



Biological and Environmental Research (BER)
2021 Genomic Sciences Program Annual PI Meeting
February 22-24, 2021

Monday, February 22nd

10:00 am EST
7:00 am PST

WELCOME AND INTRODUCTION TO THE MEETING

- | | |
|----------------|---|
| 10:00-10:10 am | Sharlene Weatherwax – Associate Director, DOE Office of Biological and Environmental Research (BER)
Opening Remarks |
| 10:10-10:25 am | Todd Anderson – Director, Biological Systems Science Division (BSSD)
Meeting Introduction |
| 10:25-10:30 am | Science Division Logistics |

11:00 am EST
8:00 am PST

KEYNOTE PRESENTATION

Moderator: Prem Srivastava

- | | |
|----------------|--|
| 11:00-12:00 am | Eva Nogales – Professor of Biochemistry, Biophysics and Structural Biology, Molecular, and Cell Biology Department, University of California, Berkeley
The Power of Cryo-EM and the Challenges and Opportunity Ahead |
|----------------|--|

12:00 pm EST
9:00 am PST

BREAK

12:30 pm EST
9:30 am PST

PLENARY SESSION 1

**Bioenergy Research Centers:
Feedstocks: Where we are. Where we need to be and how are we going to get there.**

Moderator: Kent Peters

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|---------------|--|
| 12:30-1:00 pm | Federica Brandizzi – Michigan State University, Great Lakes Bioenergy Research Center
Genomics-enabled development of the next-generation bioenergy feedstocks |
|---------------|--|

- 1:00-1:30 pm **Henrik Scheller – Lawrence Berkeley National Laboratory, Joint BioEnergy Institute**
Engineering of bioenergy crops for reduced recalcitrance and accumulation of bioproducts
- 1:30-2:00 pm **Wellington Muchero – Oak Ridge National Laboratory, Center for Bioenergy Innovation**
Deploying computationally predicted genomic targets to engineer bioenergy traits in *Populus*, rice and switchgrass
- 2:00-2:30 pm **Emily Heaton – University of Illinois, Center for Advanced Bioenergy and Bioproducts Innovation**
Progress towards using grasses as efficient, sustainable factories for bioenergy and bioproducts

2:30 pm EST
11:30 am PST **BREAK**

3:00 pm EST
12:00 pm PST **BREAKOUT SESSION A**

Closed Captioning (CC) link:

<https://www.captionedtext.com/client/event.aspx?EventID=4710267&CustomerID=321>

Microbial Modification of Plant Phenotypes

Moderator: Kent Peters

Session Description: All plants live in symbiotic relationship with a multitude of microbes. This session will explore how those microbes influence the expressed phenotypes of host plants.

- 3:00-3:15 pm **Sarah Evans – Michigan State University**
Do microbes shape switchgrass phenotype through changes in N- cycling?
- 3:15-3:30 pm **Christine Hawkes – North Carolina State University**
Microbiome mediation of switchgrass phenotypes: the role of fungal symbionts in plant host physiology
- 3:30-3:45 pm **Kabir Peay – Stanford University**
Ectomycorrhizal fungal modification of host plant growth across contrasting environmental conditions
- 3:45-4:00 pm **Jessy Labbe – Oak Ridge National Laboratory**
Insights on the impact of a mycorrhizal-bacterium assembled community on the phenotypic responses of *Populus*
- 4:00-4:15 pm **Break**
- 4:15-4:30 pm **Adina Howe – Iowa State University**
Phyllosphere microbiome activities in perennial biofuel feedstocks
- 4:30-4:45 pm **Jennifer Morell-Falvey – Oak Ridge National Laboratory**
Uncovering the mechanisms that promote plant association by microbes

4:45-5:00 pm **Jenny Mortimer – Joint BioEnergy Institute**
Using fabricated ecosystems to bridge the lab-field scale gap

5:00 pm **Adjourn**

3:00 pm EST
12:00 pm PST

BREAKOUT SESSION B

KBase User Science

Moderator: Ramana Madupu

Session Description: 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.

3:00-3:10 pm **Christopher Henry – Argonne National Laboratory**
Introduction

3:10-3:25 pm **Ellen Dow – Lawrence Berkeley National Laboratory**
KBase for Educators: Building community and empowering teaching (in KBase)

3:25-3:40 pm **Jia Wang – Oak Ridge National Laboratory**
Formation and Characterization of Emergent Microbial Communities

3:40-3:55 pm **Patrik D'haeseleer – Livermore National Laboratory**
Improving metabolic models by integrating output from multiple annotation algorithms

3:55-4:10 pm **Lauren Liu, Lawrence Berkeley National Laboratory**
Utilizing KBase apps to obtain high quality assemblies of isolate genomes and metagenome-assembled genomes

4:10-4:25 pm **Ben Boldoc – Ohio State University**
Viral Tools in KBase

4:25-4:30 pm **Break**

4:30-4:45 pm **Pamela Weisenhorn – Argonne National Laboratory**
Improved Amplicon Analysis Tools and Sample Data Integration in KBase

4:45-5:00 pm **Aimee Kessell – University of Nebraska**
Metabolic Network and Metabolomics Integration to Predict the Shifts in Microbial Processes across Globally-Distributed River Corridors

5:00-5:15 pm **Kelly Wrighton – Colorado State University**
Putting the BIO into geochemistry with KBase: linking genome annotations to biogeochemical models

- 5:15-5:30 pm **Neeraj Kumar – Pacific Northwest National Laboratory**
Quantum Mechanical Methods to Improve Genome-Scale Modeling
- 5:30-5:45 pm **Pryia Ranjan – Oak Ridge National Laboratory**
Framework for modeling plant genotype to phenotype relationships in KBase
- 5:45-6:00 pm **Dan Jacobson – Oak Ridge National Laboratory**
Embracing Complexity: Progress on Exa- and Peta-scale Networks for *Arabidopsis* in KBase
- 6:00 pm **Adjourn**

6:00 pm EST
3:00 pm PST

POSTER SESSION A

Location: Please visit meeting website for additional information and links.

Duration: 2h (6-8pm ET)

Tuesday, February 23rd

10:00 am EST
7:00 am PST

PLENARY SESSION 2

USDA-DOE Plant Feedstocks Genomics for Bioenergy

Moderators: Cathy Ronning (DOE BER) and Daniel Cassidy (USDA NIFA)

Session Description: Since 2006 the joint USDA-DOE Plant Feedstocks Genomics for Bioenergy program has supported genomics-based research leading to the development of improved and more sustainable plant feedstocks for biofuels and biobased products. With the conclusion of this program in 2019, this year marks the final Plant Feedstocks PI/PD meeting. The session will include presentations by the 2018 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.

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|------------------|---|
| 10:00-10:20 am | John Carlson – Pennsylvania State University
Breeding resilient, disease-resistant switchgrass cultivars for marginal lands |
| 10:20-10:40 am | Hugo Cuevas – USDA-ARS Mayaguez
Uncovering novel sources of anthracnose resistance in populations of genetically diverse sorghums [<i>Sorghum bicolor</i> (L.) Moench] |
| 10:40-11:00 am | Tiffany Jamann – University of Illinois
Conserved genetic mechanisms for biotic stress in <i>Sorghum</i> |
| 11:00-11:20 am | Zenith Tandukar (presenting for Jim Anderson – University of Minnesota)
Genetic Improvement of seed yield and oil content in field pennycress |
| 11:20-11:40 am | Gary Peter – University of Florida
Enhanced resistance pines for improved renewable biofuel and chemical production |
| 11:40 – 12:00 pm | Posy Busby – Oregon State University
Identifying plant genetic variation associated with microbiome composition and pathogen antagonism in <i>Populus trichocarpa</i> |

12:00 pm EST
9:00 am PST

BREAK

12:30 pm EST
9:30 am PST

PLENARY SESSION 3

DOE 2020 Early Career Awards

Moderator: Pablo Rabinowicz

Session Description: The 2020 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:

- 12:30-12:50 pm **Erin Nuccio – Lawrence Livermore National Laboratory**
Crosstalk: Interkingdom interactions in the mycorrhizal hyphosphere and ramifications for soil C cycling
- 12:50-1:10 pm **Simon Roux – Lawrence Berkeley National Laboratory**
Characterizing virus-driven alterations of microbial metabolism in model soil ecosystems
- 1:10 -1:30 pm **Joanne Emerson – University of California, Davis**
Infective viruses and inert virions: illuminating abundant unknowns in terrestrial biogeochemical cycles

1:30 pm EST
10:30 am PST

BREAK

2:00 pm EST
11:00 am PST

KBASE 1-ON-1 CONSULTATION & HELP

Maximum 4 per hour (15 min zoom sessions; advance registration required)

Registration: <https://calendly.com/kbase/gsp2021>

Session Description: The KBase booth offers 1-on-1 information and consultation help. 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 pm EST
11:00 am PST

KBASE TRAINING SESSIONS

Maximum: No limit to registration, but advance registration required

Registration: <https://forms.gle/pX2AKezhCg3UpNAz6>

- 2:00-2:50 pm **Introduction to Genome Analysis in KBase**
Host: Ben Allen
Description: Learn the basics of KBase and how it can help your research. This session will introduce users to the platform, including data upload, building Narratives, running apps, creating organizations, and sharing your analysis. Attendees will learn how to find data and use tools for processing NGS reads, assembly, and annotation to construct genomes. The workshop will demonstrate basic workflows for analyzing genomes in KBase, including searching for features and performing comparative analysis. We'll also cover any new features and developments to support your research.
- 3:00-3:50 pm **Communities and Metagenomics Analysis**

Host: Dylan Chivian and Sean Jungbluth

Description: From metagenomes to MAGs (metagenome assembled genomes), this workshop will introduce users to KBase's microbiome analysis tools. Genome extraction and species predictions are just the beginning of how metagenomic samples can be analyzed within KBase. We will also demonstrate how these extracted genomes can be used as input for downstream analysis with our powerful tools for community modeling.

4:00-4:50 pm

Metabolic Modeling

Host: José Faria and Janaka Edirisinghe

Description: KBase has a suite of Apps and data that support the reconstruction, prediction, and design of metabolic models in microbes and plants. Genome-scale metabolic models are primarily reconstructed from protein functional annotations. These genome-scale metabolic models can be used to explore an organism's growth in specific media conditions, determine which biochemical pathways are present, optimize production of an important metabolite, identify high flux pathways, and more. In this workshop we will use metabolic models to evaluate an organism's metabolic capability by simulating growth under different conditions to answer important biological questions.

2:00 pm EST
11:00 am PST

BREAKOUT SESSION C

Advancing the Bioeconomy with Safely Designed Biosystems

Moderator: Pablo Rabinowicz

Session Description: Gaining a systems-level understanding of fundamental biological processes that occur within and between plants and microbes, along with the development of biological design technologies, will allow us to harness the enormous potential of biological systems for beneficial purposes. Engineered plants and microbes that can be safely contained will not only enable the biological conversion of biomass into fuels and valuable chemicals but will also advance towards deploying biological systems for environmental applications. This session will present BER's efforts in systems and synthetic biology as well as secure biosystems design aimed at achieving a robust bioeconomy.

SPEAKERS

2:00-2:25 pm

Neal Stewart – University of Tennessee, Knoxville

Rational Design and Testing of Abiotic Stress Inducible Synthetic Promoters from Poplar Cis-regulatory Elements

2:25-2:40 pm

Michael Guarnieri – National Renewable Energy Laboratory

IMAGINE BioSecurity: Integrative Modeling and Genome-scale Engineering for Biosystems Security

2:40-3:05 pm

Nanette Boyle – Colorado School of Mines

Data-driven Multiscale Metabolic Modeling of Diurnal Growth in *Chlamydomonas*

3:05-3:20 pm

Joe Schoeniger – Sandia National Laboratory

Harnessing Horizontal Gene Transfer for Secure Biodesign

3:20-3:30 pm	Break
3:30-3:55 pm	Pamela Soltis and Matias Kirst – University of Florida, Gainesville Comparative Phylogenomics and Single-Cell Transcriptomic Dissection of Nitrogen Fixation for Synthetic Biology Engineering of Nodules in Bioenergy Crops
3:55-4:10 pm	Yongqin Jiao – Lawrence Livermore National Laboratory From Sequence to Cell to Population: Secure and Robust Biosystems Design for Environmental Microorganisms
4:10-4:35 pm	Danny Schnell – Michigan State University, East Lansing A Systems Approach to Increasing Oil Yields in <i>Camelina sativa</i>
4:35-5:00 pm	Carrie Eckert – University of Colorado, Boulder, and National Renewable Energy Laboratory Understanding and Engineering Regulatory Networks to Improve Microbial Bioproduction Systems

2:00 pm EST
11:00 am PST

BREAKOUT SESSION D

Sustainable Bioenergy Cropping Systems

Moderators: Cathy Ronning and Shing Kwok

Session Description: Recent advances in systems biology and omics technologies are allowing researchers to map the complex networks of plants' responses to abiotic stresses and plant-microbial interactions that control plant growth, development, and metabolism. Awardees of the Systems Biology Research to Advance Sustainable Bioenergy Crop Development program will apply these tools to examine the ecological impacts of a fully sustainable, bioenergy crop production. This session features seven new projects that seek to develop a mechanistic understanding of how candidate biofuel plants interact with environmental factors to affect long-term plant feedstock performance.

SPEAKERS

2:00-2:05 pm	Shing Kwok and Cathy Ronning, DOE BER Introduction
2:05-2:25 pm	Tom Juenger – University of Texas Austin Project Title: Testing Predictions of Plant-Microbe-Environment Interactions to Optimize Climate Adaptation and Improve Sustainability in Switchgrass Feedstocks
2:25-2:45 pm	Jeff Bennetzen – University of Georgia Project Title: Systems Analysis of the Beneficial Associations of <i>Sorghum</i> with Arbuscular Mycorrhizal Fungi Studied with Genetics, Genomics, Imaging and Microbiomics
2:45-3:05 pm	Jean-Michel Ané – University of Wisconsin Madison Project Title: A Systems Understanding of Nitrogen Fixation on the Aerial Roots of <i>Sorghum</i>
3:05-3:25 pm	Karsten Zengler – University of California San Diego

Project Title: Integration of Experimental and Modeling Approaches to Understand, Predict, and Modulate Rhizosphere Processes for Improved Bioenergy Crop Productivity

3:25-3:35 pm **BREAK**

3:35-3:55 pm **Sharon Doty – University of Washington Seattle**

Project Title: Elucidation of the Roles of Diazotrophic Endophyte Communities in Promoting Productivity and Resilience of *Populus* through Systems Biology Approaches

3:55-4:15 pm **Chaofu Lu – Montana State University**

Project Title: ECON: Enhancing Camelina Oilseed Production with Minimum Nitrogen Fertilization in Sustainable Cropping Systems

4:15-4:35 pm **John Sedbrook – Illinois State University**

Project Title: Interrogating Pennycress Natural and Induced Variation to Improve Abiotic Stress Tolerance and Oilseed Bioenergy Crop Resilience

4:35-5:00 pm **Live Q&A/Discussion with Presenters**

5:00 pm **ADJOURN**

**2:00 pm EST
11:00 am PST**

BREAKOUT SESSION E

Environmental Microbiology

Moderator: Boris Wawrik

Session Description: Microbial communities and their interactions are a fundamental feature of natural systems. From the bedrock below our feet to the upper reaches of the troposphere, the environment contains microbiomes that respond to and shape the conditions surrounding them in ways that profoundly affect the physical world. Increasingly sophisticated molecular tools coupled to computational techniques and high-resolution analytical technologies offer exciting and growing opportunities for investigating the functional properties of microbes in their natural context. Much has been learned from the characterization of the natural world vis-à-vis the application of molecular tools and we are beginning to understand the plethora connections that exist among microbial activities in nature. This session highlights DOE's support for studies that leverage integrated, multidisciplinary research to assess microbial cycling of elements in the environment and will seek to explore future trends and challenges in environmental microbiome research.

SPEAKERS

2:00-2:25 pm **John Dunbar – Los Alamos National Lab**

Michaeline Albright – Los Alamos National Lab

Microbial Mediocrity and Pursuit of the Extraordinary – A forward looking perspective on modeling and management of soil C.

2:25-2:50 pm **Thea Whitman – University of Wisconsin, Madison**

Matt Trexler – University of California, Berkeley

Wildfire's effects on carbon and nitrogen cycling: A mechanistic approach

- 2:50-3:15 pm **Jeremy Semrau – University of Michigan**
Copper competition between microbes: Implications for greenhouse gas emissions
- 3:15-3:40 pm **Zach Hallberg (PI: Michiko Taga) – University of California, Berkeley**
Digging for B12: Unraveling microbial nutritional interactions in soil
- 3:40-4:05 pm **Alicia Purcell (PI: Bruce Hungate) – Northern Arizona University**
Presentation Title: Quantifying microbes: warming effects, field responses, and element transformations
- 4:05-4:30 pm **Jean P. Gibert – Duke University**
Simple traits predict complex temperature responses across scales
- 4:30-4:55 pm **Kathleen Treseder (PI: Steven Allison) – University of California, Irvine**
How evolution and trait trade-offs in fungi could mediate carbon cycling under climate change
- 4:55-5:15 pm **Live Q&A**
Discussion with Presenters
- 5:15 pm **Adjourn**

5:00 pm EST
2:00 pm PST

POSTER SESSION B

Location: Please visit meeting website for additional information and links.
Duration: 2h (5-7pm ET)

Wednesday, February 24th

10:00 am EST
7:00 am PST

PLENARY SESSION 4

Facilities and Resources

Moderator: Ramana Madupu

Session Description: Towards advancing its research goals the Biological Systems Science Division (BSSD) supports National Scientific User Facilities, Community Resources and Computational resources. These world-class facilities and resources provide access to a suite of enabling capabilities and technologies to BER researchers and the broader user community. They also foster multidisciplinary research efforts through cross facility integrative programs. In this session speakers will provide an overview of joint collaborative efforts among user facilities to advance Genomic Science research.

SPEAKERS

10:30-10:15 am **Nigel Mouncey – Director Joint Genome Institute, Lawrence Berkeley National Laboratory**
Integrative Genome Science at and with the JGI

10:15-10:30 am **Douglas Mans – Director of the Environmental Molecular Sciences Laboratory (EMSL)**
Molecular Phenotyping in EMSL

10:30-10:45 am **Riti Sarangi – SLAC National Accelerator Laboratory, Stanford University**
Biological Systems Science Research at DOE Lightsources

10:45-11:00 am **Emiley Eloe-Fadrosh – Joint Genome Institute, Lawrence Berkeley National Laboratory**
The National Microbiome Data Collaborative: Integrative Infrastructure & Inclusive Engagement

11:00-11:15 am **Adam Arkin – KBase, Lawrence Berkeley National Laboratory**
KBase: Bringing the BER community together to understand biological ecosystems

11:15-11:50 am **Panel Discussion and Q&A**

11:50 am EST
12:00 pm PST

BREAK

12:00 pm EST
9:00 am PST

PLENARY SESSION 5

Emerging Technologies – Computing and Data Science

Moderator: Amy Swain

Session Description: The broad range of Genomic Science research presented throughout the PI meeting requires and drives the development of sophisticated mathematics, algorithms, computing and data analysis capabilities. Genomic Science research is further enhanced and advanced using these approaches to incorporate information from literature, imaging studies, structural biology and computational models and simulations. Some emerging technologies and their applications that inform and enrich BER genomic science will be presented in this session. After each recorded presentation, there will be five minutes for live Q/A with the speaker.

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|----------------|---|
| 12:00-12:20 pm | Esther Singer – Lawrence Berkeley National Laboratory
EcoPODs - an Opportunity for Standardizing Plant-microbiome Research |
| 12:20-12:40 pm | James Sethian – UC Berkeley, Lawrence Berkeley National Laboratory
Developing and Applying New Mathematics for Computer Vision and Autonomous Self-Driving Experiments: The Center for Advanced Mathematics for Energy Research Applications (CAMERA) |
| 12:40-1:00 pm | Mary Dunlop – Boston University
Single cell methods for Rapid Image Analysis and Detection of Biofuel Production in Individual Bacteria |
| 1:00-1:20 pm | Shinjae Yoo – Brookhaven National Laboratory
Automated Knowledge Harvesting from Literature text, tables, and figures using Natural Language Processing and Machine Learning |
| 1:20-1:40 pm | Chris Henry – Argonne National Laboratory
KBase and PDB Infrastructure for Bringing Structural Biology Insights to Systems and Synthetic Biology Applications |

1:45 pm EST
10:45 am PST

CLOSE-OUT AND ADJOURNMENT