

## JGI/KBase Project-Related Presentations

### International Plant & Animal Genome XXVII Conference

January 12 – 16, 2019 San Diego, CA, USA

The Department of Energy (DOE) Office of Science supports both a large-scale genomics user facility at the DOE Joint Genome Institute (JGI: <http://jgi.doe.gov/>) and a large-scale computational resource for comparative functional genomics and systems biology of microbes, plants and their communities called the DOE Systems Biology Knowledgebase (KBase: <http://kbase.us/>). The core mission of both of these endeavors is to help scientists carry out experiments and analyses in areas such as improving biofuel development, understanding plant model systems, advancing plant comparative science and investigating global element cycling. In the BER Plant Genomic Science Workshop (#4850), Monday, January 14, from 6:20 PM – 8:30 PM at the Town and Country, Royal Palm Salon 3-4 (<http://bit.ly/BER-PAGXXVII>) (see details inside), we will present current and ongoing developments from both the Plant Program at JGI and KBase toward integrative biology. We will also hear from researchers who are applying genomic sequence information from JGI to elucidate functions of plant systems and from users who are working to apply KBase computational infrastructure to plant biological inquiries.

visit us  
at Booth  
509

see talks  
schedule  
inside



## The Plant Program @ DOE Joint Genome Institute

The Plant Program focuses on understanding how plant genes function in the context of the whole organism and how these genes drive the interaction with a plant's environment. Focus areas include:

- Feedstocks for biofuels, e.g., next-generation cellulosic biofuels from perennial grasses and forest plantation trees.
- Ecosystems and the role of terrestrial plants and oceanic phytoplankton in carbon sequestration.
- The role of plants in coping with toxic pollutants in soils by hyper-accumulation and detoxification.
- The ability to respond to environmental change (e.g., loss of diversity from monoculture produces vulnerabilities; nitrogen-fixing nodules in legumes reduce fertilizer need).
- The generation of useful secondary metabolites (produced largely for disease resistance) for positive/negative control in agriculture, with attendant influence on the global carbon cycle.

The Plant Program accomplishes the above through the following activities:

1. **Sequence.** Produce genome sequences of key plant (and algal) species to accelerate biofuel development and understand response to climate change.
2. **Function.** Develop data sets (and synthetic biology tools) to elucidate functional elements in plant genomes, with special focus on handful of "flag-ship" genomes.
3. **Variation.** Characterize natural genomic variation in plants (and their associated microbiomes), and relate to biofuel sustainability and adaptation to climate change.
4. **Integration.** Provide a centralized hub for the retrieval and deep integrated analysis of plant genome data sets.



## Saturday, January 12, 2019

### Forage, Feedstocks & Turf

Time: 9:00 AM  
Room: Town and Country, Pacific Salon 4-5 (2nd Floor)  
Title: Polymorphism of Genes Involved with Regulation of Flowering Time in *Miscanthus* as C4 Bioenergy Crop  
Presenter: **Lindsay V. Clark**, CABB

### Ecological Genomics

Time: 10:50 AM  
Room: Town and Country, Royal Palm Salon 5-6  
Title: The GWAS Times: A Time-Series Aware GWAS to Detect Natural Climate Adaptations in *Arabidopsis* and *Populus*  
Presenter: **Ashley Cliff**, ORNL

### Functional Genomics of C4 and CAM photosynthesis

Time: 11:10 AM  
Room: Town and Country, Towne - Meeting House  
Title: Using a C3+CAM Hybrid to Elucidate Genetic Regulation of CAM  
Presenter: **Karolina Heyduk**, Yale University

### Grasslands (Lolium Genome Initiative)

Time: 11:30 AM  
Room: Town and Country, Esquire - Meeting House  
Title: Molecular Breeding for Freezing Tolerance in Lowland Switchgrass  
Presenter: **Mike Casler**, GLBRC

### Non-Seed Plants

Time: 4:40 PM  
Room: Town and Country, Esquire - Meeting House  
Title: Sexually Antagonistic Selection in an Ancient Interaction between Moss and Microarthropods  
Presenter: **Leslie M. Kollar**, University of Florida

### Genomic Selection and Genome-Wide Association Studies

Time: 4:50 PM  
Room: Town and Country, Golden West  
Title: PanGWAS: GWAS of the Pan-Genome Provides New Insights into *P. trichocarpa* Phenotypic Variation  
Presenter: **David Kainer**, ORNL

### Bioenergy Grasses Genomics

Time: 5:00 PM  
Room: Town and Country, Pacific Salon 2  
Title: Development of Genomic Resources to De-tangle the Complex Genome of Sugarcane  
Presenter: **Adam Healey**, HudsonAlpha

## Sunday, January 13, 2019

### Forest Tree

Time: 8:25 AM  
Room: Town and Country, Sunrise - Meeting House  
Title: Expression Quantitative Trait Locus Mapping in *Populus*  
Presenter: **Jay Chen**, ORNL

### Sorghum/Millet

Time: 9:43 AM  
Room: Town and Country, Pacific Salon 6-7 (2nd Floor)  
Title: Leveraging Multiple Genomic Resources to Dissect Nonstructural Sugar Accumulation in *Sorghum bicolor*  
Presenter: **Zachary Brenton**, Clemson University

### Abiotic Stress

Time: 11:50 AM  
Room: Town and Country, Golden Ballroom  
Title: A Novel NAC83 Transcription Factor from *Kalanchoe fedtschenkoi* Enhances Drought and Salt Tolerance in *Arabidopsis*  
Presenter: **John Cushman**, University of Nevada, Reno

### Plant Reproductive Genomics

Time: 3:10 PM  
Room: Town and Country, Sunset - Meeting House  
Title: Phylogenomic Analyses Uncover Ancient but Highly Dynamic Moss Sex Chromosomes  
Presenter: **Sarah Carey**, University of Florida

### Sex Chromosomes and Sex Determination

Time: 5:40 PM  
Room: Town and Country, Royal Palm Salon 5-6  
Title: Structural Variation between the U and V Sex Chromosomes in the Moss *Ceratodon purpureus*  
Presenter: **Stuart McDaniel**, University of Florida

## Monday, January 14, 2019

### Population and Conservation Genomics 2

Time: 5:25 PM  
Room: Town and Country, Sunset - Meeting House  
Title: Your Daily GWAS: A Time-Series Aware GWAS to Detect Natural Climate Adaptations in North American *Populus trichocarpa*  
Presenter: **Ashley Cliff**, ORNL

## Tuesday, January 15, 2019

### Brachypodium Genomics

Time: 11:45 AM  
Room: Town and Country, Pacific Salon 2  
Title: Wild Monocots are Wired Differently: Hormone Action in *Brachypodium*  
Presenter: **Christian S. Hardtke**, University of Lausanne

### Brachypodium Genomics

Time: 12:10 PM  
Room: Town and Country, Pacific Salon 2  
Title: Revisiting *Brachypodium* Genomes through Whole-Genome Optical Maps  
Presenter: **Tingting Zhu**, University of California, Davis

### Gene Expression Analysis

Time: 4:00 PM  
Room: Town and Country, Royal Palm Salon 1-2  
Title: Dynamic Transcriptional Landscape of Polyploid Plants  
Presenter: **Avinash Sreedasyam**, HudsonAlpha

### Perennial Grasses

Time: 4:40 PM  
Room: Town and Country, Pacific Salon 1  
Title: Comparative Sequence and Synteny Analysis across 13 Complete *de novo* Grass Genomes  
Presenter: **John Lovell**, HudsonAlpha

### Perennial Grasses

Time: 5:40 PM  
Room: Town and Country, Pacific Salon 1  
Title: Transgenic Pollen Containment in *Brachypodium sylvaticum* and *Panicum virgatum*  
Presenter: **Jonathan Willis**, USDA-ARS



Monday, January 14, 2019

DOE Office of Biological and Environmental Research (BER) Plant Genomic Science

Time: 6:20 PM – 8:30PM  
Room: Royal Palm Salon 3-4  
Organizers: DOE Joint Genome Institute (JGI) & DOE Systems Biology Knowledgebase (KBase)

Time: 6:20 PM  
Room: Royal Palm  
Title: Overview and Joint Genome Institute Plant Program Update  
Presenter: **Jeremy Schmutz**, Joint Genome Institute

Time: 6:33 PM  
Room: Royal Palm  
Title: Comparative Genomic and Transcriptomic Analyses for Bioprospecting in the Green Lineage using KBase  
Presenter: **Crysten Blaby**, Brookhaven National Laboratory

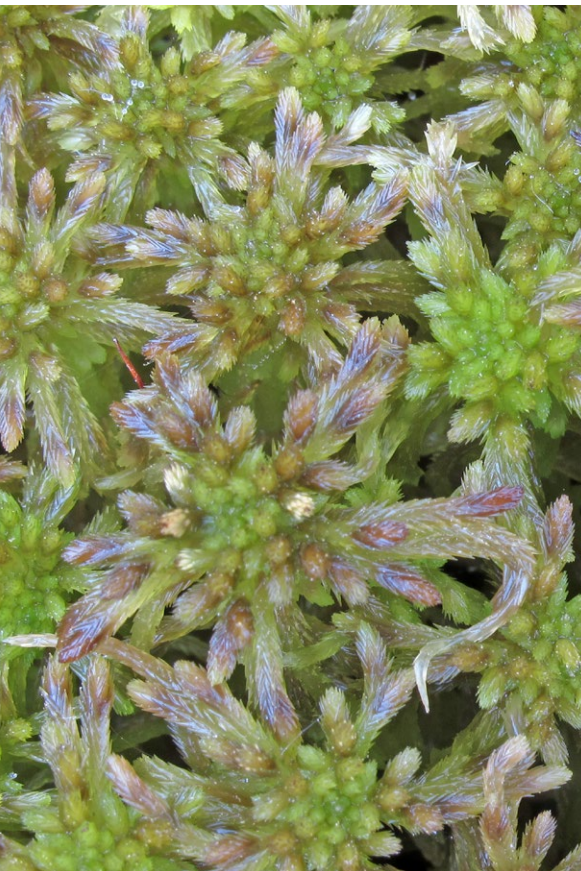
Time: 6:51 PM  
Room: Royal Palm  
Title: Evolution of Sex Chromosomes in the Moss *Ceratodon*  
Presenter: **Stuart McDaniel**, University of Florida

Time: 7:09 PM  
Room: Royal Palm  
Title: Bioinformatic Approach to Discovering Promoters Regulating Poplar Drought Response  
Presenter: **Austin Wyer**, UT-Knoxville

Time: 7:27 PM  
Room: Royal Palm  
Title: Highlights from Genome of *Miscanthus*  
Presenter: **Therese Mitros**, University of California, Berkeley

Time: 7:45 PM  
Room: Royal Palm  
Title: Transcriptome Changes during Leaf Senescence in *Populus*  
Presenter: **Haiwei Lu, Steven Strauss** (presenter), Oregon State University

Time: 8:03 PM  
Room: Royal Palm  
Title: Natural Diversity in *Setaria* and a Novel Gene for Shattering  
Presenter: **Elizabeth Kellogg**, Danforth Center



## JGI Plant Program and Related Initiatives:

**Phytozome** facilitates comparative genomic studies among green plants. Families of genes that represent the modern descendants of ancestral gene sets are constructed at key phylogenetic nodes. These families allow easy access to clade-specific relationships as well as clade-specific genes and gene expansions.

<http://phytozome.jgi.doe.gov>

**Plant Flagship Genomes** are the most important set of plant genomes to DOE's mission and to plant science. They have been selected to focus our computational and experimental efforts in order to move beyond sequence and function and to provide the most direct benefit for enabling world-class science.

<http://bitly.com/JGI-Plants>

**Plant Gene Atlas** is a major initiative to develop gene expression catalogs for five species, sampling a wide variety of relevant developmental and experimental conditions (uniform nitrogen application and metabolism, etc.) using deep-coverage RNA-seq methods and small RNA sequencing. In addition to facilitating direct comparisons of gene expression patterns within a species of interest, these data will enable broad inferences of shared gene function across phyla, focusing on applications to address mission-oriented research within DOE-relevant plants.

<http://bit.ly/JGI-PGA>

**KBase**, the Department of Energy Systems Biology Knowledgebase, is a knowledge discovery and creation environment designed for both biologists and bioinformaticians. KBase integrates a large variety of public data and analysis tools into an easy-to-use graphical user interface and leverages DOE computational infrastructure to perform sophisticated systems biology analyses. KBase is a freely available system that enables scientists to upload their own data, analyze it alongside collaborator and public data, build validated systems biology models, and share workflows and conclusions.

<http://kbase.us>



# Join us in San Francisco...

FOR THE 14<sup>TH</sup> ANNUAL  
**Genomics of Energy &  
Environment Meeting**

**Hilton San Francisco Union Square**

**APRIL 2-5, 2019**

**REGISTRATION NOW OPEN!**  
[usermeeting.jgi.doe.gov](http://usermeeting.jgi.doe.gov)

HOSTED BY THE  
**U.S. Department of Energy  
Joint Genome Institute**

The Meeting brings together scientists pursuing challenges in energy and environmental genomics, data science, and tech development. Workshops include microbiome analyses using KBase, and JGI strategic technologies: e.g., single-cell omics, DNA synthesis, metabolomics, and *in vitro* transcription and translation. Register by February 19 and submit an abstract to be considered for a short talk. The NeLLi 2019 Symposium will feature innovations that are enabling researchers to move from identification of microbial novelty to assigning metabolic and functional capabilities.



<http://kbase.us>

<http://jgi.doe.gov>