & ANIMAL GENOME RESEARCH

FINAL PROGRAM & EXHIBIT GUIDE



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from earth to life

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Mark Your Calendar For:

PAG Asia 2017 – May 29-31, 2017 – Seoul, South Korea

PAG XXVI – January 13-17, 2018 – San Diego, CA

Plant & Animal Genome XXV
Registration & Meeting Schedule

Registration - ATLAS FOYER

Friday	January 13	12:00pm - 9:00pm
Saturday - Sunday	January 14-15	7:00am - 8:00pm
Monday	January 16	7:00am - 5:00pm
Tuesday	January 17	7:00am - 3:00pm
Wednesday	January 18	7:00am - 12:00pm

Plenary Session - ATLAS BALLROOM

Sunday	January 15	6:15pm - 7:00pm
Monday	January 16	8:00am - 10:00am
Tuesday-Wednesday	January 17-18	8:00am - 9:30am

Poster Access Hours – GRAND EXHIBIT HALL & LOWER LEVEL

Saturday	January 14	7:00am - 9:00pm
Sunday	January 15	7:00am - 9:00pm
Monday	January 16	7:00am - 9:00pm
Tuesday	January 17	7:00am - 3:00pm
Wednesday	January 18	7:00am - 12:00pm

ALL POSTERS MUST BE REMOVED BY 12:00PM WEDNESDAY, JANUARY 18.

Speaker Ready Room – TERRACE SALON 2

Friday	January 13	12:00pm - 8:00pm
Saturday - Tuesday	January 14-17	7:00am - 8:00pm
Wednesday	January 18	7:00am - 12:00pm

Poster Sessions - GRAND EXHIBIT HALL & LOWER LEVEL

Monday (Even Numbers)	January 16	10:00am - 11:30am
Monday (Odd Numbers)	January 16	3:00pm - 4:30pm

Exhibit Hours - GRAND EXHIBIT HALL

Sunday	January 15 **(Reception: 7:00-8:30)**	3:00pm - 8:30pm
Monday	January 16	9:30am - 5:00pm
Tuesday	January 17	9:30am - 3:00pm

Computer Room - CALIFORNIA

Friday	January 13	12:00pm - 10:00pm
Saturday - Tuesday	January 14-17	6:00am - 10:00pm
Wednesday	January 18	6:00am - 3:00pm

Computer Demonstrations: Computer system demonstrations will be conducted Sunday - Wednesday in the "computer room", located in the California Room, see Computer Demo schedule for times.

Welcome Reception - GRAND EXHIBIT HALL & LOWER LEVEL

Sunday	January 15	7:00pm - 8:30pm

Closing Banquet Dinner – GRAND EXHIBIT HALL

Wednesday	January 18	7:00pm - 12:00am

Meeting Schedule Table

	Friday January 13	Saturday January 14	Sunday January 15	Monday January 16	Tuesday January 17	Wednesday January 18
Poster Session Access		7:00-9:00	7:00-9:00	7:00-9:00	7:00-3:00	7:00-2:00
Registration (Atlas Foyer)	12:00-9:00	7:00-8:00	7:00-8:00	7:00-5:00	7:00-3:00	7:00-12:00
Continental Breakfast (Golden Ballroom)		7:00-8:00	7:00-8:00	7:00-8:00	7:00-8:00	7:00-8:00
Workshops		8:00-10:10	8:00-10:10			
Plenary Lectures (Town & Country)				8:00-10:00 DuPont Pioneer	8:00-9:30 DuPont Pioneer	8:00-9:30 DuPont Pioneer
Exhibits				9:30-5:00	9:30-3:00	Closed
Coffee Break		9:30-10:30 Atlas Foyer	9:30-10:30 Atlas Foyer	9:30-11:30 Exhibit Hall	9:30-10:30 Exhibit Hall	9:30-10:30 Atlas Foyer
Poster Session (Grand Exhibit Hall)				10:00-11:30 Even Numbers		
Workshops		10:20-12:30	10:20-12:30		10:20-12:30	10:20-5:00
Computer Demos (California Room)					10:30-12:40	
Lunch (Lion Fountain Courtyard & Grand Exhibit Hall)		12:30-1:30	12:30-1:30	12:00-12:50	12:30-1:30	12:30-1:30
Workshops		1:30-3:40	1:30-3:40	12:50-3:00	1:30-3:40	
Computer Demos (California Room)		1:30-3:50		12:50-3:00		
Exhibits			3:00-8:30 Reception: 7:00-8:30			
Coffee Break		3:00-4:00 Atlas Foyer	3:00-4:00 Atlas Foyer	3:00-5:00 Exhibit Hall	2:00-3:00 Exhibit Hall	
Poster Session (Grand Exhibit Hall)				3:00-4:30 Odd Numbers		
Workshops		4:00-6:10	4:00-6:10	6:10-8:20	4:00-6:10	
Plenary Lecture (Town & Country)			6:15-7:00 Pioneer DuPont			
Welcome Reception (Grand Exhibit Hall)			7:00-8:30			
Coffee Break				7:00-7:30		
Conference Banquet (Grand Exhibit Hall)						7:00-12:00

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Plenary Talks Schedule

Sponsored by: DuPont Pioneer

Sunday, January 15, 2017

6:15 pm - 7:00 pm **TOWN & COUNTRY BALLROOM**
Scott Hamilton Kennedy, Black Valley Films
"Food and Film: A Search for Nuance in the Struggle Between Art and Activism"

Monday, January 16, 2017

8:00 am - 9:45 am **TOWN & COUNTRY BALLROOM**
Clare M. Fraser, University of Maryland School of Medicine
"The Gut Microbiome in Health and Disease"

8:45 am - 9:30 am **TOWN & COUNTRY BALLROOM**
Rob Martienssen, HHMI-GBMF Cold Spring Harbor Laboratory
"Germline Reprogramming and Epigenetic Inheritance in Plants: How to Avoid Bad Karma"

Tuesday, January 17, 2017

8:00 am - 8:45 am **TOWN & COUNTRY BALLROOM**
Alan Cooper, University of Adelaide
"Ancient DNA Records of Genome Evolution"

8:45 am - 9:30 am **TOWN & COUNTRY BALLROOM**
Seth Bordenstein, Vanderbilt University
"Microbes and the Origin of Animal Species"

Wednesday, January 18, 2017

8:00 am - 8:45 am **TOWN & COUNTRY BALLROOM**
Rebecca N. Johnson, Australian Museum Research Institute
"Genomics and Wildlife Conservation"

8:45 am - 9:30 am **TOWN & COUNTRY BALLROOM**
Thomas Mitchell-Olds, Duke University
"Dissecting Genotype-Environment Interactions and Trait Correlations"

Computer Demos Schedule

Saturday - January 14, 2017

1:30pm - 3:40pm **Computer Demo 1 - CALIFORNIA**
Organizers: Monica C. Munoz-Torres, Lawrence Berkeley National Laboratory and Brian Smith-White, National Center for Biotechnology Information (NCBI/NLM/NIH)

1:30pm Pierre Larmande,IRD, UMR DIADE, Institut de Biologie Computationnelle
"The Agronomic Linked Data (AgroLD) Project" (C01)

1:45pm Célia Michotey,INRA - URGI
"Forest Tree GnpIS: an Information System Dedicated to Forest Tree Genetics, Genomics and Phenomics" (C02)

2:00pm Marco Moretto,Fondazione Edmund Mach
"Exploring Grapevine Gene Expression Patterns with Vespucci." (C03)

2:15pm Carol Lushbough,University of South Dakota
"Bio -TDS : BioQuery Tool Discovery System" (C04)

2:30pm Damien Leroux,MIAT, Institut National de la Recherche Agronomique
"Spell-QTL, a New Tool for QTL Analysis on Modern Datasets" (C05)

2:45pm Jorge Duitama,Universidad de los Andes
"Analysis of Genomic Variability within Inbred Populations with NGSEP" (C06)

3:00pm Lon Phan,NIH/NLM/NCBI
"NCBI Genomic Data Viewer" (C07)

3:15pm Richard J Challis,Edinburgh University
"Easymirror and Easyimport: Set up Your Own Ensembl Site in 2 Hours for Your Favourite Taxa" (C08)

12:50pm - 3:00pm **Computer Demo 2 - CALIFORNIA**
Organizers: Monica C. Munoz-Torres, Lawrence Berkeley National Laboratory and Brian Smith-White, National Center for Biotechnology Information (NCBI/NLM/NIH)

12:50pm Kelly Robbins,Cornell University
"GOBII: Genomic Open-source Breeding Informatics Initiative " (C09)

1:05pm Manuel Ruiz,CIRAD, UMR AGAP / CIAT
"Gigwa - Genotype Investigator for Genome-Wide Analyses." (C10)

1:20pm Annemarie Eckes,Earlham Institute
"The Brassica Information Portal: Towards Integrating Phenotype and Genotype Data." (C11)

1:35pm Guillaume Cornut,INRA - URGI
"GnpIS-Ephesis, Plant Phenotype Field Experimentations Resources – Data Discovery and Dataset Building Use Cases." (C12)

1:50pm Richard Michael Bruskiewich,STAR Informatics / Delphinai Corporation
"Knowledge.Bio: A Web Application for Collaboratively Building and Exploring Networks of Biological Relationships." (C13)

2:05pm Clay Birkett,USDA-ARS
"The Triticeae Toolbox (T3): Connecting Phenotypes, Genotypes, and Biological Knowledge" (C14)

2:20pm Matthias Lange,Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Gatersleben
"e!Dal - a Open Source Software to Store, Share and Publish Research Data" (C15)

2:35pm Jeffrey Grover,University of Arizona
"User-Friendly Whole Genome DNA Methylation Analysis With FlowGe" (C16)

10:30am - 12:40pm **Computer Demo 3 - CALIFORNIA**
Organizers: Monica C. Munoz-Torres, Lawrence Berkeley National Laboratory and Brian Smith-White, National Center for Biotechnology Information (NCBI/NLM/NIH)

10:30am Taner Z. Sen,USDA -ARS / GrainGenes
"GrainGenes: Supporting the Small Grains Community" (C17)

10:50am Hiromasa Ono,Database Center for Life Science
"RefEx, a Reference Gene Expression Dataset As a Web Tool for the Functional Analysis of Genes." (C18)

11:10am Sook Jung,Washington State University
"Newly Designed Genome Database for Rosaceae (GDR)" (C19)

11:30am Felipe A. Simão,University of Geneva Medical School & Swiss Institute of Bioinformatics
"Quality Assessment Using BUSCO v2" (C20)

11:50am Peifen Zhang,Carnegie Institution for Science
"PMN, A Unified Resource For Plant Metabolism" (C21)

12:10pm Austin Meier,Oregon State University
"Planteome: Reference Ontologies and a Platform for Integrative Plant Genomics" (C22)

10:30am - 12:40pm **Computer Demo 4 - CALIFORNIA**
Organizers: Monica C. Munoz-Torres, Lawrence Berkeley National Laboratory and Brian Smith-White, National Center for Biotechnology Information (NCBI/NLM/NIH)

10:30am Felix Shaw,Earlham Institute
"COPO: A Data Stewardship Platform for Plant Scientists" (C23)

10:45am Prashant S Hosmani,Boyce Thompson Institute
"Systems Biology Resources for the Citrusgreening Disease Complex." (C24)

11:00am Locedie Mansueto,International Rice Research Institute
"SNP-Seek Resource for Rice Research" (C25)

11:15am Ming Chen,University of Tennessee
"Elasticsearch Indexing/Search and Expression Data Visualization with Two New Tripal Extension Modules" (C26)

11:30am Christine Tranchant-Dubreuil,IRD - UMR DIADE
"Toggle-3 : A Framework to Build Quickly Pipelines and to Perform Large-Scale NGS Analysis" (C27)

11:45am Frederic B. Bastian,SIB Swiss Institute of Bioinformatics - University of Lausanne
"Bgee: Database and R Package for Retrieving the Preferred Anatomical Expression Localization of a List of Genes, or of a Single Gene, in Animals." (C28)

12:00pm Hans Vasquez-Gross,University of California Davis
"Using the Wheat Tilling Resource to Find Mutations of Interest" (C29)

12:15pm Reinhard Simon,International Potato Center (CIP)
"Using the Public Plant Breeding API (BrAPI) to Access Data from the Statistical Platform R" (C30)

Industry Workshop Schedule

10x Genomics	Monday, Jan 16	12:50 pm - 3:00 pm	Pacific Salon 1
Addressing the Challenges of Nucleic Acid Extraction, Quantitation and Amplification	Tuesday, Jan 17	1:30 pm - 3:40 pm	Golden West
AgriPlex Genomics – Bridging the Gap Between Singleplex Screening and High Density Arrays	Monday, Jan 16	12:50 pm - 3:00 pm	Sunrise - Meeting House
BioNano Genomics Education Workshop: Next-Generation Mapping Reveals Large Structural Variations: So What?	Monday, Jan 16	6:10 pm - 8:20 pm	Pacific Salon 3
Computomics - From genomes to insight	Monday, Jan 16	6:10 pm - 8:20 pm	Royal Palm Salon 1-2
Doriane Research Software And Consulting: Why build An All-In-One Tool For Collaborative Work	Tuesday, Jan 17	4:00 pm - 6:10 pm	Pacific Salon 1
Douglas Scientific - Accelerating Trait Discovery	Monday, Jan 16	6:10 pm - 8:20 pm	San Diego
Dovetail Genomics - In vitro Proximity Ligation - The Path to Better Genomes	Tuesday, Jan 17	1:30 pm - 3:40 pm	Pacific Salon 1
Examples of New NGS-Enabled Plant Research and Opportunities for Global Gen Banking Partnerships	Monday, Jan 16	6:10 pm - 8:20 pm	Sunset - Meeting House
For Smarter Genomics in Agriculture, Partnering is the Answer	Monday, Jan 16	12:50 pm - 3:00 pm	Golden West
GeneSeek, A Neogen Company - Genomic Solutions for Agri-Research	Monday, Jan 16	12:50 pm - 3:00 pm	Pacific Salon 2
Genestack - Applying High-throughput Bioinformatics Technologies to Crop Reserach	Tuesday, Jan 17	1:30 pm - 3:40 pm	Sunset - Meeting House
Illumina, Inc.	Tuesday, Jan 17	4:00 pm - 6:10 pm	Golden West
KeyGene: Expediting Innovation in Agriculture	Monday, Jan 16	12:50 pm - 3:00 pm	Royal Palm Salon 3-4
Knowledge Management and Data Integration in Plant Research	Monday, Jan 16	6:10 pm - 8:20 pm	Pacific Salon 2
Kyazma's JoinMap and MapQTL Demonstration	Monday, Jan 16	12:50 pm - 3:00 pm	Pacific Salon 4-5 (2nd Floor)
Lexogen - QuantSeq 3' mRNA-Seq technology as an efficient tool for gene expression profiling	Tuesday, Jan 17	1:30 pm - 3:40 pm	Sunrise - Meeting House
Metagenomics & more – bioinformatics solutions for plant and animal research	Monday, Jan 16	12:50 pm - 3:00 pm	Royal Palm Salon 5-6
MYcroarray - Advances in Target Capture for NGS	Tuesday, Jan 17	1:30 pm - 3:40 pm	Royal Palm Salon 1-2
NAPPN - Technologies and Applications in Digital Plant Phenotyping	Tuesday, Jan 17	1:30 pm - 3:40 pm	Pacific Salon 2
New England Biolabs - New NEBNext methods to enhance your NGS performance	Monday, Jan 16	12:50 pm - 3:00 pm	Royal Palm Salon 1-2
Novogene: Latest NGS Applications in Agricultural Research	Monday, Jan 16	6:10 pm - 8:20 pm	Pacific Salon 1
NRGene - From Multiple genome assemblies to accurate pangenome view	Tuesday, Jan 17	1:30 pm - 3:40 pm	Golden Ballroom
NRGene DeNovoMAGIC 3.0 - Complete assembly & phasing of heterozygote and polyploid genomes	Monday, Jan 16	6:10 pm - 8:20 pm	Golden Ballroom
NuGEN - Trait to Table: NGS Solutions to Advance Agrigenomics	Tuesday, Jan 17	1:30 pm - 3:40 pm	Royal Palm Salon 5-6
PacBio Workshop: SMRT Sequencing for Complete Genomes	Monday, Jan 16	12:50 pm - 3:00 pm	San Diego
Translational Agriculture: Opportunities, Technologies and Products	Tuesday, Jan 17	1:30 pm - 3:40 pm	Royal Palm Salon 3-4

PLANT AND ANIMAL GENOME XXV CONFERENCE
Workshop List - By Name

4337	**10x Genomics**	**16-Jan-17**	**12:50 pm**	**-3:00 pm**	**Sara Agee Le**	**Pacific Salon 1**
4161	**Abiotic Stress**	**15-Jan-17**	**10:30 am**	**-12:40 pm**	**Henry T. Nguyen**	**Golden Ballroom**
4158	**Addressing the Challenges of Nucleic Acid Extraction,**	**17-Jan-17**	**1:30 pm**	**-3:40 pm**	**Mary Jo Martinson**	**Golden West**
4413	**AgriPlex Genomics**	**16-Jan-17**	**12:50 pm**	**-3:00 pm**	**Scott Weigel**	**Sunrise - Meeting House**
4162	**Allele Mining**	**14-Jan-17**	**1:30 pm**	**-3:40 pm**	**Jeremy D. Edwards**	**Pacific Salon 2**
4163	**Analysis of Complex Genomes**	**14-Jan-17**	**1:30 pm**	**-3:40 pm**	**Boulos Chalhoub**	**Golden Ballroom**
4164	**Animal Epigenetics**	**17-Jan-17**	**1:30 pm**	**-3:40 pm**	**Hasan Khatib**	**San Diego**
4165	**Animal Genomics and Adaptation to Climate Change**	**18-Jan-17**	**10:30 am**	**-12:40 pm**	**Susan J. Lamont**	**Sunrise - Meeting House**
4166	**Aquaculture**	**14-Jan-17**	**8:00 am**	**-6:10 pm**	**Nathan Campbell**	**Royal Palm Salon 3-4**
4167	**Arabidopsis Information Portal & Intl Arabidopsis Informatics Consortium**	**16-Jan-17**	**12:50 pm**	**-3:00 pm**	**Christopher D. Town**	**Pacific Salon 6-7 (2nd Floor)**
4168	**Arthropod Genomics**	**14-Jan-17**	**8:00 am**	**-10:10 am**	**Lindsey Perkin**	**Esquire - Meeting House**
4169	**Avian Genomics - Going Wild!**	**17-Jan-17**	**4:00 pm**	**-6:10 pm**	**Robert H. S. Kraus**	**Towne - Meeting House**
4170	**Banana Genomics**	**17-Jan-17**	**10:30 am**	**-12:40 pm**	**Mathieu Rouard**	**Pacific Salon 6-7 (2nd Floor)**
4172	**Bioenergy Grass Genomics**	**14-Jan-17**	**4:00 pm**	**-6:10 pm**	**Kankshita Swaminathan**	**Pacific Salon 2**
4173	**Bioinformatics**	**17-Jan-17**	**10:30 am**	**-12:40 pm**	**Tatiana Tatusova**	**Golden West**
4140	**BioNano Genomics**	**16-Jan-17**	**6:10 pm**	**-8:20 pm**	**Gail Lamangan**	**Pacific Salon 3**
4174	**Brachypodium Genomics**	**17-Jan-17**	**10:30 am**	**-12:40 pm**	**David F. Garvin**	**Pacific Salon 2**
4175	**Brassicas**	**14-Jan-17**	**10:30 am**	**-12:40 pm**	**Ian Bancroft**	**Pacific Salon 2**
4176	**Buffalo genome**	**14-Jan-17**	**10:30 am**	**-12:40 pm**	**John Williams**	**Royal Palm Salon 1-2**
4177	**Cacao Advanced Omics Workshop**	**15-Jan-17**	**10:30 am**	**-12:40 pm**	**Siela Maximova**	**Royal Palm Salon 3-4**
4179	**Cassava Genomics**	**17-Jan-17**	**4:00 pm**	**-6:10 pm**	**Steve Rounsley**	**Sunrise - Meeting House**
4180	**Cat & Dog Workshop**	**15-Jan-17**	**10:30 am**	**-12:40 pm**	**Barbara Gandolfi**	**Royal Palm Salon 5-6**
4181	**Cattle/Sheep/Goat 1**	**14-Jan-17**	**1:30 pm**	**-6:10 pm**	**Jared E. Decker**	**San Diego**
4182	**Cattle/Sheep/Goat 2**	**15-Jan-17**	**8:00 am**	**-12:40 pm**	**Jared E. Decker**	**San Diego**
4183	**Cattle/Swine**	**14-Jan-17**	**8:00 am**	**-12:40 pm**	**Jared E. Decker**	**San Diego**
4171	**Challenges and Opportunities in Plant Science Data Management - an International Workshop**	**14-Jan-17**	**4:00 pm**	**-6:10 pm**	**Darwin Campbell**	**Pacific Salon 4-5 (2nd Floor)**
4184	**Citrus Genome**	**14-Jan-17**	**1:30 pm**	**-3:40 pm**	**Concetta Licciardello**	**Pacific Salon 6-7 (2nd Floor)**
4188	**Coffee Genomics**	**15-Jan-17**	**4:00 pm**	**-6:10 pm**	**Marcela Yepes**	**Pacific Salon 3**
4189	**Comparative Genomics**	**15-Jan-17**	**8:00 am**	**-10:10 am**	**Yong Q. Gu**	**Golden West**
4190	**Components of Apomixis**	**17-Jan-17**	**4:00 pm**	**-6:10 pm**	**Emidio Albertini**	**Esquire - Meeting House**
4191	**Compositae**	**17-Jan-17**	**1:30 pm**	**-3:40 pm**	**John M. Burke**	**Pacific Salon 4-5 (2nd Floor)**
4192	**Computational Gene Discovery**	**15-Jan-17**	**10:30 am**	**-12:40 pm**	**Mark Borodovsky**	**Pacific Salon 3**
	Computer Demo 1	**14-Jan-17**	**1:30 pm**	**-3:40 pm**	**Monica C. Munoz-Torres**	**California**
	Computer Demo 2	**16-Jan-17**	**12:50 pm**	**-3:00 pm**	**Monica C. Munoz-Torres**	**California**
	Computer Demo 3	**17-Jan-17**	**10:30 am**	**-12:40 pm**	**Monica C. Munoz-Torres**	**California**
	Computer Demo 4	**18-Jan-17**	**10:30 am**	**-12:40 pm**	**Monica C. Munoz-Torres**	**California**
4333	**Computomics - From genomes to insight**	**16-Jan-17**	**6:10 pm**	**-8:20 pm**	**Venkatesh Balakrishnan**	**Royal Palm Salon 1-2**
4249	**Connecting Crop Phenotype Data**	**14-Jan-17**	**10:30 am**	**-12:40 pm**	**Clay Birkett**	**Golden Ballroom**
4193	**Cool Season Legumes**	**14-Jan-17**	**1:30 pm**	**-3:40 pm**	**Kirstin Bett**	**Pacific Salon 1**
4320	**Crop Evolution Genomics & Future Agricultural Productivity**	**14-Jan-17**	**1:30 pm**	**-3:40 pm**	**Shahal Abbo**	**Esquire - Meeting House**
4194	**Crop Genomics for Global Food Security**	**17-Jan-17**	**4:00 pm**	**-6:10 pm**	**Antonio Costa De Oliveira**	**Golden Ballroom**
4195	**CSSA: Translational Genomics**	**14-Jan-17**	**8:00 am**	**-10:10 am**	**Robert M. Stupar**	**Pacific Salon 1**
4196	**Cucurbit Genomics**	**15-Jan-17**	**4:00 pm**	**-6:10 pm**	**Yaakov (Kobi) Tadmor**	**Pacific Salon 4-5 (2nd Floor)**
4198	**CyVerse - Software, Tools, and Services for Data-Driven Discovery**	**16-Jan-17**	**6:10 pm**	**-8:20 pm**	**Jason Williams**	**California**
4244	**CyVerse Education: Scaling Genomics and Data Science for the Biology Classroom**	**14-Jan-17**	**8:00 am**	**-10:10 am**	**Dave Micklos**	**California**
4325	**Data Resource Sustainability and Funding**	**18-Jan-17**	**10:30 am**	**-2:00 pm**	**Tanya Z. Berardini**	**Pacific Salon 1**
4199	**Degraded DNA and Paleogenomics**	**15-Jan-17**	**1:30 pm**	**-3:40 pm**	**Greger Larson**	**Pacific Salon 3**
4200	**Development and Application of Transgenic Technology in Agriculture**	**15-Jan-17**	**8:00 am**	**-10:10 am**	**Ashok Shrawat**	**Royal Palm Salon 3-4**
4317	**DivSeek – Addressing the challenges and opportunities for information and data sharing associated with plant germplasm**	**18-Jan-17**	**10:30 am**	**-12:40 pm**	**Ruth Bastow**	**Pacific Salon 2**
4201	**Domestication Genomics**	**15-Jan-17**	**4:00 pm**	**-6:10 pm**	**Briana L. Gross**	**Pacific Salon 2**
4403	**Doriane Research Software And Consulting**	**17-Jan-17**	**4:00 pm**	**-6:10 pm**	**Tristan Duminil**	**Pacific Salon 1**
4135	**Douglas Scientific - Accelerating Trait Discovery**	**16-Jan-17**	**6:10 pm**	**-8:20 pm**	**Jill Walerius**	**San Diego**
4143	**Dovetail Genomics - In vitro Proximity Ligation**	**17-Jan-17**	**1:30 pm**	**- 3:40 pm**	**Michelle Vierra**	**Pacific Salon 1**
4202	**Ecological Genomics**	**14-Jan-17**	**10:30 am**	**-12:40 pm**	**Katrina Dlugosch**	**Royal Palm Salon 5-6**
4203	**Engineering NUE**	**14-Jan-17**	**10:30 am**	**-12:40 pm**	**David A. Lightfoot**	**Pacific Salon 4-5 (2nd Floor)**
4204	**EPIC: the Plant Epigenome Project**	**18-Jan-17**	**10:30 am**	**-12:40 pm**	**Craig Pikaard**	**San Diego**
4205	**Equine 1**	**14-Jan-17**	**1:30 pm**	**-6:10 pm**	**Carrie J. Finno**	**Royal Palm Salon 5-6**
4206	**Equine 2**	**15-Jan-17**	**8:00 am**	**-10:10 am**	**Carrie J. Finno**	**Royal Palm Salon 5-6**

4207	**Evolution of Genome Size**	**14-Jan-17**	**8:00 am**	**-10:10 am**	**William S. Sanders**	**Golden West**
4138	**Examples of New NGS-Enabled Plant Research and Opportunities for Global Gen Banking Partnerships**	**16-Jan-17**	**6:10 pm**	**-8:20 pm**	**Johan Christiaanse**	**Sunset - Meeting House**
4208	**Exploring Phytobiomes**	**18-Jan-17**	**10:30 am**	**-12:40 pm**	**Kellye Eversole**	**Royal Palm Salon 3-4**
4322	**Farm Animal Genome Editing**	**15-Jan-17**	**4:00 pm**	**-6:10 pm**	**C. Bruce Whitelaw**	**Esquire - Meeting House**
4209	**Flax Genomics**	**18-Jan-17**	**10:30 am**	**-12:40 pm**	**Sylvie Cloutier**	**Towne - Meeting House**
4160	**For Smarter Genomics in Agriculture, Partnering is the Answer**	**16-Jan-17**	**12:50 pm**	**-3:00 pm**	**Delaney Wermuth**	**Golden West**
4210	**Forage, Feedstocks & Turf**	**14-Jan-17**	**8:00 am**	**-10:10 am**	**German Spangenberg**	**Pacific Salon 4-5 (2nd Floor)**
4211	**Forest Tree**	**15-Jan-17**	**8:00 am**	**-6:10 pm**	**Amy Brunner**	**Sunrise - Meeting House**
4212	**Fruit/Nuts**	**14-Jan-17**	**8:00 am**	**-12:40 pm**	**Veronique Decroocq**	**Pacific Salon 3**
4213	**Functional Annotations of Animal Genomes (FAANG)**	**16-Jan-17**	**6:10 pm**	**-8:20 pm**	**Huaijun Zhou**	**Golden West**
4214	**Functional Genomics**	**15-Jan-17**	**10:30 am**	**-12:40 pm**	**David A. Lightfoot**	**Pacific Salon 1**
4215	**Functional Genomics of C_4 and CAM photosynthesis**	**14-Jan-17**	**10:30 am**	**-12:40 pm**	**Thomas P. Brutnell**	**Towne - Meeting House**
4216	**Fungal Genomics**	**15-Jan-17**	**4:00 pm**	**-6:10 pm**	**Stephen B. Goodwin**	**Royal Palm Salon 3-4**
4218	**Gene Expression Analysis**	**17-Jan-17**	**4:00 pm**	**-6:10 pm**	**David W. Galbraith**	**Royal Palm Salon 1-2**
4219	**Gene Introgression**	**15-Jan-17**	**8:00 am**	**-10:10 am**	**Julie King**	**Pacific Salon 2**
4146	**GeneSeek, A Neogen Company - Genomic Solutions for Agri-Research**	**16-Jan-17**	**12:50 pm**	**-3:00 pm**	**Jeremy Walker**	**Pacific Salon 2**
4338	**Genestack - Applying High-throughput Bioinformatics Technologies to Crop Reserach**	**17-Jan-17**	**1:30 pm**	**-3:40 pm**	**Kalina Cetnar**	**Sunset - Meeting House**
4220	**Genome annotation resources at the EBI**	**15-Jan-17**	**8:00 am**	**-12:40 pm**	**Sandra Orchard**	**California**
4217	**Genome Annotation with Galaxy**	**17-Jan-17**	**4:00 pm**	**-6:10 pm**	**Dave Clements**	**California**
4316	**Genome Database for Rosaceae Training**	**14-Jan-17**	**4:00 pm**	**-6:10 pm**	**Dorrie Main**	**California**
4321	**Genome-wide variation in rhinoceros species for evolutionary and conservation assessments**	**17-Jan-17**	**10:30 am**	**-12:40 pm**	**Oliver Ryder**	**Royal Palm Salon 5-6**
4222	**Genomic features and chromosome functionality**	**14-Jan-17**	**10:30 am**	**-12:40 pm**	**Xiyin Wang**	**Sunrise - Meeting House**
4223	**Genomic Selection and Genome-Wide Association Studies**	**14-Jan-17**	**4:00 pm**	**-6:10 pm**	**Jianming Yu**	**Golden West**
4224	**Genomics of Genebanks**	**14-Jan-17**	**10:30 am**	**-12:40 pm**	**Christopher M. Richards**	**Pacific Salon 1**
4225	**Genomics of Non-Classical Model Animals**	**15-Jan-17**	**10:30 am**	**-12:40 pm**	**Aaron Avivi**	**Pacific Salon 4-5 (2nd Floor)**
4226	**Genomics of Plant Development**	**15-Jan-17**	**4:00 pm**	**-6:10 pm**	**Khalid Meksem**	**Pacific Salon 6-7 (2nd Floor)**
4227	**Genomics of Tissue Regeneration in Plants and Animals**	**16-Jan-17**	**12:50 pm**	**-3:00 pm**	**Moshe Reuveni**	**Esquire - Meeting House**
4228	**Genomics-Assisted Breeding**	**17-Jan-17**	**10:30 am**	**-12:40 pm**	**Rajeev K Varshney**	**Town and Country**
4229	**GMOD**	**18-Jan-17**	**10:30 am**	**-2:30 pm**	**Scott Cain**	**Golden West**
4230	**Graft Genetics and Genomics**	**15-Jan-17**	**10:30 am**	**-12:40 pm**	**Gan-Yuan Zhong**	**Towne - Meeting House**
4231	**Gramene Database: A resource for comparative plant genomics, pathways and phylogenomics analyses**	**17-Jan-17**	**1:30 pm**	**-3:40 pm**	**Doreen Ware**	**California**
4232	**Grape Genome Initiative**	**15-Jan-17**	**1:30 pm**	**-3:40 pm**	**Grant R. Cramer**	**Pacific Salon 6-7 (2nd Floor)**
4234	**Grasslands (Lolium Genome Initiative)**	**14-Jan-17**	**10:30 am**	**-12:40 pm**	**Reed E. Barker**	**Esquire - Meeting House**
4235	**Host-Microbe Interactions**	**17-Jan-17**	**4:00 pm**	**-6:10 pm**	**Brett Tyler**	**Sunset - Meeting House**
4319	**Hybridization, heterosis and balancing selection**	**17-Jan-17**	**10:30 am**	**-12:40 pm**	**Eyal Fridman**	**Sunset - Meeting House**
4147	**Illumina, Inc.**	**17-Jan-17**	**4:00 pm**	**-6:10 pm**	**Lauren Brock**	**Golden West**
4236	**Increasing Genetic Gains for Food Security in the Developing World**	**17-Jan-17**	**10:30 am**	**-1:00 pm**	**Angela Records**	**Golden Ballroom**
4237	**Integrated Breeding Platform: Tools, Databases and Applications for Plant Breeding**	**16-Jan-17**	**12:50 pm**	**-3:00 pm**	**Graham McLaren**	**Golden Ballroom**
4238	**International Cotton Genome Initiative (ICGI)**	**15-Jan-17**	**4:00 pm**	**-6:10 pm**	**John Z. Yu**	**Sunset - Meeting House**
4239	**International Goat Genome Consortium**	**16-Jan-17**	**5:00 pm**	**-8:00 pm**	**Gwenola Tosser-Klopp**	**Sunrise - Meeting House**
4242	**International Sheep Genomics Consortium**	**16-Jan-17**	**11:30 am**	**-3:00 pm**	**Noelle Cockett**	**Towne - Meeting House**
4243	**International Wheat Genome Sequencing Consortium (IWGSC)**	**14-Jan-17**	**8:00 am**	**-10:10 am**	**Kellye Eversole**	**Town and Country**
4221	**Interoperability and Federation Across Bioinformatic Platforms and Resources**	**14-Jan-17**	**10:30 am**	**-12:40 pm**	**Eric Lyons**	**California**
4241	**IRIC: Rice Informatics for the Global Community**	**18-Jan-17**	**10:30 am**	**-12:40 pm**	**Kenneth L. McNally**	**Royal Palm Salon 5-6**
4245	**IWGSC - Standards and Protocols**	**17-Jan-17**	**1:30 pm**	**-6:10 pm**	**Jane Rogers**	**Pacific Salon 3**
4246	**JBrowse, a Next Generation Genome Browser**	**15-Jan-17**	**1:30 pm**	**-3:40 pm**	**Scott Cain**	**California**
4150	**KeyGene: Expediting Innovation in Agriculture**	**16-Jan-17**	**12:50 pm**	**-3:00 pm**	**Sireen Khan**	**Royal Palm Salon 3-4**
4335	**Knowledge Management and Data Integration in Plant Research**	**16-Jan-17**	**6:10 pm**	**-8:20 pm**	**Mercedes Ames Sevillano**	**Pacific Salon 2**
4151	**Kyazma's JoinMap and MapQTL Demonstration**	**16-Jan-17**	**12:50 pm**	**-3:00 pm**	**Johan Van Ooijen**	**Pacific Salon 4-5 (2nd Floor)**
4247	**Legumes**	**14-Jan-17**	**8:00 am**	**-10:10 am**	**Marc Libault**	**Royal Palm Salon 5-6**
4336	**Lexogen - QuantSeq 3' mRNA-Seq technology as an efficient tool for gene expression profiling**	**17-Jan-17**	**1:30 pm**	**-3:40 pm**	**Jekaterina Aleksejeva**	**Sunrise - Meeting House**
4248	**Maize**	**14-Jan-17**	**1:30 pm**	**-3:40 pm**	**Patrick S. Schnable**	**Golden West**

4250	**Mango genomics**	**16-Jan-17**	**6:10 pm**	**-8:30 pm**	**Amir Sherman**	**Towne - Meeting House**
4159	**Metagenomics & more – bioinformatics solutions for plant and animal research**	**16-Jan-17**	**12:50 pm**	**-3:00 pm**	**Nonna Druker**	**Royal Palm Salon 5-6**
4251	**Mutation Screening**	**14-Jan-17**	**10:30 am**	**-12:40 pm**	**Abdel Bendahmane**	**Golden West**
4153	**MYcroarray - Advances in Target Capture for NGS**	**17-Jan-17**	**1:30 pm**	**-3:40 pm**	**Alison Devault**	**Royal Palm Salon 1-2**
4157	**NAPPN - Technologies and Applications in Digital Plant Phenotyping**	**17-Jan-17**	**1:30 pm**	**-3:40 pm**	**Todd M. DeZwaan, PhD**	**Pacific Salon 2**
4252	**National Plant Genome Initiative Workshop - Challenges and Opportunities in High-Throughput Phenotyping and Data Management**	**15-Jan-17**	**1:30 pm**	**-3:40 pm**	**Jack K. Okamuro**	**San Diego**
4253	**NCBI Genome Resources**	**16-Jan-17**	**12:50 pm**	**-3:00 pm**	**Kim D. Pruitt**	**Sunset - Meeting House**
4254	**New Approaches for Developing Disease Resistance in Cereals**	**15-Jan-17**	**8:00 am**	**-10:10 am**	**Jesse Poland**	**Pacific Salon 4-5 (2nd Floor)**
4323	**New breeding technologies: Prospects and regulatory hurdles**	**15-Jan-17**	**4:00 pm**	**-6:10 pm**	**Thorben Sprink**	**Royal Palm Salon 1-2**
4411	**New England Biolabs - New NEBNext methods to enhance your NGS performance**	**16-Jan-17**	**12:50 pm**	**-3:00 pm**	**Kari Goodwin**	**Royal Palm Salon 1-2**
4255	**Next Generation Genome Annotation and Analysis**	**14-Jan-17**	**4:00 pm**	**-6:10 pm**	**Carson Holt**	**Sunrise - Meeting House**
4256	**Non-coding RNA**	**15-Jan-17**	**1:30 pm**	**-3:40 pm**	**Jan Gorodkin**	**Royal Palm Salon 3-4**
4257	**Non-Seed Plants**	**14-Jan-17**	**4:00 pm**	**-6:10 pm**	**Stefan A. Rensing**	**Towne - Meeting House**
4395	**NRGene - From Multiple genome assemblies to accurate pangenome view**	**17-Jan-17**	**1:30 pm**	**-3:40 pm**	**Moran Ofer**	**Golden Ballroom**
4155	**NRGene DeNovoMAGIC 3.0 - Complete assembly & phasing of heterozygote and polyploid genomes**	**16-Jan-17**	**6:10 pm**	**-8:20 pm**	**Moran Ofer**	**Golden Ballroom**
4258	**NRSP-8 Animal Genome**	**15-Jan-17**	**1:30 pm**	**-6:10 pm**	**Huaijun Zhou**	**Golden West**
4331	**NuGEN - Trait to Table: NGS Solutions to Advance Agrigenomics**	**17-Jan-17**	**1:30 pm**	**-3:40 pm**	**Kate Karfilis**	**Royal Palm Salon 5-6**
4259	**Oats**	**14-Jan-17**	**4:00 pm**	**-6:10 pm**	**Eric N. Jellen**	**Pacific Salon 6-7 (2nd Floor)**
4261	**Organellar Genetics**	**15-Jan-17**	**10:30 am**	**-12:40 pm**	**Michael J. Havey**	**Pacific Salon 6-7 (2nd Floor)**
4262	**Ornamentals**	**15-Jan-17**	**1:30 pm**	**-3:40 pm**	**Mohammed Bendahmane**	**Esquire - Meeting House**
4156	**PacBio Workshop: SMRT Sequencing for Complete Genomes**	**16-Jan-17**	**12:50 pm**	**-3:00 pm**	**Donal Murphy**	**San Diego**
4263	**Palm Genetics and Genomics**	**15-Jan-17**	**1:30 pm**	**-3:40 pm**	**Frederique Aberlenc-Bertossi**	**Towne - Meeting House**
4264	**Perennial Grasses**	**17-Jan-17**	**4:00 pm**	**-6:10 pm**	**Malay C. Saha**	**Pacific Salon 2**
4197	**Planning, Executing and Cultivating Broader Impact Programs: Tools, Communities**	**17-Jan-17**	**10:30 am**	**-12:40 pm**	**Michael D. Gonzales**	**Esquire - Meeting House**
4265	**Plant Chromosome Biology**	**15-Jan-17**	**10:30 am**	**-12:40 pm**	**Fangpu Han**	**Pacific Salon 1**
4266	**Plant Cytogenetics**	**15-Jan-17**	**1:30 pm**	**-3:40 pm**	**James Higgins**	**Pacific Salon 4-5 (2nd Floor)**
4267	**Plant Dormancy Workshop**	**17-Jan-17**	**4:00 pm**	**-6:10 pm**	**Anne Fennell**	**Royal Palm Salon 3-4**
4268	**Plant Genome Engineering**	**15-Jan-17**	**1:30 pm**	**-3:40 pm**	**Dan Voytas**	**Town and Country**
4269	**Plant Interactions with Pests and Pathogens**	**14-Jan-17**	**1:30 pm**	**-3:40 pm**	**Christie Williams**	**Sunrise - Meeting House**
4270	**Plant Molecular Breeding**	**14-Jan-17**	**1:30 pm**	**-3:40 pm**	**Jinguo Hu**	**Pacific Salon 3**
4271	**Plant Phenotypes**	**15-Jan-17**	**8:00 am**	**-10:10 am**	**Darwin Campbell**	**Pacific Salon 3**
4272	**Plant Reproductive Genomics**	**15-Jan-17**	**1:30 pm**	**-3:40 pm**	**Jim Leebens-Mack**	**Sunset - Meeting House**
4273	**Plant Science at the JGI and KBase**	**17-Jan-17**	**4:00 pm**	**-6:10 pm**	**Doreen Ware**	**San Diego**
4274	**Plant Transgene Genetics**	**16-Jan-17**	**12:50 pm**	**-3:00 pm**	**Gan-Yuan Zhong**	**Town and Country**
4275	**Polyploidy**	**15-Jan-17**	**10:30 am**	**-12:40 pm**	**Boulos Chalhoub**	**Town and Country**
4276	**Population and Conservation Genomics 1**	**14-Jan-17**	**4:00 pm**	**-6:10 pm**	**Om P. Rajora**	**Pacific Salon 3**
4394	**Population and Conservation Genomics 2**	**16-Jan-17**	**12:50 pm**	**-3:00 pm**	**Om P. Rajora**	**Pacific Salon 3**
4278	**Poultry 1**	**14-Jan-17**	**8:00 am**	**-6:10 pm**	**Huaijun Zhou**	**Sunset - Meeting House**
4279	**Poultry 2**	**15-Jan-17**	**8:00 am**	**-12:40 pm**	**Behnam Abasht**	**Sunset - Meeting House**
4280	**Proteomics**	**17-Jan-17**	**10:30 am**	**-12:40 pm**	**Madan K. Bhattacharyya**	**Pacific Salon 3**
4281	**QTL Cloning**	**15-Jan-17**	**8:00 am**	**-10:10 am**	**Roberto Tuberosa**	**Town and Country**
4318	**Quinoa and close relatives**	**15-Jan-17**	**10:30 am**	**-12:40 pm**	**David E Jarvis**	**Esquire - Meeting House**
4282	**Recombination - mechanisms**	**15-Jan-17**	**4:00 pm**	**-6:10 pm**	**Wojtek Pawlowski**	**Pacific Salon 1**
4283	**Resources and Programs for Undergraduate Education in Genomics**	**15-Jan-17**	**8:00 am**	**-10:10 am**	**Scott T Woody**	**Towne - Meeting House**
4284	**Rice Functional Genomics**	**15-Jan-17**	**1:30 pm**	**-3:40 pm**	**Mingsheng Chen**	**Royal Palm Salon 5-6**
4285	**Root Genomics**	**17-Jan-17**	**1:30 pm**	**-3:40 pm**	**Antonio Costa De Oliveira**	**Pacific Salon 6-7 (2nd Floor)**
4286	**Sequencing Complex Genomes**	**15-Jan-17**	**4:00 pm**	**-6:10 pm**	**Robert Henry**	**Golden Ballroom**
4287	**Sex Chromosomes and sex determination**	**15-Jan-17**	**4:00 pm**	**-6:10 pm**	**Abdelhafid Bendahmane**	**Royal Palm Salon 5-6**
4288	**SGN and RTB Databases: Genomes, Pathways and Breeder Tools.**	**17-Jan-17**	**10:30 am**	**-12:40 pm**	**Isaak Y. Tecle**	**Towne - Meeting House**
4289	**Small RNA**	**14-Jan-17**	**4:00 pm**	**-6:10 pm**	**Blake Meyers**	**Pacific Salon 1**
4290	**Solanaceae**	**15-Jan-17**	**8:00 am**	**-10:10 am**	**Shelley Jansky**	**Pacific Salon 1**
4291	**Somatic Genome**	**14-Jan-17**	**1:30 pm**	**-3:40 pm**	**Xiu-Qing Li**	**Pacific Salon 4-5 (2nd Floor)**
4292	**Sorghum/Millet**	**15-Jan-17**	**8:00 am**	**-10:10 am**	**Yinghua Huang**	**Pacific Salon 6-7 (2nd Floor)**
4293	**Soybean Genomics**	**17-Jan-17**	**10:30 am**	**-12:40 pm**	**Suk-Ha Lee**	**Royal Palm Salon 1-2**
4294	**Speciation Genomics**	**14-Jan-17**	**8:00 am**	**-10:10 am**	**Michael S. Barker**	**Towne - Meeting House**
4295	**Statistical Genomics**	**15-Jan-17**	**10:30 am**	**-12:40 pm**	**Zhenyu Jia**	**Golden West**
4296	**Sugar Beet Workshop**	**14-Jan-17**	**1:30 pm**	**-3:40 pm**	**Imad Eujayl**	**Towne - Meeting House**

4297	**Sugar Cane (ICSB)**	**15-Jan-17**	**8:00 am**	**-12:40 pm**	**Paul H. Moore**	**Royal Palm Salon 1-2**
4298	**Sugar Cane Sequencing Initiative**	**15-Jan-17**	**1:30 pm**	**-3:40 pm**	**Robert Henry**	**Royal Palm Salon 1-2**
4299	**Sweet Potato and Yam Genomics**	**18-Jan-17**	**10:30 am**	**-2:00 pm**	**Ranjana Bhattacharjee**	**Sunset - Meeting House**
4300	**Swine**	**14-Jan-17**	**1:30 pm**	**-6:10 pm**	**Kiho Lee**	**Royal Palm Salon 1-2**
4301	**Synthetic Biology**	**17-Jan-17**	**10:30 am**	**-12:40 pm**	**Elibio Rech**	**Pacific Salon 4-5 (2nd Floor)**
4302	**Systems Biology and Ontologies**	**14-Jan-17**	**8:00 am**	**-10:10 am**	**Sushma Naithani**	**Pacific Salon 2**
4303	**Systems Genomics**	**17-Jan-17**	**10:30 am**	**-12:40 pm**	**Hong-Bin Zhang**	**Sunrise - Meeting House**
4304	**Teaching Genetics, Genomics, Biotechnology, and Bioinformatics**	**14-Jan-17**	**4:00 pm**	**-6:10 pm**	**Abdelmajid Kassem**	**Esquire - Meeting House**
4305	**The Analysis and Role of the Microbiome**	**14-Jan-17**	**8:00 am**	**-10:10 am**	**Paola Mariani**	**Sunrise - Meeting House**
4306	**The Phytoremediation Genome**	**17-Jan-17**	**10:30 am**	**-12:40 pm**	**Adel M. Zayed**	**Pacific Salon 1**
4328	**Translational Agriculture: Opportunities, Technologies and Products**	**17-Jan-17**	**1:30 pm**	**-3:40 pm**	**Sireen Khan**	**Royal Palm Salon 3-4**
4308	**Transposable Elements**	**15-Jan-17**	**1:30 pm**	**-3:40 pm**	**Jianxin Ma**	**Golden Ballroom**
4309	**Tripal Database Network and Initiatives**	**15-Jan-17**	**4:00 pm**	**-6:10 pm**	**Stephen P. Ficklin**	**California**
4310	**Triticeae Genetics and Genomics, Session 1: Progress in structural and functional genomics**	**14-Jan-17**	**10:30 am**	**-12:40 pm**	**Justin D. Faris**	**Town and Country**
4311	**Triticeae Genetics and Genomics, Session 2: Trait genetics and gene identification**	**14-Jan-17**	**1:30 pm**	**-3:40 pm**	**Justin D. Faris**	**Town and Country**
4312	**Triticeae Genetics and Genomics, Session 3: Application of genomic resources to Triticeae improvement**	**14-Jan-17**	**4:00 pm**	**-6:10 pm**	**Justin D. Faris**	**Town and Country**
4313	**UCSC Genome Browser - a home for all organisms**	**18-Jan-17**	**10:30 am**	**-12:40 pm**	**Robert Kuhn**	**Royal Palm Salon 1-2**
4314	**Weedy and Invasive Plant Genomics**	**17-Jan-17**	**1:30 pm**	**-3:40 pm**	**Patrick Tranel**	**Towne - Meeting House**

Friday - January 13, 2017

12:00pm - 9:00pm **Registration - ATLAS FOYER**

Saturday - January 14, 2017

7:00am - 8:00am **Continental Breakfast - GOLDEN BALLROOM**

7:00am - 8:00pm **Registration - ATLAS FOYER**

7:00am - 9:00pm **Poster Access - GRAND EXHIBIT HALL**

8:00am - 10:10am **Arthropod Genomics - ESQUIRE - MEETING HOUSE**
Organizers: Joachim Nwezeobi, University of Greenwich and Lindsey Perkin, USDA ARS Center for Grain & Animal Health Research

8:00am Introductory Remarks

8:05am Surya Saha,Boyce Thompson Institute
"Using Long Reads, Optical Maps and Long-Range Scaffolding to Improve the *Diaphorina citri* Genome" (W051)

8:25am Scott Geib,USDA-ARS
"Using Sequencing-Based Approaches to Characterize Genetic Sexing Systems in Tephritid Fruit Flies" (W052)

8:45am Erin D. Scully,USDA-ARS Center for Grain and Animal Health Research
"Investigation of Genes Linked to Polyphagy and Xylophagy in Asian Longhorned Beetle (*Anoplophora glabripennis*) through Comparative Genomics and Transcriptome Profiling" (W053)

9:05am Marcé D. Lorenzen,North Carolina State University Entomology department
"Basic Steps for Developing Genetic Technologies in a Non-Model Organism" (W054)

9:25am Joanna Chiu,University of California
"Delivery of dsRNA Biopesticide Using Engineered Microbes" (W055)

9:45am Wayne Hunter,USDA Agricultural Research Service
"FANA and Morpholino's, Novel Molecules for Gene-Targeting in Plants and Arthropods" (W056)

10:05am Concluding Remarks

Saturday - January 14, 2017

8:00am - 10:10am **Camelids - ROYAL PALM SALON 1-2**
Chair: Terje Raudsepp, Texas A&M UniversityCo-Chair: Pamela A. Burger, Research Institute of Wildlife Ecology, Vetmeduni Vienna, Austria

8:00am Introductory Remarks

8:05am Heather M. Holl,University of Florida
"*De novo* Assembly of a Dromedary Camel" (W103)

8:20am Ciani Elena,University of Bari "Aldo Moro"
"Genetic Structure of *Camelus dromedarius* Populations through Genome-Wide RAD Sequencing" (W104)

8:35am Hussain Mahdi Bahbahani,Kuwait University
"Exploring the Full Genome Sequence of Dromedary Camels from the Arabian Penninsula" (W105)

8:50am Liang Ming,Inner Mongolia Agricultural University
"Constructing Genetic Variation Maps in the Bactrian Camel" (W106)

9:05am Mark F. Richardson,Deakin University
"VicPac 3.0: A New and Improved Alpaca Reference Genome" (W107)

9:20am Felipe Avila,University of Minnesota
"Application of Molecular Cytogenetic Tools in Camelids: Characterization of an Autosomal Translocation in an Infertile Llama" (W108)

9:35am Petr Horin,N/A
"The Major Histocompatibility Complex in Old World Camelids" (W109)

9:50am Panel Discussion; Moderators Pamela Burger, Samantha Brooks, Mark Richardson and Terje Raudsepp; Topics include but are not limited to: - Genome assembly issues: anchoring; other - Genome annotation: inclusion of alpaca and dromedary in FAANG - Phenotype

Saturday - January 14, 2017

8:00am - 10:10am **CSSA: Translational Genomics - PACIFIC SALON 1**
Organizer: Robert M. Stupar, Department of Agronomy and Plant Genetics, University of MinnesotaCo-Chair: David A. Lightfoot, Southern Illinois University

8:00am Peggy Ozias-Akins,University of Georgia
"Fertilization-Independent Embryo Development As a Component of Apomixis" (W225)

8:20am Sally Mackenzie,University of Nebraska
"Phenotypic Plasticity and Epigenetic Memory Are Associated with Circadian Dysregulation" (W226)

8:40am Nigel J. Taylor,Donald Danforth Plant Science Center
"TBD" (W227)

9:00am Christopher Dardick,USDA-ARS Appalachian Fruit Research Station
"Translational Genomic Approaches for Genetic Modification of Plant Architecture" (W228)

9:20am Gunvant Patil,University of Missouri
"Genomic-Assisted Haplotype Analysis and Trait Discovery in Soybean" (W229)

9:40am Sarah D. Turner,University of Wisconsin-Madison
"Insights into the Heritability and Genetic Basis of Carrot Shoot Growth Using Bayesian Diallel Analysis" (W230)

8:00am - 10:10am **Evolution of Genome Size - GOLDEN WEST**
Organizer: William S. Sanders, The Jackson Laboratory

8:00am Roy N Platt,Texas Tech University
"Transposable Elements and Their Role in Genome Evolution" (W312)

8:25am Adam Session,DOE Joint Genome Institute
"Repetitive Elements Reveal the Evolutionary History of Polyploid Grass Genomes" (W313)

8:50am Xianran Li,Iowa State University
"Knowledge Discovery and Data Mining: Dynamics of Genome's Size and Composition" (W314)

9:15am Ivan Liachko,Phase Genomics Inc.
"End-to-End Assembly of Genomes of Any Size using *in vivo* Chromatin Proximity Data" (W315)

9:40am Daojun Yuan,Brigham Young University
"Transcriptome Comparison Reveals Patterns of Selection in Domesticated and Wild Cotton" (W316)

Saturday - January 14, 2017

8:00am - 10:10am **Forage, Feedstocks & Turf - PACIFIC SALON 4-5 (2ND FLOOR)**
Organizers: German Spangenberg, Biosciences Research, DEDJTR and Reed E. Barker, Grass Genomic Testing, Inc.

8:00am Kirankumar S. Mysore,The Samuel Roberts Noble Foundation
"Over-Expression of MYB Transcription Factor Imparts Multi Stress Tolerance in Alfalfa" (W329)

8:20am Hans Daetwyler,Agriculture Victoria
"Exploring the Potential of Polyploid Forages through Computer Simulation" (W330)

8:40am Elisabeth Veeckman,ILVO Plant Sciences Unit - Growth and Development
"Perennial Ryegrass: Unravelling the Structure and Content of a Many-Faced Genome" (W331)

9:00am David Kopecky,Institute of Experimental Botany
"Dynamic Changes in Genomes of Newly Developed Allopolyploid Grasses" (W332)

9:20am Xiangyu Guo,Aarhus University
"Genomic Prediction in Tetraploid Ryegrass" (W333)

9:40am Rachel F. Begheyn,ETH Zurich
"Inheritance Patterns of the Response to *in vitro* Doubled Haploid Induction in Perennial Ryegrass (*Lolium perenne* L.)" (W334)

8:00am - 10:10am **International Wheat Genome Sequencing Consortium (IWGSC) - TOWN AND COUNTRY**
Organizer: Kellye Eversole, IWGSCCo-Chair: Rudi Appels, Murdoch Univ.

8:00am Nils Stein,Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)
"The IWGSC Reference Genome Sequence" (W554)

8:30am Naeela Qureshi,University of Sydney
"Fine Mapping of the Chromosome 5B Region Carrying Closely Linked Rust Resistance Genes *Yr47* and *Lr52* in Wheat" (W555)

8:50am Luigi Cattivelli,CREA Genomics research centre
"High Quality Assembly of the Durum Wheat Genome cv. Svevo" (W556)

9:10am Raj K Pasam,DEDJTR, Biosciences Research, AgriBio
"Using Advanced Wheat Genomic Resources and Metabolite Fingerprinting to Address Complex Traits" (W557)

9:30am Guangyao Zhao,Institute of Crop Sciences, Chinese Acadamy of Agricultural Sciences
"The Reference Genomes for *Aegilops tauschii* (AL8/78), *Ae. speltoides* (Y2032) and *Triticum aestivum* (AK58)" (W558)

9:50am Dr. Gil Ronen,NRGene
"From Multi-Genome Assembly to Capturing Full Diversity Using Denovomagic 3.0" (W559)

Saturday - January 14, 2017

8:00am - 10:10am **CyVerse Education: Scaling Genomics and Data Science for the Biology Classroom - CALIFORNIA**
Organizers: Dave Micklos, DNA Learning Center and Jason Williams, Cold Spring Harbor Laboratory

8:00am Stacia E. Rodenbusch,University of Texas at Austin
"The Freshman Research Initiative: Results from a Model Cure" (W237)

8:40am Oliver Hyman,James Madison University
"Large-Scale Implementation of DNA Barcoding in Freshman Biology" (W238)

9:10am Maria Brown,Sayville High School
"Microbiome Studies in the High School Research in Science & Engineering Program: A Primer in Workforce Development" (W239)

9:40am Joslynn Lee,Cold Spring Harbor Laboratory
"Data Science Challenges and Solutions for Student Microbiome Research" (W240)

8:00am - 10:10am **Legumes - ROYAL PALM SALON 5-6**
Organizers: Jamie A. O'Rourke, USDA-ARS and Marc Libault, University of Oklahoma

8:00am Zhenzhen Qiao,University of Oklahoma
"-Omic Analysis at the Level of One Single Legume Cell Type to Reveal the Conservation and Divergence of the Regulatory Mechanisms of Gene Transcription" (W585)

8:20am Robert Schmitz,University of Georgia
"Integration of ATAC-seq and DAP-seq Data to Uncover Gene Regulatory Networks in Soybean" (W586)

8:40am Chantal McCabe,United States Department of Agriculture
"Characterization of Resistant and Susceptible Responses to *Phialophora gregata* in Soybean using RNA-Seq" (W587)

9:00am Senthil Subramanian,South Dakota State University
"Regulation of Local Auxin Metabolism during Soybean Nodule Development" (W588)

9:20am Josh Clevenger,University of Georgia
"Novel Pipelines for Marker Discovery in Allotetraploid *Arachis hypogaea* Lead to Advances in Peanut Genomics" (W589)

9:40am K. Peter Pauls,University of Guelph
"Applied Bean Genomics - Insights from Genome Mapping, Sequencing and Analysis Relevant to Bean Breeding" (W590)

Saturday - January 14, 2017

8:00am - 10:10am **Systems Biology and Ontologies - PACIFIC SALON 2**
Organizers: Pankaj Jaiswal, Department of Botany & Plant Pathology, Oregon State University, Laurel Cooper, Department of Botany & Plant Pathology, Oregon State University and Sushma Naithani, Department of Botany & Plant Pathology, Oregon State University

8:00am Welcoming Remarks

8:03am Christopher Mungall,Lawrence Berkeley National Laboratory
"Phenopackets: An Ontology-Based Expressive Exchange Format for Phenotype and Trait Data" (W929)

8:23am Thomas Sharpton,Oregon State University
"The Gut Metagenome Across Health and Evolution" (W930)

8:43am Kusum Naithani,University of Arkansas
"Use of Mechanistic and Empirical Models of Photosynthesis to Explore Genetic Variation in Rice" (W931)

9:03am David Hendrix,School of Electrical Engineering and Computer Science, Oregon State University and Dept of Biochemistry and Biophysics, Oregon State University
"Identification and Pathway Association of Abiotic Stress-Responsive Long Noncoding RNAs in *Populus trichocarpa*" (W932)

9:23am Song Li,Virginia Tech
"Integrated Transcriptome and Proteome Analyses Reveal Cell Type-Specific Regulation of Alternative Splicing in Arabidopsis" (W933)

9:43am Brent Kronmiller,Oregon State University
"Draft Genome of the North American Beaver (*Castor canadensis).* " (W934)

9:58am Brett Tyler,Oregon State University
"Plant Science Research Network's Draft 10 Year Strategic Plan for Plant Science Cyberinfrastructure" (W935)

8:00am - 10:10am **The Analysis and Role of the Microbiome - SUNRISE - MEETING HOUSE**
Organizer: Paola Mariani, PTP Science Park

8:00am Introductory Remarks

8:05am Barbara F. Nowak,University of Tasmania
"Investigations of Microbiome in Aquaculture Species" (W946)

8:30am Charlotte Lindqvist,University at Buffalo
"Divergent Gut Microbiomes of Toothed and Baleen Whales" (W947)

8:55am Suzanne Rowe,AgResearch, Invermay Agricultural Centre
"Genomic Host Control of the Rumen Microbiome, Breeding for Optimal Productivity and Low Environmental Impact in Pastoral Livestock Systems" (W948)

9:20am Alessandra Stella,Fondazione Parco Tecnologico Padano and ADAPTMAP Consortium

"Effect of Italian "Grana Padano" Cheese on the Oral Microbiota Composition: A 16S rRNA Metabarcoding Approach" (W949)

9:45am Mick Watson,The Roslin Institute and R(D)SVS, University of Edinburgh

"Comparison of Methods for Functional and Phylogenetic Charactersiation of Rumen Metagenomic Data" (W950)

8:00am - 12:40pm Cattle/Swine - SAN DIEGO

Organizers: Jared E. Decker, Division of Animal Sciences, University of Missouri and Kiho Lee, Virginia Tech

8:00am Welcoming Remarks

8:10am Daniela A.L. Lourenco,University of Georgia

"How Large-Scale Genomic Evaluations Are Possible: A Look into the Dimensionality of Genomic Information" (W135)

9:05am Vanmathy Kasimanickam,Washington State University

"Genome to Phenome Integration in the Context of Boar Sperm microRNAs" (W136)

10:00am Break

10:20am Alan L. Archibald,The Roslin Institute and R(D)SVS, University of Edinburgh

"Exploiting Long Read Sequencing Technologies to Establish High Quality Highly Contiguous Pig Reference Genome Assemblies" (W137)

11:15am Benjamin D. Rosen,ARS, USDA

"Updating the Bovine Reference Genome Assembly" (W138)

8:00am - 12:40pm **Fruit/Nuts - PACIFIC SALON 3**
Organizer: Veronique Decroocq, UMR BFP1332 - INRA-Universite de Bordeaux

8:00am Dario Grattapaglia,Embrapa Recursos Genéticos e Biotecnologia and Graduate Program in Genomic Sciences - Catholic University of Brasília
"A Chromosome-Scale Assembly of the Cashew Tree Genome: Leveraging the Combined Power of PacBio, DNA-Chromatin Proximity Ligation and SNP Linkage Maps" (W354)

8:19am Concetta Licciardello,Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria (CREA)
"Evaluation of Variability in the Sweet Orange Germplasm through Next Generation Clonal Fingerprinting" (W355)

8:38am Na Wei,University of Pittsburgh, Department of Biological Sciences
"A Combination of Genetic Mapping and Phylogenetics Untangles the Cryptic Hybrid Origin of a Decaploid Strawberry" (W356)

8:57am Julie Caruana,University of Maryland
"Genomic Analyses Linking Genes and Gene Networks to Fruit Traits in Wild Strawberry" (W357)

9:16am Robert Schaffer,New Zealand Institute for Plant and Food Research Ltd.
"How Much Should We Rely on Computer Annotation for Identifying Genes in New Genomes?" (W358)

9:35am Dorrie Main,Washington State University
"GDR: New Data and New Functionality" (W359)

9:54am Mareike Knäbel,The New Zealand Institute for Plant & Food Research Limited
"Genetics of Red Flesh Colouration in Kiwifruit (*Actinidia chinensis*)" (W360)

10:13am Soichiro Nishiyama,Graduate School of Agriculture, Kyoto University
"Toward Isolation of a Gene Conferring Astringency Loss in Persimmon Fruit" (W361)

10:32am Jessica Guseman,USDA-ARS Appalachian Fruit Research Station
"DEEPER ROOTING 1 Controls Root Architecture in *Arabidopsis* and *Prunus* Species" (W362)

10:51am Michael Wisniewski,USDA-ARS
"Functional Analysis of the CBF Transcription Factor in Apple: A Model for Studying the Interaction Between Cold Hardiness, Dormancy, and Growth" (W363)

11:10am Ryutaro Tao,Graduate School of Agriculture, Kyoto University
"Sex Determination in Oriental Persimmon (*Diospyros kaki*)" (W364)

11:29am Andréa M. Almeida,Universidad Andrés Bello, Centro de Biotecnología Vegetal
"New Insights in the Epigenetic Regulation of Floral Bud Dormancy and Cold Accumulation in Sweet Cherry (*Prunus avium*)" (W365)

11:48am Humberto Prieto,Instituto de Investigaciones Agropecuarias - La Platina Station
"Plum Pox Virus and *Prunus spp*: The Small RNA Talk" (W366)

Saturday - January 14, 2017

8:00am - 6:10pm **Aquaculture - ROYAL PALM SALON 3-4**
Organizer: Nathan Campbell, Columbia River Inter-Tribal Fish Commission

8:00am Welcoming Remarks

8:05am Louis Bernatchez,Université Laval
"Epigenetics in Salmonids: Impacts of Rearing Environment, Hybridization and Inbreeding " (W026)

8:45am Tom Goldammer,Leibniz Institute for Farm Animal Biology (FBN)
"Genome Biology of Maraena Whitefish (Coregonus maraena, BLOCH, 1779) for Preservation of Baltic Fish Biodiversity" (W027)

9:05am Rachael Ashby,AgResearch Ltd, Invermay Agricultural Centre and University of Otago, Department of Anatomy
"A Genomic Toolbox (genome, transcriptome and GBS) for the New Zealand Greenshell™ Mussel (*Perna canaliculus*)" (W028)

9:25am James Kijas,CSIRO Agriculture
"Genome Sequencing of 20 Tasmanian Atlantic Salmon Used to Characterize Multiple Loci Associated with Sex Determination" (W029)

9:45am Cristian Araneda,Universidad de Chile, Depto. de Produccion Animal
"Development of a Genotyping-in-Thousand By Sequencing (GT-seq) Panel for Traceability in Chilean Blue Mussel" (W030)

10:05am AM Break

10:20am Anna K Sonesson,Nofima AS
"Using Pooled DNA of a Reference Population in Genomic Selection for a Disease Trait in Atlantic Salmon"

10:40am Albert Caballero-Solares,Department of Ocean Sciences, Memorial University of Newfoundland
"Applying Transcriptomic Profiling to the Formulation of Sustainable Feeds for Atlantic Salmon (*Salmo salar*)" (W032)

11:00am Sixin Liu,USDA-ARS-NCCCWA
"Identification of Commercial Rainbow Trout Strains Using a SNP Panel" (W033)

11:20am Nawar Al-Janabi,Mississippi State University
"The Intestinal Immune Responses of Channel Catfish Against Live-Attenuated *Edwardsiella Ictaluri* Vaccines" (W034)

11:40am Daniel Powell,University of the Sunshine Coast
"Progress on the Genome Characterisation of the Sydney Rock Oyster *(Saccostrea glomerata)*" (W035)

12:00pm Lunch Break

Saturday - January 14, 2017

1:10pm	Sigbjørn Lien,Centre of Integrative Genetics (CIGENE), Department of Animal and Aquacultural Sciences, Norwegian University of Life Sciences **"Salmonid genomics to advance our understanding of genome evolution, adaptation and the genetic architecture of complex traits" (W036)**
1:50pm	Michelle T.T. Crown,Simon Fraser University, Molecular Biology and Biochemistry Department and Fisheries and Oceans Canada, Centre for Aquaculture and Environmental Research **"Identification of Genomic Loci Associated with Maturation in Pacific Coho Salmon (*Oncorhynchus kisutch*)" (W037)**
2:10pm	Sylvie M.A. Quiniou,USDA-ARS **"Third Generation Sequencing: Unraveling the Genome and the Immunoglobulin Superfamily Genes in Catfish (*Ictalurus punctatus*)" (W038)**
2:30pm	Ross D. Houston,The Roslin Institute and R(D)SVS, University of Edinburgh **"Genotype Imputation to Improve the Efficiency of Genomic Selection in Atlantic Salmon" (W039)**
2:50pm	PM Break
3:05pm	Yniv Palti,USDA-ARS-NCCCWA **"GWAS of Bacterial Cold Water Disease Resistance in Rainbow Trout Reveals the Potential for a Combined Approach Between Genomic Selection and Marker Assisted Selection" (W040)**
3:25pm	Jacob Seiloe Torgersen,AquaGen **"The Genetics of Muscle Color in Atlantic Salmon" (W041)**
3:45pm	Matthew A. Conte,University of Maryland **"A High Quality Assembly of the Nile Tilapia (*Oreochromis niloticus*) Genome Provides Insights into the Structure of Two Sex Determination Regions" (W042)**
4:05pm	Zihao Yuan,Auburn University; The Fish Molecular Genetics and Biotechnology Laboratory **"Comparative Genome Analysis of 52 Fish Species Suggests Differential Associations of Repetitive Elements with Their Living Aquatic Environments" (W043)**
4:25pm	Christina C. Yildirimer,Portland State University **"Gut Microbiota Diversity of Pre-Smolt Hatchery Steelhead (*Oncorhynchus mykiss)* Across the Cascade Divide" (W044)**
4:45pm	James M. Reecy,Department of Animal Science, Iowa State University **"NSRP-8 Bioinformatics Coordinator" (W045)**
5:05pm	Business Meeting
5:35pm	Break
6:40pm	Aquaculture Reception and Poster Session

Saturday - January 14, 2017

8:00am - 6:10pm	**Poultry 1 - SUNSET - MEETING HOUSE** **Organizers: Behnam Abasht, Department of Animal and Food Sciences, University of Delaware and Huaijun Zhou, University of California, Davis**
8:00am	Introductory Remarks
8:20am	Carl J. Schmidt,University of Delaware **"Systemic Transcriptome Responses to Heat Stress in the Chicken" (W754)**
8:40am	Huaijun Zhou,University of California, Davis **"Genetic Improvement of Resistance to NDV and Heat Stress in Chickens" (W755)**
9:00am	Susan J. Lamont,Iowa State University, Department of Animal Science **"Transcriptome Response to Newcastle Disease Virus in Resistant and Susceptible Inbred Chicken Lines" (W756)**
9:20am	Jack C.M. Dekkers,Iowa State University, Department of Animal Science **"Response to Newcastle Disease Virus in Indigenous Chickens in Africa" (W757)**
9:40am	Cobb Travel Award winner
10:00am	AM Break
10:20am	Samuel E. Aggrey,University of Georgia **"Gene Expression and Cellular Analyses of Genes in the Protein Biosynthesis Pathway in Meat-Type Chickens Under Heat Stress" (W758)**
10:40am	Wayne Kuenzel,University of Arkansas **"The Neuroendocrine Regulation of Stress in Birds Involves a New Structure Called the Nucleus of the Hippocampal Commissure" (W759)**
11:00am	Hans Cheng,USDA, ARS, ADOL and USDA, ARS, ADOL **"Characterization of Marek's Disease Tumors for Driver Mutations" (W760)**
11:20am	Mary E. Delany,Animal Science, University of California **"Host Chromosome Integration Profiles of Marek's Disease (MD) Virus and Vaccine Strains Differ Between MD Resistant and Susceptible Lines of Chicken" (W761)**
11:40am	Huanmin Zhang,USDA-ARS, Avian Disease & Oncology Laboratory **"NGS Analysis Identified Differentially Expressed Coding and microRNA Genes in ALV-like Spontaneous Tumors Potentially Contributing to Tumorigenicity in Susceptible Chickens" (W762)**
12:00pm	Saturday Lunch Break
1:20pm	William Muir,Purdue University **"Design and Analysis of Reference Populations to Detect Signatures of Selection from Genomic Data" (W763)**

1:40pm Brynn Voy,University of Tennessee
"Programming Reduced Fatness in Broilers" (W764)

2:00pm Kent M. Reed,University of Minnesota
"Temperature Effects on Differential Gene Expression in Turkey Satellite Cells during Proliferation and Differentiation" (W765)

2:20pm Gale M. Strasburg,Michigan State University
"Effect of Embryonic and Post-Hatch Thermal Challenge on Turkey Muscle Development" (W766)

2:40pm Break

3:20pm Update on NRSP8 Bioinformatics

3:40pm Walter Bottje,University of Arkansas
"Evidence of Enhanced Energy Production and Transfer, Synthesis of Nucleotides, Ribosome Assembly, and Protein Translation in Breast Muscle in High *vs* Low Feed Efficiency Pedigree Broiler Males: Hypotheses Worth Pursuing?" (W767)

4:00pm Eric A. Wong,Virginia Tech
"Expression of Nutrient Transporters and Host Defense Peptides in the Intestine and Yolk Sac of Chickens" (W768)

4:20pm Alia Parveen,University of Arkansas, Cell and Molecular Biology Program
"Identification of Copy Number Variations Associated with Ascites Phenotype in Broilers" (W769)

4:40pm Neal A. Jorgenson Travel Award winner

5:00pm Students and Postdocs Lightning Talks

9:30am - 10:30am Coffee Break - ATLAS FOYER

10:30am - 12:40pm Brassicas - PACIFIC SALON 2
Organizers: Ian Bancroft, Department of Biology, University of York and J. Chris Pires, Division of Biological Sciences, University of Missouri

10:30am Charlotte Noelle Miller,John Innes Centre
"Identification of a Novel Regulator of *Brassica napus* Seed Development By Associative Transcriptomics" (W086)

10:50am Michael S. Barker,University of Arizona
"Genetic Variation from Ancient Hexaploidy Preferentially Selected during Domestication of *Brassica rapa* Crops" (W087)

11:10am Stephen J. Robinson,Agriculture and Agri-Food Canada
"Exploring Epigenetic Variation in the Brassicas" (W088)

11:30am David M Jones,John Innes Centre
"Redundancy, Subfunctionalization and Neofunctionalization in the Gene Regulatory Network Underlying Flowering in *Brassica napus*" (W089)

11:50am David Edwards,University of Western Australia
"The Pangenome of *Brassica oleracea*" (W090)

12:10pm Rod Snowdon,Justus Liebig University
"Structural Genome Variation and Adaptive Potential in *Brassica napus*" (W091)

10:30am - 12:40pm **Buffalo genome** - ROYAL PALM SALON 1-2
Organizer: John Williams, Davies Research Centre, University of AdelaideChair: John Williams, Davies Research Centre, Univ. of Adelaide

10:30am John Williams,Davies Research Centre, University of Adelaide
"Introduction" (W092)

10:35am Richard E. Green,Dovetail Genomics
"Improving the Buffalo Genome using Chicago Data" (W093)

11:00am Rachel Young,The Roslin Institute and R(D)SVS, University of Edinburgh
"The Buffalo Expression Atlas" (W094)

11:25am Jesus Rommel V. Herrera,Philippine Carabao Center
"Disequilibrium in the Four Riverine Buffalo Populations in the Philippines" (W095)

11:50am Nicolò P. P. Macciotta,University of Sassari
"Analysis of Genetic Diversity in River Buffalo Populations using a Multivariate Approach" (W096)

12:15pm Theodore S. Kalbfleisch,University of Louisville
"Triallelic SNPs for Estimating Cattle Introgression, Inbreeding and Determining Parentage in North American Yak" (W097)

10:30am - 12:40pm **Ecological Genomics - ROYAL PALM SALON 5-6**
Organizers: Katrina Dlugosch, University of Arizona and Nolan Kane, University of Colorado

10:30am Nolan Kane,University of Colorado
"Genetic Regulation and Evolution of Alternative Splicing Changes during Sunflower Domestication" (W277)

10:50am David L. Des Marais,Harvard University
"Topological Features of a Plant Gene Regulatory Network Predict Patterns of Natural Diversity in Environmental Response" (W278)

11:10am Huey Tyng Lee,University of Queensland
"Comparison of Gene Loss and Adaptation Between Two Independent Return to the Sea Events in Seagrasses" (W279)

11:30am Craig Primmer,University of Turku
"The Genetic Architecture of Age at Maturity in Atlantic Salmon: A Large-Effect Locus with Sex Dependent Dominance Reduces Sexual Conflict and Shows Signals of Local Adaptation" (W281)

11:50am Qingshun Quinn Li,Xiamen University
"*De novo* Transcriptome Analysis of a Cold Tolerant Mangrove, *Kandelia obovata*" (W282)

10:30am - 12:40pm **Engineering NUE - PACIFIC SALON 4-5 (2ND FLOOR)**
Organizers: David A. Lightfoot, Southern Illinois University and Ashok Shrawat, Monsanto

10:30am John Davies,Dow AgroSciences
"Nitrogen Use Efficiency Differentially Influences Grain Yield in Old and New Era Maize Hybrids" (W283)

10:50am Anne Laperche,AGROCAMPUS OUEST
"Genetic Basis of Nitrogen Use Efficiency and Yield Stability Across N Conditions in Rapeseed: Combining Quantitative Genetic and Functional Genomic Approaches" (W284)

11:10am Ling Li,Mississippi State University
"The Arabidopsis QQS Orphan Gene Modulates Carbon and Nitrogen Allocation Across Species" (W285)

11:30am Rodrigo A. Gutiérrez,Pontificia Universidad Católica de Chile
"Systems Biology to Identify New Regulators of Nitrogen Use Efficiency in Plants" (W286)

10:30am - 12:40pm **Functional Genomics of C_4 and CAM photosynthesis - TOWNE - MEETING HOUSE**
Organizers: Thomas P. Brutnell, Donald Danforth Plant Science Center and John C. Cushman, Department of Biochemistry and Molecular Biology, University of Nevada, Reno

10:30am Carla P. Coelho,Donald Danforth Plant Science Center
"Unraveling the Molecular Basis of Kranz Anatomy in C4 Grasses" (W382)

10:50am Robert VanBuren,Michigan State University
"Genomics of Crassulacean Acid Metabolism (CAM) Species" (W383)

11:10am Christopher R. Myers,Cornell University
"Multiscale Modeling of Metabolism and Its Regulation in C4 Plants" (W384)

11:30am Victor A. Albert,University at Buffalo
"Using the Genome of the Orchid *Erycina pusilla* as a Model to Study Crassulacean Acid Metabolism in Monocots" (W385)

11:50am Andrea Braeutigam,Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK)
"Regulation of C4 Photosynthesis" (W386)

12:10pm Karolina Heyduk,University of Georgia
"Variation in Gene Expression and Regulation of CAM in *Yucca* (Asparagaceae)" (W387)

10:30am - 12:40pm **Interoperability and Federation Across Bioinformatic Platforms and Resources - CALIFORNIA**
Organizer: Eric Lyons, University of Arizona; BIO5 Institute; CyVerseCo-Chair: Haibao Tang, University of Arizona

10:30am Eric Lyons,University of Arizona; BIO5 Institute; CyVerse
"Welcome and Introductory Remarks" (W560)

10:40am Ramona Walls,CyVerse, University of Arizona
"Exploring Identifier Services for Large, Distributed Biological Datasets" (W561)

10:55am Paul J. Kersey,EMBL - The European Bioinformatics Institute
"Guiding Users through Diverse, Dispersed Data Ecosystems" (W562)

11:10am Matthew Vaughn,Texas Advanced Computing Center
"TBD" (W563)

11:25am Bonnie Hurwitz,University of Arizona
"iVirus and iMicrobe" (W564)

11:40am Christopher D. Town,J. Craig Venter Institute
"Araport: Baby Steps Towards a Federated Data Portal" (W565)

11:55am Ethalinda Cannon,Iowa State University
"Legume Federation" (W566)

12:10pm Ian Holmes,Department of Bioengineering
"JBrowse" (W567)

10:30am - 12:40pm **Genomic features and chromosome functionality - SUNRISE - MEETING HOUSE**
Organizers: Xiyin Wang, School of Life Sciences and Xiu-Qing Li, Agriculture and Agri-Food Canada

10:30am Welcoming Remarks

10:35am Wei Feng,Carnegie Institution for Science, Department of Plant Biology
"Large-Scale Heterochromatin Remodeling Facilitates Overreplicatin-Associated DNA Damage in Plant " (W430)

10:55am Jinyu Wang,Iowa State University
"Genome Divergence Pattern and its Correlation to DNA Repairing Pathway" (W431)

11:15am Ainong Shi,University of Arkansas
"Genetic Diversity and Association Analysis in Spinach" (W432)

11:35am Rachit Kumar Saxena,ICRISAT
"Whole Genome Re-Sequencing of 300 Cajanus Accessions Provides Genome-Wide Variations, Targets for Domestication and Genomic Regions Associated with Agronomic Traits for Pigeonpea Improvement" (W433)

11:55am Ainong Shi,University of Arkansas
"Association Analysis of Seed Antioxidant Content and Aphid Resistance in Cowpea" (W434)

11:46am Rachit Kumar Saxena,ICRISAT
"Whole Genome Re-Sequencing of 300 *Cajanus* Accessions Provides Targets for Domestication and Genomic Regions Associated with Agronomic Traits" (W435)

12:15pm Shengyi Liu,Oil Crops Research Institute of CAAS
"Asymmetrical Evolution of Polyploid Genomes: The Role of Recombination Linking Genomic Variation to Traits in *Brassica napus*" (W436)

10:30am - 12:40pm Genomics of Genebanks - PACIFIC SALON 1
Organizers: Clare Coyne, Washington State University and Christopher M. Richards, USDA ARS National Laboratory for Genetics Resources

10:30am Adnan Riaz,Queensland Alliance for Agriculture and Food Innovation
"Mining Vavilov's Treasure Chest of Wheat Diversity for Resistance to Leaf Rust" (W450)

10:55am Cécile Berthouly-Salazar,IRD and LMI LAPSE
"Investigating Genes Linked to Adaptations in Pearl Millet" (W451)

11:20am Martin Mascher,Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)
"Twenty Thousand Accessions Under Analysis: From Cold Room to GWAS" (W452)

11:45am Joanne A Labate,USDA ARS
"High-Throughput Genotyping of Vegetable Crops for Germplasm Conservation" (W453)

12:10pm Xiaoqing Yu,Iowa State University
"Genomic Prediction Contributing to a Promising Global Strategy to Turbocharge Gene Banks" (W454)

10:30am - 12:40pm Grasslands (Lolium Genome Initiative) - ESQUIRE - MEETING HOUSE
Organizers: Iain Donnison, Institute of Biological, Environmental and Rural Sciences (IBERS), Aberystwyth University and Reed E. Barker, Grass Genomic Testing, Inc.

10:30am Sai Krishna Arojju,Teagasc, Crop Science Department and Trinity College Dublin
"Genomic Prediction of Heading Date and Crown Rust Resistance in Perennial Ryegrass" (W491)

10:50am Timothy Sykes,ETH Zurich
"Identification of Candidate Genes for Fertility Restoration in Cytoplasmic Male Sterile Perennial Ryegrass (*Lolium perenne* L.)" (W492)

11:10am Isabel Roldan-Ruiz,ILVO Plant Sciences Unit and Department of Plant Biotechnology and Bioinformatics, Ghent University
"Genetic Dissection of Cell Wall Digestibility in Perennial Ryegrass" (W493)

11:30am Charlotte M Jones,IBERS, Aberystwyth University
"Large Scale SNP Analysis Reveals Genomic Diversity within European and Asian Red Clover (*Trifolium pratense* L.) Germplasm" (W494)

11:50am Andrew Griffiths,AgResearch, Grasslands Research Centre and Pastoral Genomics c/o AgResearch Grasslands
"Developing Genomic Selection in White Clover (*Trifolium repens* L.)" (W495)

12:10pm Silvio Salvi,Department of Agricultural Sciences, University of Bologna
"Mutagenesis and Genomic Analysis in *Arundo donax*" (W496)

10:30am - 12:40pm Connecting Crop Phenotype Data - GOLDEN BALLROOM
Organizers: Clay Birkett, USDA-ARS and Jean-Luc Jannink, USDA-ARS

10:30am Keywan Hassani-Pak,Rothamsted Research
"KnetMiner - Interrogate Plant and Animal Knowledge Networks" (W200)

10:50am Jan Erik Backlund,Integrated Breeding Program
"BrAPI, a Standard Interface for Plant Databases" (W201)

11:10am David Marshall,The James Hutton Institute
"Visualizations of Phenotypic and QTL Data" (W202)

11:30am Ramona Walls,CyVerse
"CyVerse Data Commons" (W203)

11:50am Paul J. Kersey,EMBL - The European Bioinformatics Institute
"Transplant Integrated Search using Apache Solr" (W204)

12:10pm Hadi Quesneville,INRA - URGI
"WheatIS : A Genetics and Genomics Information System for the Wheat Research Community" (W205)

10:30am - 12:40pm Mutation Screening - GOLDEN WEST
Organizer: Abdel Bendahmane, INRA

10:30am Robert M. Stupar,Department of Agronomy and Plant Genetics, University of Minnesota
"Identification of Functional Variants in Soybean Using Fast Neutron and CRISPR-Based Mutagenesis" (W601)

10:50am Thomas Jacobs,VIB
"High-Throughput CRISPR Vector Construction and Mutant Characterization in Plants" (W602)

11:10am Norbert Bollier,INRA
"CRISPR/Cas9-Mediated Mutagenesis of Floral Termination Genes: A Way to Control Fruit Size" (W603)

11:30am Naoufal Lakhssassi,Department of Plant Soil and Agricultural Systems, SIUC
"Mutational Analysis and *in silico* Modeling Identify a Novel Molecular Cross-Talk Between SNAP and SHMT in Soybean" (W604)

11:50am Jinrui Shi,DuPont Pioneer
"Novel Genetic Variation Generated By CRISPR-Cas System for Improving Drought Tolerance in Maize" (W605)

12:10pm Magdy Mahfouz,Biological and Environmental Sciences and Engineering Division
"Plant Genome Editing *via* CRISPR/Cas9" (W606)

12:30pm Seiichi Toki,National Institute of Agrobiological Sciences
"Precision Mutagenesis in Plants *via* Genome Editing" (W607)

10:30am - 12:40pm Triticeae Genetics and Genomics, Session 1: Progress in structural and functional genomics - TOWN AND COUNTRY
Organizers: Justin D. Faris, USDA-ARS, Gary J. Muehlbauer, Department of Plant and Microbial Biology, University of Minnesota and Michael Bevan, John Innes Centre

10:30am Eduard Akhunov,Kansas State University, Department of Plant Pathology, Manhattan, KS
"Genetic Architecture of Recombination Rate Variation in Wheat Revealed By Analyzing a Nested-Association Mapping Population and Reverse Genetic Screens" (W964)

10:50am Elodie Rey,Institute of Experimental Botany AS CR
"The Impact of Genomic Interactions on Gene Expression in a Wheat-Barley 7HL Addition Line" (W965)

11:10am Thomas Wicker,Department of Plant and Microbial Biology, University of Zurich
"The Repetitive Landscape of the Barley Genome" (W966)

11:30am Sara G. Milner,IPK Gatersleben
"Developing a Toolkit for Barley Genebank Genomics" (W967)

11:50am Bernardo J. Clavijo,Earlham Institute
"From Zero to Many: Assembling Wheat Genomes with w2rap" (W968)

12:30pm - 1:30pm Lunch (Vouchers Provided) - ROYAL PALM COURT & TIKI PAVILION COURT

1:30pm - 3:40pm **Allele Mining - PACIFIC SALON 2**
Organizer: Jeremy D. Edwards, USDA-ARS Dale Bumpers National Rice Research Center

1:30pm David M. Francis,The Ohio State University, Horticulture and Crop Science
"Allele Mining: From Sequence Variation to Functional Evaluation in Tomato" (W007)

1:51pm Aureliano Bombarely,Virginia Polytechnic Institute and State University, Department of Horticulture
"Analysis of the *Sinningia speciosa* Diversity under Domestication" (W008)

1:30pm - 3:40pm **Analysis of Complex Genomes - GOLDEN BALLROOM**
Organizers: David M. Stelly, Texas A&M University, Hong-Bin Zhang, Department of Soil and Crop Sciences, Texas A&M University and Boulos Chalhoub, UEVE-INRA

1:30pm Welcoming Remarks

1:35pm Bhavna Hurgobin,University of Western Australia
"Towards a Pangenome for *Brassica napus* Canola" (W009)

1:55pm Julia Naumann,Penn State University
"Tremendous Transfer – Intracellular and Horizontal Gene Transfer in the Genome of the Basal Angiosperm *Amborella trichopoda*" (W010)

2:15pm Jill Herschleb,10x Genomics Inc.
"Deciphering Complex Structural Variation with Linked-Reads" (W011)

2:35pm Amanda M. Hulse-Kemp,University of California
"A New Pepper Genome Built Using Long-Range Short-Read Technology Allows Direct Comparison of Pungent and Non-Pungent Types" (W012)

2:55pm Tony Bolger,RWTH Aachen University - Institute for Biology 1
"Sequence Analysis Using the LOGAN (LOssless Graph-based ANalysis) Framework" (W013)

3:15pm Doane Chilcoat,DuPont Pioneer
"Maize Genome Modification: Technology and Applications" (W014)

3:35pm Concluding Remarks

1:30pm - 3:40pm **Citrus Genome - PACIFIC SALON 6-7 (2ND FLOOR)**
Organizer: Concetta Licciardello, Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria (CREA)

1:30pm Manuel Talon,Centro de Genomica, Instituto Valenciano de Investigaciones Agrarias, IVIA
"Genomics Illuminates the Origin and Dispersal of Citrus" (W146)

1:50pm Tokurou Shimizu,Institute of Fruit Tree and Tea Science, NARO
"Genomic Selection in Citrus Breeding: Improved Accuracy with Additional Population Data" (W147)

2:10pm Yoko Eck,University of California Riverside
"Application of High Throughput Genotyping SNP Array for Citrus" (W148)

2:30pm Javier Terol,Centro de Genomica, Instituto Valenciano de Investigaciones Agrarias, IVIA
"RNA-SEQ Analysis of Fruit Ripening in 3 Clementine Varieties" (W149)

2:50pm Surya Saha,Boyce Thompson Institute
"CitrusCyc: Metabolic Pathway Databases for the *C. clementina* and *C. sinensis* Genomes" (W150)

3:10pm Qibin Yu,University of Florida, IFAS-CREC
"Transcriptional Profiling of Rough Lemon and Sweet Orange Reveals Critical Involvement of Reprogramming of Signaling Pathways in Early Response and Strong Quantitative Nature of Defense to '*Candidatus* Liberibacter asiaticus'" (W151)

1:30pm - 3:40pm **Cool Season Legumes - PACIFIC SALON 1**
Organizer: Kirstin Bett, University of Saskatchewan

1:30pm Eric von Wettberg,International Center for Tropical Botany, Florida Intl Univ.
"Temporal and Spatial Variation in a Large Collection of Chickpea (*Cicer arietinum*) Landraces" (W206)

1:50pm Alan H. Schulman,LUKE & University of Helsinki
"TBA on Faba Bean" (W207)

2:10pm Jonathan Kreplak,INRA, UMR1347 Agroécologie
"Updates on Pea Genomics" (W208)

2:30pm James L. Weller,School of Biological Sciences, University of Tasmania
"Comparative Genetics of Flowering Time Control in Legume" (W209)

2:50pm Ezgi Ogutcen,University of Saskatchewan
"Capturing Variation in *Lens spp.*" (W210)

3:10pm Mandeep Sagi,University of Saskatchewan
"Chickpea NBS-LRR Expression when Challenged with *Ascocyta rabei*" (W211)

3:20pm Kirstie Hetherington,Earlham Institute
"Genotype-to-Phenotype Associations in Common Pea and Wild Relatives" (W212)

Saturday - January 14, 2017

1:30pm - 3:40pm **Maize - GOLDEN WEST**
Organizer: Patrick S. Schnable, Iowa State UniversityChair: Patrick S. Schnable, Iowa State University

1:30pm Patrick S. Schnable,Iowa State University
"Introduction" (W591)

1:35pm Steven Briggs,University of California, San Diego
"Complementarity of the Transcriptome and Proteome" (W592)

2:05pm Bill Gordon-Kamm,DuPont Pioneer
"Expression of Bbm and WUS2 Extends Monocot Transformation into New Target Explants and Genotypes" (W593)

2:35pm Jason G Wallace,The University of Georgia
"Exploring the Other Maize Genome: Quantitative Analysis of How Maize Plants Interact with their Microbial Communities" (W594)

2:55pm Zhiwu Zhang,Washington State University
"BLUP Alphabet for Genomic Prediction" (W595)

3:15pm Sébastien Praud,LIMAGRAIN
"Remote Sensing for Crop Improvement: From Research to Industry" (W596)

1:30pm - 3:40pm **Plant Interactions with Pests and Pathogens - SUNRISE - MEETING HOUSE**
Organizer: Christie Williams, USDA-ARS at Purdue University

1:30pm Claude dePamphilis,Penn State University
"Parasitic Plants Steal Genes from their Host Plants through Horizontal Gene Transfer and use them in Parasite Processes" (W700)

1:50pm Brandon Schemerhorn,USDA-ARS/Purdue University
"Spatial Population Genetic Structure and Genetic Diversity of *Phytopthera sojae* in Indiana" (W701)

2:10pm Vincent P. Klink,Mississippi State University
"Co-Regulation of the SNARE-Containing Regulon Occurs during Plant Defense" (W702)

2:30pm Eduard Akhunov,Kansas State University, Department of Plant Pathology, Manhattan, KS
"Unraveling the Mechanisms of Stem Rust Resistance Conferred by the *Sr35* Gene against *Puccinia graminis f. sp. tritici* (*Pgt*)" (W703)

2:50pm Kai Voss-Fels,Justus Liebig University
"From Head to Foot: Genetics of Wheat Seedling Resistance Against Root Rot Caused by *Fusarium graminearum*" (W704)

3:10pm Jin-Ying Gou,School of Life Sciences, Fudan University
"Biosynthesis of Flavonoids Protects Wheat from Powdery Mildew Infection" (W705)

1:30pm - 3:40pm **Plant Molecular Breeding - PACIFIC SALON 3**
Organizers: Jinguo Hu, USDA ARS, Zhi-Kang Li, Institute of Crop Sciences/National Key Facility for Crop Gene Resources and Genetic Improvement and Yunbi Xu, CIMMYT/CAASChair: Yunbi Xu, CIMMYT/CAASCo-Chair: Zhi-Kang Li, Institute of Crop Sciences/National Key Facility for Crop Gene Resources and Genetic Improvement

1:30pm Long-Xi Yu,USDA-ARS-Plant Germplasm Introduction and Testing
"Molecular Markers Associated with Resistance to Drought and High Salinity in Alfalfa (*Medicago sativa* L.)" (W706)

1:50pm Fabio Cericola,Molecular Biology and Genetics, Aarhus University
"Optimizing Training Population Size and Genotyping Strategy for Genomic Prediction Using Association Study Results and Pedigree Information. a Case of Study in Advanced Wheat Breeding Lines" (W707)

2:10pm Christian R. Werner,Department of Plant Breeding, Justus Liebig University
"Genomic Prediction for Hybrid Performance in Rapeseed" (W708)

2:30pm Shuyu Liu,Texas A&M AgriLife Research
"Application of Array SNP and GBS in Genetics and Breeding of Hard Red Winter Wheat" (W709)

2:50pm John Baison,Umea Plant Science Center (UPSC)
"Exome Genotyping and Association Mapping in Conifers: Focusing on Norway Spruce" (W710)

3:10pm Janina Braatz,Christian Albrechts University of Kiel
"Towards the Production of Shatter Resistant Rapeseed by use of Mutations in Dehiscence Zone Identity Genes" (W711)

1:30pm - 3:40pm **Somatic Genome - PACIFIC SALON 4-5 (2ND FLOOR)**
Organizer: Xiu-Qing Li, Agriculture and Agri-Food Canada

1:30pm Xiu-Qing Li,Agriculture and Agri-Food Canada
"Introduction to Somatic Genome Variation and Manipulation" (W850)

1:55pm Pal Maliga,Rutgers University
"Cell-to-Cell Movement of Plastids and Mitochondria in Plants" (W851)

2:20pm Yinping Jiao,USDA-ARS/Cold Spring Harbor Laboratory
"Genomic Landscape of Induced Mutations in Sorghum" (W852)

2:45pm Richard J. Morris,John Innes Centre
"Signaling through Mobile mRNA: Lost in Translation?" (W853)

3:10pm Scott C. Lenaghan,Center for Renewable Carbon, University of Tennessee
"TBD" (W854)

1:30pm - 3:40pm **Sugar Beet Workshop - TOWNE - MEETING HOUSE**
Organizer: Imad Eujayl, USDA-ARS, Northwest Irrigation and Soils Res. Lab.

1:30pm Piergiorgio Stevanato,University of Padova, Italy
"Targeted Next-Generation Sequencing (NGS) of Disease Resistance Gene Analogs (RGAs) in Wild and Cultivated Beet" (W883)

1:47pm Andy Funk,Mihcigan State University
"Organization of a Resistance Gene Cluster Linked to Rhizomania Resistance in Sugar Beet" (W884)

2:04pm Kazunori Taguchi,NARO, Hokkaido Agricultural Research Center(HARC)
"Dynamic Analysis of Leaf Growth in Sugar Beet F1s Using UAV over Breeding Research Field" (W885)

2:21pm Subhashini Srinivasan,Institute of Bioinformatics and Applied Biotechnology
"Differential Genome Organization of Some Species in the Caryophyllales Order" (W886)

2:38pm Ilia Shilov,Institute of Agricultural Biotechnology
"Progress of Marker Assisted Selection on Sugar Beet in Russia" (W887)

2:55pm Chiara Broccanello,DAFNAE, Università degli Studi di Padova
"Ionomic and Openarray Profiling to Detect Effects of Biostimulants in Sugar Beet" (W888)

1:30pm - 3:40pm **Triticeae Genetics and Genomics, Session 2: Trait genetics and gene identification - TOWN AND COUNTRY**
Organizers: Michael Bevan, John Innes Centre, Gary J. Muehlbauer, Department of Plant and Microbial Biology, University of Minnesota and Justin D. Faris, USDA-ARS

1:30pm Sarah M McKim,University of Dundee at the James Hutton Institute
"Developmental Genetics of Reproductive Architecture in Barley" (W969)

1:50pm Helmy M. Youssef,IPK-Gatersleben
"VRS2 Regulates Hormone-Mediated Inflorescence Patterning in Barley" (W970)

2:10pm Robert S. Brueggeman,Department of Plant Pathology, North Dakota State University
"Wall Associated Kinases; Subversion by Necrotrophs to Cause Disease in the Cereals" (W971)

2:30pm Juan M. Debernardi,University of California, Davis
"miR172 Plays a Critical Role in the Origin of Free-Threshing Wheat" (W972)

2:50pm Simon Griffiths,John Innes Centre
"Extracting New and Useful Alleles from Wheat Landrace Cultivars of the AE Watkins Collection" (W973)

1:30pm - 3:40pm **Crop Evolution Genomics & Future Agricultural Productivity - ESQUIRE - MEETING HOUSE**
Organizer: Shahal Abbo, The Hebrew University of JerusalemCo-Chair: Yong-Bi Fu, Plant Gene Resources of Canada

1:30pm Brandon S. Gaut,University of California, Irvine
"Crop Genomic Diversity: A Contrast Between Annual and Perennial Systems" (W213)

1:50pm Paul Gepts,University of California
"Origin, Evolution, and Adaptation of Wild *Phaseolus vulgaris*" (W214)

2:10pm Zvi Peleg,The Hebrew University of Jerusalem
"Differential Selection of Grain and Embryo Weight during Wheat Evolution under Domestication" (W215)

2:30pm Martin Mascher,Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)
"Barley Diversity Now and 6000 Years Ago" (W216)

2:50pm Assaf Distelfeld,Tel Aviv University
"Genome-Wide Diversity Analysis using Wild Emmer Wheat Reference Assembly" (W217)

3:10pm Pat Heslop-Harrison,University of Leicester
"Domestication, Polyploidy and Genomics of Crops" (W218)

1:30pm - 3:40pm **Computer Demo 1 - CALIFORNIA**
Organizers: Monica C. Munoz-Torres, Lawrence Berkeley National Laboratory and Brian Smith-White, National Center for Biotechnology Information (NCBI/NLM/NIH)

1:30pm Pierre Larmande,IRD, UMR DIADE, Institut de Biologie Computationnelle
"The Agronomic Linked Data (AgroLD) Project" (C01)

1:45pm Célia Michotey,INRA - URGI
"Forest Tree GnpIS: an Information System Dedicated to Forest Tree Genetics, Genomics and Phenomics" (C02)

2:00pm Marco Moretto,Fondazione Edmund Mach
"Exploring Grapevine Gene Expression Patterns with Vespucci." (C03)

2:15pm Carol Lushbough,University of South Dakota
"Bio -TDS : BioQuery Tool Discovery System" (C04)

2:30pm Damien Leroux,MIAT, Institut National de la Recherche Agronomique
"Spell-QTL, a New Tool for QTL Analysis on Modern Datasets" (C05)

2:45pm Jorge Duitama,Universidad de los Andes
"Analysis of Genomic Variability within Inbred Populations with NGSEP" (C06)

3:00pm Lon Phan,NIH/NLM/NCBI
"NCBI Genomic Data Viewer" (C07)

3:15pm Richard J Challis,Edinburgh University
"Easymirror and Easyimport: Set up Your Own Ensembl Site in 2 Hours for Your Favourite Taxa" (C08)

1:30pm - 6:10pm **Cattle/Sheep/Goat 1 - SAN DIEGO**
Organizer: Jared E. Decker, Division of Animal Sciences, University of Missouri

1:30pm Kim C. Worley,Baylor College of Medicine
"Rambouillet Sheep Genomic Resources" (W123)

2:00pm Derek M. Bickhart,Dairy Forage Research Center, USDA-ARS
"The New Goat Long-Read Assembly Enables Interrogation of Genomic Dark Matter" (W124)

2:30pm Kim D. Pruitt,National Center for Biotechnology Information (NCBI/NLM/NIH)
"Bovidae Genome Data at NCBI – from Genome Annotation to Gene Curation" (W125)

3:00pm Break

3:30pm Ran Blekhman,University of Minnesota
"Host Genomic Control of the Microbiome" (W126)

4:15pm George E. Liu,Animal Genomics and Improvement Laboratory, USDA-ARS
"Systematic Profiling of Short Tandem Repeats in the Cattle Genome" (W127)

4:45pm Christine G. Elsik,Division of Animal Sciences, University of Missouri
"Annotating the New Bovine Reference Genome Assembly" (W128)

5:15pm James M. Reecy,Department of Animal Science, Iowa State University
"NRSP8 Bioinformatics Update" (W129)

1:30pm - 6:10pm **Equine 1 - ROYAL PALM SALON 5-6**
Organizer: Carrie J. Finno, University of California-DavisChair: Carrie J. Finno, University of California-DavisCo-Chair: Jessica L. Petersen, University of Nebraska

1:30pm Introductory Remarks

1:35pm Douglas Antczak,Cornell University
"Expression Signatures of Equid Lymphocyte Subsets Defined By Single Cell Sequencing" (W292)

1:50pm SK Beeson,University of Minnesota
"Identification of Candidate Genes for Recurrent Exertional Rhabdomyolysis in Thoroughbreds and Standardbreds" (W293)

2:05pm Brittni Ming-Whitfield,University of California - Davis
"Genome Wide Association Study of Juvenile Idiopathic Epilepsy (JIE) in Egyptian Arabian Foals" (W294)

2:20pm Maura Mack,University of California-Davis
"Two Mutations in Solute Carrier Family 24 Member 5 Are Associated with "Tiger Eye" Iris Pigmentation in Puerto Rican Paso Fino Horses" (W295)

2:35pm Vidhya Jagannathan,Institute of Genetics, University of Bern
"Naked Foal Syndrome (NFS) in Akhal-Teke Horses" (W296)

2:50pm Ernest Bailey,Maxwell H. Gluck Equine Research Center, Veterinary Science Department, University of Kentucky
"Natural History of CXCL16 in Horses: Evidence for Caballine, Non-Caballine Hybridization" (W297)

3:05pm Victor Mason,Swiss Institute of Equine Medicine, University of Bern and Agroscope
"Recurrent Airway Obstruction and eQTLs in Horses" (W298)

3:20pm Break

3:35pm Felipe Avila,University of Minnesota
"Identification of Genomic Signatures of Selection Associated with Cranial Morphology and Conformation in Arabian Horses" (W299)

3:50pm Annette M McCoy,University of Illinois
"Validation of Genetic Variants Predictive of Pacing in Standardbred Horses" (W300)

4:05pm Ann Kemper,University of Minnesota and University of Illinois
"Differential Expression Analysis of the Subchondral Bone and Articular Cartilage Transcriptomes in Neonatal and Adult Horses" (W301)

4:20pm Nicole Wanner,University of Minnesota College of Veterinary Medicine
"Impact of Paternal Inheritance of an Allele for Type I Polysaccharide Storage Myopathy on Exertional Rhabdomyolysis and Muscle Glycogen Concentration" (W302)

4:35pm Erica Scott,School of Veterinary Medicine, UC Davis
"Annotating Long Non-Coding RNA in the Horse Transcriptome" (W303)

4:50pm Erin Burns,University of California - Davis
"Generation of an Equine Tissue Biobank for Functional Annotation" (W304)

5:05pm Break

5:15pm RJ Schaefer,University of Minnesota
"Unraveling Gene Function Using Gene Coexpression Networks in the Domestic Horse" (W305)

5:30pm Michael S. DePriest,University of Louisville
"Protein-Coding Gene Sequences Quantify Progress Toward the New Equine Reference Genome Assembly" (W306)

5:45pm Douglas Antczak,Cornell University
"Expression Signatures of Equid Lymphocyte Subsets Defined by Single Cell Sequencing" (W307)

6:00pm Elspeth Bruford,European Bioinformatics Institute (EMBL-EBI)
"HGNC: Vertebrate Gene Nomenclature Resource" (W308)

6:15pm Discussion and Station Reports

1:30pm - 6:10pm Swine - ROYAL PALM SALON 1-2
Organizer: Kiho Lee, Virginia Tech

1:30pm Introductory Remarks

1:35pm Mary Ranketse,Agricultural Research Council-Biotechnology Platform
"Whole Genome Sequence Analysis Reveals Antimicrobial Resistance Genes, Plasmids and Potentially Unique Sequence Types of Enterotoxigenic *Escherichia coli* Isolates Causing Colibacillosis in Neonatal and Weaning Piglets of South Africa" (W911)

2:00pm Alex Clop,Center for Research in Agricultural Genomics (CRAG) CSIC-IRTA-UAB-UB
"A Whole-Genome Association Scan Detects Several Genetic Regions Influencing Semen Quality Traits in the Boar’s Sperm." (W912)

2:25pm Kiho Lee,Virginia Tech
"Use of CRISPR/Cas9 to Induce Targeted Mutagenesis during Porcine Embryogenesis" (W913)

2:40pm Dan Nonneman,USDA, ARS, USMARC
"Usmarc Update on Swine Reproduction Research" (W914)

2:55pm Francesca Bertolini,Iowa State University
"A Genomic Investigation of Porcine Periweaning Failure to Thrive Syndrome (PFTS)" (W915)

3:10pm Jorgenson Genome Travel Award Winner

3:20pm Administrator and Coordinator Reports

3:35pm Discussion of Community Needs and Resources

3:50pm Break

4:05pm James M. Reecy,Department of Animal Science, Iowa State University
"Reecy" (W916)

4:20pm Christopher K. Tuggle,Iowa State University, Department of Animal Science
"Tuggle " (W917)

4:35pm Joan K. Lunney,APDL, BARC, ARS, USDA
"Lunney USDA" (W918)

4:50pm Daniel C. Ciobanu,University of Nebraska - Lincoln
"Integration of Genomic Resources to Uncover Pleiotropic Regions Associated with Age at Puberty and Reproductive Longevity in Sows" (W919)

5:05pm Christian Maltecca,NCSU
"NCSU Update" (W920)

5:20pm Catherine W. Ernst,Department of Animal Science, Michigan State University
"Evaluation of Four US Pig Breeds Using the Affymetrix Axiom Pig HD Array" (W921)

5:35pm Zhihua Jiang,Washington State University
"Whole Transcriptome Termini Site Sequencing Reveals Gender Differences in Genome-Wide Usage of Alternative Polyadenylation Sites" (W922)

5:50pm Election of Officers and Other Business

3:00pm - 4:00pm Coffee Break - ATLAS FOYER

4:00pm - 6:10pm Challenges and Opportunities in Plant Science Data Management - an International Workshop - PACIFIC SALON 4-5 (2ND FLOOR)
Organizers: Ruth Bastow, GARNet, Carolyn J. Lawrence-Dill, Department of Genetics, Development and Cell Biology, Iowa State University and Darwin Campbell, Iowa State University

4:00pm Robert P. Davey,Earlham Institute
"Data Stewardship in the Life Sciences" (W139)

4:15pm Kelly Robbins,Cornell University
"The GOBII Project: Genomic Data Management for the Implementation of Genomic Selection" (W140)

4:30pm Margaret R. Krause,Cornell University
"Diverse Data Integration for Exploiting Genotype-by-Environment-by-Management Interactions" (W141)

4:45pm Elizabeth Arnaud,Bioversity International
"Annotation of Crop Data with Ontologies to Support Fitness for Use" (W142)

5:00pm Baskar Ganapathysubramanian,Iowa State University
"High Throughput Plant Phenotyping in the Field: Machine Learning Enabled by Data from Crowdsourcing" (W143)

5:15pm Uwe Scholz,Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Gatersleben
"Data Publication Using e!Dal" (W144)

5:30pm Medha Devare,CGIAR Consortium Office
"CGIAR's Big Data Platform: Leveraging Data for Impact" (W145)

4:00pm - 6:10pm **Bioenergy Grass Genomics - PACIFIC SALON 2**
Organizers: Kankshita Swaminathan, HudsonAlpha Institute for Biotechnology and Dan Smith, Aberystwyth University

4:00pm Kankshita Swaminathan,University of Illinois Urbana-Champaign
"Miscanthus Genome Update" (W069)

4:10pm Dan Smith,Aberystwyth University
"Analysis of Phenotype and Transcriptome Changes in *Miscanthus* Responding to Drought Stress" (W070)

4:30pm Isabel Roldan-Ruiz,ILVO Plant Sciences Unit and Department of Plant Biotechnology and Bioinformatics, Ghent University
"How Low Can You Go? Chilling and Frost Tolerance in *Miscanthus* Germplasm" (W071)

4:55pm David M. Braun,University of Missouri
"Sugar Transporters Controlling Sucrose Accumulation in Bioenergy Grasses" (W072)

5:20pm Jeremy Schmutz,HudsonAlpha Institute for Biotechnology
"Sequencing and Analysis of the Switchgrass Reference Genome and the Diversity of Switchgrass Wild Accessions" (W073)

5:45pm Shavannor M. Smith,University of Georgia
"TBA" (W074)

4:00pm - 6:10pm **Climate Change and ICRCGC 1 - GOLDEN BALLROOM**
Chair: Chittaranjan Kole, International Climate Resilient Crop Genomics ConsortiumCo-Chair: Jeffrey D. Ehlers, The Bill and Melinda Gates Foundation

4:00pm Chittaranjan Kole,International Climate Resilient Crop Genomics Consortium
"Combating Climate Change for FNEE Security" (W152)

4:10pm Prasanna Boddupalli,International Maize and Wheat Improvement Center
"TBA" (W153)

4:30pm Jauhar Ali,PBD, International Rice Research Institute
"Securing Food through Climate-Resilient Rice Varieties for Asia and Africa" (W154)

4:50pm Roberto Tuberosa,Department of Agricultural Sciences, University of Bologna
"A Collaborative Effort for Mining Allelic Diversity Toward the Selection of Climate-Resilient Durum Wheat" (W155)

5:10pm Manoj Prasad,National Institute of Plant Genome Research
"TBA" (W156)

5:30pm Bill Payne,University of Nevada-Reno
"TBA" (W157)

5:50pm Robert J. Henry,University of Queensland/QAAFI
"C4 Photosynthesis in Seeds may Contribute to Climate Adaptation" (W158)

4:00pm - 6:10pm **Genomic Selection and Genome-Wide Association Studies - GOLDEN WEST**
Organizers: Jianming Yu, Iowa State University and Dorian J. Garrick, Department of Animal Science, Iowa State University

4:00pm Welcoming Remarks

4:05pm Susan McCouch,Cornell University
"Linking Genome Wide Association Studies (GWAS) and Genomic Selection (GS) to better utilize Natural Variation in Rice" (W445)

4:30pm Bertrand Servin,INRA, UMR1388 GenPhySe
"QTL Detection using Genome Scans for Selection on Resequencing Data: Illustration in Cattle" (W446)

4:55pm Zhongwei Lin,National Maize Improvement Center, China Agricultural University
"The Genetic Architecture of Maize Nodal Root Number during Domestication" (W447)

5:15pm Rohan L. Fernando,Iowa State University
"Strategies to Improve Numerical Stability of Equations used for Genomic Prediction of Genetic Merit" (W448)

5:40pm Edward S. Buckler,USDA-ARS-Cornell University
"Direction of GWAS and GS" (W449)

6:05pm Concluding Remarks

4:00pm - 6:10pm **Next Generation Genome Annotation and Analysis - SUNRISE - MEETING HOUSE**
Organizer: Carson Holt, University of Utah

4:00pm Welcoming Remarks

4:05pm Steven B. Cannon,USDA-ARS-CICGRU
"Evaluating MAKER-P in the Context of Two Closely Related Peanut Genomes" (W626)

4:30pm Upendra Devisetty,CyVerse
"WQ-Maker: A Flexible and Scalable Genome Annotation Pipeline on Jetstream Cloud" (W627)

4:55pm Daniel Standage,University of California, Davis
"Genome Annotation of the Primitively Eusocial Paper Wasp *Polistes dominula*: Challenges and Insights" (W628)

5:20pm Nathan A Dunn,Lawrence Berkeley National Laboratory
"Apollo: Collaborative and Scalable Manual Genome Annotation" (W629)

5:45pm Michael S. Campbell,Cold Spring Harbor Laboritory
"High-Throughput Assessment of Gene Structure Changes in Resequencing Data, Using ACE" (W630)

4:00pm - 6:10pm **Non-Seed Plants - TOWNE - MEETING HOUSE**
Organizer: Stefan A. Rensing, Faculty of Biology, University of Marburg

4:00pm Jan de Vries,Dalhousie University
"Land Plant Terrestrialization and What We Can Learn from *Chara*" (W637)

4:20pm Daniel Lang,Helmholtz Center Munich
"Extraordinary Moss Genome Structure and Evolution uncovered by the *Physcomitrella* V3 Chromosome-Scale Assembly" (W638)

4:40pm Nico van Gessel,Plant Biotechnology, University of Freiburg
"Sequencing Funariaceae: First Insights from Seven Draft Genomes of *Physcomitrella's* Closest Relatives" (W639)

5:00pm Peter Szovenyi,University of Zurich
"The Genome of the Hornwort, *Anthoceros agrestis*" (W640)

5:20pm Harald Schneider,Natural History Museum and Sun Yat-Sen University
"Rate Homo- and Rate Heterogeneity in the Genome Size Evolution Across the Phylogeny of Land Plants" (W641)

5:40pm Fay-Wei Li,Boyce Thompson Institute
"Fern Genomes on the Horizon" (W642)

4:00pm - 6:10pm **Oats - PACIFIC SALON 6-7 (2ND FLOOR)**
Organizers: Nicholas A. Tinker, Agriculture and Agri-Food Canada and Eric N. Jellen, Brigham Young University

4:00pm Nicholas A. Tinker,Agriculture and Agri-Food Canada
"Avena Origins and Futures: Workshop Introduction and Summary" (W650)

4:10pm Anne Osbourn,John Innes Centre
"*Avena strigosa* – from Biosynthetic Gene Clusters to Genomics" (W651)

4:30pm Adam Whaley,University of North Carolina at Charlotte
"A Hexaploid Oat Genome: The Long and the Short of It" (W652)

4:50pm Elena Prats,Spanish National Research Council (CSIC)
"Genetic Diversity and GxE Interactions for Drought and Disease Tolerance in Oat" (W653)

5:10pm Vahid Omidvar,University of Minnesota
"Oat Crown Rust Disease Resistance: Two Sides to the Story" (W654)

4:00pm - 6:10pm **Population and Conservation Genomics 1 - PACIFIC SALON 3**
Organizer: Om P. Rajora, University of New Brunswick

4:00pm Introductory Remarks

4:05pm Sam Yeaman,University of Calgary
"Using Comparative Population Genomics to Find the Genes Driving Convergent Local Adaptation" (W742)

4:25pm Marjorie F. Oleksiak,University of Miami
"Rapid Adaptation through Standing Genetic Variation" (W743)

4:45pm Mackenzie Gavery,University of Washington
"Characterization of Genetic and Epigenetic Variation in Hatchery and Natural-Origin Steelhead, *Oncorhynchus mykiss*" (W744)

5:05pm Wenbin Mei,University of California, Davis
"Population Genomics of Copy Number Variation in a Natural Population of Teosinte" (W745)

5:25pm Eleftheria Palkopoulou,Department of Genetics, Harvard Medical School
"Genomics of Elephants and their Extinct Relatives" (W746)

5:45pm Ying Zhen,University of California, Los Angeles
"Genomic Divergence across Ecological Gradients in a Central African Songbird (*Andropadus virens*)" (W747)

6:05pm Concluding Remarks

4:00pm - 6:10pm **Small RNA - PACIFIC SALON 1**
Organizers: Blake Meyers, Donald Danforth Plant Science Center and Pamela J. Green, University of Delaware

4:00pm Craig Pikaard,Indiana University/HHMI
"Transcribing the RNAs of RNA-Directed DNA Methylation" (W838)

4:20pm Rebecca A. Mosher,University of Arizona
"Dynamic Nucleocytoplasmic Trafficking of Argonaute 4 Enables RNA-Directed DNA Methylation" (W839)

4:40pm Amy Pasquinelli,University of California, San Diego
"Elucidating the Dark Side of the MicroRNA" (W840)

5:00pm Wenbo Ma,University of California
"*Phytophthora* Pathogens Manipulate Plant Small RNAs to Promote Infection" (W841)

5:20pm Olivia Rissland,University of Toronto
"Reorganization of mRNA-Protein Complexes during microRNA-Mediated Repression" (W842)

5:40pm Lila Vodkin,University of Illinois
"A Mutation in an Argonaute Protein Explains the Epistatic Interactions of the K and I Loci which Control Soybean Seed Color Patterns through Levels of Chalcone Synthase siRNAs" (W843)

4:00pm - 6:10pm **Teaching Genetics, Genomics, Biotechnology, and Bioinformatics - ESQUIRE - MEETING HOUSE**
Organizer: Abdelmajid Kassem, Fayetteville State University

4:00pm Noel Chen,Novogene Corporation
"Genotyping By Sequencing (GBS) Based Approach in Ultra-Density Genetic Mapping, SNP Discovery and Population Evolution" (W942)

4:20pm Etienne Gnimpieba,University of South Dakota
"Bio-Question Driven Bioimage Informatics Workflow Design Using Bio-TDS" (W943)

4:40pm David A. Lightfoot,Southern Illinois University
"Teaching Bioinformatics By Social Networking: The Pokémon Factor" (W944)

5:00pm Khalid Meksem,Department of Plant Soil and Agricultural Systems, SIUC
"Teaching Introductory Genetics to Agricultural Science Students" (W945)

4:00pm - 6:10pm **Triticeae Genetics and Genomics, Session 3: Application of genomic resources to Triticeae improvement - TOWN AND COUNTRY**
Organizers: Michael Bevan, John Innes Centre, Gary J. Muehlbauer, Department of Plant and Microbial Biology, University of Minnesota and Justin D. Faris, USDA-ARS

4:00pm Cyrille Saintenac,INRA / UBP GDEC
"*Stb6* is a Wall-Associated Kinase Gene that provides Gene-for-Gene Resistance against *Zymoseptoria tritici* in Wheat"

4:20pm Matthew J. Moscou,The Sainsbury Laboratory
"Genomics of the Barley Immune System" (W974)

4:40pm Cyrille Saintenac,INRA/UBP
"*Stb6* is a Wall-Associated Kinase Gene that provides Gene-for-Gene Resistance against *Zymoseptoria tritici* in Wheat" (W975)

5:00pm Tatiana V. Danilova, Kansas State University
"Major structural genomic alterations are associated with hybrid speciation in Aegilops markgrafii (Triticeae)"

5:20pm Kevin P. Smith,University of Minnesota
"Barley Breeding using Genomic Selection" (W977)

5:40pm Jochen Kumlehn,Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)
"Mutual Benefits of Genome Engineering and Haploid Technology" (W978)

4:00pm - 6:10pm **Genome Database for Rosaceae Training - CALIFORNIA**
Organizer: Dorrie Main, Washington State University

4:00pm Sook Jung,Washington State University
"Using GDR: An Overview" (W418)

4:20pm Richard J. Harrison,NIAB EMR
"Use of Strawberry Genomic Resources in GDR" (W419)

4:40pm Riccardo Velasco,Research and Innovation Centre, Edmund Mach Foundation
"Using the New Apple Genome Assembly v4.0 Data in GDR" (W420)

5:00pm Cameron Peace,Washington State University
"The GDR Is a Critical Resource for Developing and Refining Trait-Predictive DNA Tests" (W421)

5:20pm Ksenija Gasic,Clemson University
"Using Field Book App and Bims in GDR for Peach Breeding" (W422)

5:40pm Michael Coe,Cedar Lake Research Group
"Open Discussion on GDR" (W423)

5:30pm - 7:30pm **Canadian Genomics Enterprise Reception - TIKI PAVILION TERRACE**

5:30pm - 7:30pm **CyVerse User Meeting: Tools and Resources Demos - STRATFORD**
Organizers: Jason Williams, Cold Spring Harbor Laboratory and Kapeel Chougule, Cold Spring Harbor Laboratory

5:30pm User-guided demonstrations and discussion

6:20pm - 8:20pm **IWGSC Business Meeting - PACIFIC SALON 4-5 (2ND FLOOR)**

6:30pm - 8:30pm **Africa Biosciences Networking Dinner - GARDEN BALLROOM**

Organized by Steve Rounsley (Dow Agrosciences), Kathy Kahn and Christina Owen (Bill & Melinda Gates Foundation). Please join colleagues who have an interest in African agriculture to network and consider how your research might help increase the sustainable productivity of smallholder farmers. We welcome those who have already worked extensively on these issues, as well as new or simply curious colleagues. We will be highlighting the interests and accomplishments of Africa-based scientists who are partnering with Dow Agrosciences and/or the Bill & Melinda Gates Foundation. Each registered participant will be encouraged to share their expertise and/or questions. Dinner and drinks will be provided! Due to limited space, RSVP is recommended to kelly.thoma@gatesfoundation.org by January 5, 2016.

Sunday - January 15, 2017

7:00am - 8:00am **Continental Breakfast - GOLDEN BALLROOM**

7:00am - 8:00pm **Registration - ATLAS FOYER**

7:00am - 9:00pm **Poster Access - GRAND EXHIBIT HALL**

8:00am - 10:10am **Comparative Genomics - GOLDEN WEST**
Organizers: Yong Q. Gu, USDA ARS, Western Regional Research Center and Nathan M. Springer, Department of Plant and Microbial Biology, University of Minnesota

8:00am Blake Meyers,Donald Danforth Plant Science Center
"A Comparative Genomic Analysis of Plant Reproductive phasiRNAs" (W177)

8:20am Jim Leebens-Mack,University of Georgia
"Plant Phylogenomics: Comparative Analyses of Plant Genes and Genomes" (W178)

8:40am Huey Tyng Lee,University of Queensland
"Understanding Marine Adaptation through the Genome of a Southern Hemisphere Seagrass Species (*Zostera muelleri*)" (W179)

9:00am Hong-Qing Ling,Institute of Genetics and Developmental Biology, CAS
"Comparative Analysis of *Triticum urartu* Genome with other Grass Genomes" (W180)

9:20am Brad Barbazuk,University of Florida
"Genome Wide Discovery of Alternative Splice Isoforms Across Multiple Plant Species and the Identification of Conserved Events" (W181)

9:40am Matthew B. Hufford,Iowa State University
"Evolutionary Insights from *de novo* Genome Assembly of Wild Maize" (W182)

8:00am - 10:10am **Development and Application of Transgenic Technology in Agriculture - ROYAL PALM SALON 3-4**
Organizer: Ashok Shrawat, Monsanto

8:00am Nian Wang,University of Florida, IFAS-CREC
"Generating Disease Resistant Citrus Varieties using Cas9/sgRNA" (W262)

8:20am Cara L Soyars,Univeristy of North Carolina at Chapel Hill
"Cas9 Targeting and Specificity in Higher-Order CRISPR Multiplexed Plants" (W263)

8:40am Ming Luo,CSIRO
"Genome Editing in Cereals" (W264)

9:00am Bing Yang,Iowa State University
"SWEET Promoter Editing Produces Rice Lines Resistant to Bacterial Blight" (W265)

9:20am Justin M. McGrath,University of Illinois, Urbana-Champaign
"Chloroplast Transformation for High-Level Expression of Useful Proteins" (W266)

8:00am - 10:10am Equine 2 - ROYAL PALM SALON 5-6
Organizer: Carrie J. Finno, University of California-Davis

8:00am Elizabeth A. Maga,University of California, Davis
"Does the Microbiome Matter? Microbiome Profiling in the Horse and Other Livestock Species" (W309)

8:50am James M. Reecy,Department of Animal Science, Iowa State University
"Update on NRSP8 Activities" (W310)

9:00am Theodore S. Kalbfleisch,University of Louisville
"EquCab3: An Improved Genomic Reference for the Domestic Horse" (W311)

9:30am Discussion

8:00am - 10:10am Gene Introgression - PACIFIC SALON 2
Organizers: Julie King, The University of Nottingham and Theresa A. Musket, University of MissouriCo-Chair: Julie King, The Univ of Nottingham

8:00am Julie King,The University of Nottingham
"Introduction" (W401)

8:05am Narinder Singh,Kansas State University
"Simultaneous Introgression and Mapping of Hessian Fly Resistance from *Aegilops tauschii* in Wheat" (W402)

8:25am Ji Zhou,Earlham Institute
"Scalable-Infield Phenotyping for DNA Measurements of Performance Related Traits to Study Gene Introgression in Bread Wheat" (W403)

8:45am George Fedak,Agriculture and Agri-Food Canada
"Introgression of Alien Genes for Resistance to Fusarium Head Blight and Race *Ug99* of Stem Rust" (W404)

9:05am Tim Langdon,IBERS, Aberystwyth University
"Introgressions in an Oat Nested Assoc. Mapping Population" (W405)

9:25am Delphine Fleury,University of Adelaide
"Characterization of a *Thinopyrum ponticum* Introgressions into Durum Wheat Chromosome 7A for Tolerance to Drought and Heat" (W406)

9:45am André Schönhofen,University of California, Davis
"Combined Mutations in *SBEII* Genes Affect Grain Yield and Quality in Pasta and Bread Wheat" (W407)

8:00am - 10:10am **New Approaches for Developing Disease Resistance in Cereals - PACIFIC SALON 4-5 (2ND FLOOR)**
Organizers: Jesse Poland, Kansas State University, Maricelis Acevedo, North Dakota State University and Jessica Rutkoski, Cornell University & CIMMYT

8:00am Roger Wise,Corn Insects and Crop Genetics Research, USDA-Agricultural Research Service, Iowa State University
"Inter-Chromosomal Transfer of Immune Regulation during Infection of Barley with the Powdery Mildew Pathogen" (W614)

8:20am Christian D Cruz,Kansas State University
"Developing Strategies for Identifying Novel Sources of Resistance for the Intractable Wheat Blast Disease" (W615)

8:40am Adnan Riaz,Queensland Alliance for Agriculture and Food Innovation
"Speeding up the Discovery of Novel Leaf Rust Resistance in Wheat" (W616)

9:00am Burkhard Steuernagel,John Innes Centre
"New Approaches for Gene Cloning in Triticeae" (W617)

9:20am Simon Krattinger,University of Zurich
"Rapid Isolation of a Disease Resistance Gene in Hexaploid Wheat By Generating a Cultivar-Specific Long-Range Chromosome Assembly" (W618)

8:00am - 10:10am **Plant Phenotypes - PACIFIC SALON 3**
Organizers: Carolyn J. Lawrence-Dill, Department of Genetics, Development and Cell Biology, Iowa State University, Darwin Campbell, Iowa State University and Ruth Bastow, Global Plant Council

8:00am Mitch Tuinstra,Purdue University
"Introduction to the North American Plant Phenotyping Network" (W712)

8:18am Ulrich Schurr,Forschungszentrum Jülich GmbH
"Integrated Phenotyping Concepts and News from Emphasis - the European Infrastructure for Multi-Site Plant Phenotypingand Simulation for Food Security in a Changing Climate" (W713)

8:36am Steven A. Whitham,Iowa State University
"Developing the Enviratron: A Facility for Automated Phenotyping of Plants Growing under Varied Conditions" (W714)

8:54am Francisco Pinto,International Maize and Wheat Improvement Centre (CIMMYT)
"Phenotyping for Breeding and Physiological Pre-Breeding" (W715)

9:12am Ramona Walls,University of Arizona
"Merging Data Across Continents and Scales with the Plant Phenology Ontology" (W716)

Sunday - January 15, 2017

8:00am - 10:10am **QTL Cloning - TOWN AND COUNTRY**
Organizer: Roberto Tuberosa, Department of Agricultural Sciences, University of Bologna

8:00am Beat Keller,University of Zurich
"Genomic Approaches Provide Novel Tools for Rapid Cloning of Major QTL in Large Cereal Genomes" (W784)

8:20am Francesco Emanuelli,DipSA - University of Bologna
"Cloning of *Vgt3*, a Major QTL for Flowering Time in Maize" (W785)

8:40am Enrico Francia,Department of Life Sciences, University of Modena and Reggio Emilia
"Copy Number Variation of *CBF* Genes Rules the Effect of *FR-H2* QTL for Frost Tolerance in Barley" (W786)

9:00am Assaf Distelfeld,Tel Aviv University
"Genetic Dissection of QTLs Controlling Brittle Rachis on Chromosomes 3A and 3B in Tetraploid Wheat" (W787)

9:20am Jemima Brinton,John Innes Centre
"Two Tightly Linked Genes Controlling Grain Length Underlie a Major Grain Weight QTL in Polyploid Wheat" (W788)

9:40am Vasu Kuraparthy,North Carolina State University
"Modifications to a LATE MERISTEM IDENTITY-1 Gene Are Responsible for the Major Leaf Shapes of Cotton" (W789)

8:00am - 10:10am **Resources and Programs for Undergraduate Education in Genomics - TOWNE - MEETING HOUSE**
Organizer: Scott T Woody, UW-Madison

8:00am Scott Woody,UW-Madison
"Introductory remarks" (W802)

8:10am Sarah Elgin,Washington University in St Louis
"The Genomics Education Partnership: An Introduction to Bioinformatics in a Course-based Undergraduate Research Experience (CURE)" (W803)

8:30am Anne G. Rosenwald,Georgetown University
"The Genome Solver Project: Faculty Training in Bioinformatics for a Cure" (W804)

9:10am Ray A. Enke,James Madison University
"Enke title" (W805)

9:30am Dave Micklos,DNA Learning Center
"Student DNA Genotyping by Mass Spectrometry: An Affordable Look into DNA Ancestry and Profiling" (W806)

9:50am Burnette Jim,UC-Riverside
"NIBLSE: A Network to Fully Integrate Bioinformatics into the Undergraduate Curriculum." (W807)

8:00am - 10:10am **Solanaceae - PACIFIC SALON 1**
Organizers: Shelley Jansky, University of Wisconsin-Madison and Mathilde Causse, INRA GAFL

8:00am Richard E. Veilleux,Virginia Tech
"Genomic Heterogeneity of Potato" (W844)

8:20am Antonio Granell,IBMCP
"Digging in the European Tomato Variabiltiy Pool (TRADITOM)" (W845)

8:40am Laurie Grandont,Biosystematics, Wageningen University & Research
"The High-Quality Genome Sequence of *Solanum etuberosum* provides Insights into Genome and Trait Evolution of the *Solanum* Genus" (W846)

9:00am Prashant S Hosmani,Boyce Thompson Institute
"Improvements in the Tomato Reference Genome (SL3.0) and Annotation (ITAG3.0)" (W847)

9:20am Spela Baebler,National Institute of Biology, Department of Biotechnology and Systems Biology
"Novel Hormonal Cross - Talks in Potato Discovered By Network Analysis" (W848)

9:40am Mohamed Zouine,INPT-ENSAT
"Tomexpress, a Unified Tomato RNA-Seq Platform for Visualization of Expression Data, Clustering and Correlation Networks" (W849)

8:00am - 10:10am **Sorghum/Millet - PACIFIC SALON 6-7 (2ND FLOOR)**
Organizer: Yinghua Huang, USDA ARS

8:00am Yinghua Huang,USDA ARS
"Introduction: Sorghum & Millet Workshop" (W855)

8:05am Ian Godwin,School of Agriculture and Food Sciences, The University of Queensland
"Genome-Informed Genetic Engineering and Gene Editing in *Sorghum*" (W856)

8:25am Takashi Sazuka,Nagoya Univ.
"*Dw1*, an Important Gene for Lodging Resistance and Mechanical Harvesting of Sorghum, Encodes a Novel Protein Involved in Cell Proliferation" (W857)

8:45am Yongfu Tao,Queensland Alliance for Agriculture and Food Innovation, The University of Queensland
"Dissecting the Genetic Basis of Seed Size in *Sorghum bicolor*" (W858)

9:05am Patrick S. Schnable,Iowa State University
"High Resolution Phenotyping: Semi-Automated Feature Extraction from RGB Images of *Sorghum* Panicles" (W859)

9:25am Sandeep R. Marla,Kansas State University
"Functional Genomic Analyses Reveal Molecular Systems Underlying Chilling Response in Cold-tolerant and Cold-susceptible Sorghums" (W860)

9:45am Song Weining,Northwest A&F University
"TBD" (W861)

8:00am - 12:40pm Cattle/Sheep/Goat 2 - SAN DIEGO
Organizer: Jared E. Decker, Division of Animal Sciences, University of Missouri

8:00am Hans D. Daetwyler,Agriculture Victoria and La Trobe University
"Meta-Analyses Approaches to Prioritise Pleiotropic Sequence Variants from Global Sequence Consortia" (W130)

8:30am Simon Forsberg,Uppsala Universitet
"Simon Update: Yeast Interactions" (W131)

9:15am Julie Demars,INRA-GenPhySE-Génétique, Physiologie et Systèmes d'Elevage-UMR1388
"*EIF2S2* Retroposition into *IRF2BP2* Underlies Fleece Variation in Sheep through the Formation of a Long Endogenous Double-Stranded RNA" (W132)

9:45am Break

10:15am Megan M. Rolf,Kansas State University
"Heritability and Test Duration for Water Intake in Beef Cattle" (W133)

10:45am Jesse L. Hoff,Division of Animal Sciences, University of Missouri
"Enhancement of QTL Mapping and Genomic Prediction for Bovine Respiratory Disease Using Sequence Imputation and Feature Selection" (W134)

8:00am - 12:40pm Genome annotation resources at the EBI - CALIFORNIA
Organizer: Sandra Orchard, EMBL-EBI

8:00am Helen Sparrow,European Bioinformatics Institute (EMBL-EBI)
"Ensembl and EnsemblGenomes" (W408)

9:00am Jane Loveland,Wellcome Trust Sanger Institute
"Manual Genome Annotation" (W409)

9:30am Elspeth Bruford,European Bioinformatics Institute (EMBL-EBI)
"VGNC: The Vertebrate Gene Nomenclature Committee" (W410)

9:50am Ramona Britto,EMBL-EBI
"Comprehensive Coverage and Annotation of Proteome Space" (W411)

10:20am Laura Clarke,European Molecular Biology Laboratory, European Bioinformatics Institute, Vertebrate Genomics
"Submitting Data to EMBL-EBI Resources" (W412)

10:50am Amy Tang,EMBL-European Bioinformatics Institute
"Expression Atlas - a Gene and Protein Expression Look-up Tool" (W413)

11:20am Gary Saunders,EMBL-EBI
"Drilling into Experimental Data at the EMBL-EBI Archives" (W414)

11:50am Sandra Orchard,EMBL-EBI
"Omics-DI : Searching the Omics Space" (W415)

12:10pm Dominic Clark,EMBL-EBI
"The EMBL-EBI Industry Program and Ontologies for Agriculture" (W416)

8:00am - 12:40pm Poultry 2 - SUNSET - MEETING HOUSE
Organizers: Behnam Abasht, Department of Animal and Food Sciences, University of Delaware and Huaijun Zhou, University of California, Davis

8:00am Wesley Warren,Washington University School of Medicine-McDonnell Genome Institute
"A Improved Chicken Genome Reference: Recovery of Missing Autosomes and Addition of a New W Chromosome" (W770)

8:20am Thibaut Hourlier,European Molecular Biology Laboratory - EBI
"Genome Annotation of the New Chicken Assembly Gallus_Gallus-5.0" (W771)

8:40am Fiona McCarthy,University of Arizona
"Beyond Annotation: Assigning Function to Chicken ncRNAs" (W772)

9:00am Richard Kuo,Roslin Institute, University of Edinburgh
"Iso-Seq Sequencing and the Chicken Genome Annotation" (W773)

9:20am Behnam Abasht,Department of Animal and Food Sciences, University of Delaware
"RNA-Seq Analyses Reveals High Frequency of Allele Specific Expression and No Evidence of Genomic Imprinting in Specific Embryonic Tissues of Chicken" (W774)

9:40am Martien A.M. Groenen,Wageningen University
"Identification of Deleterious Alleles in Poultry" (W775)

10:00am Break

10:30am Richard Crooijmans,Wageningen University
"EU-Project Horizon 2020: Innovative Management of Animal Genetic Resources (IMAGE) Specific for Chicken" (W776)

10:50am Michèle Tixier-Boichard,GABI, INRA, AgroParisTech, Université Paris-Saclay
"Disentangling Genetic Exchanges Between *Gallus gallus* and *Gallus sonneratii* in Order to Better Understand the Domestication of Chickens" (W777)

11:10am NC1170 Business Meeting

8:00am - 12:40pm **Sugar Cane (ICSB) - ROYAL PALM SALON 1-2**
Organizers: Paul H. Moore, Centro de Tecnologia Canavieira, Brazil and Nathalie Piperidis, Sugar Research Australia

8:00am Introductory Remarks

8:10am Olivier Garsmeur,CIRAD, UMR AGAP
"A Reference Sequence of the Monoploid Genome of Sugarcane" (W889)

8:40am Frederik C Botha,Sugar Research Australia Limited
"Development and Plasticity of Photosynthesis in Sugarcane" (W890)

9:10am Annelie Marquardt,Queensland Alliance of Agriculture and Food Innovation - The University of Queensland - Sugar Research Australia
"Yellow Canopy Syndrome Is Associated with Changes in Primary and Secondary Metabolism" (W891)

9:40am Intermission

9:50am Jianping Wang,Agronomy Department, University of Florida
"Identifying Quantitative Trait Loci Controlling Sugarcane Orange Rust Resistance *via* Genotyping by Sequencing" (W892)

10:20am Ray Ming,University of Illinois at Urbana-Champaign
"Cell Wall Metabolism and Hexose Allocation Contribute to Biomass Accumulation in Sugarcane" (W893)

10:50am Robert J. Henry,University of Queensland/QAAFI
"The Long and Short of the Sugarcane Transcriptome" (W894)

11:20am Mona B. Damaj,Texas A&M AgriLife Research and Extension
"The CBF1/DREB1C Transcription Factor is a Common Regulator of Hormonal, Biotic and Abiotic Stress Responses in Sugarcane" (W895)

11:50am Concluding Remarks

8:00am - 6:10pm **Forest Tree - SUNRISE - MEETING HOUSE**
Organizers: Steve Hanley, Rothamsted Research, Jill L. Wegrzyn, Department of Ecology and Evolutionary Biology - University of Connecticut and Amy Brunner, Department of Forest Resources and Environmental Conservation, Virginia Tech

8:00am Introductory Remarks

8:05am Timothy J. Tschaplinski,Oak Ridge National Laboratory
"Metabolomic Responses of Down-Regulated p-Coumaroyl Quinate/Shikimate 3'-Hydroxylase (C3'H) and Cinnamate 4-Hydroxylase (C4H) Genes in the Lignin Biosynthetic Pathway of *Eucalyptus urophylla* X *E. grandis* with Reduced Recalcitrance" (W349)

8:25am David Kainer,Australian National University
"Genome-Wide Association of Essential Oil Traits in *Eucalyptus polybractea* using a Low-Depth WGS Pipeline" (W348)

8:45am Craig H. Carlson,Cornell University
"Differential Expression, Regulatory Divergence, and Sex Dimorphism Pervade the Shrub Willow (*Salix* spp.) Transcriptome" (W337)

9:05am Dario Grattapaglia,Embrapa Recursos Genéticos e Biotecnologia and Graduate Program in Genomic Sciences - Catholic University of Brasília
"Differential Patterns of Genome-Wide Methylation within and between *Eucalyptus* Clones across Variable Environments" (W339)

9:25am Albert G. Abbott,Forest Health Research and Education Center, University of Kentucky
"Genetic Mapping of Resistance to *Phytophthora cinnamomi* for American Chestnut Restoration in the Southeastern United States" (W340)

9:45am Break

10:10am Jerald D. Noble,University of Florida
"Integrating Genome and Transcriptome Data to Predict Growth and Development Traits in *Populus deltoides*" (W341)

10:30am Héloïse Bastiaanse,US Forest Service
"A Genome-Wide Screen for Genomic Regions Influencing Gravitropism and Tension Wood Formation in *Populus*" (W343)

10:50am Evandro Novaes,Universidade Federal de Goias
"The Transcriptome of Savanna Species are Less Responsive to Drought Compared to Forest Species of the Neotropical Tabebuia Alliance" (W344)

11:10am Barbara S. F. Muller,University of Brasília - EMBRAPA
"Joint GWAS Analysis for Growth Traits Across Four *Eucalyptus* Breeding Populations" (W338)

11:30am Matthew Zinkgraf,UC Forest Service
"Comparative Genomics Analysis of Gravitropic Response in a Phylogenetic Survey of Angiosperm Trees" (W345)

11:50am Jarkko T Salojärvi,University of Helsinki
"Population Genomics of Silver Birch" (W346)

12:10pm Gancho T. Slavov,Institute of Environmental Biological and Rural Sciences (IBERS), Aberystwyth University and Rothamsted Research
"Predicting the Forest, but not the Trees: Genomecology of *Populus trichocarpa*" (W350)

12:30pm Lunch

2:00pm C. Donovan Bailey,New Mexico State University
"*Leucaena* (Leguminosae: Mimosoideae) Genomic Resources and a Novel Means of Recovering Hybrid Parentage from a Combination of Data Sources" (W342)

2:20pm Hairong Wei,Michigan Technological University
"Genome and Evolution of *Betula platyphylla*" (W347)

2:40pm Daniela Puiu,Johns Hopkins University, School of Medicine
"Preliminary Studies of a Genome Assembly of the California Endemic Oak, *Quercus lobata* Née (Fagaceae) using Pacific Biosciences and Illumina Sequencing Data" (W351)

3:00pm U. Uzay Sezen,Department of Ecology and Evolutionary Biology, University of Connecticut
"A Reference Draft Genome for Douglas-fir (*Pseudotsuga menziesii* (Mirb.) Franco)" (W352)

3:20pm David Chagne,Plant and Food Research
"Manuka Genome Assembly using Chromosome Conformation Capture Hi-C Analysis" (W353)

3:40pm Nanette Christie,Department of Genetics, Forestry and Agricultural Biotechnology Institute (FABI), Genomics Research Institute (GRI), University of Pretoria
"A Systems Genetics Browser for Genome-Wide Expression Association Data in Forest Trees" (W335)

4:00pm Discussion

9:30am - 10:30am Coffee Break - ATLAS FOYER

10:30am - 12:40pm Abiotic Stress - GOLDEN BALLROOM
Organizer: Henry T. Nguyen, University of Missouri

10:30am Seyedehmahsa Mousaviderazmahalleh,University of Western Australia
"From Climate to the Genome: An Insight Towards Genome-Wide Changes of Wild Narrow-Leafed Lupin in Different Climates" (W001)

10:50am Sandra K. Truong,Texas A&M University
"Bioenergy Sorghum Crop Model Predicts VPD-Limited Transpiration Traits Enhance Biomass Yield in Water-Limited Environments" (W002)

11:10am Heng Ye,University of Missouri
"Genetic Improvement and Molecular Mechanisms of Waterlogging Tolerance in Soybean" (W003)

11:30am Rupesh Deshmukh,University Laval
"Elucidation of Molecular Mechanisms Involved in Silicon Uptake and Derived Stress Tolerance in Plants" (W004)

11:50am Wenwei Xu,Texas A&M University
"Breeding for Drought Tolerance in Maize" (W005)

12:10pm Francis Kusi,CSIR - Savanna Agricultural Research Institute and CSIR-Savanna Agricultural Research Institute (CSIR-SARI)
"Breeding for Abiotic Stress Tolerance Cowpea in West Africa" (W006)

Sunday - January 15, 2017

10:30am - 12:40pm **Cacao Advanced Omics Workshop - ROYAL PALM SALON 3-4**
Organizers: Mark Guiltinan, The Pennsylvania State University and Siela Maximova, The Pennsylvania State University

10:30am Xavier Argout,CIRAD, UMR AGAP
"The Cacao Criollo Genome v2.0 : An Improved Version of the Genome for Genetic and Functional Genomic Studies" (W098)

10:55am Claude dePamphilis,Penn State University
"Population Genomics of Tropical Tree Species: Implications for Identification of Genetic Components of Disease Resistance in Theobroma Cacao" (W099)

11:20am Ranjana Bhattacharjee,International Institute of Tropical Agriculture
"True-to-Type DNA Fingerprinting of West and Central African Cocoa Germplasm: Implications Towards Cocoa and Chocolate Economy and Sustainability" (W100)

11:45am Judith K Brown,University of Arizona
"Characterization of 21 Cacao Swollen Shoot Viral Genomes Reveals Multiple Species with Diverse Genome Organizations" (W101)

12:10pm Andrew Fister,The Pennsylvania State University
"CRISPR/Cas9 Mediated Mutagenesis of a Supressor of Defense Response in *T. cacao*" (W102)

10:30am - 12:40pm **Cat & Dog Workshop - ROYAL PALM SALON 5-6**
Organizer: Barbara Gandolfi, University of Missouri-Columbia
Co-Chair: Brian W. Davis, NHGRI

10:30am Eva-maria Geigl,Institut Jacques Monod - University Paris Diderot
"Ancient DNA to Explore Origin and Spread of the Domestic Cat" (W116)

10:48am Adam R. Boyko, Cornell University
"Contrasting the Genetic Architecture of Complex Traits Between Village Dog Populations and Purebred and Mixed-Breed Dog Cohorts" (W117)

11:06am Mohini Patil,Affymetrix
"Dogs Un-Leashed-New Analysis Tools for the Canine Community" (W118)

11:16am Fabiana H. G. Farias,Washington University School of Medicine-McDonnell Genome Institute
"A Survey of Whole-Genome Variation in Domestic Cats" (W119)

11:34am Ana Leticia Kolicheski,University of Missouri
"Many Kissed Frogs and a Few Princes: Searching Dog Genomes for Causal Variants, Incidental Findings, and Reverse Genetics Associations" (W120)

11:52am Francesca Bertolini,Iowa State University
"A Cat’s Eye on Madagascar" (W121)

12:10pm Dayna L. Dreger,National Human Genome Research Institute,
"The Fonni's Dog as a Means to Define 'Breed' and Inform Inter-Species Island Colonization" (W122)

10:30am - 12:40pm Climate Change and ICRCGC 2 - PACIFIC SALON 2
Chair: Chittaranjan Kole, International Climate Resilient Crop Genomics ConsortiumCo-Chair: Jeffrey D. Ehlers, The Bill and Melinda Gates Foundation

10:30am Loren H. Rieseberg,University of British Columbia
"Adapting Sunflower to Climate Change by Tapping Variation in Its Wild Relatives" (W159)

10:50am Rajeev K Varshney,ICRISAT
"Translational Genomics for Developing Superior and Climate-Change Ready Varieties in Semi-Arid Legume Crops" (W160)

11:10am Michael Baum,ICARDA
"Crop Breeding for the Development of Climate Resilient Crops: Approaches at ICARDA" (W161)

11:30am Phillip Roberts,University of California-Riverside
"TBA" (W162)

11:50am Paul Gepts,University of California
"Exploration of *Phaseolus* Germplasm for Heat and Drought Tolerance" (W163)

10:30am - 12:40pm Computational Gene Discovery - PACIFIC SALON 3
Organizer: Mark Borodovsky, Georgia Institute of Technology

10:30am Mihaela Pertea,McKusick-Nathans Institute of Genetic Medicine, JHU
"Efficient and Robust Transcriptome Reconstruction with StringTie" (W194)

10:50am Felipe A. Simão,University of Geneva Medical School & Swiss Institute of Bioinformatics
"Orthodb: Genomics Data in the Light of Evolution" (W195)

11:10am Anindya Bhattacharya,University of California San Diego
"Validation of Proteogenomic Annotations" (W196)

11:30am Daniel Lang,Helmholtz Center Munich
"Integration of Theorectical and Experimental Data on Gene Regulation and Gene Evolution for Improved Genome Annotation" (W197)

11:50am Oren Tzfadia,Ghent University
"High-Throughput 3' End Sequencing Reveals Novel Features in the Tomato Genome" (W198)

12:10pm Vsevolod Makeev,Vavilov Institute for General Genetics, Russian Academy of Sciences
"Predicting Transcription Factor Tissue Specific Binding Profiles" (W199)

10:30am - 12:40pm **Functional Genomics - PACIFIC SALON 1**
Organizer: David A. Lightfoot, Southern Illinois University

10:30am Stefania Giacomello,SciLifeLab
"Spatially Resolved Transcriptome Profiling in Model Plant Species" (W376)

10:50am Vincent Colantonio,Southern Illinois University
"Machine Learning Algorithms for Functional Genomics: Soybean Genomics for Pathogen Resistance" (W377)

11:10am Baohong Zhang,East Carolina University
"MicroRNA Roles in Cotton Fiber Initiation and Early Development" (W378)

11:30am David Jordan,University of Queensland
"Sorghum Root Research" (W379)

11:50am Shaun J Curtin,USDA-ARS
"Crop Functional Genomics Made Easy with CRISPR/Cas9" (W380)

12:10pm Stig Uggerhøj Andersen,Aarhus University
"The Non-Transgenic *LORE1* Insertion Mutant Collection for Legume Genetics" (W381)

10:30am - 12:40pm **Genomics of Non-Classical Model Animals - PACIFIC SALON 4-5 (2ND FLOOR)**
Organizer: Aaron Avivi, Institute of Evolution, Haifa University, Israel

10:30am Jennifer A. Maier,Department of Animal Biology, University of Illinois at Urbana-Champaign
"The Gray Short-Tailed Opossum (*Monodelphis domestica*) in Biomedical Research" (W455)

11:00am Leslie A. Lyons,University of Missouri-Columbia and University of Missouri
"Cats Genome as a Potential Model for Human Disease" (W456)

11:30am Brian W. Davis,NHGRI
"Transmissible Tumors Represent a Unique Evolutionary Paradigm in Multiple Species" (W457)

12:00pm Marc Tollis,Arizona State University
"The Evolution of Cancer Suppression: Solutions to Peto's Paradox Revealed by Genomic Analyses of Elephants and Whales" (W458)

10:30am - 12:40pm **Graft Genetics and Genomics - TOWNE - MEETING HOUSE**
Organizers: Gan-Yuan Zhong, USDA-ARS and Yingzhen Yang, USDA-ARS Grape Genetics Research Unit

10:30am Welcoming Remarks

10:35am Margaret Frank,Donald Danforth Plant Science Center
"Investigating the Molecular, Physiological, and Architectural Changes that underlie Grafting-Induced Vigor" (W474)

10:55am Guo-Qing Song,Michigan State University
"The Use of Transgenic Rootstock for Improving Nontransgenic Scion Cultivars: Opportunities and Challenges" (W475)

11:15am Mathew G. Lewsey,La Trobe University
"Mobile Small RNAs Regulate Genome-Wide DNA Methylation" (W476)

11:35am Gennaro Fazio,USDA-ARS
"Graft Union Strength of Apple Rootstocks and Hormone Flux through Graft Unions" (W477)

11:55am Allison Miller,Saint Louis University
"Grapevine Rootstock Impacts on Shoot System Phenotypes: Preliminary Data from an Experimental Vineyard in Mount Vernon, MO" (W478)

12:15pm Liping Chen,Zhejiang University
"Heritability and Reversibility of DNA Methylation Induced by *in vitro* Grafting between Tuber Mustard (*Brassica juncea)* and Red Cabbage (*B. oleracea)*" (W479)

10:30am - 12:40pm **Organellar Genetics - PACIFIC SALON 6-7 (2ND FLOOR)**
Organizer: Michael J. Havey, USDA-ARS and University of Wisconsin

Current research on organellar (chloroplast or mitochondrial) genetics and genomics will be presented and discussed.

10:30am Maureen Hanson,Cornell University
"The Organelle RNA Recognition Motif (RRM) Proteins in Plants" (W655)

11:00am Jesus Beltran,Center for Plant Science Innovation, University of Nebraska,
"Evidence of Plastid Influence on Epigenetic Reprogramming in Arabidopsis and Crop Plants" (W656)

11:30am Renate Horn,University of Rostock
"Cytoplasmic Male Sterility Based on the PET2 Cytoplasm in Sunflower" (W657)

12:00pm Shaun D Jackman,BC Cancer Agency Genome Sciences Centre
"Mitochondrial Genome of Sitka Spruce Assembled Using Chromium Reads" (W658)

10:30am - 12:40pm **Plant Chromosome Biology - PACIFIC SALON 1**
Organizer: Fangpu Han, Chinese Academy of Sciences

10:30am R. Kelly Dawe,University of Georgia
"Spontaneous and RNAi-Induced Epimutants of a Kinesin Gene Family in Maize" (W677)

10:50am Gernot Presting,University of Hawaii
"Neocentromere Formation and Rapid Turnover of Centromere Repeats are Linked to Maize Domestication" (W678)

11:10am Youping Wang,Yangzhou University
"Cytology and Molecular Analysis on Sterile Mechanism of SaNa-1A CMS derived from Somatic Hybrid between *Brassica napus* and *Sinapis alba*" (W679)

11:30am Bao Liu,Northeast Normal University
"Deciphering the Molecular Basis Underlying Rapid Phenotypic Diversity in Plant Allopolyploids" (W680)

11:50am Adele Zhou,Cornell University
"Chromatin Landscape of Meiotic Recombination in Maize" (W681)

12:10pm Yongbiao Xue,Beijing Institute of Genomics
"TBA" (W682)

10:30am - 12:40pm **Polyploidy - TOWN AND COUNTRY**
Organizer: Boulos Chalhoub, UEVE-INRACo-Chair: Corrinne E. Grover, Iowa State University

10:30am Xiyin Wang,School of Life Sciences
"A Gold Standard to Deconvolute Complicated Structures of Plant Genomes with Recursive Polyploidizations" (W736)

10:50am Z. Jeffrey Chen,The University of Texas at Austin
"Dosage and Epigenetic Regulation Contributes to Gene Expression and Evolutionary Novelty in Plant Polyploids" (W737)

11:10am Julie Ferreira de Carvalho,Netherlands Institute of Ecology (NIOO-KNAW)
"Unravelling the Importance of Transposable Elements for Phenotypic Divergence in Triploid Asexual Dandelions" (W738)

11:30am Xueying Guan,Nanjing Agricultural University
"The lncRNA Landscape of Diploid *vs.* Allotetraploid Cotton Genomes" (W739)

11:50am Jonathan P. Spoelhof,University of Florida
"Chromosomal Composition and Fertility in the Early Generations of Two Resynthesized Allopolyploids in Tragopogon (Asteraceae)" (W740)

12:10pm John P. Vogel,DOE Joint Genome Institute and University of California, Berkeley
"The Genus *Brachypodium* as a Tool to Study Polyploidy" (W741)

10:30am - 12:40pm **Statistical Genomics - GOLDEN WEST**
Organizers: Shizhong Xu, Department of Botany & Plant Sciences, University of California - Riverside and Zhenyu Jia, University of California Riverside

10:30am William Muir,Purdue University
"Detection Signatures of Selection in Genomic Data, Lessons Learned from a Replicated Rat Model" (W877)

10:50am Rong-Cai Yang,University of Alberta
"A Tutorial of F-Statistics for Genome-wide Analysis of Population Differentiation" (W878)

11:10am Gustavo de los Campos,Michigan State University
"What Fraction of the Information Contained in an Omic Set Can Be Explained by Other Omics? Theory and Application of Penalized Analysis of Variance for Multi-Layered High Dimensional Inputs" (W879)

11:30am Huihui Li,CIMMYT
"Statistical Genomics in a World of Complete Genome Sequencing" (W880)

11:50am James Baldwin-Brown,University of California, Irvine
"Detecting Quantitative Trait Loci *via* Experimental Evolution: an Analysis of Power." (W881)

12:10pm Quan Long,University of Calgary
"Improving Genotype-based Phenotype Prediction by Integrating 3D Conformational Information" (W882)

10:30am - 12:40pm **Quinoa and close relatives - ESQUIRE - MEETING HOUSE**
Organizer: David E Jarvis, King Abdullah University of Science and Technology

10:30am Peter J. Maughan,Brigham Young University
"A PacBio and Hi-C based proximity-guided assembly of Amaranth pseudo chromosomes" (W790)

10:50am Michael K. Deyholos,University of British Columbia
"Betalains and Other Specialized Metabolites of *Amaranth spp.* Explored using Transcriptomics and Reverse Genetics" (W791)

11:10am Eibertus N. van Loo,Plant Breeding, Wageningen University & Research
"The Chromosome Scaffold Based Quinoa Genome: Its Building and its use to Find the Non-Bitter Mutations in Quinoa" (W792)

11:35am Hajime Ohyanagi,School of Agriculture, Meiji University
"ChenopodiumDB: An Integrated Repository for Population Genomics in genus *Chenopodium*" (W793)

11:55am Malia Gehan,Donald Danforth Plant Science Center
"High-Throughput Phenotyping of Chenopodium Quinoa Seed, Shoots, and Roots" (W794)

12:15pm Rick Jellen,Brigham Young University and Brigham Young University
"Future Directions for Quinoa and Related Species" (W795)

12:30pm - 1:30pm **Lunch (Vouchers Provided) - ROYAL PALM COURT & TIKI PAVILION COURT**

1:30pm - 3:40pm **Climate Change and ICRCGC 3 - PACIFIC SALON 2**
Chair: Chittaranjan Kole, International Climate Resilient Crop Genomics ConsortiumCo-Chair: Jeffrey D. Ehlers, The Bill and Melinda Gates Foundation

1:30pm Gary Atlin,Bill & Melinda Gates Foundation
"TBA" (W165)

1:55pm Nora Lapitan,U.S. Agency for International Development
"Advancing the Use of Genomics in Breeding for Climate Resilient Crops in the Developing World" (W166)

2:20pm Shadrack R Moephuli,Agricultural Research Council
"Strategies for Increasing Resilience to Climate Change and Variability in Southern African Agriculture" (W167)

2:40pm Antonio Costa De Oliveira,Universidade Federal de Pelotas
"Climate Change Genomics in South America" (W164)

3:00pm Appolinaire Djikeng,BecA-ILRI Hub
"TBA" (W168)

3:20pm Jeffrey D. Ehlers,The Bill and Melinda Gates Foundation
"Concluding Remarks" (W170)

1:30pm - 3:40pm **Degraded DNA and Paleogenomics - PACIFIC SALON 3**
Organizer: Greger Larson, University of Oxford

1:30pm Robin G. Allaby,University of Warwick
"3,000 Years of Sorghum Genome Evolution: The Birth of a New Crop" (W254)

1:48pm James Haile,University of Oxford
"Tracking Gene Flow Between Wild Boar and Domestic Pigs in (Time and) Space" (W255)

2:06pm Jessica Hendy,Max Planck Institute for the Science of Human History
"Dietary Protein Preservation on Archaeological Pottery" (W256)

2:24pm Ian Barnes,Natural History Museum
"Ancient DNA of Extinct Mammals" (W257)

2:42pm Daniel G. Bradley,Trinity College Dublin
"Ancient Human Genomes, Transitions, Farmers and Language at the Edge of Europe" (W258)

3:00pm Love Dalen,Swedish Museum of Natural History
"Quantifying the Genomic Consequences of Demographic Declines" (W259)

3:18pm Pontus Skoglund,Harvard Medical School
"Population Genomics of Ice Age Gray Wolves" (W260)

3:36pm Beth Shapiro,Department of Ecology and Evolutionary Biology, University of California Santa Cruz
"Passenger Pigeon Genomics: Take III" (W261)

1:30pm - 3:40pm Grape Genome Initiative - PACIFIC SALON 6-7 (2ND FLOOR)
Organizer: Grant R. Cramer, University of Nevada, Reno

1:30pm Grant R. Cramer,University of Nevada, Reno and University of Nevada, Reno
"Network Analysis of the Late Stages of Grape Berry Ripening" (W485)

1:50pm Carlos M Rodriguez Lopez,University of Adelaide
"Multi-Omics Data Integration for Genome by Environment Interactions Analysis in *Vitis vinifera*" (W486)

2:10pm Dario Cantu,University of California
"Beyond the Grape Genome: Construction of a Vineyard Metagenome Reference" (W487)

2:30pm Yongfeng Zhou,University of California, Irvine
"Domestication Genomics of Grapes" (W488)

2:50pm Davide Scaglione,IGA Technology Services
"Pan Genome and Structural Variation Analysis using different Approaches for *de novo* Assembly and Haplotype Reconstruction" (W489)

3:10pm Sushma Naithani,Department of Botany & Plant Pathology, Oregon State University
"Resources for Comparative Pathway Analysis for Grapevine" (W490)

1:30pm - 3:40pm JBrowse, a Next Generation Genome Browser - CALIFORNIA
Organizer: Scott Cain, Ontario Institute for Cancer Research

A Hands on Workshop for Installing, Configuring and Using Your Own JBrowse

1:30pm Scott Cain,Ontario Institute for Cancer Research
"Jbrowse Workshop" (W584)

1:30pm - 3:40pm National Plant Genome Initiative Workshop - Challenges and Opportunities in High-Throughput Phenotyping and Data Management - SAN DIEGO
Organizers: Catherine Ronning, U.S. Dept. of Energy, Diane Jofuku Okamuro, National Science Foundation, Jack K. Okamuro, USDA ARS and Ed Kaleikau, USDA NIFA

1:30pm Catherine Ronning,U.S. Dept. of Energy
"Welcome and Ws Goals"

1:45pm Natalia de Leon,University of Wisconsin-Madison
"Genomes to Field"

2:00pm Jesse Poland,Kansas State University
"Automated Field-Based Phenotyping"

2:15pm Todd C. Mockler,Donald Danforth Plant Science Center
"Automated Field-Based Phenotyping"

2:30pm Kelly Robbins,Cornell University
"Gobii"

2:45pm Joe Cornelius,ARPA-E
"Roots"

3:00pm Edward S. Buckler,USDA-ARS-Cornell University
"Innovations in Crop Functional Diversity Analysis"

1:30pm - 3:40pm **Non-coding RNA - ROYAL PALM SALON 3-4**
Organizers: Jan Gorodkin, Center for non-coding RNA in Technology and Health, Department of Veterinary Clinical and Animal Sciences, University of Copenhagen and Keith Adams, University of British Columbia

1:30pm Zhihua Jiang,Washington State University
"Non-Coding RNAs: Striking Features in Use of Alternative Polyadenylation Sites" (W631)

1:50pm J. Allan Feurtado,National Research Council Canada
"Wax-on, Wax-Off: ncRNA Mediate Control of Glaucousness in Wheat" (W632)

2:10pm Sarah Djebali,INRA
"A Study of Pig Chromosome X lncRNA Expression" (W633)

2:30pm Adam Frankish,Wellcome Trust Sanger Institute
"Annotating Non-Coding Loci in Ensembl and Ensembl Genomes" (W634)

2:50pm Andrew DL Nelson,School of Plant Sciences, University of Arizona
"Comparative Genomic and Transcriptomic Analysis of lincRNA Evolution in Plants and Mammals using Evolinc" (W635)

3:10pm Tasia M. Taxis,USDA/ARS
"Differential Expression of Small Non-Coding RNAs in Serum from Cattle Challenged with Viruses Causing Bovine Respiratory Disease" (W636)

1:30pm - 3:40pm **Ornamentals - ESQUIRE - MEETING HOUSE**
Organizer: Mohammed Bendahmane, Ecole Normale Supérieure

1:30pm Aureliano Bombarely,Virginia Polytechnic Institute and State University, Department of Horticulture
"Analysis of the Genome Architectures for *Petunia hybrida* and its Wild Relatives" (W659)

1:48pm Jeremy Just,Ecole Normale Superieure
"Rose Genome Sequencing" (W660)

2:06pm Tom Ruttink,ILVO Plant Sciences Unit
"Building Bridges: Integrating *in situ* HiC and Molecular Cytogenetics to Reconstruct *Rosa wichurana* Pseudochromosomes" (W661)

2:24pm Marinus J. M. Smulders,Wageningen University & Research, Plant Breeding
"High-Density SNP Maps in Garden Rose and Cut Rose, and Synteny with *Fragaria*" (W662)

2:42pm David Byrne,Texas A&M University, Department of Horticultural Sciences
"The Development of a Dense SNP-Based Consensus Map and QTL Detection for Black Spot Resistance in Five Diploid Rose Populations" (W663)

3:00pm Paul Arens,Wageningen UR
"Mapping of *Botrytis* Resistance in *Gerbera* and Validation of Candidate Genes" (W664)

3:18pm Arwa Shahin,Royal van Zanten Company
"Breeding Signature and Mode of Inheritance in the Tetraploid *Alstroemeria*" (W665)

1:30pm - 3:40pm Palm Genetics and Genomics - TOWNE - MEETING HOUSE
Organizer: Frederique Aberlenc-Bertossi, IRD

1:30pm Emira Cherif,IRD: French National Research Institute for Sustainable Development
"Genetic Structuration of Date Palm Populations" (W666)

1:50pm Michael D. Purugganan,New York University
"Population Genomics of Date Palms" (W667)

2:10pm Joel A. Malek,Weill Cornell Medical College
"Genomics of Commercially Important Traits in Date Palm (*Phoenix dactylifera*)" (W668)

2:30pm Craig F. Barrett,West Virginia University
"Genome Evolution and Diversification in Palms" (W669)

2:50pm Alix Augusto Armero,Centre de coopération internationale en recherche agronomique pour le développement (CIRAD)
"Improving Genomic Resources in Coconut and Finding Clues to Plant Breeding Using Comparative Genomics" (W670)

1:30pm - 3:40pm Plant Cytogenetics - PACIFIC SALON 4-5 (2ND FLOOR)
Organizers: James Higgins, University of Leicester and Eugenio Sanchez-Moran, University of Birmingham

1:30pm Kulvinder Gill,Washington State University
"Unique Expression Pattern, Insertions/Deletions and Alternate Splicing Evolved the Novel Function of the Ph1 Gene of Wheat" (W683)

1:50pm Mischa Olson,Cornell University
"Mechanisms of Meiotic Prophase are Disrupted in Neopolyploid Maize" (W684)

2:10pm Chris Franklin,University of Birmingham
"Evolution of Chiasma Patterning: A Route to Stable Polyploids?" (W685)

2:30pm Isabelle Colas,The James Hutton Institute
"Bringing Light to Barley Meiosis" (W686)

2:50pm Wanqi Liang,Shanghai JiaoTong University
"Function of an E3 Ligase in Rice Meiotic Progression" (W687)

3:10pm Marina Martinez Garcia,University of Birmingham
"Topoisomerase II is Required for Programmed Chromosome Reorganization during Meiosis and Mitosis in Plants" (W688)

1:30pm - 3:40pm Plant Genome Engineering - TOWN AND COUNTRY
Organizers: Dan Voytas, University of Minnesota and Yinong Yang, Pennsylvania State University

1:30pm Keiji Nishida,Kobe University
"Genome Editing by Targeted Deaminase" (W695)

1:55pm Steve Jacobsen,University of California at Los Angeles
"Targeted Epigenetic Modification in Plants" (W696)

2:20pm Rene Ruiter,Bayer Crop Science
"Crop Improvement Through Targeted Genome Optimization Requires More Than Scissors" (W697)

2:45pm Bing Yang,Iowa State University
"Talen- and CRISPR/Cas9-Based Gene Editing in Maize and Rice" (W698)

3:10pm Fredy Altpeter,Agronomy Department, University of Florida
"Genetic Improvement of Sugarcane by Targeted Loss- or Gain of Function Mutations using TALEN or CRISPR-Cas9" (W699)

1:30pm - 3:40pm Plant Reproductive Genomics - SUNSET - MEETING HOUSE
Organizer: Jim Leebens-Mack, University of Georgia

1:30pm Abdelhafid Bendahmane,INRA
"Sex Determination Pathway in Cucurbits" (W717)

1:50pm Alex Harkess,Donald Danforth Plant Science Center
"Divergence of X and Y Chromosomes in Asparagus" (W718)

2:10pm Brian Sanderson,Texas Tech University
"Sexual Dimorphism and the Evolution of Sex-Biased and Sex-Limited Genes in the Dioecious Tree *Populus balsamifera*" (W719)

2:30pm Stuart McDaniel,University of Florida
"Sexual Dimorphism in Growth, Gene Expression, and Metabolite Profile in Early Moss Development" (W720)

2:50pm Frederic Berger,Gregor Mendel Institute of Molecular Plant Biology
"Towards the Origin of Sexual Reproduction in Plants: Neofunctionalization of a MYB Transcription Factor Is Linked to Male Gametogenesis in Land Plant Ancestors" (W721)

3:10pm Zhongchi Liu,University of Maryland
"The Making of Fruit: Genomic Approaches to Understand Fruit Set in Wild Strawberry" (W722)

1:30pm - 3:40pm **Rice Functional Genomics - ROYAL PALM SALON 5-6**
Organizers: Mingsheng Chen, IGDB, Chinese Academy of Sciences, Guo-Liang Wang, The Ohio State University and Hiroyuki Tsuji, Kihara Institute for Biological Research, Yokohama City University

1:30pm Rod A. Wing,Arizona Genomics Institute, University of Arizona
"Harnessing 15 Million Years of *Oryza* Genome Evolution to Help Solve the 10-Billion People Question?" (W808)

1:50pm Manyuan Long,University
"Rapid Evolution of New Genes in Oryza Genomes" (W809)

2:10pm Kenji Yano,The University of Tokyo
"Genome-Wide Association Study using Whole-Genome Sequencing Rapidly Identifies New Genes Influencing Agronomic Traits in Rice" (W810)

2:30pm Jie Luo,Huazhong Agricultural University
"Dissection of Metabolic and Phenotypic Traits in Major Crops" (W811)

2:50pm Yuese Ning,Institute of Plant Protection, Chinese Academy of Agricultural Sciences
"Dissection of the Molecular Mechanism of Rice Immunity Against *Magnaporthe oryzae*" (W812)

3:10pm Jinfeng Chen,University of Riverside, California
"On the Origin of Burst of MITE Element mPing in Rice Population" (W813)

1:30pm - 3:40pm **Sugar Cane Sequencing Initiative - ROYAL PALM SALON 1-2**
Organizers: Glaucia M. Souza, Universidade de São Paulo (USP), Robert Henry, University of Queensland QAAFI and Ray Ming, University of Illinois at Urbana-Champaign

1:30pm Milton Y. Nishiyama Junior,Special Laboratory of Applied Toxicology, Butantan Institute
"Insights into Signaling and Regulation of Gene Expression in the Highly Polyploid Sugarcane" (W896)

1:50pm Anete P Souza,University of Campinas - UNICAMP
"Genetic Variations in a Complex Polyploid: Unveiling the Sugarcane Allelic Dynamics" (W897)

2:10pm Jeremy Shearman,National Center for Genetic Engineering and Biotechnology
"The *Saccharum* Mitochondrial Genome" (W898)

2:30pm Jianping Wang,Agronomy Department, University of Florida
"Target Enrichment Sequencing of 300 Representative Accessions in the Sugarcane World Germplasm Collection" (W899)

2:50pm Jisen Zhang,Center for Genomics and Biotechnology, Fujian Provincial Key laboratory of Haixia applied plant systems biology, Haixia Institute of Science and Technology,Fujian Agriculture and Forestry University
"Ultra High Density Mapping of the *Saccharum spontaneum* Genome" (W900)

3:10pm Marcio C Silva-Filho,Laboratório de Biologia Molecular de Plantas, ESALQ, USP.
"Structural and Functional Characterization of SUGARWINs and their Role in Plant Defense" (W901)

1:30pm - 3:40pm Transposable Elements - GOLDEN BALLROOM
Organizers: Jianxin Ma, Purdue University and Olivier Panaud, University of Perpignan

1:30pm Marie-Anne Van Sluys,Universidade de Sao Paulo
"Virus-like Attachment Sites as Structural Landmarks of Plants Retrotransposons" (W954)

1:48pm Hadi Quesneville,URGI, Versailles
"*De novo* Annotation of Transposable Elements: Tackling the Fat Genome Issue" (W951)

2:06pm Etienne Bucher,Institut de Recherche en Horticulture et Semences
"Mobilized Transposable Elements As a Tool for Crop Improvement" (W952)

2:24pm Sophie Lanciano,Institut of Research for Development (IRD)
"Specific Sequencing of Mobilomes Reveals Real Time Transposable Element Activity in Rice" (W953)

2:42pm Sarah N Anderson,University of Minnesota, Twin Cities
"Dynamic Transposable Element Expression Across Development in Maize" (W955)

1:30pm - 6:10pm NRSP-8 Animal Genome - GOLDEN WEST
Organizer: Huaijun Zhou, University of California, Davis

1:30pm Zhanjiang Liu,Auburn University; The Fish Molecular Genetics and Biotechnology Laboratory
"Underwater Genomics: Exploiting Fishes'€™ Unique Biology to Meet the Needs of the Aquaculture Industry" (W643)

2:15pm Noelle Cockett,Utah State University
"Recent Advancements in Sheep Genomics Research" (W644)

2:55pm Claire Rogel-Gaillard,GABI, INRA, AgroParisTech, Université Paris-Saclay
"Microbiomes As Actors of Host Phenotype Variability: An Increasing Research Field in Animal Biology" (W645)

3:35pm Huaijun Zhou,University of California, Davis
"Break" (W646)

3:55pm Gerald Quon,University of California, Davis
"Computational Integration of Epigenomic and Functional Genomic Data for Fine-Mapping Complex Trait Loci" (W647)

4:35pm Trey Ideker,University of California, San Diego
"Building Hierarchical Models of the Cell from Genomics Data" (W648)

5:15pm Huaijun Zhou,University of California, Davis
"NRSP-8 Business meeting" (W649)

3:00pm - 4:00pm Coffee Break - GRAND EXHIBIT HALL

3:00pm - 8:30pm Exhibits Open - GRAND EXHIBIT HALL

4:00pm - 6:10pm Coffee Genomics - PACIFIC SALON 3
Organizers: Marcela Yepes, Cornell University/ School of Integrative Plant Sciences/ Plant Pathology and Plant Microbe Biology Section and Philippe Lashermes, Institut de Recherche pour le Développement

4:00pm Carlos Ernesto Maldonado,Centro Nacional de Investigaciones de Café, CENICAFE
"Using PACBio Long-Reads to Generate High Quality References for the Allotetraploid *Coffea arabica* and Its Diploid Maternal Ancestor *C. eugenioides:* characterization of Genomic Regions Containing QTLs for Yield, Plant Height, and Bean Size" (W171)

4:40pm Lucio Navarro,Centro Nacional de Investigaciones de Cafe, CENICAFE
"Insights from the Genome of the Major Coffee Insect Pest Worldwide: The Coffee Berry Borer" (W172)

4:56pm Alan C. Andrade,Embrapa Café/INOVACAFÉ - UFLA
"Towards GWAS and Genomic Prediction in Coffee: Development and Validation of a 26K SNP Chip for *Coffea canephora*" (W173)

5:12pm Luis Felipe V. Ferrão,University of São Paulo (ESALQ/USP)
"Comparison of Statistical Methods and Reliability of Genomic Prediction in *Coffea canephora* Populations" (W174)

5:28pm Kassahun Tesfaye,Addis Ababa University
"Coffee Forest Biodiversity and Implications for Multi-Site *in situ* Conservation Approach in the Afromontane Rainforests of Ethiopia" (W175)

5:44pm Allen Van Deynze,University of California
"Update on the Sequencing of the *Coffea arabica* Variety, Geisha" (W176)

4:00pm - 6:10pm **Cucurbit Genomics - PACIFIC SALON 4-5 (2ND FLOOR)**
Organizers: Amnon Levi, USDA-ARS, U.S. Vegtable Laboratory and Yaakov (Kobi) Tadmor, Agricultural Research Organization, Newe Ya'ar Research CenterCo-Chair: Patrick Wechter, USDA-ARS

4:00pm Heather Rose Kates,University of Florida
"Determining Genetic Relationships among all Wild and Domesticated *Cucurbita* species Provides a Framework for Domestication Genetics Studies in *Cucurbita*" (W231)

4:20pm Shaogui Guo, Beijing Academy of Agriculture and Forestry Sciences
"Genome Variation Elucidates Evolution and Domestication of Fruit Ripening and Quality Traits in Watermelon" (W232)

4:40pm Yi Ren,National, Beijing Academy of Agriculture and Forestry Sciences
"A Tonoplast Sugar Transporter Mediates Sugar Accumulation in Dessert Watermelon (*Citrullus lanatus*) Fruit" (W233)

5:00pm Sandra E. Branham,USDA-ARS
"Quantitative Trait Loci Mapping of Resistance to *Fusarium oxysporum* f. sp. *niveum* race 2 in *Citrullus lanatus* var. *Citroides* using Genotyping-by-Sequencing (GBS)" (W234)

5:20pm Ryoichi Yano,Faculty of Life and Environmental Sciences, Univ of Tsukuba
"Development of "Melonet-DB" Gene Expression Database for Functional Genomics Research of Muskmelon" (W235)

5:40pm Yiqun Weng,USDA ARS/ Universtiy of Wisconsin
"Cucumber Hypocotyl Elongation Mutants Reveal New Players in Plant UVB Signaling" (W236)

4:00pm - 6:10pm **Domestication Genomics - PACIFIC SALON 2**
Organizers: Allison Miller, Saint Louis University and Briana L. Gross, University of Minnesota Duluth

4:00pm J. Chris Pires,Division of Biological Sciences, University of Missouri
"The Origin and Diversity of *Brassica napus* from *Brassica rapa* and *Brassica oleracea*" (W271)

4:20pm Briana L. Gross,University of Minnesota Duluth
"Patterns of Variation in Wild and Domesticated Apple" (W272)

4:40pm Emily Warschefsky,Florida International University
"Domestication Genetics of the Mango *(Mangifera indica* L.)" (W273)

5:00pm Nyree Zerega,Northwestern University and the Chicago Botanic Garden
"Domestication, Diversity, and Distribution History of Breadfruit (*Artocarpus altilis*, Moraceae), a Priority Underutilized Staple Crop" (W274)

5:20pm Laurent Frantz,University of Oxford
"Decoding Animal Domestication with Palaeogenetics" (W275)

5:40pm Martien A.M. Groenen,Wageningen University
"Evolutionary History, Selective Sweeps and Deleterious Variation in the Pig" (W276)

4:00pm - 6:10pm **Fungal Genomics - ROYAL PALM SALON 3-4**
Organizer: Stephen B. Goodwin, USDA ARS

4:00pm Introductory Remarks

4:05pm Eduard Akhunov,Kansas State University, Manhattan, KS
"Dissecting the Genomic Architecture of *Puccinia graminis* f. sp. *tritici* – Wheat Interaction" (W388)

4:25pm Carlos M Rodriguez Lopez,University of Adelaide
"*Botrytis cinerea* Loss and Restoration of Virulence during *in vitro* Culture Follows Flux in Global DNA Methylation" (W389)

4:45pm Burt H. Bluhm,University of Arkansas
"Genomics of *Cercospora*" (W390)

5:05pm Daniel Cullen,USDA Forest Products Laboratory
"Basidiomycete Genomics" (W391)

5:25pm Robert Riley,U.S. Department of Energy Joint Genome Institute
"A New Genetic Code in Yeasts" (W392)

5:45pm Hala Badr Khalil,Agriculture and Agrifood canada
"A New Approach: Detection of Fungal and Wheat Genes Involved in Leaf Rust Disease by Transcript Expression Associations" (W393)

4:00pm - 6:10pm **Genomics of Plant Development - PACIFIC SALON 6-7 (2ND FLOOR)**
Organizer: Khalid Meksem, Department of Plant Soil and Agricultural Systems, SIUC

4:00pm James L. Weller,School of Biological Sciences, University of Tasmania
" Identification of Late BLOOMER2 As a Cycling Dof Factor Homolog Reveals Conserved and Divergent Features of the Flowering Response to Photoperiod in Pea" (W459)

4:25pm Dr. Senthil Subramanian,South Dakota State University
"microRNA and Gene Regulatory Networks Governing Soybean Nodule Development" (W460)

4:50pm Silvio Salvi,Department of Agricultural Sciences, University of Bologna
"A New Maize Tassel-Seed Mutant is under the Control of a Two-Locus System" (W461)

5:15pm Raju Datla,National Research Council Canada
"Developmental and Gene Expression Programs in Wheat Grain" (W462)

5:40pm Moussa Benhamed,Institute of Plant Sciences - Paris-Saclay
"Chromatin Architecture: A New Dimension in the Dynamic Control of Gene Expression" (W463)

6:05pm Baohong Zhang,East Carolina University
"MicroRNA Roles in Cotton Fiber Initiation and Early Development" (W464)

4:00pm - 6:10pm International Cotton Genome Initiative (ICGI) - SUNSET - MEETING HOUSE
Organizers: John Z. Yu, USDA-ARS, Southern Plains Agricultural Research Center and David M. Stelly, Texas A&M University

4:00pm Don C. Jones,Cotton Incorporated
"Introduction and Update" (W521)

4:10pm Yuxian Zhu,College of Life Sciences, Peking University
"Sequence Assembly, Evolution and Functional Application of the Cotton Genomes" (W522)

4:30pm Brian G. Ayre,University of North Texas
"Functional and Genomic Analysis of Cotton Growth Habit: Branching Architecture is Regulated by the *Gossypium hirsutum* *Single Flower Truss* and *Self Pruning* Orthologs" (W523)

4:50pm Xiao-Ya Chen,Shanghai Institute of Plant Physiology and Ecology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences.
"Characterization of Transcription Factors Regulating Cotton Fiber Elongation" (W524)

5:10pm Gregory Thyssen,Cotton Chemistry and Utilization Unit, USDA-ARS-SRRC
"The GhTT2_A07 Gene Is Linked to the Brown Color and Natural Flame Retardancy Phenotypes of *Lc1* Cotton (*Gossypium hirsutum* L.) Fibers" (W525)

5:30pm Shuangxia Jin,Huazhong Agricultural University
"The Application of T-DNA Insertion and CRISPR/Cas 9 System in Cotton for Functional Genomic Research" (W526)

5:50pm John Z. Yu,USDA-ARS, Southern Plains Agricultural Research Center
"1-Minute Oral Presentations on Cotton Genomics" (W527)

4:00pm - 6:10pm Recombination - mechanisms - PACIFIC SALON 1
Organizer: Wojtek Pawlowski, Cornell University - Section of Plant Biology, School of Integrative Plant Science

4:00pm Charles White,Centre National de Recherche Scientifique
"DMC1, RAD51 and Meiotic Recombination in Arabidopsis" (W796)

4:20pm Marie-Therese Kurzbauer,Department of Chromosome Biology, Max F. Perutz Laboratories, University of Vienna
"Understanding and Controlling Meiotic Recombination in Plants" (W797)

4:40pm Eugenio Sanchez-Moran,University of Birmingham
"Control of Meiotic Recombination by the Phosphorylation of Chromosome Axis ASY1 Protein" (W798)

5:00pm Cathy Melamed-Bessudo,Weizmann Institute of Science
"What Makes DNA Recombination Hot" (W799)

5:20pm Jiyue Huang,State Key Lab of Genet Eng, Sch of Life Sci., Fudan Univ.
"DNA Polymerase Epsilon Is a Key Component of the Meiotic Recombination Pathway" (W800)

5:40pm Penny Kianian,University of Minnesota
"Investigating Differences in Meiotic Recombination Patterns Between Male and Female Meiosis Using High-Resolution Crossover Mapping in Maize" (W801)

4:00pm - 6:10pm Sequencing Complex Genomes - GOLDEN BALLROOM
Organizer: Robert Henry, University of Queensland QAAFI

4:00pm Yinping Jiao,Cold Spring Harbor Laboratory/USDA-ARS
"The Complex Sequence Landscape of Maize Revealed by Single Molecule Technologies" (W820)

4:20pm Jianwei Zhang,Arizona Genomics Institute and Huazhong Agricultural University
"A Case Study from Reseq to Refseq-Two High-Quality Reference Genome Sequences for *indica* Rice" (W821)

4:40pm Adam Healey,University of Queensland
"Sequencing the Branches of the Eucalypt Tree: Comparison Between *Eucalyptus* and *Corymbia* Genomes" (W822)

5:00pm Susan R. Strickler,Boyce Thompson Institute
"The Genome of the Tetraploid *arabica* Coffee and its Diploid Ancestors" (W823)

5:20pm Giovanni Giuliano,Italian National Agency for New Technologies, Energy and Sustainable Development
"The Eggplant Genome Reveals Key Events in Solanaceae Evolution" (W824)

5:40pm Karen S. Aitken,CSIRO Agriculture and Food
"Update on the Sugarcane Genome Sequence" (W825)

4:00pm - 6:10pm Sex Chromosomes and sex determination - ROYAL PALM SALON 5-6
Organizers: Ray Ming, University of Illinois at Urbana-Champaign and Abdelhafid Bendahmane, INRA

4:00pm Catherine Montchamp-Moreau,Évolution, Génomes, Comportement, Écologie, CNRS, IRD, Université Paris-Sud and Université Paris-Saclay
"Rapid Evolution of a Y-Chromosome Heterochromatin Protein Underlies Sex Chromosome Meiotic Drive" (W826)

4:20pm Wansheng Liu,Department of Animal Science, Penn State University
"The Bovine PRAMEY - an Example of Autosome-to-Y-Chromosome Transposition to Enhance Male Reproduction" (W827)

4:40pm Dmitry A. Filatov,University of Oxford
"Evolution of Sex Chromosomes in Silene" (W828)

5:00pm William Wadlington,University of Illinois at Urbana-Champaign
"Genomic Analysis of the Sex Determining Region of the Sex Chromosomes in Spinach" (W829)

5:20pm Jacob A. Tennessen,Oregon State University
"Homologous Sex Determination across Octoploid Strawberry Species *via* a Conserved Gene with a Shifting Genomic Location" (W830)

5:40pm Frederique Aberlenc-Bertossi,IRD
"Sex Determination in Date Palm" (W831)

4:00pm - 6:10pm Tripal Database Network and Initiatives - CALIFORNIA
Organizers: Stephen P. Ficklin, Washington State University and Lacey-Anne Sanderson, University of Saskatchewan

4:00pm Stephen P. Ficklin,Washington State University
"Tripal Introduction and Core Development Efforts" (W956)

4:25pm Katheryn Buble,Washington State University
"Development of TripalMap" (W957)

4:40pm Lacey-Anne Sanderson,University of Saskatchewan
"Extending Tripal for Community-Based Management and Distribution of Genotypic and Phenotypic Data" (W958)

4:55pm Nic Herndon,University of Connecticut
"CartograTree Workflows with Tripal API for Association Mapping in Forest Trees" (W959)

5:10pm Sook Jung,Washington State University
"Mainlab Chado Loader, Chado Data Display and Chado Search for Sequence, Map, Marker, QTL, Genotype, Phenotype and Germplasm Data" (W960)

5:25pm Sudhansu Dash,National Center for Genome Resources (NCGR)
"Customizing Tripal Sites with Non-Tripal Components at the Legume Information System and Peanutbase" (W961)

5:40pm Christopher Childers,USDA/Agricultural Resarch Service/National Agricultural Library
"The i5k Workspace@Nal" (W962)

5:55pm Margaret Staton,University of Tennessee, Knoxville
"New Tripal Extensions: Elasticsearch and Gene Expression Visualization" (W963)

4:00pm - 6:10pm Farm Animal Genome Editing - ESQUIRE - MEETING HOUSE
Organizer: C. Bruce Whitelaw, The Roslin Institute and R(D)SVS, University of Edinburgh

Sunday - January 15, 2017

4:00pm - 6:10pm **New breeding technologies: Prospects and regulatory hurdles - ROYAL PALM SALON 1-2**
Organizer: Thorben Sprink, Julius Kühn InstitutCo-Chair: Frank Hartung, Julius Kühn Institut

4:00pm Frank Hartung,Julius Kühn Institut
"Introduction to New Breeding Techniques" (W619)

4:10pm Alison Van Eenennaam,University of California, Davis
"Do Kingdoms Matter? Regulation of Animal Breeding Technologies. " (W620)

4:30pm Friedrich Fauser,Princeton University
"Genome Engineering & High-Throughout Phenotyping in Plants" (W621)

4:50pm Werner Schenkel,Federal Office of Consumer Protection and Food Safety Germany
"To be or not to be GMO? Application of European GMO Regulation in Times of Genome Editing" (W622)

5:10pm Sol Ortiz García,Intersecretarial Commission on Biosafety of Genetically Modified Organisms CIBIOGEM
"NPBT: Building Consensus for Regulatory Approaches in Mexico" (W623)

5:30pm Neil E. Hoffman,USDA-APHIS-BRS
"USDA Regulation of Products of Biotechnology" (W624)

5:50pm Heather Shearer,Canadian Food Inspection Agency
"Environmental Release of Plants with Novel Traits in Canada: A Product-Based Approach to Regulatory Oversight" (W625)

6:15pm - 7:00pm **Plenary Lecture: Scott Kennedy - TOWN & COUNTRY BALLROOM**
Chair: Alison Van Eenennaam, University of California, Davis

This is the opening plenary lecture

6:15pm Scott Hamilton Kennedy,Black Valley Films
"Food and Film: A Search for Nuance in the Struggle Between Art and Activism"

7:00pm - 8:30pm **Opening Reception - GRAND EXHIBIT HALL**

Monday - January 16, 2017

7:00am - 8:00am	**Continental Breakfast - GOLDEN BALLROOM**
7:00am - 5:00pm	**Registration - ATLAS FOYER**
7:00am - 9:00pm	**Poster Access - GRAND EXHIBIT HALL**
8:00am - 8:45am	**Plenary Lecture: Clare M. Fraser - TOWN & COUNTRY BALLROOM** **Chair: Catherine Feuillet, Bayer CropScience**
8:00am	Clare M. Fraser,University of Maryland School of Medicine **"The Gut Microbiome in Health and Disease"**
8:45am - 9:30am	**Plenary Lecture: Rob Martienssen - TOWN & COUNTRY BALLROOM** **Chair: Catherine Feuillet, Bayer CropScience**
8:45am	Rob Martienssen,HHMI-GBMF Cold Spring Harbor Laboratory **"Germline Reprogramming and Epigenetic Inheritance in Plants: How to Avoid Bad Karma"**
9:30am - 11:30am	**Coffee Break - GRAND EXHIBIT HALL**
9:30am - 12:30pm	**AgBioData Workshop - GARDEN SALON 1** **Organizer: Lisa Harper, USDA ARS**
9:30am - 5:00pm	**Exhibits Open - GRAND EXHIBIT HALL**
10:00am - 11:30am	**Poster Session - Even Numbers - GRAND EXHIBIT HALL**
11:30am - 3:00pm	**International Sheep Genomics Consortium - TOWNE - MEETING HOUSE** **Organizer: Noelle Cockett, Utah State UniversityCo-Chair: James Kijas, CSIRO Agriculture**
11:30am	Kim C. Worley,Baylor College of Medicine **"Update on Rambouillet Assembly, the v5.0 Reference, and Plans for FAANG RNA Sequencing" (W544)**
11:50am	Emily L. Clark,The Roslin Institute and R(D)SVS, University of Edinburgh **"Functional Annotation of the Sheep (*Ovis aries*) Genome" (W545)**
12:10pm	James Kijas,CSIRO Agriculture **"A Comparative Functional Annotation and Enrichment in Selection Sweeps" (W546)**
12:30pm	Michael P. Heaton,USDA, ARS, U.S. Meat Animal Research Center (USMARC) **"Using an Online Genome Resource to Identify Protein Variants in U.S. Sheep" (W547)**

12:50pm Alisha T. Massa,Washington State University
"Genome-Wide Landscape of Active Enhancers in Sheep Alveolar Macrophages" (W548)

1:10pm Matthew M. Hindle,The Roslin Institute
"Genome Wide Transcript and Methylation Changes in the Sheep Seasonal Clock" (W549)

1:30pm Francois Pompanon,Université Grenoble Alpes
"Transpecific Signatures of Selection Related to Domestication in Sheep and Goats" (W550)

1:50pm Tristan Cumer,Université Grenoble Alpes
"Old Origin of a Protective Endogenous Retrovirus (enJSRV) in the *Ovis* Genus" (W551)

2:10pm Suzanne Rowe,AgResearch, Invermay Agricultural Centre
"Health Traits and Work with the NZ Dairy Sheep Industry" (W552)

2:30pm Badr Benjelloun,Laboratoire d'Ecologie Alpine CNRS France / CRRA of Tadla INRA Morocco
"Landscape Genomics of Local Adaptation in Sheep and Goats" (W553)

12:00pm - 12:50pm Lunch (Vouchers Provided) - ROYAL PALM COURT, EXHIBIT HALL & TIKI PAVILION COURT

12:50pm - 3:00pm GeneSeek, A Neogen Company - Genomic Solutions for Agri-Research - PACIFIC SALON 2
Organizer: Jeremy Walker, GeneSeek

12:50pm Stewart Bauck,Neogen/GeneSeek
"Geneseek Update: New Genomic Tools"

1:10pm José B. S. Ferraz,University of Sao Paulo
"Creation of a New Bos Indicus 35k SNP Genotyping Array

1:30pm George Sofronidis,Orivet Genetic Pet care
"Building a Successful and Innovative Canine Genetic Testing Business - No Equipment Required!"

1:50pm Yulin Jin,Auburn University
"Utilizing a Custom Catfish 250K SNP Array for Linkage Mapping, Genome Sequence Validation, and GWAS Analysis of Performance Traits"

12:50pm - 3:00pm **KeyGene: Expediting Innovation in Agriculture - ROYAL PALM SALON 3-4**
Organizer: Sireen Khan, KeyGeneChair: Fayaz Khazi, KeyGene USA

KeyGene is a leader in technology innovation. Over the last 28 years, KeyGene scientists have made significant contributions leading to advances in the food and agriculture industry. As the Company continues to maintains its lead in the industry as a key player, this annual workshop is themed towards showcasing new developments within the KeyGene technology pipeline, its strategic partnerships and a sneak preview of its disruptive, virtual reality based breeding tool.

12:50pm Fayaz Khazi,KeyGene USA
"Keygene: The Crop Innovation Company"

1:10pm Michiel J.T. van Eijk,KeyGene
"Crop Innovation Using Sequence Based Genotyping"

1:30pm Michiel Reessink,GENALICE
"GENALICE MAP: Getting the Best Possible Yield out of Your NGS Data, Faster, Better, Easier and More Cost-Effective"

1:50pm Marco van Schriek,KeyGene
"Virtual Reality Breeding : A Powerful New Tool in Crop Phenotyping"

2:10pm Anker Sørensen,KeyGene
"Croppedia, Big Data & Crop Innovation"

12:50pm - 3:00pm **Kyazma's JoinMap and MapQTL Demonstration - PACIFIC SALON 4-5 (2ND FLOOR)**
Organizer: Johan Van Ooijen, Kyazma B.V.

Live demonstration of the genetic mapping and QTL analysis software of Kyazma ®
- JoinMap ® – Genetic mapping made easy
- MapQTL ® – User-friendly power in QTL analysis

12:50pm Welcoming Remarks

12:55pm JoinMap 5 – General Demonstration

1:45pm Break

1:50pm MapQTL 6 – General Demonstration

12:50pm - 3:00pm **PacBio Workshop: SMRT Sequencing for Complete Genomes - SAN DIEGO**
Organizer: Donal Murphy, PacBio

Join us to hear the latest and greatest in SMRT Sequencing. Our workshop will open with the 2017 roadmap for Sequel System enhancements, followed by an engaging scientific program highlighting insect, animal, and plant genome projects. Learn how scientists are employing long reads to complete even the most complex genomes.

12:50pm Jonas Korlach,Pacific Biosciences
"Welcome and Introductory Comments"

1:10pm Rod A. Wing,Arizona Genomics Institute, University of Arizona
"Introducing 5 New High-Quality Pacbio Genome Assemblies for Rice to Help Solve the 10-Billion People Question "

1:30pm Erich Jarvis,Rockefeller University
"Comparative Analyses of Next Generation Technologies for Generating Chromosome-Level Reference Genome Assemblies"

1:50pm Rebecca N. Johnson,Australian Museum Research Institute, Science & Learning
"*De Novo* Sequencing of the Koala Genome"

2:10pm Ben Matthews,HHMI-Rockefeller University
"Genome Assembly and Molecular Genetics of the Dengue, Yellow Fever, and Zika Vector Aedes Aegypti"

12:50pm - 3:00pm **Metagenomics & more – bioinformatics solutions for plant and animal research - ROYAL PALM SALON 5-6**
Organizer: Nonna Druker, QIAGEN

QIAGEN bioinformatics offers genome scientists continuity in their research. CLC Genomics Workbench and a series of specialized modules integrate all NGS data analysis capabilities required to power modern plant and animal research into a single platform – from DNA-Seq and variant detection, advanced RNA-Seq and Epigenomics capabilities, to a comprehensive toolbox for metagenomics or plant pathogen analysis. The direct integration with Ingenuity Pathway Analysis (IPA) allows researchers to explore the biological consequences of the results of RNA-Seq or Epigenomics experiments.

12:50pm Jamie Hill,QIAGEN
"Make Lasting Expressions with Your Research – One Integrated Solution for Your RNA-Seq Analysis"

1:50pm Mark Borodovsky,Georgia Institute of Technology
"Metagenemark: Analysis of NGS Sequences with Clc Genomic Workbench"

12:50pm - 3:00pm **For Smarter Genomics in Agriculture, Partnering is the Answer - GOLDEN WEST**
Organizer: Delaney Wermuth, Thermo Fisher Scientific

Underlying agribusiness fundamentals point to abundant opportunities for development and profitable growth- as the often dynamic, volatile, and complex agriculture industry continues its transformation. Fueled by economic and technological drivers, the new conditions emphasize efficiency, innovation and creativity- producing opportunities for those savvy enough to recognize and seize them. Thermo Fisher Scientific is a partner who understands your business by providing you with a broad, deep portfolio of agrigenomic solutions – including AgriSeq and Eureka GBS technology, TaqMan assays and master mixes, Axiom microarray technologies, and Ion Torrent Sequencers. Attend our workshop to learn how we are partnering with agribusiness leaders to help address agricultural challenges and revolution.

12:50pm Ravi Ramadhar,Thermo Fisher Scientific
"Welcome & Introduction"

12:55pm Thomas P. Scott,Informa Agribusiness Business Intelligence IEG
"Thermo Fisher Scientific and Informa –Agribusiness Insights and Outlook: Challenges and Opportunities in Agribusiness- an Economic Perspective on Global and Technological Factors Transforming and Impacting Agribusiness"

1:20pm Thomas C. Osborn,Monsanto
"Yield Testing in the Lab"

1:35pm Wim van Haeringen,VHLGenetics
"Enabling More Accurate Animal Parentage and Genetic Testing through Targeted Genotyping By Sequencing (GBS) and CE Approaches"

2:00pm Dario Grattapaglia,EMBRAPA Brazilian Corporation of Agricultural Research and Graduate Program in Genomic Sciences - Catholic University of Brasília
"A Five-Species 50K Axiom SNP Microarray Allows High Quality Genotyping of Coffee, Cashew, Cassava, Brazilian Pine and Eucalyptus"

2:30pm Emily Rose,Neogen-GeneSeek Lab
"Applications of Axiom Microbiome Array in Food Safety"

12:50pm - 3:00pm **Arabidopsis Information Portal & Intl Arabidopsis Informatics Consortium - PACIFIC SALON 6-7 (2ND FLOOR)**
Organizers: Christopher D. Town, J. Craig Venter Institute and Blake Meyers, Donald Danforth Plant Science Center

12:50pm Welcoming Remarks

1:00pm Agnes P. Chan,J. Craig Venter Institute
"What's New at Araport" (W046)

1:20pm Detlef Weigel,Max Planck Institute for Developmental Biology
"1001 Genomes Plus (1001G+)" (W047)

1:45pm Andrew Farmer,National Center for Genome Resources (NCGR)
"A Versatile, User-Configurable Micro-Synteny Viewer for Comparative and Pan- Genomics of Arabidopsis and its Relatives" (W048)

2:10pm Asher Pasha,University of Toronto / CAGEF
"Integrating Visual Analytic Tools from the Bio-Analytic Resource into Araport" (W049)

2:35pm Weijia Xu,Texas Advanced Computing Center
"Enriching Information Content and Accessibility of Journal Publication with Text Mining and Biological Ontologies" (W050)

12:50pm - 3:00pm Genomics of Tissue Regeneration in Plants and Animals - ESQUIRE - MEETING HOUSE
Organizer: Moshe Reuveni, ARO, Volcani Center

12:50pm Hiroshi Hisano,Institute of Plant Science and Resources, Okayama University
"Identification of *TFA* Genomic Regions that confer Amenability to *Agrobacterium*-Mediated Transformation in Barley" (W465)

1:20pm Patricia Springer,Department of Botany and Plant Sciences
"Leaf Initiation, Patterning, Organ Separation from the Meristem" (W466)

1:50pm Venugopala Reddy Gonehal,Botany and Plant Sciences
"Cell Type Specific Whole Genome Approaches to Understand Transcriptional Control of Stem Cell Maintenance" (W467)

12:50pm - 3:00pm Integrated Breeding Platform: Tools, Databases and Applications for Plant Breeding - GOLDEN BALLROOM
Organizer: Graham McLaren, Integrated Breeding Platform

12:50pm Jean-Marcel Ribaut,Integrated Breeding Platform
"Integrated Breeding Platform Deployment in Africa (I.): The Digital Revolution Has Already Started!" (W515)

1:10pm Graham McLaren,Integrated Breeding Platform
"Breeding Management System (II.): Managing Breeding Data in the Cloud" (W516)

1:30pm Michel Ragot,Integrated Breeding Platform and Nouvelle France Genetics
"Reversing the Trend: Bottom-Up Approach to Increasing Plant Breeding Efficiency in Africa" (W517)

1:50pm Abhishek Rathore,ICRISAT
"BMS (IV.) - Enterprise Solution for Public Breeding Programmes: ICRISAT Case Study" (W518)

2:10pm Lukas Mueller,Boyce Thompson Institute
"The Cassavabase System, a Web-Based Breeding Platform Adaptable for Many Crops" (W519)

2:30pm Reinhard Simon,International Potato Center (CIP)
"Using the Public Plant Breeding API (BrAPI) to Access Data from the Statistical Platform R (VI.)" (W520)

Monday - January 16, 2017

12:50pm - 3:00pm **NCBI Genome Resources - SUNSET - MEETING HOUSE**
Organizers: Kim D. Pruitt, National Center for Biotechnology Information (NCBI/NLM/NIH) and Terence D. Murphy, National Center for Biotechnology Information (NCBI/NLM/NIH)

12:50pm Kim D. Pruitt,National Center for Biotechnology Information (NCBI/NLM/NIH)
"Workshop Overview and Welcome" (W608)

12:55pm Karen Clark,National Center for Biotechnology Information (NCBI/NLM/NIH)
"Genbank Submission Improvements and Contamination Checks" (W609)

1:15pm Shashikant Pujar,NCBI, National Institutes of Health
"Curated Content of RefSeq Genomes" (W610)

1:35pm Francoise Thibaud-Nissen,National Center for Biotechnology Information (NCBI/NLM/NIH)
"Annotating Genomes, Assessing Quality, and Dowloading Data" (W611)

2:05pm Tao Tao,NIH/NLM/NCBI
"E-Utilities and EDirect: NCBI Entrez Programming Interface" (W612)

2:25pm Lon Phan,NIH/NLM/NCBI
"NCBI Variation Resources" (W613)

12:50pm - 3:00pm **Plant Transgene Genetics - TOWN AND COUNTRY**
Organizers: Yingzhen Yang, USDA-ARS Grape Genetics Research Unit and Gan-Yuan Zhong, USDA-ARS

12:50pm Maureen Hanson,Cornell University
"Engineering Carboxysomes into C3 Plants" (W730)

1:10pm Lanqin Xia,Institute of Crop Sciences, Chinese Academy of Agricultural Sciences
"CRISPR/Cas9-Mediated Gene Targeting for Crop Improvement" (W731)

1:30pm James Thomson,USDA-WRRC
"Development of Site-Specific Recombinase Technology for Targeted Integration with Marker Removal" (W732)

1:50pm Jay Chen,Oak Ridge National Laboratory
"Simultaneous Knockdown of Six Non-Family Genes using a Single Synthetic RNAi Fragment in *Arabidopsis thaliana*" (W733)

2:10pm Dominique Van Der Straeten,Ghent University
"Towards a Solution for Hidden Hunger: Folate Biofortification of Crop Plants" (W734)

2:30pm Hailing Jin,University of California
"Cross-Kingdom RNAi and Plant Disease Control" (W735)

12:50pm - 3:00pm **10x Genomics - PACIFIC SALON 1**
Organizer: Sara Agee Le, 10x Genomics
Chair: Deanna Church, 10x Genomics Inc.

12:50pm Jill Herschleb,10x Genomics Inc.
"The Chromium System: Delivering Linked-Reads and Single Cell Gene Expression for Improved Genomics"

1:10pm Benjamin E.R. Rubin,Lewis-Sigler Institute for Integrative Genomics, Princeton University
"Comparative Genomics of Bee Sociality Using 10x Linked-Read Sequencing"

1:30pm Patrick S. Schnable,Iowa State University
"Applications of Linked-Reads to Maize Genome Assembly"

1:50pm Michael Scanlon,Cornell University
"Single Cell RNA-Seq: A Tool to Decipher the Influences of Cell Signaling, Cell Lineage, and Cell Position on Gene Expression during Plant Development"

12:50pm - 3:00pm **Population and Conservation Genomics 2 - PACIFIC SALON 3**
Organizer: Om P. Rajora, University of New Brunswick

12:50pm Introductory Remarks

12:55pm Loretta C Johnson,Kansas State University
"Predicting Phenotypic and Genotypic Response of the Dominant Prairie Grass *Andropogon gerardii* to Climate Change in the US Central Grasslands" (W748)

1:15pm Paul F. Gugger,University of Maryland Center for Environmental Science
"Landscape Genomics of California Valley Oak (*Quercus lobata*)" (W749)

1:35pm Brittany Barker,University of Arizona
"Landscape Genomic Analyses Reveal Rapid Adaptation to Climate in Introduced Biocontrol Weevils despite Multiple Founder Events" (W750)

1:55pm Michael Russello,University of British Columbia
"Genomic Changes Associated with Sockeye Salmon Ecotype Divergence Provide Insights into Life History Evolution and Tools for Fisheries Management" (W751)

2:15pm Eben Gering,Michigan State University
"Rapid Life History Evolution in Feral Chickens (*Gallus gallus*) Involves both Ancestral and Artificially-Selected Traits" (W752)

2:35pm Tanja Slotte,Stockholm University
"Demography and Mating System Shape the Genome-Wide Impact of Natural Selection in *Arabis alpina*" (W753)

2:55pm Concluding Remarks

12:50pm - 3:00pm **New England Biolabs - New NEBNext methods to enhance your NGS performance - ROYAL PALM SALON 1-2**
Organizer: Kari Goodwin, New England Biolabs

With its unprecedented throughput, scalability, and speed, next-generation sequencing (NGS) is expanding its applications; addressing an increasingly diverse range of biological problems. As the use of Next Generation Sequencing (NGS) is becoming more widespread there is a need for faster protocols that perform reliably even with reduced input amounts. To address these challenges the new NEBNext® Ultra™ II library prep solutions have optimized every step in the workflows to enable high quality of sequencing data even from few picograms (gDNA) and low nanograms (RNA) of input material. Enzymatic fragmentation has also been included to streamline the library prep workflow and to avoid the sample lost involved in mechanical shearing. Genome editing is enabled by the development of tools to make precise, targeted changes to the genome of living cells. Recently a new tool based on a bacterial CRISPR-associated protein-9 nuclease (Cas9) from Streptococcus pyogenes has generated considerable excitement. CRISPR-based genome editing workflows vary considerably depending on experimental design. NEB reagents support multiple workflows enabling researcher's flexibility in their genome editing strategy. In this presentation, we will introduce NEB's RNA synthesis products, novel assembly methods for generation of sgRNA templates and homologous repair templates, recombinant Cas9 protein, and reagents for downstream mutation analysis.

12:50pm Daniela B Munafo,New England Biolabs
"The Latest in DNA Library Preparation: Superior Performance from Picogram Input Amounts with Nebnext® Ultra™ II, Plus New Enzymatic DNA Fragmentation."

1:10pm Keerthana Krishnan,New England Biolabs
"The Next Generation of RNA Library Preparation. "

1:30pm Breton Hornblower,New England Biolabs
"Genome Editing: Tools to Support CRISPR/Cas9 Applications"

12:50pm - 3:00pm **AgriPlex Genomics – Bridging the Gap Between Singleplex Screening and High Density Arrays - SUNRISE - MEETING HOUSE**
Organizer: Scott Weigel, AgriPlex Genomics

PlexSeq™: a new targeted amplicon based focused sequencing method. Our workshop will focus on our PlexSeq™ system and how assays are multiplexed and applied to large number of samples simultaneously to create an ultra-high throughput, NGS based, ligation free sequencing and genotyping platform. PlexSeq™ works well with crude extraction methods, has a high assay design and conversion success rate for insertions, deletions and other difficult regions. Multiplexed SSR/STR assays can also be robustly analyzed. Various multiplexing levels and the ability to run large population studies rapidly and inexpensively will be discussed. As an example, we will present data on simultaneous analysis of 9 SNP's in 20,000 samples on one Illumina MiSeq run. Data can be robustly analyzed using our fully automated genotype calling PlexCall™ proprietary software. The combination of PlexSeq™ and PlexCall™ enables several other applications including quantitative pathogen detection and focused RNAseq in large number of samples.

12:50pm Alex Miron,AgriPlex Genomics

12:50pm - 3:00pm **Computer Demo 2 - CALIFORNIA**
Organizers: Monica C. Munoz-Torres, Lawrence Berkeley National Laboratory and Brian Smith-White, National Center for Biotechnology Information (NCBI/NLM/NIH)

12:50pm Kelly Robbins,Cornell University
"GOBII: Genomic Open-source Breeding Informatics Initiative" (C09)

1:05pm Manuel Ruiz,CIRAD, UMR AGAP / CIAT
"Gigwa - Genotype Investigator for Genome-Wide Analyses." (C10)

1:20pm Annemarie Eckes,Earlham Institute
"The Brassica Information Portal: Towards Integrating Phenotype and Genotype Data." (C11)

1:35pm Guillaume Cornut,INRA - URGI
"GnpIS-Ephesis, Plant Phenotype Field Experimentations Resources – Data Discovery and Dataset Building Use Cases." (C12)

1:50pm Richard Michael Bruskiewich,STAR Informatics / Delphinai Corporation
"Knowledge.Bio: A Web Application for Collaboratively Building and Exploring Networks of Biological Relationships." (C13)

2:05pm Clay Birkett,USDA-ARS
"The Triticeae Toolbox (T3): Connecting Phenotypes, Genotypes, and Biological Knowledge" (C14)

2:20pm Matthias Lange,Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Gatersleben
"e!Dal - a Open Source Software to Store, Share and Publish Research Data" (C15)

2:35pm Jeffrey Grover,University of Arizona
"User-Friendly Whole Genome DNA Methylation Analysis With FlowGe" (C16)

3:00pm - 4:30pm **Poster Session - Odd Numbers - GRAND EXHIBIT HALL**

3:00pm - 5:00pm **Coffee Break - GRAND EXHIBIT HALL**

4:30pm - 6:30pm **Brachypodium Community Organizational Meeting - SHEFFIELD**
Organizer: John P. Vogel, Department of Energy Joint Genome Institute

5:00pm - 8:00pm **International Goat Genome Consortium - SUNRISE - MEETING HOUSE**
Organizer: Gwenola Tosser-Klopp, INRACo-Chair: Alessandra Stella, PTP Science Park

5:00pm Gwenola Tosser-Klopp,INRA
"Introduction" (W528)

5:05pm Licia Colli,Research Center on Biodiversity and Ancient DNA – BioDNA and Inst. of Zootechnics, Università Cattolica del S. Cuore
"Adaptmap WG7 & 8 - Global Diversity and Selection Signatures in Goats" (W529)

5:25pm Kevin Daly,Trintiy College Dublin
"Ancient Whole Mitochondrial Genomes and Insights into the Prehistory of Goats" (W530)

5:40pm Suzanne Rowe,AgResearch, Invermay Agricultural Centre
"Genomic Selection in Dairy Goats (*Capra hircus*) using Genotyping by Sequencing" (W531)

6:00pm Stephen N. White,USDA, ARS, Animal Disease Research Unit
"Goats Singly Heterozygous for PRNP S146 or K222 Substitutions Each Show Extended Scrapie Incubation Time Beyond Common Commercial Productive Lifetime" (W532)

6:20pm Ramadimetja Prescilla Mohlatlole,Agricultural Research Council and University KwaZulu-Natal
"Whole-genome Sequence and Genetic Variant Analysis of the Tankwa Feral Goat of South Africa" (W533)

6:40pm M.J. Woodward-Greene,USDA-ARS
"ADAPTMap and Points Methods for Livestock Digital Phenotyping and Weight Prediction" (W534)

7:00pm Thibaut Hourlier,European Molecular Biology Laboratory - EBI
"Goat Genome Assembly Annotation" (W535)

7:20pm Gwenola Tosser-Klopp,INRA
"Conclusion" (W536)

6:10pm - 8:20pm **Douglas Scientific - Accelerating Trait Discovery - SAN DIEGO**
Organizer: Jill Walerius, Douglas Scientific

6:10pm Michiel van Eijk,KeyGene
"Sequence Based Genotyping: From Marker Discovery to Targeted Detection"

6:30pm Romy Morrin O'Donnell,Weatherbys Ireland Ltd DNA Laboratory
"“Genomic DNA Extraction - 1 Million Cattle” Application of the Oktopure™ Robot and Sbeadex™ Chemistry for High through-Put DNA Extraction"

6:50pm Martin W. Ganal,TraitGenetics GmbH
"Optimized Marker Sets for Array-Based Plant Genotyping – a Continuous Improvement Process"

7:10pm David M. Francis,The Ohio State University, Horticulture and Crop Science

"Rapid Assessment of Novel Alleles and QTL through Background Genome Selection: From Sequence Variation to Functional Characterization in Tomato"

7:30pm Kellie Watson,University of Edinburgh

"Flexible, Low Density SNP Information in Animal Breeding"

6:10pm - 8:20pm Examples of New NGS-Enabled Plant Research and Opportunities for Global Gen Banking Partnerships - SUNSET - MEETING HOUSE
Organizer: Johan Christiaanse, BGI Americas

Our speakers will present recent work on the genetic diversity of cotton, revealed through NGS and a strategy to combine methylome and gene expression data in plant genomes. In addition, we will present a new open-data gene banking initiative that presents new opportunities for global cooperation.

6:10pm Joshua A. Udall,Brigham Young University

"Re-Sequenced Genomes Reveal the Genetic Diversity of Polyploid Cotton."

6:30pm Sally Mackenzie,Beadle Center for Genetic Research, University of Nebraska

"Integrating Genome-Wide Methylome and Gene Expression Data in Plant Genomes"

6:50pm Xin Liu,Beijing Genomics Institute-Shenzhen

"Large Scale Genomic Studies at China National Genebank”

6:10pm - 8:20pm BioNano Genomics Education Workshop: Next-Generation Mapping Reveals Large Structural Variations: So What? - PACIFIC SALON 3
Organizer: Gail Lamangan, BioNano Genomics

Learn how colleagues have used next-generation mapping to enhance their research.

6:10pm Alex R. Hastie,BioNano Genomics

"Genome Wide Detection of Large Structural Variation - Latest Advances from Bionano Genomics"

6:35pm Florian Jupe,Salk Institute for Biological Studies & Howard Hughes Medical Institute

"Next Generation Arabidopsis Genomics"

7:05pm Alex Harkess,Donald Danforth Plant Science Center

"Optical Maps Finish Homologous X and Y Sex Determination Regions in Asparagus"

7:35pm Parwinder Kaur,Centre for Plant Genetics & Breeding, Univ. of Western AU

"Assessing Structural Variation at the Subspecies Level within *Trifolium Subterraneum* L. — Towards a Trifolium Pangenome"

8:00pm Matthias Weissensteiner,Uppsala University

"Repetive but Not Redundant - Revealing Structural Genomic Features with Tandem Repeat Arrays in Optical Maps"

6:10pm - 8:20pm **NRGene DeNovoMAGIC 3.0 - Complete assembly & phasing of heterozygote and polyploid genomes - GOLDEN BALLROOM**
Organizer: Moran Ofer, NRGene

6:10pm Sachiko Isobe,Kazusa DNA Research Institute
"*De novo* Whole Genome Assembly in Allo-Octoploid Strawberry"

6:30pm Jizeng Jia,Chinese Academy of Agricultural Sciences
"Wheat Genome De Novo Assembly: Diploid and Hexaploid

6:50pm R. Kelly Dawe,University of Georgia
"Validation of PacBio and NRgene Maize Genome Assemblies by BioNano Genome Mapping"

7:10pm Dr. Gil Ronen,NRGene
"Complete Phasing of Heterozygote and/or Polyploid Genomes to Create Very Long and Accurate Scaffolds Using Denovomagic 3.0"

6:10pm - 8:20pm **CyVerse - Software, Tools, and Services for Data-Driven Discovery - CALIFORNIA**
Organizer: Jason Williams, Cold Spring Harbor Laboratory

6:10pm Parker Antin,University of Arizona
"Overview of the CyVerse" (W241)

6:25pm Naser Alkhalifah,Iowa State University
"The Maize Genomes to Fields Initiative: Data Discovery and Reuse" (W242)

6:45pm Zain A. Alvi,Seton Hall University
"Genomic and Expression Analysis of Spermatid Nuclear Transition Proteins in Sequenced *Drosophila* Species " (W243)

7:05pm Matthew Vaughn,Texas Advanced Computing Center
"Jetstream: On-Demand Cloud Computing for Life Sciences Research and Education" (W244)

7:25pm Annemarie H. Eckes,Earlham Institute
"CyVerse for Brassica: Performing Associative Transcriptomics by Integrating with Sequence and Phenotype Repositories" (W245)

7:45pm Liya Wang,Cold Spring Harbor Laboratory
"A CyVerse Powered Data Coordination Center (DCC) for MaizeCODE" (W246)

8:05pm Jawon Song,Texas Advanced Computing Center
"Methylation Pipelines in CyVerse" (W247)

6:10pm - 8:20pm **Functional Annotations of Animal Genomes (FAANG) - GOLDEN WEST**
Organizer: Huaijun Zhou, University of California, Davis

6:10pm Pablo J. Ross,Animal Science, University of California Davis
"Update on Functional Annotation of Regulatory Elements in Chicken, Pig and Cattle" (W367)

6:22pm Huaijun Zhou,University of California, Davis
"Fr-Agencode Update" (W368)

6:27pm Hans D. Daetwyler,Agriculture Victoria and La Trobe University
"Identification and Use of Regulatory Variation in Dairy Cattle" (W369)

6:39pm Martien A.M. Groenen,Wageningen University
"FAANG Reference Data Datasets for the Pig Ipec-J2 and Chicken SL-29 Epithelial Cell Lines" (W370)

6:51pm James M. Reecy,Department of Animal Science, Iowa State University
"Update on FAANG Bioinformatics Pipeline Analysis" (W371)

7:11pm Laura Clarke,European Molecular Biology Laboratory, European Bioinformatics Institute, Vertebrate Genomics
"Updates on the FAANG M&DS Committee and the FAANG DCC at EMBL-EBI" (W372)

7:21pm Stephen N. White,USDA, ARS, Animal Disease Research Unit
"FAANG-Related Project Update" (W373)

7:41pm Christopher K. Tuggle,Iowa State University, Department of Animal Science
"Update on Coordination of FAANG-Related Proposals to AFRI-Tools and Resources" (W374)

7:46pm Huaijun Zhou,University of California, Davis
"FAANG Coordination Discussion" (W375)

6:10pm - 8:20pm **Computomics - From genomes to insight - ROYAL PALM SALON 1-2**
Organizer: Venkatesh Balakrishnan, Computomics GmbH

Computomics is a team of world-leading experts in bioinformatics, offering next-generation sequencing (NGS) analyses for agriculture biotech companies and research scientists. Whether the concern is genomics research, breeding improvement, or plant protection, Computomics helps navigate the complexities of plant genomes. Our advanced bioinformatics services provide our customers with high-quality NGS data interpretation from state-of-the-art genomics tools and technologies

6:10pm Dr. Detlef Weigel,Max Planck Institute for Developmental Biology
"Genomics of a. thaliana: Beyond Resequencing"

6:30pm Dr. Andre Kahles,ETH- Institute for Machine Learning
"Graph Genomes"

6:50pm Dr. Timothy P.L. Smith,USDA, ARS, USMARC
"Multiple Reference Genomes"

7:10pm Dr. George Wang,Computomics Corp
"Cropscore: High-Throughput Phenotypic Data Simplified"

6:10pm - 8:20pm **Knowledge Management and Data Integration in Plant Research - PACIFIC SALON 2**
Organizer: Mercedes Ames Sevillano, Biomax Informatics AGCo-Chair: Maximilian Peters, Biomax Informatics AG

Efficient data integration, exploration and interpretation are indispensable to research in the plant and animal sciences. This workshop will address the major challenges and current computational solutions that scientists are using to extract knowledge from diverse data resources. We will examine how to best integrate diverse content, including public and private databases, ontologies, methods and analytical tools, into centralized repositories that represent an organization's collective knowledge. The goal of the workshop is to foster open discussion of how the abundance of data, information and tools, are being utilized and translated into knowledge and opportunity in an organized and systematic way. Renowned presenters from industry, academic and research institutions will share their experiences and insight.

6:10pm Welcoming Remarks

6:15pm Introductory Remarks

6:20pm Julie Green,Syngenta
"Gene-Centric Knowledgebases for Identification of Agronomic Trait Lead Candidates"

6:45pm Mercedes Ames Sevillano,Biomax Informatics AG
"Data Integration and Knowledge Management to Facilitate Research on Plant-Pathogen Interactions: Case Study *Solanum tuberosum*−Verticillium Wilt"

7:10pm Tatiana Tatarinova,University of Southern California
"Whole-Genome Approach to Plant Phenotype Prediction"

7:35pm Reinhard Simon,International Potato Center (CIP)
"Tentative Title: Building Data Repositories for Crop Genetic Resources"

8:00pm Concluding Remarks

6:10pm - 8:20pm **Novogene: Latest NGS Applications in Agricultural Research - employing PacBio, 10X Genomics, & Illumina HiSeq X Ten - PACIFIC SALON 1**

6:10pm Wenkai Jiang,Novogene
"De Novo Assembly of Plant and Animal Genomes: From Next Generation to Next-Next Generation"

6:30pm M. Brian Couger,Oklahoma State University
"Evolution of Molecular Biology Investigation during the Disruptive Growth of Sequencing"

6:50pm David D. Fang,Cotton Fiber Biosciences Unit, USDA-ARS-SRRC
"Intraspecific Polymorphic SNP and Indel Marker Discovery Based on Whole Genome Sequencing of a MAGIC Population in Upland Cotton"

7:10pm Ainong Shi,University of Arkansas
"Whole Genome Sequencing and Resequencing for Genome-Wide Study in Cowpea"

7:30pm L. Augusto Becerra Lopez-Lavalle,International Center for Tropical Agriculture, CIAT
"TBD"

6:10pm - 8:30pm Mango genomics - TOWNE - MEETING HOUSE
Organizers: Yuval Cohen, Volcani Research Center and Amir Sherman, ARO

6:10pm Kobi Baruch,NRGENE LTD.
"*De novo* Assembly of the Tommy Atkins Mango Genome" (W597)

6:30pm Nagendra K. Singh,ICAR-National Research Centre on Plant Biotechnology
"A Reference Genome of Mango (*Mangifera indica* L. cv Amrapali)" (W598)

6:50pm Amy Groh,USDA-ARS
"Mango Germplasm Characterization using SNPs Markers" (W599)

7:10pm Noam Alkan,Agricultural Research Organization, Volcani Center
"Transcriptome and Metabolome Dynamics of Mango Fruit Response to Cold Storage" (W600)

7:00pm - 7:30pm Coffee Break - ATLAS FOYER

8:30pm - 10:30pm Bioinformatics Ice Cream Social – Collaborating and networking across complex projects - STRATFORD
Organizers: Jason Williams, Cold Spring Harbor Laboratory and Matthew Vaughn, Texas Advanced Computing Center

Calling all bioinformaticians and bioinformatics enthusiasts! CyVerse is hosting a small get together on a variety of topics relevant to making bioinformatics accessible and open to all communities. We will also have time to cover more questions on the new CyVerse project - specifically how developers can participate and how collaborative science projects can make use of CyVerse. If you are working on a collaborative science projects, have ever contributed code to an open source project, helped with documentation, or trained students and colleagues we'd like to invite you down to this late-night event.

Tuesday - January 17, 2017

7:00am - 8:00am **Continental Breakfast - GOLDEN BALLROOM**

7:00am - 3:00pm **Poster Access - GRAND EXHIBIT HALL**

7:00am - 3:00pm **Registration - ATLAS FOYER**

8:00am - 8:45am **Plenary Lecture: Alan Cooper - TOWN & COUNTRY BALLROOM**
Chair: Huaijun Zhou, University of California, Davis

8:00am Alan Cooper, University of Adelaide
"Ancient DNA Records of Genome Evolution"

8:45am - 9:30am **Plenary Lecture: Seth Bordenstein - TOWN & COUNTRY BALLROOM**
Chair: Huaijun Zhou, University of California, Davis

8:45am Seth Bordenstein, Vanderbilt University
"Microbes and the Origin of Animal Species"

9:30am - 10:30am **Coffee Break - GRAND EXHIBIT HALL**

9:30am - 3:00pm **Exhibits Open - GRAND EXHIBIT HALL**

10:30am - 12:40pm **Banana Genomics - PACIFIC SALON 6-7 (2ND FLOOR)**
Organizers: Mathieu Rouard, Bioversity International and
Angelique D'Hont, CIRAD, UMR AGAP

10:30am James Dale,Centre for Tropical Crops and Biocommodities
"Golden Bananas for Africa and Asia" (W063)

10:50am Guillaume Martin,CIRAD, UMR AGAP
"Characterization of a Large Reciprocal Chromosomal Translocation in Banana (*Musa acuminata*) and its Impact on Chromosomal Segregation using NGS" (W064)

11:10am Robert N. G. Miller,Universidade de Brasília
"Transcriptome Analysis in *Musa acuminata* during Compatible Interaction with the Root-Knot Nematode *Meloidogyne incognita*" (W065)

11:30am Trude Schwarzacher,Department of Genetics, University of Leicester
"Comparative Genomic Analysis in Zingiberales: What Can We Learn from Banana to Enable Ensete and Boesenbergia to Reach Their Potential?" (W066)

11:50am Nicolas Roux,Bioversity International
"Revision of the Global Strategy for the Conservation and Use of *Musa* Genetic Resources" (W067)

12:10pm Mathieu Rouard,Bioversity International
"Banana Genome Hub and MGIS : Managing Banana Germplam Data in the NGS Era" (W068)

10:30am - 12:40pm **Bioinformatics - GOLDEN WEST**
Organizers: Tatiana Tatusova, National Center for Biotechnology Information (NCBI/NLM/NIH) and Aleksey Zimin, Institute for Physical Science and Technology, University of Maryland

10:30am Sergey Koren,National Human Genome Research Institute, National Institutes of Health
"Combining Nanopore Sequencing and Conformation Capture for the Reconstruction of Complete Chromosomes" (W075)

10:50am Deanna M. Church,10x Genomics Inc.
"Using Linked-Reads to Enable Efficient *de novo* Diploid Assembly" (W076)

11:10am Maria Nattestad,Cold Spring Harbor Laboratory
"Visualization and Analysis Tools for Comparing Genomes and Assemblies" (W077)

11:30am Heiko Schoof,INRES Crop Bioinformatics, University of Bonn
"Function Prediction: Using Ahrd to Annotate Human Readable Descriptions and Gene Ontology Terms." (W078)

11:50am Tatiana Tatarinova,University of Southern California
"Analysis of Nucleotide Diversity in *Oryza sativa* Across Functionally Important Genomic Regions" (W079)

12:10pm Jodi L. Humann,Washington State University
"Structural and Functional Annotation of Model and Non-Model Organisms with GenSAS v5.0, a Web-Based Annotation Platform" (W080)

10:30am - 12:40pm **Brachypodium Genomics - PACIFIC SALON 2**
Organizer: David F. Garvin, USDA-ARS, PSRU

10:30am Matthew J. Moscou,The Sainsbury Laboratory
"Accessing Natural Variation in *Brachypodium distachyon*: Development of the ABR6 x Bd21 RIL Population" (W081)

10:55am Kyria A. Roessler,UC Irvine
"Differential Methylation and Gene Expression Between Leaf and Floral Tissues in *Brachypodium*" (W082)

11:20am Daniel Woods,University of Wisconsin-Madison
"Genetic Architecture of Flowering Time Variation in *Brachypodium distachyon*" (W083)

11:45am Lifeng Liu,DOE Joint Genome Institute
"Epigenetics of Cold Acclimation and Vernalization in *Brachypodium distachyon*" (W084)

12:10pm Boulos Chalhoub,UEVE-INRA
"Development and Characterization of an Original *Brachypodium* Polyploid Model" (W085)

10:30am - 12:40pm **Planning, Executing and Cultivating Broader Impact Programs: Tools, Communities and Resources to GET ORGANIZED, GET CONNECTED, GET NOTICED and GET FUNDED. - ESQUIRE - MEETING HOUSE**
Organizer: Michael D. Gonzales, University of South Dakota

10:30am Carol Lushbough,University of South Dakota
"Getbio-PGR: The Gateway for Education, Training, Broader Impacts and Outreach in Plant Genome Research" (W869)

11:00am Etienne Gnimpieba,University of South Dakota
"Bio-TDS - the Bioquery Tool Discovery System" (W870)

11:25am Susan Cato,American Society of Plant Biologists
"Plantae: The Digital Ecosystem for Plant Science" (W871)

11:50am Joslynn Lee,Cold Spring Harbor Laboratory
"The Importance of Making a Presence at Diversity-Focused Conferences" (W872)

12:15pm Jennifer Weller,University of North Carolina at Charlotte
"Nurturing Strong Broader Impacts: Developing Plans for Executing a Successful Program to Incorporate in Grant Applications" (W873)

10:30am - 12:40pm **Genomics-Assisted Breeding - TOWN AND COUNTRY**
Organizer: Rajeev K Varshney, ICRISAT

10:30am Rajeev K Varshney,ICRISAT
"Welcome & Introduction" (W437)

10:35am Andreas Graner,Leib-Inst Plant Gen & Crop Plant Res
"T B A" (W438)

10:55am Shawn Kaeppler, University of Wisconsin - Madison
"Connecting the Genome and Phenome to Develop Stress-Tolerant Maize Cultivars" (W439)

11:15am Thomas Lubberstedt,Iowa State University
"Use of Doubled Haploids in the Context of Genetic Resource Exploitation in Maize" (W440)

11:35am Rod Snowdon,Justus Liebig University
"Genome-Based Gene Pool Expansion and Heterotic Haplotype Capture in Rapeseed" (W441)

11:55am Yusaku Uga,National Agriculture and Food Research Organization
"Genomics-Based Ideotype Breeding for Root System Architecture to Enhance Rice Production" (W442)

12:15pm Jean-Luc Jannink,USDA-ARS / Cornell University
"Genomic Prediction Meets Transcriptomics: An RNA-Seq Experiment Improves Cassava Brown Streak Disease Prediction Accuracy" (W443)

12:35pm Rajeev K Varshney,ICRISAT
"Summary and Wrap-up" (W444)

10:30am - 12:40pm **International Phytomedomics and Nutriomics Consortium (ICPN) - ROYAL PALM SALON 3-4**
Chair: Phullara Kole, Kole's Foundation for Science and SocietyCo-Chair: Chittaranjan Kole, International Climate Resilient Crop Genomics Consortium

10:30am Phullara Kole,Kole's Foundation for Science and Society
"Genomic Intervention for Amelioration of Bioactive Profiles in Plants for Health Security" (W537)

10:45am Byoung-Cheorl Kang,Seoul National University
"GWAS of fruit related quantitative traits in Capsicum" (W538)

11:00am Massimo Iorizzo,Plants for Human Health Institute, Department of Horticulural Science, North Carolina State University,
"TBA" (W539)

11:15am Yuxing Deng,the Institute of Medicinal Plant Development, Chinese Academy of Medical Sciences & Peking Union Medical College
"Sm-miR828 is a Negative Regulator of the Flavonoid Pathway in *Salvia miltiorrhiza*" (W540)

11:30am Herman Silva,Lab Gen Func & Bioinfo - Fac Ciencias Agro - U de Chile
"Functional Genomics as a Tool to Unveil Bioactives Compounds in Commercial and Andean Natives Plants" (W542)

11:45pm Yong Pyo Lim,Chungnam National University
"Genome-Wide Association Analysis of 14 Glucosinolate Compounds Reveals the Multiple Association Loci's and Related Candidate Genes in Chinese Cabbage" (W543)

10:30am - 12:40pm **Proteomics - PACIFIC SALON 3**
Organizers: Madan K. Bhattacharyya, Iowa State University and Michael A. Djordjevic, Australian National University

10:30am David A. Lightfoot,Southern Illinois University
"Proteomic Profiling and the Predicted Interactome of Host Proteins in Compatible and Incompatible Interactions Between Soybean and *Fusarium virguliforme*" (W778)

10:50am Wende Liu,Institute of Plant Protection, Chinese Academy of Agricultural Sciences
"Proteomic Insights into Lysine-Acetylation Mediated Innate Immunity in Rice (*Oryza sativa*)" (W781)

11:10am Hong Lin,Crop Diseases, Pests and Genetics Research , USDA ARS
"Proteome Analysis of Host Responses: Investigation of Molecular Mechanisms Associated with Citrus Huanglongbing" (W782)

11:30am Karina L Lopes,Esalq/ Universidade de Sao Paulo
"FIP, a Putative Regulator of FtsH5 in Chloroplasts, is involved with Abiotic Stress Response in Arabidopsis" (W783)

11:50am Yuri R. Montanholi,Dalhousie University
"Seminal Plasma Proteomics vary with Feed Efficiency and Fertility-Related Measures in the Bovine" (W779)

12:10pm Xinyun Li,Key Laboratory of Agricultural Animal Genetics, Breeding, and Reproduction of the Ministry of Education & Key Laboratory of Swine Genetics and Breeding of Ministry of Agriculture, Huazhong Agricultural University
"Proteiomics Analysis Indicated that Mitochondrial Energy Metabolism in Skeletal Muscle Tissue was Negatively Correlated with Feed Efficiency in Pigs" (W780)

10:30am - 12:40pm SGN and RTB Databases: Genomes, Pathways and Breeder Tools. - TOWNE - MEETING HOUSE
Organizers: Isaak Y. Tecle, Boyce Thompson Institute and Lukas Mueller, Boyce Thompson Institute

10:30am Lukas Mueller,Boyce Thompson Institute
"Breeder Tools on SGN and RTB Databases" (W832)

10:50am Surya Saha,Boyce Thompson Institute
"Sol Genomics Network Bioinformatics Web Tools" (W833)

11:10am Prashant S Hosmani,Boyce Thompson Institute
"ITAG3.0 Annotation for the New Tomato Reference Genome SL3.0" (W834)

11:30am Mirella Flores-Gonzalez,Boyce Thompson Institute
"Improved Tomato Genome Reference using Full-Length BACs, BioNano Genome Maps and SGN Community Resources" (W835)

11:50am Anjana Raina Vatsan,National Center for Biotechnology Information (NCBI/NLM/NIH)
"Tomato Genome Annotation and Curation at NCBI" (W836)

12:10pm Hartmut Foerster,Boyce Thompson Institute
"Pathway/Genome Databases of the Solanaceae: Capturing Metabolic Data in Taxon - Specific Databases" (W837)

10:30am - 12:40pm Soybean Genomics - ROYAL PALM SALON 1-2
Organizer: Suk-Ha Lee, Department of Plant Science and Research InstituteChair: Suk-Ha Lee, Seoul National University

10:30am Michelle A. Graham,USDA-ARS-CICGRU
"Iron Deficiency Signaling in Soybean: Root and Shoot Interactions" (W862)

10:50am Zhixi Tian,Chinese Academy of Sciences
"Genetic Dissection of Agronomic Traits and Molecular Design Breeding in Soybean" (W863)

11:10am Xuelu Wang,Huazhong Agricultural University
"Co-Expression Network Analysis of Nodule Development in Soybean" (W864)

11:30am Xia Li,Huazhong Agricultural University
"Nodule Number Regulation of Soybean" (W865)

11:50am Kyung Do Kim,University of Georgia
"Reduced Abundance of 24 nt Small RNA in Soybean is Associated with a Missense Mutation in Dicer-like (DCL) 3" (W866)

12:10pm Bao-Hua Song,University of North Carolina at Charlotte
"Apply Untapped Genetic Diversity of Crop Wild Relatives to Meet Global Challenges" (W867)

12:25pm Ju Seok Lee,Seoul National University
"Multi-Genome-Wide Association Study and Novel Gene Identification in Korean Soybean Using a 391 Core Collection" (W868)

10:30am - 12:40pm Synthetic Biology - PACIFIC SALON 4-5 (2ND FLOOR)
Organizer: Elibio Rech, EMBRAPA

10:30am Yang Liu,Iowa State University
"Targeted Gene Editing in Tetraploid Switchgrass (*Panicum virgatum* L.) by CRISPR/Cas9" (W923)

10:48am Sateesh Kagale,National Research Council Canada
"WheatCRISPR: A Web-Based Optimized sgRNA Designer for CRISPR-Cas9-Mediated Genome Editing in Wheat" (W924)

11:06am Wei Chen,Dow AgroSciences
"A Simple Way to Detect in Planta ZFN Activity and Chimerism in Gene Targeting" (W925)

11:24am Dheeraj Singh Rathore,Teagasc
"Enhancing the Utility of Plant Associated Bacterium; *Ensifer adhaerens* strain OV14, as a Vector for Plant Transformation" (W926)

11:42am Hiroshi Hisano,Institute of Plant Science and Resources, Okayama University
"TFA Genomic Regions Confer Amenability to Agrobacterium-Mediated Transformation in Barley " (W927)

12:00pm Melissa Huang Liu,Agilent Technologies
"Monitoring Guide RNA Synthesis for CRISPR/Cas9 Genome Editing Workflow Using the Agilent 2100 Bioanalyzer System" (W928)

10:30am - 12:40pm **Systems Genomics - SUNRISE - MEETING HOUSE**
Organizers: Meiping Zhang, Department of Soil and Crop Sciences, Texas A&M University and Hong-Bin Zhang, Texas A&M University

10:30am Mathilde Causse,Génétique et Amélioration des Fruits et Légume
"Integration of QTL, eQTL and Allele Specific Expression to Unravel Genotype by Watering Regime Interaction in Cultivated Tomato" (W936)

10:50am Hikmet Budak,Montana State University
"A Large Scale microRNA and Long-Noncoding RNA Annotation and Network Analysis in Plants" (W937)

11:10am Yun-Hua Liu,Texas A&M University
"Development of a Gene-Based Breeding System in Cotton: A New Method Powerful and Efficient for Enhanced Fiber Quality Breeding" (W938)

11:30am Shahid Mukhtar,University of Alabama at Birmingham
"Network Biology Discovers Pathogens' Contact Points in Host Protein-Protein Interaction Networks" (W939)

11:50am Yuling Jiao,Institute of Genetics and Developmental Biology, CAS
"A Gene Expression Map of Shoot Cell Types Reveals New Regulatory Mechanisms" (W940)

12:10pm Daifeng Wang,State University of New York at Stony Brook
"Dreiss: Using State-Space Models to Infer the Dynamics of Gene Expression Driven by External and Internal Regulatory Networks" (W941)

10:30am - 12:40pm **The Phytoremediation Genome - PACIFIC SALON 1**
Organizer: Adel M. Zayed, Supply Chain, Monsanto Company

10:30am Sharon L. Doty,University of Washington
"Endophyte-Assisted Phytoremediation: Genomic Analysis to Successful Field Trial" (W874)

11:00am Ivan Baxter,USDA-ARS, Danforth Plant Science Center
"Ionomics" (W875)

11:30am Bjoern Pietzenuk,Ruhr-Universität Bochum
" *Arabidopsis halleri* – a Hyperaccumulator of Zinc, Cadmium and Lead" (W876)

10:30am - 12:40pm **Hybridization, heterosis and balancing selection - SUNSET - MEETING HOUSE**
Organizer: Eyal Fridman, The Volcani CenterChair: Eyal Fridman, The Volcani CenterCo-Chair: Jianming Yu, Iowa State University

10:30am Michael Lenhard,University of Potsdam
"Dissecting the Heterostyly Supergene in *Primula* (primrose)" (W501)

10:50am Leonie Moyle,Indiana University
"Pervasive 'Less-Than-Additive' Interactions Characterize Fitness Effects in Wide *Solanum* Crosses" (W502)

11:10am Jode Edwards,USDA-ARS and Iowa State University, Ames, IA
"History and Modern Synthesis of Heterosis" (W503)

11:30am Jacob D Washburn,Division of Biological Sciences, University of Missouri
"Progressive Heterosis in Tetraploid Maize" (W504)

11:50am Bin Han,National Center for Gene Research,SIBS,CAS
"Characterizing Genetic Basis of Complex Traits and Heterosis in Rice" (W505)

12:10pm Detlef Weigel,Max Planck Institute for Developmental Biology
"Long-Term Balancing Selection Drives Evolution of Immunity in *Capsella*" (W506)

12:30pm Eyal Fridman,The Volcani Center and Volcani Agricultural Research Organization (ARO)
"Segregation Distortion and Heterozygous Advantage in Barley Multi-Parent Populations" (W507)

10:30am - 12:40pm **Genome-wide variation in rhinoceros species for evolutionary and conservation assessments - ROYAL PALM SALON 5-6**
Organizer: Oliver Ryder, San Diego Zoo Institute for Conservation Research

10:30am Yoshan Moodley,University of Venda
"The Divergent Evolutionary Histories of the Black and White Rhinoceros" (W424)

10:50am Tate Tunstall,San Diego Zoo Institute for Conservation Research
"Evaluating Genome Wide Measures of Variation in Northern White Rhinoceros" (W425)

11:10am Alfred L. Roca,University of Illinois at Urbana-Champaign
"Developing Genetic Tools for Conservation Management of Asian Rhinos" (W426)

11:30am Love Dalen,Swedish Museum of Natural History
"A Status Update on Rhino Reference Genome Assemblies" (W427)

11:50am M Thomas P Gilbert,Natural History Museum of Denmark, Univ. of Copenhagen
"Whole Genome Analysis of Rhinoceros Evolution" (W428)

12:10pm Elinor K. Karlsson,Broad Institute of MIT and Harvard
"The 200 Mammals Genome Project: Understanding Evolutionary Conservation at the Single Base Level" (W429)

10:30am - 12:40pm **Computer Demo 3 - CALIFORNIA**
Organizers: Monica C. Munoz-Torres, Lawrence Berkeley National Laboratory and Brian Smith-White, National Center for Biotechnology Information (NCBI/NLM/NIH)

10:30am Taner Z. Sen,USDA -ARS / GrainGenes
"GrainGenes: Supporting the Small Grains Community" (C17)

10:50am Hiromasa Ono,Database Center for Life Science
"RefEx, a Reference Gene Expression Dataset As a Web Tool for the Functional Analysis of Genes." (C18)

11:10am Sook Jung,Washington State University
"Newly Designed Genome Database for Rosaceae (GDR)" (C19)

11:30am Felipe A. Simão,University of Geneva Medical School & Swiss Institute of Bioinformatics
"Quality Assessment Using BUSCO v2" (C20)

11:50am Peifen Zhang,Carnegie Institution for Science
"PMN, A Unified Resource For Plant Metabolism" (C21)

12:10pm Austin Meier,Oregon State University
"Planteome: Reference Ontologies and a Platform for Integrative Plant Genomics" (C22)

10:30am - 1:00pm **Increasing Genetic Gains for Food Security in the Developing World - GOLDEN BALLROOM**
Organizers: Nora Lapitan, U.S. Agency for International Development, Jennifer Long, U.S. Agency for International Development, Angela Records, U.S. Agency for International Development and Paul Tanger, U.S. Agency for International Development

10:30am Overview and Purpose of Workshop

10:40am Kelvin Kamfwa,University of Zambia
"Harnessing PhotosynQ-Connected Phenotyping Technologies for Common Bean Breeding in Zambia" (W508)

11:00am Chiedozie Egesi,National Root Crops Research Institute (NRCRI)
"Delivering Genetic Gain in Cassava to Smallholder Farmers in Africa" (W509)

11:20am Gael Pressoir,Chibas - Quisqueya University
"Implementing a Sorghum Genomics Assisted Breeding Program in Haiti" (W510)

11:40am Panel Discussion

11:41am Appolinaire Djikeng,BecA-ILRI Hub
"Panelist" (W511)

11:42am Damaris Achieng Odeny,ICRISAT
"Panelist" (W512)

11:43am Peggy Ozias-Akins,University of Georgia
"Panelist" (W513)

11:44am Jesse Poland, Kansas State University
"Panelist" (W514)

11:45am Panel Discussion

12:49pm Summary and Next Steps

12:30pm - 1:30pm Lunch (Vouchers Provided) - ROYAL PALM COURT, EXHIBIT HALL & TIKI PAVILION COURT

1:30pm - 3:40pm Dovetail Genomics - In vitro Proximity Ligation - The Path to Better Genomes - PACIFIC SALON 1
Organizer: Michelle Vierra, Dovetail Genomics, LLC

1:30pm Richard E. Green,Dovetail Genomics
"In Vitro Proximity Ligation Techniques for Genome Assembly"

1:50pm John P. Vogel,DOE Joint Genome Institute
"A Reference Assembly for Brachypodium Hybridum As a Tool to Study Polyploidy"

2:10pm M Thomas P Gilbert,Natural History Museum of Denmark, University of Copenhagen
"A High-Quality Genome Assembly for Giant Squid"

1:30pm - 3:40pm MYcroarray - Advances in Target Capture for NGS - ROYAL PALM SALON 1-2
Organizers: Alison Devault, MYcroarray and Jake Enk, MYcroarray

Here we aim to provide attendees with tools and strategies for successful targeted sequencing using in-solution hybridization capture. We also discuss provocative new applications that demonstrate the breadth of sample types and target types that can be studied with the technology. We address probe design when starting with reference genomes, RADseq data, or transcriptomes; library preparation and quality assessment strategies; sequence data assembly and locus reconstruction; and even how to capture massive inserts for 3rd generation sequencing. Aspiring and veteran NGS users alike are sure to benefit from this broad-based but practical workshop. Visit us at exhibitor booth #615 to discuss your next project.

1:30pm Introductory Remarks

1:35pm Alison Devault,MYcroarray
"Designing Target Enrichment Baits from any Sequence Source"

1:50pm Matthew Johnson,Chicago Botanic Garden
"Targeted Exon Sequencing (HybSeq) in Non-Model Organisms: Best Practices for Probe Design and Data Analysis with HybPiper"

2:20pm Michael Giolai,Earlham Institute
"Improved Methodology for Large Fragment Plant Resistance-Gene Capture"

2:40pm Jake Enk,MYcroarray
"Complexity Made Simple: Maximizing Library Performance in Targeted NGS"

2:55pm Travis C. Glenn,University of Georgia
"Reducing Sequence Capture Costs with Universal Library Preparation Methods (Adapterama) and Ultraconserved Element (UCE) Bait Sets"

3:15pm Sandra Hoffberg,University of Georgia
"Sequence Capture of RADseq Libraries with Identifiable Duplicates (RADcap) Improves Genotyping and Reduces Costs"

1:30pm - 3:40pm **NAPPN - Technologies and Applications in Digital Plant Phenotyping - PACIFIC SALON 2**
Organizers: Gregoire Hummel, Phenospex, Bas van Eerdt, PhenoKey, Klara Panzarova, Photon Systems Instruments (PSI), Didier Neuzeret, Phenoware, Todd M. DeZwaan, PhD, LemnaTec Corporation and April Agee Carroll, Purdue University

In this workshop, the North American Plant Phenotyping Network (NAPPN) will provide a venue for researchers to learn the “who’s who,” and “what’s what” in phenotyping technology from researchers using the latest techniques and vendors representing >80% of the phenotyping market. Two high impact keynotes plus five scientific lightning talks will highlight applications of phenomics technology in plant science research. Sponsoring companies will present five-minute briefs on their latest successes and future directions. Digital phenomic data is crucial to fully benefit from the advances in genetic analysis and molecular engineering. However, the evolution from manual to digital and high throughput phenotyping proves to be difficult. Choosing where to start and understanding possibilities of the latest developments is a scientific discipline in itself. This workshop will provide space to accelerate inspiration, matchmaking and implementation of these cutting edge technologies by breeders and scientists into their day-to-day operations. It is a great opportunity to learn more about plant phenotyping applications, concepts and commercial state of the art technologies. If you are interested in presenting a five-minute lightning talk on a cutting-edge application of digital phenotyping technology, send a brief abstract (200 words or less) to the NAPPN before 23-Dec, 2016.

1:30pm April Carroll from NAPPN – **Welcome Remarks**

1:40pm David M. Kramer,Michigan State Univeristy
"What Do We Learn from Phenotyping Tools That Bridge the Gaps Between the Lab and the World?"

2:10pm Gregoire Hummel,Phenospex
"Planteye F500: Combine 3D and Multsipectral Information in One Sensor"

2:15pm Bas van Eerdt,PhenoKey
"Phenokey Translates Your Phenotyping Needs into a Real World Solutions That Work"

2:20pm Martin Trtílek,Photon Systems Instruments (PSI)
"New Tools for Automated Image-Based High-Throughput Phenotyping"

2:25pm Solmaz Hajmohammadi,LemnaTec Corporation

"Quantification of Plant Morphological and Physiological Traits with Lemnatec's Scanalyzer Suite of Sensors"

2:30pm Didier Neuzeret,Phenoware

"Phenotyping in Green House : Opening the Possibilities with Phenoware Technology"

2:35pm Mitchell Tuinstra,Purdue University

"MULTI-Scale Analysis of FIELD-Grown Sorghum Using RGB, Lidar, and Hyperspectral Imaging"

1:30pm - 3:40pm Addressing the Challenges of Nucleic Acid Extraction, Quantitation and Amplification - GOLDEN WEST
Organizer: Mary Jo Martinson, Promega Corporation

Nucleic acid extraction, quantitation and amplification are key processes in the molecular monitoring of plant genotypes and plant health. The diversity of input materials from seeds, embryos, woody mature tissues and the presence of substances that may inhibit nucleic acid amplification create many challenges. Once nucleic acid is isolated, success in DNA/RNA analysis applications often comes down to using the appropriate amount of input nucleic acid, but common nucleic acid quantitation methods provide only minimal information about nucleic acid quality. In this workshop, we will review extraction of nucleic acid from a wide range of plant materials using manual to high throughput automated protocols and the relative strengths of absorbance, fluorescent nucleic acid-binding dyes and qPCR quantitation of purified nucleic acids to allow you to select the appropriate methods for your sample type and downstream application.

1:30pm Chris Moreland,Promega Corporation

"Paramagnetic Cellulose DNA Isolation Improves DNA Yield and Quality Among Diverse Plant Taxa "

2:10pm Eric B. Vincent,Promega Corporation

"Choosing Appropriate Quantitation Methods for Nucleic Acids, a Review of Absorbance, Fluorescent Nucleic Acid-Binding Dyes and qPCR Quantitation Methods and What They Do and Do Not Tell You "

2:50pm Doug Wieczorek,Promega Corporation

"Purification of Plant Nucleic Acids from *Arabidopsis* to *Zea mays* using Manual, Bench Top and High Throughput Automation"

1:30pm - 3:40pm Animal Epigenetics - SAN DIEGO
Organizer: Hasan Khatib, University of Wisconsin Madison

1:30pm Jiuzhou Song,University of Maryland

"Epigenetic Regulation in Chicken Germ Stem Cell Differentiation" (W015)

1:50pm Eli Sellem,Allice R&D Department

"Small Non Coding RNA from Frozen Bull Sperm Cells: A Biomarker Panel of Male Fertility" (W016)

2:10pm Tasia M. Taxis,USDA/ARS

"Differential Expression of miRNA-423-5p in Cattle Challenged with Bovine Viral Diarrhea Virus" (W017)

2:30pm Eveline M. Ibeagha-Awemu,Agriculture and Agri-Food Canada, Sherbrooke Research and Development Centre
"Long Non-Coding RNA- Occurrence and Emerging Roles in the Bovine Genome" (W018)

2:50pm Helene Jammes,UMR BDR, INRA, ENVA, Université Paris Saclay
"Methylation Analysis in Blood Cells: Epigenetic Marks of Health in Dairy Cattle" (W019)

3:10pm Stephanie McKay,University of Vermont
"Whole Genome Bisulfite Sequencing of Three Tissues Related to the Bovine Reference Genome" (W020)

1:30pm - 3:40pm Compositae - PACIFIC SALON 4-5 (2ND FLOOR)
Organizers: John M. Burke, Department of Plant Biology, University of Georgia and Richard Michelmore, Genome Center, University of California Davis

1:30pm Hélène Badouin,INRA-LIPM
"The Reference Genome of the Common Sunflower *Helianthus annuus* Sequenced by Single Molecule, Real-Time Sequencing" (W188)

1:50pm Lien Bertier,Genome Center, University of California Davis
"Genome Editing in Lettuce" (W189)

2:10pm Koen J.F. Verhoeven,Netherlands Institute of Ecology
"Epigenetic Inheritance and Divergence within Apomictic Dandelion Lineage" (W190)

2:30pm Dan G. Bock,University of British Columbia
"Multiple Genetic Routes to the Evolution of Invasiveness in a Perennial Sunflower" (W191)

2:50pm Katherine Denby,University of York
"A Systems Approach to Breeding Disease Resistance in Lettuce Against Necrotrophic Fungal Pathogens" (W192)

3:10pm Stacey L. Harmer,University of California, Davis
"Interactions Between Circadian and Photoreceptor Signaling Networks to Produce Complex Behaviors" (W193)

1:30pm - 3:40pm Gramene Database: A resource for comparative plant genomics, pathways and phylogenomics analyses - CALIFORNIA
Organizer: Doreen Ware, Cold Spring Harbor Laboratory

1:30pm Marcela Karey Tello-Ruiz,Cold Spring Harbor Laboratory
"Overview of Gramene's Ensembl Genome Browser" (W480)

1:50pm Joshua Stein,Cold Spring Harbor Laboratory
"Mining Rice Disease Resistance Genes Using Gramene" (W481)

2:10pm Pankaj Jaiswal,Department of Botany & Plant Pathology, Oregon State University
"Plant Reactome: A Resource for Comparative Analysis of Plant Pathways" (W482)

2:30pm Matthew Geniza,Oregon State University
"High Resolution Transcriptome Analysis of Rice Salt Response Enabled by Gramene Resources" (W483)

2:50pm Maria Keays,European Bioinformatics Institute (EMBL-EBI)
"Plant Gene Expression in EMBL-EBI Expression Atlas" (W484)

1:30pm - 3:40pm Root Genomics - PACIFIC SALON 6-7 (2ND FLOOR)
Organizer: Antonio Costa De Oliveira, Universidade Federal de Pelotas

1:30pm Ajay Kohli,IRRI
"Recurrent Evolutionary Selection of the Epigenome Modulating Dysfunctional Guanine Deaminase Protein for Root Traits Favorable Under Water Stress" (W814)

1:50pm Shelby Ellison,Department of Horticulture, University of Wisconsin
"Utilizing 2D Imaging to Map Root System Architecture QTL in Carrot (*Daucus carota* L.)" (W815)

2:10pm Lee Hickey,QAAFI, The University of Queensland
"Dissecting the Genetics of Cereal Root System Architecture" (W816)

2:30pm Le Khanh Nguyen,USTH, LMI RICE-2
"Crown Root Development, from QTL Detected by GWAS using a Vietnamese Rice Collection to Candidate Gene" (W817)

2:50pm Joseph A. Edwards,UC Davis
"The Plant Root-Associated Microbiome Viewed Across Diverse Plant Species and Developmental Stages" (W818)

3:10pm Antonio Costa De Oliveira,UFPel
"Changes in the Rice Transcriptome Under Abiotic Stress Responses" (W819)

1:30pm - 3:40pm Weedy and Invasive Plant Genomics - TOWNE - MEETING HOUSE
Organizers: Patrick Tranel, University of Illinois and C. Neal Stewart Jr., Department of Plant Sciences, University of Tennessee

1:30pm Kathryn A. Hodgins,Monash University
"The Genomics of *Ambrosia artemisiifolia*: Invasion History and the Genetics of Glyphosate Resistance in a Notorious Weed" (W981)

1:50pm James H. Westwood,Virginia Tech
"RNA Exchange Between the Parasitic Plant *Cuscuta* and Its Hosts" (W982)

2:10pm Mithila Jugulam,Educational
"Mechanism of Genome Adaptive Response to Glyphosate Challenge in *Amaranthus tuberculatus*" (W983)

2:30pm Eric Lloyd Patterson,Colorado State University
"The Draft Genome of *Kochia scoparia* : A Foundation for Studying Adaptive Evolution and Its Impacts on Genome Architecture" (W984)

2:50pm Regina S. Baucom,University of Michigan
"Is Convergence at the Level of the Phenotype Mirrored Across the Genome? the Repeated Evolution of Glyphosate Resistance in the Common Morning Glory, *Ipomoea purpurea*" (W985)

3:10pm Kenneth Olsen,Washington University
"Whole Genome Resequencing Provides Insights into Adaptation through De-Domestication in Weedy Rice (*Oryza sativa*)" (W986)

1:30pm - 3:40pm Translational Agriculture: Opportunities, Technologies and Products - ROYAL PALM SALON 3-4
Organizer: Sireen Khan, KeyGene
Chair: Fayaz Khazi, KeyGene USA

This annual workshop by KeyGene on Translational Agriculture is focused on the impact of innovative technologies and their integration into the product development process by the industry. Invited speakers from multiple industries in food, agriculture and forestry will showcase how their companies view technological advances and discuss the overall impact on the industry and consumers.

1:30pm Fayaz Khazi,KeyGene USA
"Translational Agriculture: Promises and Practice"

1:50pm Vonnie Estes,Caribou Biosciences
"Gene Editing - Pathway to Commercialization "

2:10pm Gabe Gusmini,PepsiCo
"Crop Improvement at Pepsico Translates “Plant Potential” into Impact on Food Value-Chains and Consumer"

2:30pm Alexandre Missiaggia,Fibria S.A.
"Innovative and Sustainable Forest Technology"

2:50pm John Reich,Foundation for Food and Agriculture Research
"How the Foundation for Food and Agriculture Research and Partners Are Working to Nourish a Growing World"

1:30pm - 3:40pm **NuGEN - Trait to Table: NGS Solutions to Advance Agrigenomics - ROYAL PALM SALON 5-6**
Organizer: Kate Karfilis, NuGEN Technolgies

1:30pm Joe Don Heath,NuGEN Technologies
"Flexible and Cost-Effective Genotyping By Targeted Sequencing"

1:50pm Davide Scaglione,IGA Technology Services
"Targeted Genotyping-By-Sequencing with Single Primer Enrichment Technology (SPET). a Case Study in Black Poplar."

2:30pm Denise Stephens,NuGEN Technologies
"RNA-Seq, Simplified. Solutions for Every Sample."

2:50pm Sarah N Anderson,University of Minnesota, Twin Cities
"Initiation of Zygotic Genome Activation in the Unicellular Rice Zygote"

1:30pm - 3:40pm **Lexogen - QuantSeq 3' mRNA-Seq technology as an efficient tool for gene expression profiling - SUNRISE - MEETING HOUSE**
Organizer: Jekaterina Aleksejeva, Lexogen

With the rapid development of NGS technologies, RNA-Seq has become the new standard for transcriptome analysis. Although the price per base has been substantially reduced, sample preparation, sequencing, and data processing remain major cost factors in high-throughput screenings. The QuantSeq technology addresses these issues by providing an easy protocol to generate highly strand-specific NGS libraries close to the 3' end of polyadenylated RNAs within 4.5 hours, requiring only 0.1 - 500 ng of total RNA input and less bioinformatics efforts than standard RNA-Seq. It is the method of choice for fast, affordable and accurate gene expression detection, quantification and 3’ UTR studies. The protocol can be readily modified for targeted sequencing and include molecular barcoding. In our workshop users of QuantSeq will present their studies where this technology has empowered their discoveries.

1:30pm Introductory Remarks

1:40pm Karl A. Kremling,Cornell University
"Characterizing the Regulatory Impact of Rare Variants and Mapping eQTL in Zea Mays Using Nearly 2000 3' Mrnaseq Samples"

2:10pm Sheina Sim,University of Hawaii-Manoa
"An Integrative Approach to Finding the Genetic Basis of a Genetic Sexing Trait Textitwhite Pupae in Bactrocera Cucurbitae"

2:40pm Roman T Kellenberger,Institute of Systematic and Evolutionary Botany (ISEB) University of Zurich
"Dobzhansky Reloaded: Eco-Evo-Devo of a Putatively Overdominant Colour Polymorphism in the Alpine Orchid *Gymnadenia* (*Nigritella*) *Rhellicani*"

1:30pm - 3:40pm **Genestack - Applying High-throughput Bioinformatics Technologies to Crop Reserach - SUNSET - MEETING HOUSE**
Organizer: Kalina Cetnar, GenestackChair: Misha Kapushesky, Genestack

Genestack platform provides an enterprise-level infrastructure for bioinformatics R&D, with a strong focus on data and metadata management, absolute reproducibility and governance, as well as scalable computing and visualisations. It can run anywhere: on and off the cloud. Genestack has been working with Rothamsted Research, a leading UK agricultural research institute, on integrating their Ondex/KnetMiner agrigenomics suite of tools. This will enable scientists to use high-throughput bioinformatics technologies to accelerate genomics-based crop improvement and protection. Ondex allows users to build genome-scale knowledge networks: networks that integrate multi-omics datasets including ontologies, homologies, and scientific literature. KnetMiner is a tool for mining networks for specific traits. It ranks genes by different types of evidence. The discoveries can be explored using powerful network analytics and visualisations. These tools have until now been underappreciated due to high usability and technical barriers: users are limited to domain experts with access to adequate infrastructure. By integrating them into Genestack, users now have access to a simple, streamlined process from data collection, knowledge network building, to knowledge discovery. In this workshop, we will provide an overview of Ondex/KnetMiner, and its application to find candidate genes for breeding success traits in Cicer arietinum (chickpea) and Brassica oleracea (kale, cabbage, etc). Then, we'll showcase how users can easily build, combine, explore and share their own knowledge networks in Genestack, and how the results of other Genestack analytical pipelines can be integrated seamlessly to aid discovery. Lastly, we'll present ideas of integration with NDEx (Network Data Exchange).

1:30pm Keywan Hassani-Pak,Rothamsted Research
"Overview of Knetminer"

2:00pm Philipp E. Bayer,University of Western Australia
"Improving Plant Breeding Using Knetminer"

2:30pm Kevin Dialdestoro,Genestack
"Building and Exploring Knowledge Network and in Genestack"

1:30pm - 3:40pm **NRGene - From Multiple genome assemblies to accurate pangenome view - GOLDEN BALLROOM**
Organizer: Moran Ofer, NRGeneChair: Guy Kol, NRGENE Ltd.

1:30pm Curtis J Pozniak,University of Saskatchewan
"The Ten Genomes Project: Towards a Pan Genome of Wheat"

1:50pm Joseph D. Clarke,Syngenta Biotechnology Inc.
"Successfully Using Nrgene's Genomagic™ Platform to Evaluate Fit-for-Purpose Genomes and Genome Management Strategies"

2:10pm Marco Maccaferri,DipSA - University of Bologna
"Leveraging the Assembly of the Durum Wheat Genome cv. Svevo"

2:30pm Kevin M. Dorn,Kansas State University
"Developing a Genomic Toolbox for the Improvement of Intermediate Wheatgrass As a Perennial Grain Crop"

2:50pm Guy Kol,NRGENE Ltd.
"TBD"

Tuesday - January 17, 2017

1:30pm - 6:10pm **IWGSC - Standards and Protocols - PACIFIC SALON 3**
Organizers: Jane Rogers, International Wheat Genome Sequencing Consortium and Frederic Choulet, INRA GDEC

1:30pm Introductory Remarks

1:50pm Xi Wang,Bayer CropScience
"Wheat Genome Structural Annotation using a Modular and Evidence-Combined Annotation Pipeline." (W574)

2:10pm Frédéric Choulet,INRA GDEC
"Challenges of Gene and Repeat Annotation of the Wheat Genome Sequence" (W575)

2:30pm Manuel Spannagl,PGSB - Plant Genome and Systems Biology, Helmholtz Center Munich, German Research Center for Environmental Health (GmbH)
"Reference gene prediction in the hexaploid bread wheat genome" (W576)

2:50pm Jemima Brinton,John Innes Centre
"Integrating Wheat RNA-Seq Data into the expVIP Gene Expression Browser with Multiple Reference Genomes" (W577)

3:10pm Rudi Appels,Murdoch University
"The Wheat Genome Visualised in Apollo: Variation in the Clarity of Defining and Naming Gene Models." (W578)

3:30pm Pankaj Jaiswal,Department of Botany & Plant Pathology, Oregon State University
"Wheat Trait Ontologies" (W579)

3:50pm Jane Loveland,Wellcome Trust Sanger Institute
"Tools for Community Genome Annotation: ZMap and Otter" (W580)

4:10pm Brian Smith-White,National Center for Biotechnology Information (NCBI/NLM/NIH)
"Genome Curation and Maintenance at NCBI" (W581)

4:30pm Michael Alaux,INRA - URGI
"The IWGSC Reference Genome Browser, Data Mining and Beyond" (W582)

4:50pm Etienne Paux,INRA GDEC
"H3K27me3, a Key Player in Wheat Gene and Genome Organization and Regulation?" (W583)

5:10pm Jane Rogers

2:00pm - 3:00pm **Coffee Break - GRAND EXHIBIT HALL**

4:00pm - 6:10pm **Illumina, Inc. - GOLDEN WEST**
Organizer: Lauren Brock, Illumina, Inc.

4:00pm Ryan Rapp,Illumina, Inc.
"Introduction"

4:30pm Jose Fernando Garcia,IAEA Collaborating Centre for Animal Genomics
"An Assembled Map for Nellore Beef "

5:00pm Dr. Todd Mockler,Donald Danforth Plant Science Center
"Characterizing the Pan-Genome of Sorghum "

4:00pm - 6:10pm **Avian Genomics - Going Wild! - TOWNE - MEETING HOUSE**
Organizer: Robert H. S. Kraus, University of Konstanz, Department of Biology

4:00pm Lel Eory,Roslin Institute University of Edinburgh
"Signatures of Selection on 48 Bird Genomes Help Detect Functional Regions in the Chicken Genome"

4:20pm Lel Eory,Roslin Institute University of Edinburgh
"Functional Consequence of Selectively Constrained Regions in the Chicken Genome" (W057)

4:40pm Rute R. da Fonseca,University of Copenhagen
"Reticulate Evolution Influenced the Andean Hummingbird Radiation" (W058)

5:00pm Mirte Bosse,Wageningen University
"Signatures of Natural Selection in Great Tit Genomes: Past Selection, Local Adaptation or Human Imposed Change?" (W059)

5:20pm Matthias Weissensteiner,Uppsala University
"Going the Long (Molecule) Way: Detecting Structural Features Influencing Recombination Rate *via* SMRT-Seq and Optical Mapping in the Crow Genome" (W060)

5:40pm Martin Stervander,Linnaeus University
"Repeated Resource-Driven Speciation with Gene Flow in Isolated Island Finches" (W061)

6:00pm Elinor Jax,Max Planck Institute for Ornithology
"Expression Profiling of Whole Blood as a Means of Detecting an Immune Response in an Avian Non-Model Species" (W062)

4:00pm - 6:10pm **Cassava Genomics - SUNRISE - MEETING HOUSE**
Organizer: Steve Rounsley, Genus plc

4:00pm Rebecca Bart,Donald Danforth Plant Science Center
"Production, Assembly and Use of Genomic, Transcriptomic and Epigenomic Datasets to Understand the Loss of CMD2-Mediate Resistance during Cassava Tissue Culture" (W110)

4:20pm Ismail Rabbi,International Institute of Tropical Agriculture (IITA)
"Current Insights on Genomic Diversity and Genetic Architecture of Primary Breeding-Goal Traits in Africa Cassava Germplasm" (W111)

4:40pm Morag E. Ferguson,International Institute of Tropical Agriculture (IITA)
"QTL Associated with Field Resistance to Cassava Brown Streak Disease in the Context of the Genetic Relationship Among Genotypes" (W112)

5:00pm Ramu Punna,Institute for Genomic Diversity, Cornell University
"Genetic Load in Cassava" (W113)

5:20pm Cyprian Rajabu,North Carolina State University and University
"Two Novel DNAs Responsible for Enhanced Symptoms and Overcome Resistance to CMD in Plants" (W114)

5:40pm Diana Katherine Castillo Avila,CIAT
"Alternative Splicing in the GBSSI Gene Involved in Amylose-Free Cassava" (W115)

4:00pm - 6:10pm **Components of Apomixis - ESQUIRE - MEETING HOUSE**
Organizer: Emidio Albertini, University of Perugia

In this workshop we treat topics ranging from Meiosis to gametogenesis and embryogenesis related to apomixis

4:00pm Li Yuan,DuPont Pioneer
"Capturing Heterosis: Progress Towards Achieving Apomixis in Sorghum" (W183)

4:20pm Peggy Ozias-Akins,University of Georgia
"A Conserved Apomict-Derived *Babyboom* Gene Promotes Parthenogenesis in Multiple Cereals" (W184)

4:40pm Margaret L. Worthington,University of Arkansas
"Segmental Allopolyploidy and Diagnostic Markers for Apomixis in *Brachiaria*" (W185)

5:00pm John G. Carman,Utah State University
"Apomixis in Eukaryotes: An Ancient Fair-Weather Alternative to Sex" (W186)

5:20pm Emidio Albertini,University of Perugia
"Identification of Genes Showing Differential Methylation and Expression Patterns in Flowers of Apomictic and Sexual *Paspalum Spp.*" (W187)

4:00pm - 6:10pm **Crop Genomics for Global Food Security - GOLDEN BALLROOM**
Organizers: Antonio Costa De Oliveira, Universidade Federal de Pelotas and Henry T. Nguyen, University of Missouri

4:00pm Leon Kochian,Global Institute for Food Security
"Getting to the Root of the Matter: The Growing Importance of Root Biology to Global Food Security" (W219)

4:20pm Timothy J. Close,Department of Botany & Plant Sciences, University of California
"Advancing the Cowpea Genome for Food Security" (W220)

4:40pm Ivan Ingelbrecht,Plant Breeding and Genetics Laboratory - FAO/IAEA
"Crop Mutation Breeding at the Joint FAO/IAEA Program for Food Security and Enhancing Agrobiodiversity" (W221)

5:00pm Sivakumar Sukumaran,International Maize and Wheat Improvement Center (CIMMYT)
"Increasing Genetic Gains in Wheat through Physiological Genetics and Breeding" (W222)

5:20pm Vikas Belamkar,Department of Agronomy and Horticulture, University of Nebraska-Lincoln
"Translating Genomic Research into Cultivar Development in the Nebraska Wheat Program" (W223)

5:40pm Manish Roorkiwal,ICRISAT
"Genomic Selection in Chickpea" (W224)

4:00pm - 6:10pm **Genome Annotation with Galaxy - CALIFORNIA**
Organizers: Dave Clements, Johns Hopkins University and Jeremy Goecks, Oregon Health Sciences University

4:00pm Jeremy Goecks,Oregon Health Sciences University
"Genome Annotation with Galaxy" (W417)

4:00pm - 6:10pm **Gene Expression Analysis - ROYAL PALM SALON 1-2**
Organizers: David W. Galbraith, BIO5 Institute & School of Plant Sciences, University of Arizona and Gregory D. May, Pioneer HiBred

4:00pm David W. Galbraith,BIO5 Institute & School of Plant Sciences, University of Arizona
"Introduction to the workshop" (W394)

4:10pm Joanna C. Chiu,University of California, Davis, Department of Entomology and Nematology
"Accelerating Research on Spotted Wing Drosophila Management Using Genomic Technologies" (W395)

4:30pm Deanna Church,10x Genomics Inc.
"Quantitative Profiling of Large and Complex Single Cell Populations" (W396)

4:50pm Hainan Zhao,University of Wisconsin-Madison
"Recurrent Activation of a Latent Centromere in the Cericentromeric Region of Maize Chromosome 3" (W397)

5:10pm Won Cheol Yim,Department of Biochemistry and Molecular Biology, University of Nevada, Reno
"Transcriptome Analysis & Beyond: Advanced Approaches for Transcriptome Analysis in Diploid and Polyploid Plant Species." (W398)

5:30pm Bo Wang,Cold Spring Harbor Laboratory
"Unveiling the Complexity of Maize Transcriptome Using Single-Molecule Long-Read Sequencing" (W399)

5:50pm Jan Bartoš,Institute of Experimental Botany
"Gene Expression Changes in First Generations of Reciprocal Interspecific Grass Hybrids" (W400)

4:00pm - 6:10pm Host-Microbe Interactions - SUNSET - MEETING HOUSE
Organizers: Brett Tyler, Oregon State University and Christopher Barker, Genome Prairie

4:00pm Wenbo Ma,University of California
"Effectors of the Citrus Huanglongbing-Associated Bacteria" (W497)

4:30pm Anjali Iyer-Pascuzzi,Purdue University, Department of Botany and Plant Pathology
"Getting to the Root of Bacterial Wilt Resistance in Tomato" (W498)

5:00pm Matthew Links,Department of Animal and Poultry Science, University of Saskatchewan
"Microbial Profiling with cpn60 and the Collaborative Exploratory Data Environment (CEDE) " (W499)

5:30pm Joseph E Rubin,University of Saskatchewan
"The Emergence of Broad-Spectrum ß-Lactamases in *E. coli* from Canine Urinary Tract Infections in Western Canada" (W500)

4:00pm - 6:10pm Perennial Grasses - PACIFIC SALON 2
Organizers: Malay C. Saha, The Samuel Roberts Noble Foundation and Christian Tobias, USDA-ARS, Western Regional Research Center

4:00pm Thomas Juenger,University of Texas, Austin
"QTL x Environment Interactions and Latitudinal Adaptation in Switchgrass (*Panicum virgatum*)" (W671)

4:20pm Zhujia Ye,Tenneesse State University
"Proteomics Study of Switchgrass for Drought Stress" (W672)

4:40pm Kevin M. Dorn,Kansas State University
"The Intermediate Wheatgrass Genome: A Resource for Understanding Mechanisms of Perenniality and Accelerating the Development of Perennial Crops" (W673)

5:00pm Allison Miller,Saint Louis University
"Single Nucleotide Polymorphism Discovery *via* Genotyping-by-Sequencing to Assess Population Genetic Structure and Recurrent Polyploidization in *Andropogon gerardii*" (W674)

5:20pm Niranjan Baisakh,School of Plant, Environmental, and Soil Sciences, Louisiana State University Agricultural Center
"Identification of GBS-Generated Bi-Allelic SNPs Associated with Leaf Scald Resistance in Sugarcane" (W675)

5:40pm Bradley S. Bushman,USDA-ARS Forage & Range Research
"Late Flowering in Auto-Tetraploid *Dactylis glomerata*" (W676)

4:00pm - 6:10pm Plant Dormancy Workshop - ROYAL PALM SALON 3-4
Organizers: Anne Fennell, South Dakota State University and Jason Londo, USDA-ARS Grape Genetics Research Unit

4:00pm Heqiang Huo,University of Florida and Department of Plant Sciences, UC Davis
"Regulation of Seed Dormancy and Reproductive Phase Transitions By *miRNA156* and *DOG1*" (W689)

4:20pm Wun S. Chao,USDA-ARS
"Changes in Phytohormone Levels and Transcript Profiles during Seasonal Dormancy Transitions in Underground Adventitious Buds of Leafy Spurge (*Euphorbia esula* L.)" (W690)

4:40pm Anne Fennell,South Dakota State University
"Genetic Architecture of Dormancy Induction, Dormancy Release and Winter Survival in Grapevine" (W691)

5:00pm Stephanie Cornelissen,Agricultural Research Council of South Africa
"Determining the Genetic Differences within the QTL Associated with Chill Requirement; Between High and Low Chill Apple Varieties" (W692)

5:20pm Alisson P. Kovaleski,Cornell University
"Transcriptomic Analysis of Ecodormancy Release in Grapevine" (W693)

5:40pm Peter Dolan,University of Minnesota-Morris
"Solstice Party: Contrasting Transcriptional Velocity and Transcriptome Composition at Winter and Summer Solstices in Douglas-fir" (W694)

4:00pm - 6:10pm **Plant Science at the JGI and KBase - SAN DIEGO**
Organizers: Doreen Ware, Cold Spring Harbor Laboratory and Jeremy Schmutz, DOE Joint Genome Institute

4:00pm Jeremy Schmutz,DOE Joint Genome Institute and HudsonAlpha Institute for Biotechnology
"Introduction and JGI Plant Science Update" (W723)

4:15pm Priya Ranjan,Oak Ridge National Laboratory
"Kbase Plants Update" (W724)

4:30pm Gerald A. Tuskan,Oak Ridge National Laboratory
"Evolution of the *Populus* Genome: From a Reference to Holo- to Meta- to Pan-Genomes" (W725)

4:50pm Jay Chen,Oak Ridge National Laboratory
"Mining RNAseq Data to Determine Differential Gene Expression in *Populus* Transgenic Lines using Kbase" (W726)

5:10pm Richard Sibout,INRA-IJPB
"A Genome-Wide Sequence-Indexed Collection of *Brachypodium* Mutants to Accelerate Grain and Biomass Crop Breeding" (W727)

5:30pm Laura Bartley,University of Oklahoma
"Curation of Bioenergy-Relevant Families in the Switchgrass Genome" (W728)

5:50pm Yuhong Tang,The Samuel Roberts Noble Foundation
"A RNA-Seq and Microarray Combined Gene Atlas Database for Perennial Bioenergy Crop Switchgrass" (W729)

4:00pm - 6:10pm **Doriane Research Software And Consulting: Why build An All-In-One Tool For Collaborative Work And Decision Making Assistance In Genetics, Agronomy And Processing? - PACIFIC SALON 1**
Organizer: Tristan Duminil, Doriane

5:00pm - 7:00pm **Wageningen Alumni Event - TIKI PAVILION TERRACE**

We are very pleased to invite you to an informal Wageningen Alumni Meeting on Tuesday 12 January in San Diego. Each year many of our Wageningen University alumni are attending the Plant & Animal Genome conference. A great opportunity for our alumni to reconnect with each other. For that reason, we are planning to organize an informal meeting with drinks and bites for our Wageningen University alumni on Tuesday 12 January in San Diego at the conference venue from 17h - 19h. Please visit our website for more information and registration. More information on the programme and exact location will follow soon. Feel free to forward this message to any Wageningen University alumni that might be interested. In case of any further queries please do not hesitate to contact us via alumni@wur.nl.

Wednesday - January 18, 2017

7:00am - 8:00am **Continental Breakfast - GOLDEN BALLROOM**

7:00am - 12:00pm **Poster Access - GRAND EXHIBIT HALL**

7:00am - 12:00pm **Registration - ATLAS FOYER**

8:00am - 8:45am **Plenary Lecture: Rebecca N. Johnson - TOWN & COUNTRY BALLROOM**
Chair: J. Perry Gustafson, University of Missouri

8:00am Rebecca N. Johnson,Australian Museum Research Institute, Science & Learning
"Genomics and Wildlife Conservation"

8:45am - 9:30am **Plenary Lecture: Thomas Mitchell-Olds - TOWN & COUNTRY BALLROOM**
Chair: J. Perry Gustafson, University of Missouri

8:45am Thomas Mitchell-Olds,Duke University
"Dissecting Genotype-Environment Interactions and Trait Correlations"

9:30am - 10:30am **Coffee Break - ATLAS FOYER**

10:30am - 12:40pm **Animal Genomics and Adaptation to Climate Change - SUNRISE - MEETING HOUSE**
Organizer: Susan J. Lamont, Iowa State University, Department of Animal Science

10:30am Licia Colli,Inst. of Zootechnics, Università Cattolica del S. Cuore and Research Center on Biodiversity and Ancient DNA – BioDNA
"Small Ruminant Genomics and Adaptation to Climate" (W021)

11:00am James E. Koltes,Department of Animal Science, University of Arkansas
"Cattle Genoimics and Adaptation to Climate Change" (W022)

11:25am Benjamin Hale,Iowa State University
"Heat Stress Induces Autophagy in Pig Ovaries during Follicular Development" (W023)

11:50am Melissa S. Monson,Iowa State University
"Characterizing Responses to Heat Stress and Immune Stimulation Using Transcriptomics in Chicken Immune Tissues" (W024)

12:15pm Carl J. Schmidt,University of Delaware
"Integrated Analysis of Liver Transcriptome and Metabolome Response to Heat Stress" (W025)

10:30am - 12:40pm **EPIC: the Plant Epigenome Project - SAN DIEGO**
Organizer: Craig Pikaard, Indiana University/HHMI

10:30am Welcoming Remarks

10:35am Craig Pikaard,Indiana University/HHMI
"Chromosome Position-Effect in Megabase-Scale Silencing of Nucleolus Organizer Regions" (W287)

10:55am Doris Wagner,University of Pennsylvania
"Reprogramming Cell Identity or Function in the Context of Chromatin" (W288)

11:20am Roger B. Deal,Emory University
"Using Epigenomic Tools to Define the Regulatory Structure of Plant Genomes" (W289)

11:45am Julie Law,Salk Institute
"Targeting and Interpreting DNA Methylation in *Arabidopsis thaliana*" (W290)

12:10pm Rob Martienssen,HHMI-GBMF Cold Spring Harbor Laboratory
"The Maize EnCODE Project: Deciphering the Epigenetic Circuitry of Corn" (W291)

10:30am - 12:40pm **Exploring Phytobiomes - ROYAL PALM SALON 3-4**
Organizers: Isabelle Caugant, Eversole Associates, Kellye Eversole, International Alliance for Phytobiomes Research and Jan E. Leach, Colorado State University

10:30am Kellye Eversole,International Alliance for Phytobiomes Research
"From Simple to Complex - Phytobiomes and the 2050 Vision for Agriculture" (W317)

10:55am Tom Ruff,The Climate Corporation
"Layers of Field Data to Enable Better Crop Management" (W318)

11:15am Nian Wang,University of Florida, IFAS-CREC
"Citrus Microbiome" (W319)

11:35am Janne Kerovuo,NewLeaf Symbiotics, Inc
"Pink Pigmented Facultative Methylotrophs for Sustainable Agriculture - the NewLeaf Symbiotics Approach" (W320)

11:55am Todd C. Mockler,Donald Danforth Plant Science Center
"TERRA-REF and Beyond - Systems Approaches to the Sorghum Phytobiome" (W321)

12:15pm Joshua Herr,University of Nebraska
"Comparative Phytobiomes of Plants : a Tale from the Grasses" (W322)

10:30am - 12:40pm **Flax Genomics - TOWNE - MEETING HOUSE**
Organizer: Sylvie Cloutier, Agriculture and Agri-Food CanadaCo-Chair: Christopher Cullis, Case Western Reserve University

10:30am Michael K. Deyholos,University of British Columbia
"Variation in the Flax Genome and its Application to Bioproducts" (W323)

10:55am Jan Szopa-Skorkowski,University of Wroclaw,Faculty of Biotechnology
"Pleiotropic Effect of Chalcone Synthase Gene Engineering" (W324)

11:20am Yong-Bi Fu,Plant Gene Resources of Canada
"Evidence for Congruent Three-Genome Phylogenetic Signals for Four Botanical Sections of the Flax Genus *Linum*" (W325)

11:40am Raju Datla,National Research Council Canada
"The Transcriptome of Drought Response in Flax" (W326)

12:00pm Megan House,University of Saskatchewan
"Genome-wide Approaches to Identifying the Basis of Early Flowering in Epimutagenized Royal Flax" (W327)

12:20pm Khalid Rashid,Agriculture and Agri-Food Canada
"Host Pathogen Interaction between Flax and *Septoria linicola* and the Genetics of Resistance" (W328)

10:30am - 12:40pm **IRIC: Rice Informatics for the Global Community - ROYAL PALM SALON 5-6**
Organizer: Kenneth L. McNally, International Rice Research Institute

10:30am Nickolai Alexandrov,International Rice Research Institute
"International Rice Informatics Consortium: 3,000 Rice Genomes Explorations and Beyond" (W568)

10:50am David Edwards,University of Western Australia
"Development of WheatIS and Collaboration between Plant Information System" (W569)

11:10am Dario Copetti,Arizona Genomics Institute
"Development of Gap-Free Genome Assemblies to Capture and Exploit Rice Genetic Variation" (W570)

11:30am Pierre Larmande,IRD, UMR DIADE, Institut de Biologie Computationnelle
"The Rice Data Interoperability Working Group" (W571)

11:50am Tatiana Tatarinova,University of Southern California
"Genome-Wide Analysis of SNPs in Promoter Regsions of *Oryza sativa*" (W572)

12:10pm Jeremy D. Edwards,USDA-ARS Dale Bumpers National Rice Research Center
"Ricebase - a Resource for Rice Breeding" (W573)

10:30am - 12:40pm **UCSC Genome Browser - a home for all organisms - ROYAL PALM SALON 1-2**
Organizer: Robert Kuhn, U California Santa Cruz

10:30am Robert Kuhn,UC Santa Cruz
"UCSC Genome Browser - A Home for All Organisms" (W979)

11:55am Brian Lee,UCSC
"UCSC Genome Browser -- Assembly Hubs: Display Any Organism" (W980)

10:30am - 12:40pm **DivSeek – Addressing the challenges and opportunities for information and data sharing associated with plant germplasm - PACIFIC SALON 2**
Organizers: Susan McCouch, Cornell University and Ruth Bastow, Global Plant Council

10:30am Douglas R Cook,University of California-Davis
"Ecology and Community Genomics of an Important Crop Wild Relative As a Prelude to Agricultural Innovation" (W267)

10:50am Jianming Yu,Iowa State University
"Thoughts and Examples of Turbocharging the Gene Banks with Genomic Prediction" (W268)

11:10am Peter Wenzl,CIAT
"Cassava Genebank Analysis - Question and Answers"

11:30am Robert P. Davey,The Genome Analysis Centre
"Divseek Working Group - Data Standards for Interoperable Tools" (W269)

11:50am Elizabeth Arnaud,Bioversity International
"A Divseek Working Group on Semantics for Harmonizing Trait and Agronomic Data" (W270)

10:30am - 12:40pm **Computer Demo 4 - CALIFORNIA**
Organizers: Monica C. Munoz-Torres, Lawrence Berkeley National Laboratory and Brian Smith-White, National Center for Biotechnology Information (NCBI/NLM/NIH)

10:30am Felix Shaw,Earlham Institute
"COPO: A Data Stewardship Platform for Plant Scientists" (C23)

10:45am Prashant S Hosmani,Boyce Thompson Institute
"Systems Biology Resources for the Citrusgreening Disease Complex." (C24)

11:00am Locedie Mansueto,International Rice Research Institute
"SNP-Seek Resource for Rice Research" (C25)

11:15am Ming Chen,University of Tennessee
"Elasticsearch Indexing/Search and Expression Data Visualization with Two New Tripal Extension Modules" (C26)

11:30am Christine Tranchant-Dubreuil,IRD - UMR DIADE
"Toggle-3 : A Framework to Build Quickly Pipelines and to Perform Large-Scale NGS Analysis" (C27)

11:45am Frederic B. Bastian,SIB Swiss Institute of Bioinformatics - University of Lausanne
"Bgee: Database and R Package for Retrieving the Preferred Anatomical Expression Localization of a List of Genes, or of a Single Gene, in Animals." (C28)

12:00pm Hans Vasquez-Gross,University of California Davis
"Using the Wheat Tilling Resource to Find Mutations of Interest" (C29)

12:15pm Reinhard Simon,International Potato Center (CIP)
"Using the Public Plant Breeding API (BrAPI) to Access Data from the Statistical Platform R" (C30)

10:30am - 2:00pm Sweet Potato and Yam Genomics - SUNSET - MEETING HOUSE
Organizers: Craig Yencho, North Carolina State University and Ranjana Bhattacharjee, International Institute of Tropical Agriculture

10:30am Jim Lorenzen,BMGF
"Advances in Sweetpotato and Yam Genomics" (W902)

10:40am Mercy N. Kitavi,International Potato Center (CIP)
"A Multi-Modal Approach for Building Capacity in Sweetpotato Genomics-Assisted Breeding for Africa" (W903)

10:55am Asrat A. Amele,IITA
"Population Development in Yams for Integrating Genomics Application and Predicting Clone Development" (W904)

11:10am Bode Olukolu,North Carolina State University
"An Optimized Genotyping-by-Sequencing Protocol and SNP Calling Pipeline in Diploid and Hexaploid *Ipomoea sp*" (W905)

11:25am Dorcus C. Gemenet,International Potato Center (CIP)
"Quantitative Genetics in Sweetpotato: Where Are We within the Context of Genomic Tools for Sweetpotato Improvement Project?" (W906)

11:40am Sachiko Isobe,Kazusa DNA Research Institute
"Status of Sweetpotato Genome Sequencing Under TRAS Collaboration: TRAS Sweetpotato Genome Sequencing Consortium" (W907)

11:55am Thulile F. Nhlapo,Agricultural Research Council/University of the Witwatersrand
"The Status of Sweetpotato Viruses in South Africa: Using Viral Metagenomics for the Detection and Characterisation of Potyviruses, Criniviruses, Geminiviruses and Badnaviruses" (W908)

12:10pm Roland Akakpo,IRD
"African Yam Domestication: Evidences of Selection in Starch, Root and Photosynthesis Related Genes" (W909)

12:25pm Jessica B. Lyons,University of California, Berkeley
"Development of Genomic Resources for the Water Yam (*Dioscorea alata* L.) for Accelerated Breeding and Improvement" (W910)

10:30am - 2:00pm Data Resource Sustainability and Funding - PACIFIC SALON 1
Organizer: Tanya Z. Berardini, Phoenix Bioinformatics

10:30am Welcoming Remarks

10:35am Simon Hodson,CODATA
"The OECD Global Science Forum Project on Sustainable Business Models for Data Repositories" (W248)

11:00am Jennifer Lin,Crossref
"Dryad Digital Repository" (W249)

11:18am Eva Huala,Phoenix Bioinformatics
"The Arabidopsis Information Resource" (W250)

11:36am Peter D Karp,SRI International
"Transitioning BioCyc to a Subscription Model" (W251)

11:54am Dorrie Main,Washington State University
"NRSP10 Crop Databases" (W252)

12:12pm Fiona M. McCarthy,University of Arizona
"AgBase" (W253)

12:30pm Break

1:00pm Panel Discussion

10:30am - 2:30pm GMOD - GOLDEN WEST
Organizer: Scott Cain, Ontario Institute for Cancer Research

10:30am Introductory Remarks

10:35am Ian Holmes,University of California, Berkeley
"Jbrowse Update" (W468)

11:00am Brigitte T. Hofmeister,University of Georgia
"Visualizing Epigenomics in Jbrowse" (W469)

11:25am Michael S Campbell,Cold Spring Harbor Laboritory
"Maker: The Easy-to-Use Genome Annotation Pipeline" (W470)

11:50am Lunch

1:10pm Chris Mungall,Lawrence Berkeley National Lab
"Graph Chado Database" (W471)

1:35pm Dave Clements,Johns Hopkins University
"Galaxy Community Update" (W472)

2:00pm Anil S. Thanki,Earlham Institute
"Discovery and Visualisation of Homologous Genes and Gene Families Using Galaxy" (W473)

2:25pm Concluding Remarks

12:30pm - 1:30pm Lunch (Vouchers Provided) - ROYAL PALM COURT & TIKI PAVILION COURT

7:00pm - 11:55pm Closing Banquet Dinner - GRAND EXHIBIT HALL

Future Meetings

See You Next Year:

PAG XXVI
January 13-17, 2018
Town & Country Hotel
San Diego, CA

And the Year After:

PAG XXVII
January 12-16, 2019
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And the Year After:

PAG XXVIII
January 11-15, 2020
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Acknowledgements

The Plant & Animal Genome Organizing Committee and Sponsors would like to thank the following people for their time and commitment to the Plant & Animal Genome XXV Conference.

Abstracts Coordinators

Gerry Lazo
David Grant
Victoria Carollo Blake

Travel Grants Coordinator

Tom Blake
Alison L. Van Eenennaam

Special Duty Coordinators

Hans Cheng
Max Rothschild

Travel Grant Awards

Jerome P. Miksche Travel Grant

David Kainer
Australian National University, Australia
Genome-wide associations of essential oil traits in Eucalyptus polybractea using a low-depth WGS pipeline.

Earl J. Scherago Travel Grant

Katarzyna Gacek
Plant Breeding and Acclimatization Institute National Research Institute Oilseed Crops Research Centre, Poland
Genome-wide association study of genetic control of seed fatty acid biosynthesis in Brassica napus.

Mike D. Gale Travel Grant

Parimalan Rangan
Scientist and Honorary Sr. Research Fellow (QAAFI, UQ)
ICAR-National Bureau of Plant Genetic Resources, PUSA Campus, New Delhi-110012, India
Discovery of the C4 photosynthetic pathway in developing wheat grains.

Scherago International Student Travel Grant(s)

Plant:

Varena Marina Prade
Helmholtz Zentrum Munchen GmbH
A Playground for Innovation: Pseudogenes and Gene Fragments in Barley

Hormat Shadgou
New Mexico State University
The first glimpse at the timing of flower initiation in Carya Illinoinensis

Chiraq Gupta
University of Arkansas
An abiotic stress conditioned gene regulatory network in rice predicted using an ensemble of reverse-engineering solutions

Travel Grant Awards

Scherago International Student Travel Grant

Animal:

Charity Muriuki
Roslin Institute, Scotland
Transcriptomics of Innate Immune Response in The Domestic Goat and Comparative Analysis with Other Ruminants

Rachael Ashby
University of Otago, New Zealand
A Genomic Toolbox (Genome, Transcriptome and GBS) for the New Zealand Greenshell Mussel ™ *(Pema canaliculus)*

Neal A. Jorgensen Genome Travel Grants

Swine:

Haibo Liu
Iowa State University
Swine Transcriptome Characterization by Combined Iso-Seq and RNA-seq for Annotating the Emerging Long Read-based Reference Genome

Cattle:

Jesse Hoff
University of Missouri
Enhancement of QTL-Mapping and Genomic Prediction for Bovine Respiratory Disease

Bioinformatics:

Jicai Jiang
University of Maryland
A Fast and Flexible Method for Improving Genomic Prediction with Biological Information

Sheep/Goat:

Kimberly Davenport
University of Idaho
Understanding the Ramification of Recombination Variation in Sheep

Alisha T. Massa
Washington State University
Genome-wide Identification of Active Enhancers in Sheep Alveolar Macrophages

Travel Grant Awards

Horse:

Erin Burns
University of California, Davis
Generation of an Equine Tissue Biobank for Functional Annotation

Poultry:

Hao Bai
University of Maryland
Allele-Specific Expression (ASE) of CD4+ T Cells in Response to Marek's Disease Virus Infection

Aquaculture Species Group Student and Postdoctoral Fellowship Bursaries

Matthew Conte
University of Maryland
A High Quality Assembly of the Nile Tilapia (Oreochromis niloticus) Genome Provides Insights into the Structure of Two Sex Determination Regions

Michelle T.T. Crown
Simon Fraser University
Identification of Genomic Loci Associated with Maturation and Survival in Pacific Coho Salmon (Oncorhynchus kitsutch)

Albert Caballero Solares
Memorial University of Newfoundland
Applying transcriptomic profiling to the formulation of sustainable feeds for Atlantic salmon (Salmo salar)

Nawar Al-Janabi
Mississippi State University
The Intestinal Immune Responses of Channel Catfish Against Live Attenuated Edwardsiella Ictaluri Vaccines

Yulin Jin
Auburn University
A Genome-Wide Association Study of Heat Stress-Associated SNPs in Catfish

Zihao Yuan
Auburn University
Comparative Analyses of Repetitive Elements in 52 Fish Species Revealed Their Association with Evolutionary Adaptation to Aquatic Living Environments

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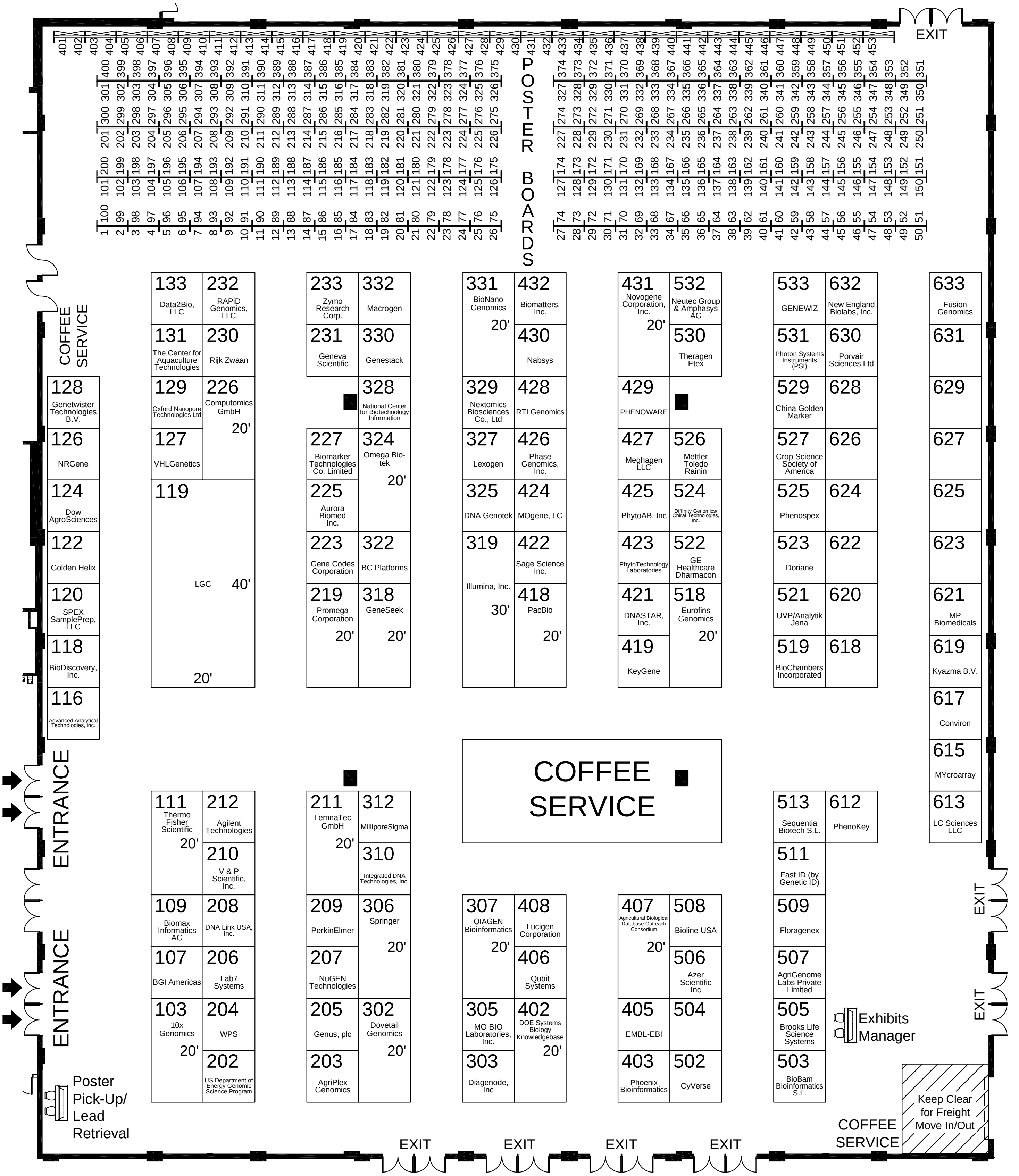

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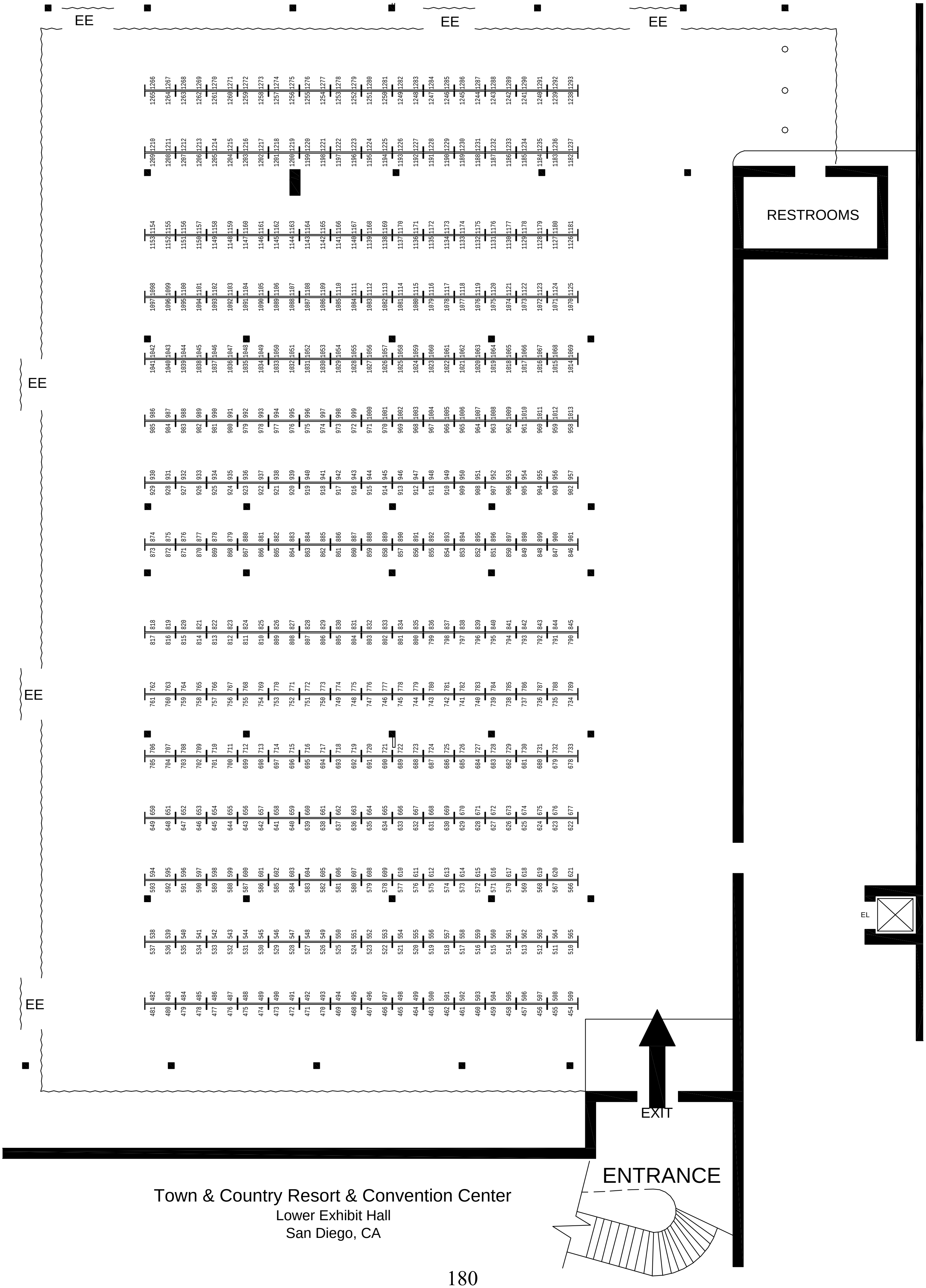

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Milestones in 2016

Initiative to construct high-quality reference genomes for important crops
构建重要农作物参考基因组计划

Participation of The National Key Research and Development Program of China
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Acquisition of the first PacBio Sequel instrument in China
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Establishment of the Clinical Laboratory
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Our Services

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Zero-gap assemblies for small genomes.

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Full Length Transcriptome

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Algorithm Engineer will be responsible for designing and developing frasergen’s advanced algorithms, performing genomic big data analysis with the latest methodologies, aiming to solve complex bioinformatics questions, such as genome assemblies. Candidates should have MS or PhD in bioinformatics, computational biology, computer science or related disciplines.

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