

2019 Genomic Sciences Program Annual PI Meeting February 24-27, 2019

Sunday, February 24th

5:00-8:00 pm **Early Registration and poster setup**
Location: Lobby outside Fairfax Ballroom

Monday, February 25th

7:00-8:30 am **Registration**
Location: Lobby outside Fairfax Ballroom

7:00-8:00 **Breakfast** (on your own)

8:00-8:30 **Welcome and Introduction to the Meeting**
Location: Fairfax Ballroom

8:00-8:10 **Sharlene Weatherwax** - Associate Director, DOE Office of Biological and Environmental Research (BER)
Opening Remarks

8:10-8:25 **Todd Anderson** - Director, Biological Systems Science Division, BER, DOE
Meeting Introduction

8:25-8:30 **Kent Peters** - Program Manager, BER, DOE
Logistics

8:30-10:30 **Plenary Session: Bioenergy Research Centers: Recent BRC Highlights**
Location: Fairfax Ballroom
Moderator: Kent Peters

Speakers:

8:30-9:00 **Tim Donohue** - University of Wisconsin, Great Lakes Bioenergy Research Center (GLBRC)
Sustainable Fuels and Bioproducts from Biomass

9:00-9:30 **Gerald Tuskan** - Oak Ridge National Laboratory, Center for Bioenergy Innovation (CBI)
Selected insights in deep data analytics of biomass feedstocks, surprising microbial ligninolytic biology and hybrid CBP

9:30-10:00 **Evan DeLucia** - University of Illinois-Urbana-Champaign, Center for Advanced Bioenergy and Bioproducts Innovation (CABBI)
The Center for Advanced Bioproduct and Bioenergy Innovation (CABBI) - building a foundation in year one for accelerating research

- 10:00-10:30 **Jay Keasling** - Lawrence Berkeley National Laboratory, Joint BioEnergy Institute (JBEI)
Building the future of low carbon biofuels and bioproducts through integrated basic science
- 10:30-11:00 **Break**
- 11:00-12:00 **Keynote Presentation: Jonathan Schilling** – University of Minnesota
From pickaxes to dynamite: Risky but rewarding fungal innovations for mining lignocellulose
- Location:** Fairfax Ballroom
Moderator: Dawn Adin
- 12:00-2:00 **Lunch** (on your own)
- 2:00-5:00 **Breakout Session A: KBase User Science Presentations**
Location: Fairfax Ballroom A
- Description of Session:** KBase users and collaborators will speak about science accomplished with the system. Research covering assembly, annotation, comparative genomics, and modeling of microbes, fungi, plants and their communities will be presented, with examples ranging from single genome modeling to large scale community analysis. Speakers will discuss how KBase enabled their research and the dissemination of their data, analyses, and algorithms. Some speakers will describe their experiences adding analysis tools as KBase apps.
- 2:00-2:10 **Christopher Henry** - Argonne National Laboratory
Introduction
- 2:10-2:24 **Kjiersten Fagnan** – DOE Joint Genome Institute
JGI-KBase co-development
- 2:24-2:36 **Patrick Chain** - Los Alamos National Laboratory
Integrating new fungal computational sequence data analysis into KBase’s capabilities
- 2:36-2:48 **Sarah Calhoun** – DOE Joint Genome Institute
Building and comparing models of diverse fungal genomes in KBase
- 2:48-3:00 **Patrik D'haeseleer** – Lawrence Livermore National Laboratory
Improving Draft Metabolic Models in KBase: Tools for Importing, Comparing and Merging Metabolic Annotations
- 3:00-3:12 **Trent Northen** - Lawrence Berkeley National Laboratory
Integration and Analysis Web of Microbes Exometabolite Data in the KBase Platform
- 3:12-3:22 **Break**
- 3:22-3:24 **Anni Zhang** - Massachusetts Institute of Technology

- Building a reference-based metagenomics workflow in KBase (ENIGMA)
- 3:24-3:36 **Daniel Segre** - Boston University
Assembly, binning, annotation, and modeling of defined microbiomes in KBase
- 3:36-3:48 **Pamela Weisenhorn** - Argonne National Laboratory
Microbiome heterogeneity across the redox dynamic zone
- 3:48-4:00 **Hyun-Seob Song** - Pacific Northwest National Laboratory
Metabolic network modeling for predicting condition-specific reaction pathways in environmental systems
- 4:00-4:10 **Break**
- 4:10-4:22 **Matt Sullivan** - Ohio State University
iVirus at KBase: Porting the viral ecogenomics toolkit to leverage the power of KBase
- 4:22-4:34 **Ada Sedova** - Oak Ridge National Laboratory
Protein Co-Evolutionary Analysis and Virtual Ligand Screening
- 4:34-4:46 **Austin Wyer** - Oak Ridge National Laboratory
Bioinformatic Approach to Discovering Promoters Regulating Poplar Drought Response
- 4:46-4:58 **Crysten Blaby** - Brookhaven National Laboratory
Comparative genomic and transcriptomic analyses for bioprospecting in the green lineage

2:00-5:00

Breakout Session B: USDA-DOE Plant Feedstock Genomics for Bioenergy

Location: Ash Grove Ballroom

Moderator: Cathy Ronning, DOE BER and Bill Goldner, USDA NIFA

Session Description: The joint USDA-DOE Plant Feedstocks Genomics for Bioenergy program supports fundamental genomics-based research leading to the development of improved and more sustainable plant feedstocks for the production of biofuels and biobased products. The session will include presentations by the 2016 awardees on their accomplishments in increasing knowledge of the molecular mechanisms underlying phenotypic traits that are critical for the development of improved, high-yielding bioenergy crops. The 2018 awardees will follow with a series of “speed talks” highlighting newly funded research spanning a variety of candidate feedstocks, from oilseeds to grasses to trees.

- 2:00-2:10 **Cathy Ronning** and **Bill Goldner**
Introduction and Program Overview

2016 Awardees

- 2:10-2:40 **Serge Edmé**, USDA-ARS, Lincoln NE
Genetics and Genomics of Pathogen Resistance in Switchgrass
- 2:40-3:10 **Jack Brown**, University of Idaho

Developing Non-Food Grade *Brassica* Biofuel Feedstock Cultivars with High Yield, Oil Content, and Oil Quality that are Suitable for Low Input Production Dryland Systems

3:10-3:30

Break

3:30-4:00

Ana Alonso, University of North Texas
Development of Resources and Tools to Improve Oil Content and Quality in Pennycress

4:00-4:30

John Dyer, USDA-ARS, Maricopa AZ
Genomics and Phenomics to Identify Yield and Drought Tolerance Alleles for Improvement of Camelina as a Biofuel Crop

2018 Awardees:

4:30-4:35

Ratan Chopra, University of Minnesota (for PI Jim Anderson)
Genetic Improvement of Seed Yield and Oil Content in Field Pennycress, a Non-Food Oilseed Feedstock

4:35-4:40

Tiffany Jamann, University of Illinois, Champaign-Urbana
Conserved Genetic Mechanisms for Biotic Stress in Sorghum

4:40-4:45

John Carlson, Pennsylvania State University
Breeding Resilient, Disease-Resistant Switchgrass Cultivars for Marginal Lands

4:45-4:50

Hugo Cuevas, USDA-ARS, Mayaguez PR
Uncovering Novel Sources of Anthracnose Resistance in Populations of Genetically Diverse Sorghums [*Sorghum bicolor* (L.) Moench]

4:50-4:55

Dan Jacobson, ORNL (for PI Posy Busby, Oregon State University)
Identifying Plant Genes Associated with Pathogen Antagonism in *Populus trichocarpa*

4:55-5:00

Gary Peter, University of Florida
Enhanced Resistance Pines for Improved Renewable Biofuel and Chemical Production

2:00-5:00

Breakout Session C: Systems Biology of Bioenergy-Relevant Microbes

Awards: Rapid Fire Project Presentations

Location: Fairfax Ballroom B

Moderator: Dawn Adin

Session Description: The Genomic Science program supports research aimed at understanding the fundamental properties of bioenergy relevant organisms at the genomic scale and aims to have researchers translate that gained knowledge to enhance the production capabilities of microbes for sustainable bioenergy. In 2018, BER made eighteen new awards spanning a diverse array of organisms, approaches, and tools for harnessing and understanding the biosynthetic processing power of the microbial world to produce advanced biofuels and bioproducts. This session provides an opportunity to briefly introduce these new projects to the Genomic Science research community.

Speakers:

2:00-2:10

Jan Westpheling - University of Georgia

- Development of emerging model microorganisms: *Megasphaera elsdenii* for biomass and organic acid upgrading to fuels and chemicals
- 2:10-2:20 **Ting Lu** - University of Illinois
Dissecting the division of labor in microbial consortia for the production of biofuels and chemicals
- 2:20-2:30 **Terry Papoutsakis** - University of Delaware
Syntrophic co-cultures of Clostridium organisms to produce higher alcohols & other C6-C8 metabolites
- 2:30-2:40 **Danielle Tullman-Ercek** - Northwestern University
Employing bacterial microcompartments to create privileged redox pools for biofuel production
- 2:40-2:50 **Howard Salis** - The Pennsylvania State University
Rapid development of acetogenic Clostridia using highly multiplexed genome engineering for control of C1 bioconversion
- 2:50-3:00 **Bob Tabita** - The Ohio State University
Novel microbial routes to synthesize industrially significant precursor compounds
- 3:00-3:10 **Ian Wheeldon** - University of California, Riverside
Establishing the thermotolerant yeast *Kluyveromyces marxianus* as a host for biobased fuels and chemicals production
- 3:10-3:30 **Break**
- 3:30-3:40 **Mary Dunlop** - Boston University
High-throughput chemical imaging for optimizing biofuel synthesis using synthetic biology
- 3:40-3:50 **Jamey Young** - Vanderbilt University
Rapid flux phenotyping to accelerate metabolic engineering of cyanobacteria
- 3:50-4:00 **Jose Avalos** - Princeton University
Biosensor and optogenetics for systems biology of yeast branched-chain alcohol production and tolerance
- 4:00-4:10 **Mike Betenbaugh** - The Johns Hopkins University
Creating multifunctional synthetic lichen platforms for sustainable biosynthesis of biofuel precursors
- 4:10-4:20 **Cong Trinh** - The University of Tennessee
Understanding and harnessing the robustness of undomesticated *Yarrowia lipolytica* strains for biosynthesis of designer bioesters
- 4:20-4:30 **Keith Tyo** - Northwestern University
Biosynthesis of bioprivileged, linear molecules via novel carboligase reactions
- 4:30-4:40 **Jin Wang** - Auburn University
Harnessing methanotroph-photoautotroph interactions for biogas conversion to fuels and chemicals using binary consortia
- 4:40-4:50 **Jonathan Schilling** - Regents of the University of Minnesota
Gene regulatory networks enabling fungi to selectively extract sugars from lignocellulose

- 4:50-5:00 **Mike Adams** - University of Georgia
Systems biology-based optimization of extremely thermophilic
lignocellulose conversion to bioproducts
- 5:00-5:10 **Chris Marx** - University of Idaho
Using gene editing and an accumulated bioproduct as a reporter for
genotypic and phenotypic heterogeneity in growth-vs-production for
Methylobacterium extorquens conversion of aromatics to butanol
- 5:10-5:20 **Himadri Pakrasi** - Washington University in St. Louis
Systems analysis of a fast growing N₂-fixing cyanobacterium for
production of advanced biofuels and nitrogen-containing
petrochemical replacement compounds

5:00-7:00 **Poster Session (Group I posters)**
Location: Tysons Ballroom

Tuesday, February 26th

7:00-8:30 **Breakfast** (on your own)

8:30-10:00 **Plenary Session: DOE User Facilities & Community Resources**

Location: Fairfax Ballroom

Moderator: Ramana Madupu

Session Description: Speakers will give overviews of the various DOE user facilities and resources.

Speakers:

8:30-8:50 **Nigel Mouncey** – Lawrence Berkeley National Laboratory, Joint Genome Institute (JGI)
Beyond a Quadrillion Bases: Integrative Genome Science at the JGI

8:50-9:10 **Kirsten Hofmockle** – Pacific Northwest National Laboratory
Advancing scientific discovery through integrated collaborations at EMSL

9:10-9:30 **George Maracas** – DOE Office of Science (BES)
Opportunities for Collaborative Research at BES Nanoscale Science Research Center User Facilities

9:30-9:50 **Adam Arkin** – Lawrence Berkeley National Laboratory
Integrative Data Discovery and Analysis: Using KBase to Collaboratively Understand Biological Systems in Context

9:50-10:10 **Gerry McDermott** – University of California at San Francisco
Soft X-ray Tomography and its potential application in BER research

10:10-10:30 **Break**

10:30-12:00 **Plenary Session: USDA-DOE Plant Feedstock Genomics for Bioenergy**

Location: Fairfax Ballroom

Moderator: Cathy Ronning and Bill Goldner

Speakers:

10:30-11:00 **Chaofu Lu** – Montana State University
Systems Biology to Improve Camelina Seed and Oil Quality Traits

11:00-11:30 **Erik Sacks** – University of Illinois at Champaign-Urbana
Introgression of Novel Disease Resistance Genes from *Miscanthus* into Energy cane

11:30-12:00 **Deanna Funnell-Harris** – USDA-ARS, Lincoln NE
Resistance to Stalk Pathogens for Bioenergy Sorghum

12:00-2:00 **Lunch** (on your own)

1:00-5:00

KBase Experience Hands-on Session

Location: Potomac

Maximum: 30 per hour. Advance registration required. [Register here.](#)

Description of Session: This session provides an opportunity to test the latest tools available in KBase in an interactive setting, and learn about the apps and workflows presented by Adam Arkin in his KBase talk Tuesday morning. KBase staff will demonstrate capabilities from the talk as a hands-on demo for more detailed Q&A. Each 40 min segment will focus on a specific topic during which individuals may try out the functionality on their own data. Members of the KBase team will be there to help you start using KBase on your laptop.

Topics:

- | | |
|-----------|---|
| 1:00-1:40 | Best practices for creating organizations and narratives on KBase |
| 1:50-2:30 | Genomes and comparative genomics |
| 2:40-3:20 | Microbiome analysis with 16S and metagenome data |
| 3:30-4:10 | Modeling and metabolomics |
| 4:20-5:00 | RNA-seq and transcriptome analysis |

2:00-5:00

KBase 1-on-1 Consultation & Help

Location: Great Falls

Maximum 10 per hour. Advance registration required. [Register here.](#)

This session is an opportunity to meet individually with KBase staff to discuss more specific questions regarding how you would use KBase in your research.

2:00-5:00

Breakout Session D: Biological Data and Computation - Challenges and Opportunities

Location: Fairfax Ballroom B

Moderator: Ramana Madupu/Amy Swain

Description of Session: The Genomic Science program supports basic research to understand the biological complexity of plant and microbial metabolism aimed at identifying the foundational principles that drive biological systems, effectively exploiting new and emerging technologies in systems biology and physical measurements to accelerate biological discoveries. Data challenges for systems biology research have increased by orders of magnitude over the past few years. The growth in data size, complexity, and heterogeneity has far outpaced existing efforts to interpret the data, and the challenges are continually escalating with the development of new instruments and sensors that stream data in real time. This breakout will feature speakers who are at the fore front of tackling the analytical and computational challenges.

Speakers:

- | | |
|-----------|---|
| 2:00-2:30 | Dan Jacobson - Oak Ridge National Laboratory
Exascale Biology: Supercomputing as an Engine for Discovery in Systems Biology |
|-----------|---|

- 2:30-3:00 **Kerstin Kleese Van Dam** – Brookhaven National Laboratory
TBA
- 3:00-3:30 **Break**
- 3:30-4:00 **Paul Adams** – Lawrence Berkeley National Laboratory
Computational challenges in imaging biological systems
- 4:00-4:30 **Todd Yeates** - University of California at Los Angeles
Computational challenges and emerging breakthroughs in EM imaging methods
- 4:30-5:00 **John Westbrook** - Rutgers University
New opportunities and challenges integrating structural biology data

2:00-5:00 **Breakout Session E: Innovative engineering of DOE-relevant organisms for biofuel and bioproduct synthesis**

Location: Fairfax Ballroom A
Moderator: Pablo Rabinowicz

Session Description: Powerful genome engineering and editing technologies that are becoming available for different organisms bring unprecedented opportunities to design and build novel pathways or organisms to address DOE missions in energy and the environment. This session will feature novel approaches to develop plant and microbial systems for biofuel and bioproduct synthesis.

Speakers:

- 2:00-2:30 **Carl Schultz** - University of Illinois at Urbana-Champaign
New Tools for Genome-Scale Metabolic Engineering of Yeast
- 2:30-3:00 **Daniel Voytas** - University of Minnesota
Overcoming Bottlenecks in Plant Gene Editing
- 3:00-3:30 **Break**
- 3:30-4:00 **Melissa Roth** - University of California, Berkeley
Systems Biology and Engineering to Improve Biofuel Production in the Emerging Model Green Alga *Chromochloris zofingiensis*
- 4:00-4:30 **John Shanklin** - Brookhaven National Laboratory
Biosystems Design for Oil Accumulation in Energycane and Duckweed
- 4:30-5:00 **Gautam Dantas** - Washington University, St. Louis
Systems Engineering of *Rhodococcus opacus* to Enable Production of Drop-in Fuels from Lignocellulose

5:00-7:00 **Poster Session (Group II posters) with Bioimaging**
Location: Tysons Ballroom

Wednesday, February 27th

7:00-8:00 **Breakfast** (on your own)

8:00-9:20 **DOE 2018 Early Career Research Awards**

Location: Fairfax Ballroom

Moderator: Pablo Rabinowicz

Session Description: The 2018 Office of Science Early Career Research Program awardees from BER's Biological Systems Science Division will present their projects to the Genomic Science Program community.

Speakers:

8:00-8:20 **Nanette Boyle** - Colorado School of Mines
Enabling Predictive Metabolic Modeling of Diurnal Growth Using a Multi-Scale Multi-Paradigm Approach

8:20-8:40 **Kolby Jardine** - Lawrence Berkeley National Laboratory
Poplar esterified cell wall transformations and metabolic integration study (PECTIN)

8:40-9:00 **Philipp Zerbe** - University of California at Davis
Improved Biofuel Production through Discovery and Engineering of Terpene Metabolism in Switchgrass

9:00-9:20 **Daniel Amador-Noguez** - University of Wisconsin at Madison
In vivo thermodynamic analysis of metabolic networks

9:20-9:40 **BER workshop Report "Breaking the Bottleneck of Genomes: Understanding Gene Function across Taxa"**

Presenter: Adam Deutschbauer

Introduction: Cathy Ronning and Dawn Adin

9:40-10:00 **BER workshop Report "Genome Engineering for Material Synthesis"**

Presenter: Brian Fox, University of Wisconsin

Introduction: Seema Singh and Pablo Rabinowicz

10:00-10:30 **Break**

10:30-12:00 **Plenary Session: Roots and their Microbes**

Location: Fairfax Ballroom

Moderator: Kent Peters

Speakers:

10:30-10:50 **Elizabeth Shank** – University of North Carolina at Chapel Hill

Bacterial interactions in the rhizosphere

10:50-11:10

Mitch Doktycz – Oak Ridge National Laboratory
The *Populus* microbiome

11:10-11:30

Ashley Shade - Michigan State University
Temporal dynamics of core microbiomes from biofuel crops

11:30-11:50

Angela Kent – University of Illinois at Urbana-Champaign
Micro-managing sustainability: Plant genotype shapes
microbiome structure and function

12:00

Close-out and Adjournment