



Biological and Environmental Research (BER)
2020 Genomic Sciences Program Annual PI Meeting
February 23-26, 2020

Sunday, February 23rd

5:00-8:00 pm **EARLY REGISTRATION AND POSTER SETUP**
Location: Lobby outside Columbia Ballroom (Terrace Level)

Monday, February 24th

7:00-8:00 am **REGISTRATION**
Location: Lobby outside Columbia Ballroom (Terrace Level)

7:00-8:00 am **BREAKFAST** (on your own)

8:00-8:30 am **WELCOME AND INTRODUCTION TO THE MEETING**
Location: Columbia Ballroom (Terrace Level)

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

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

8:25-8:30 am **Boris Wawrik** – Program Manager, Biological Systems Science Division
Logistics

8:30-9:30 am **KEYNOTE PRESENTATION**
Location: Columbia Ballroom (Terrace Level)
Moderator: Cathy Ronning

Thomas Juenger – University of Texas, Austin
Climate Adaptation and Sustainability in Switchgrass: Exploring Plant-Microbe-Soil Interactions Across Continental Scale Environmental Gradients

9:30-10:00 am **BREAK**

10:00-12:00 am **PLENARY SESSION 1**

**Bioenergy Research Centers:
Biofuels and Bioproducts from Non-Cellulosic Sources**

Location: Columbia Ballroom (Terrace Level)

Moderator: Kent Peters

Speakers:

- 10:00-10:30 am **Andrew Leakey – University of Illinois, Urbana-Champaign
Center for Advanced Bioenergy and Bioproducts Innovation (CABBI)**
Progress Toward the ‘Plants as Factories’ Paradigm for Bioenergy in
Grasses
- 10:30-11:00 am **Corinne Scown – Lawrence Berkeley National Laboratory (LBNL)
Joint BioEnergy Institute (JBEI)**
Lignin Valorization for Sustainable, Lower-Cost Biofuels and Bioproducts
- 11:00-11:30 am **Gregg Beckham – National Renewable Energy Laboratory (NREL)
Center for Bioenergy Innovation (CBI)**
Biological, Catalytic, and Computational Approaches to Valorize and
Understand Lignin
- 11:30-12:00 pm **Dan Noguera – University of Wisconsin, Madison
Great Lakes Bioenergy Research Center (GLBRC)**
Assembling a Genome-Enabled Lignin to Product Processing Chain

12:00-2:00 pm **LUNCH** (on your own)

2:00-5:00 pm **BREAKOUT SESSION A**

KBase User Science Presentations

Location: Columbia (Terrace Level) Breakout Room (TBD)

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.

- 12:00-2:00 pm KBase Lunch (Fairchild E&W)
- 2:00-2:10 pm **Christopher Henry – Argonne National Lab (ANL)**
Introduction
- 2:10-2:25 pm **Patrick Chain – Los Alamos National Lab (LANL)**
Integrating Read-Based Microbiome Taxonomy Classification Tools into
KBase
- 2:25-2:40 pm **Jeremy Zucker – Environmental Molecular Sciences Laboratory
(EMSL)**
The 2019 KBase Fungal Biochemistry Curation Jamboree: Insights and
Lessons Learned
- 2:40-2:55 pm **Patrik D'haeseleer – Lawrence Livermore National Lab (LLNL)**
Tools for Importing, Comparing and Merging Functional Annotations for
Improved Metabolic Modeling in KBase

- 2:55-3:10 pm **Eric Alm – Massachusetts Institute of Technology**
Using Reference Genomes to Interpret Metagenomic Data in KBase
- 3:10-3:25 pm **Roelof Versteeg – Subsurface Insights**
Coupling KBase with PFLOTTRAN
- 3:25-3:40 pm **Break**
- 3:40-3:50 pm **Rohan Sachdeva – University of California, Berkeley**
Rapid Automated Genome from Metagenome Curation
- 3:50-4:05 pm **José P. Faria – Argonne National Lab (ANL)**
Large-Scale Model-Driven Comparison of Metagenome Assembled Genomes from Diverse Environments
- 4:05-4:20 pm **Matthew Sullivan – The Ohio State University**
The 2020 State of Viromics Tools in KBase
- 4:20-4:35 pm **Ada Sedova – Oak Ridge National Lab (ORNL)**
Inferring Protein Structure and Function using Hints from Evolution, Biophysics, and Molecular Modeling
- 4:35-4:45 pm **Neeraj Kumar – Pacific Northwest National Lab (PNNL)**
Computational Modeling of Metabolites using NWChem in KBase
- 4:45-5:00 pm **Dan Jacobson – Oak Ridge National Lab (ORNL)**
Exascale Networks for *Arabidopsis* in KBase
- 5:00 pm **Adjourn**

2:00-5:00 pm

BREAKOUT SESSION B

DOE-USDA Plant Feedstock Genomics for Bioenergy

Location: Columbia (Terrace Level) Breakout Room (TBD)

Moderator: Cathy Ronning

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 to produce biofuels and biobased products. The session will include presentations by the 2017 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.

- 2:00-2:10 pm **Cathy Ronning - DOE BER**
Introduction
- 2:10-2:35 pm **Luca Comai – University of California, Davis**
Dosage Analysis of the Phenotypic and Regulatory Landscape of the Poplar Genome
- 2:35-3:00 pm **Ed Eisenstein – University of Maryland, College Park**
The Importance of Tobacco and Alcohol for Disentangling Poplar-Rust Interactions
- 3:00-3:25 pm **Jared LeBoldus – Oregon State University**
lecRLKs Mediators of Innate Immunity in *Populus trichocarpa*
- 3:25-3:45 pm **BREAK**
- 3:45-4:10 pm **Rebecca Bart – Donald Danforth Plant Science Center**

Optimizing Tradeoffs Implicit During Bioenergy Crop Improvement:
Understanding the Effect of Altered Cell Wall and Sugar Content on
Sorghum-Associated Pathogenic Bacteria

4:10-4:35 pm **David Lowry – Michigan State University**
QTL x Environment Interactions and Epistasis Underlie Variation in
Switchgrass Rust Pathogen Susceptibility Across Central North America

4:35-5:00 pm **John Sedbrook – Illinois State University**
Advancing Field Pennycress as a New Oilseed Biofuels Feedstock that Does
Not Require New Land Commitments

5:00 pm **Adjourn**

2:00-5:00 pm **BREAKOUT SESSION C**

Confronting the Challenges of Systems Biology in Eukaryotic Systems

Location: Columbia (Terrace Level) Breakout Room (TBD)

Moderator: Dawn Adin

Session Description: The Genomic Science Program funds a diverse range of research projects on eukaryotic organisms, given the important role these organisms might play in achieving improved energy resiliency via the production of biofuels and bioproducts. While possibly offering solutions to bio-energy related problems, eukaryotes present unique challenges due to their cellular and metabolic complexity. In this context, high-throughput experimental and computational methods are frequently paired with advanced molecular biology tools to investigate the modular architecture and complex metabolic networks essential to all eukaryotes. This session will highlight how these technologies are being leveraged to enable research and advance our fundamental knowledge of eukaryotic biology and metabolic functions.

Speakers:

2:00-2:30 pm **Jose Avalos – Princeton University**
Systems Biology of Branched-Chain Higher Alcohol Production and
Tolerance in Yeast Using Genomic Libraries, Biosensors, and Optogenetics

2:30-3:00 pm **Cong Trinh – The University of Tennessee**
Discovering Genotypes Conferring Robustness of *Yarrowia lipolytica* in
Organic Solvents for Novel Biotransformation

3:00-3:30 pm **Rhona Stuart – Lawrence Livermore National Laboratory (LLNL)**
Symbioses in Bioenergy-Relevant Crops; Perspectives from the Single Cell
to the System Scale

3:30-4:00 pm **BREAK**

4:00-4:30 pm **Crysten Blaby-Haas – Brookhaven National Laboratory (BNL)**
Integrative Approaches for Protein Function Discovery: Developing
Molecular-Level Models of Micronutrient Handling in Bioenergy Crops

4:30-5:00 pm **Wellington Muchero – Oak Ridge National Laboratory (ORNL)**
Deep Orthology Underlies Shared Molecular Functions Across Highly
Divergent Eukaryotes Including Plants and Humans

5:00-7:00 pm **POSTER SESSION A**

Location: Lobby outside Columbia Ballroom (Terrace Level)

Tuesday, February 25th

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

8:30-10:00 am **PLENARY SESSION 2**

DOE User Facilities & Community Resources

Location: Columbia Ballroom (Terrace Level)

Moderator: Amy Swain

Session Description: Speakers will discuss some DOE user facilities and resources available to advance your Genomic Science research.

Speakers:

8:30-8:50 am **Nigel Mouncey – Director Joint Genome Institute, Lawrence Berkeley National Laboratory (LBNL)**
Beyond Base Pairs: Integrative and Collaborative Genome Science at the JGI

8:50-9:10 am **Emiley Eloie-Fadrosh – Joint Genome Institute, Lawrence Berkeley National Laboratory (LBNL)**
The National Microbiome Data Collaborative (NMDC)

9:10-9:30 am **Adam Arkin – KBase, Lawrence Berkeley National Laboratory (LBNL)**
Integrating Heterogeneous Data Across Scales in KBase

9:30-9:50 am **Douglas Mans – Director of the Environmental Molecular Sciences Laboratory (EMSL)**
Functional and Systems Biology: Predicting and Controlling Biology

9:50-10:10 am **Hugh O’Neil – Oak Ridge National Lab (ORNL)**
Studies of Complex Biological Systems Using Neutrons; From the Molecular to Mesoscale

10:10-10:30 am **BREAK**

10:30-12:00 am **PLENARY SESSION 3**

Defragmenting to Accelerate Discovery: Making Better Use of Biological Data

Location: Columbia Ballroom (Terrace Level)

Moderators: Ramana Madupu, Kjiersten Fagnan, and Sujata Emani

Session Description: The Genomic Science Program (GSP) supports fundamental research on the genomic and metabolic processes important for sustainable biofuel and bioproduct development, designing improved and secure biological systems for that purpose, and understanding the impact of microbes on the environment. The unprecedented growth in volume, diversity, and complexity of biological data and the evolving methods for analyzing and using data are radically reshaping existing efforts for data interpretation. These challenges continue to escalate with the development of new instruments and sensors that stream data in real time. The vision for this session is to identify and present excellent use cases of big data

sets in biology. Presentation will focus on the integration of big data to ask and answer the bleeding edge scientific questions.

Speakers:

10:30-10:50 am **Ben Brown – Lawrence Berkeley National Laboratory (LBNL)**
How the Biological and Environmental Sciences are Driving the Evolution of Third-Wave AI

10:50-11:10 am **Jerry Parks – Oak Ridge National Laboratory (ORNL)**
Combining Metagenome Sequence Mining, Coevolution Analysis, and 3D Structural Modeling to Understand Protein Function

11:10 -11:30 am **Francis Alexander – Brookhaven National Laboratory (BNL)**
Designing Optimal Experimental Campaigns for Complex and Uncertain Biological Systems

11:30-11:50 pm **Ravi Madduri – Argonne National Lab (ANL)**
Best Practices in Research Data Management and Analysis - Experiences in Using FAIR Standards for Large-Scale biological Data Analysis

11:50-12:15 pm **Panel Discussion**

12:15-2:00 pm **LUNCH** (on your own)

1:00-5:00 pm **KBASE EXPERIENCE HANDS-ON SESSION**

Location: Fairchild (E&W)

Maximum: 30 per hour. Advance registration required. <[click here to register](#)>

Session Description: 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.

1:00-1:40 pm Navigating KBase: Narratives, Organizations, and Dashboard

1:50-2:30 pm Genomes and comparative genomics

2:40-3:25 pm Microbiome analysis with 16s and metagenome data

3:30-4:20 pm Modeling, metabolomics & functional annotation

4:25-5:00 pm RNA-seq and transcriptome analysis

2:00-5:00 pm **KBASE 1-ON-1 CONSULTATION & HELP**

Location: Embassy

Maximum 10 per hour. Advance registration required. <[click here to register](#)>

Session Description: 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 pm **BREAKOUT SESSION D**

Environmental Microbiology

Location: Columbia (Terrace Level) Breakout Room (TBD)

Moderator: Boris Wawrik

Session Description: Soil is a heterogeneous system teeming with microbial life. Much remains to be learned about soil processes driven by microbial populations and how they contribute to higher order phenomena, such as the transport, biogeochemical cycling, and fate of carbon and nutrients. Increasingly sophisticated approaches for “meta-omics” (i.e. metagenomics, metatranscriptomics, metaproteomics, metabolomics, etc.) coupled to high resolution analytical technologies offer exiting opportunities for investigating the functional properties of soil microbial communities. This session highlights DOE’s support for studies that leverage integrated, multidisciplinary research to assess microbial carbon and nutrient cycling within soil and sediment microbiomes.

Speakers:

- 2:00-2:15 pm **Thea Whitman – University of Wisconsin, Madison**
Dissection of Carbon and Nitrogen Cycling in Post-Fire Soil Environments using a Genome-Informed Experimental Community
- 2:15-2:30 pm **Jennifer Bhatnagar – Boston University**
Molecular Mechanisms of Mycorrhizal-Decomposer Interactions and Impacts on Terrestrial Biogeochemistry
- 2:30-2:45 pm **John Coates – University of California, Berkeley**
Using a Systems Biology Approach to Describe the Role of Dissimilatory Phosphite Oxidation in the Global Phosphorus Cycle
- 2:45-3:00 pm **Javier Ceja Navarro – University of California, Berkeley**
Cross-Kingdom Interactions: The Foundation for Nutrient Cycling in Grassland Soils
- 3:00-3:15 pm **Jean Philippe Gibert – Duke University**
From Viruses to Protists: Temperature Response of the Neglected Components of Microbial Controls on Peatland Nutrient Cycling
- 3:15-3:30 pm **Bruce Hungate – Northern Arizona University**
The GREEN 'omics of Nutrient Feedbacks to Soil Warming
- 3:30-3:45 pm **Karen Lloyd – The University of Tennessee**
Using Culture-Independent Methods to Link Active Compound-Specific Carbon Degradation to Greenhouse Gas Production and Recycling in Natural Populations of Permafrost Microbes
- 3:45-4:00 pm **BREAK**
- 4:00-4:15 pm **Greyson Chadwick – California Institute of Technology**
Cell to Ecosystem: Understanding Methane and Associated Nutrient Cycling by Sediment Hosted Syntrophic Consortia and their Viral Predators
- 4:15-4:30 pm **Jeremy Semrau – University of Michigan**
Microbial Competition for Copper: Impacts on Carbon and Nitrogen Cycling
- 4:30-4:45 pm **Matthew Sullivan – The Ohio State University**
Virus in soils: Key Modulators of Microbiomes and Nutrient Cycling?
- 4:45-5:00 pm **Michiko Taga – University of California, Berkeley**
Corrinoids as Model Nutrients to Probe Microbial Interactions in a Soil Ecosystem

5:00-5:15 pm **Steven Allison – University of California, Irvine**
Biogeochemical Consequences of Microbial Evolution under Drought

5:15-5:30 pm **Mari Winkler – University of Washington**
Integrating Single-Cell Wetland Microbiome Structure, Function, and Activity to Ecosystem-Scale Biogeochemical Fluxes

2:00-5:00 pm **BREAKOUT SESSION E**

Secure Biosystems Design: BER's Efforts to Engineer Risk-Free Biological Systems and to Address Biological Escapes

Location: Columbia (Terrace Level) Breakout Room (TBD)

Moderator: Pablo Rabinowicz

Session Description: The advent of synthetic biology technologies brings promising opportunities to advance towards a sustainable bioeconomy. To safely realize this promise, new engineered biological systems must be designed in a secure way to minimize any potential risks. BER has started a new initiative in Secure Biosystems Design to engineer DOE-relevant biological systems with intrinsic biocontainment measures, as well as to devise strategies to prevent, detect, and respond to escapes of newly designed biosystems.

Speakers:

2:00-2:30 pm **Trent Northen – Lawrence Berkeley National Laboratory (LBNL)**
Laboratory Assessment of Microbial Community Engineering Approaches Within Fabricated Ecosystems

2:30-3:00 pm **Andrew Allen – J. Craig Venter Institute**
Genetic and Metabolic Control of Compartmentalized Metabolic Networks in a Model Photosynthetic Eukaryotic Microbe

3:00-3:30 pm **Break**

3:30-4:00 pm **Michael Jewett – Northwestern University**
Engineering Cell-Free Systems for Secure Biomanufacturing

4:00-4:15 pm **Paul Abraham – Oak Ridge National Laboratory (ORNL)**
Improving the Safety and Outcome of Research Using Next-Generation Genome Engineering

4:15-4:30 pm **Marc Salit – SLAC National Accelerator Laboratory**
FailSafe Genomes: from Intrinsic Biocontainment to Geopolitics

4:30-4:45 pm **Philippe Noirot – Argonne National Laboratory (ANL)**
Machine Learning-Guided Design of Efficient Safeguard Systems that Operate Under Different Bacterial Physiologies

4:45-5:00 pm **Robert Egbert – Pacific Northwest National Laboratory (PNNL)**
Genome Remodeling to Control the Persistence of Engineered Functions in Soil Microbes

2:00-5:00 pm **BREAKOUT SESSION F**

Plant Research for Bioenergy: From Lab to Field

Location: Columbia (Terrace Level) Breakout Room (TBD)

Moderator: Cathy Ronning

Session Description: DOE BER has significant interest in how candidate bioenergy plant species interact with environmental factors to affect long-term plant feedstock performance. A portfolio focused on these sustainability issues was funded in 2015, with projects set out to map the complex networks of plant and microbial growth, development, and metabolism in the field environment. While the research on sustainable bioenergy crop production and ecosystem outcomes is essential, characterizing and validating gene function is still a major bottleneck to fully understand and enable development of highly productive, sustainable bioenergy crops that are resilient and adaptable to changing environments. Thus, in 2019 a new effort in plant research was initiated for integrative genomics-based research and technology leading to transformative approaches to determine and validate gene function in plants and plant processes of interest to DOE BER. In this session, awardees from the Sustainability portfolio will present results from their research to investigate the molecular and physiological mechanisms underlying bioenergy crop vigor, resource use efficiency, and adaptability to changing conditions, as well as the role of plant-microbe interactions in influencing these traits. The new Plant Biology awardees will follow with a series of “speed talks” highlighting newly funded research to advance functional characterization and validation of the vast amounts of genomic information underlying bioenergy-relevant traits. Together these two programs highlight ‘omics-driven plant research within the Genomic Science Program portfolio.

Speakers:

- 2:00-2:05 pm **Cathy Ronning - DOE BER**
Introduction
- 2:05-2:30 pm **Gloria Coruzzi – New York University**
Plant Ecological Genomics at the Limits of Life in the Atacama Desert
- 2:30-2:55 pm **Lisa Tiemann (for Sarah Evans) – Michigan State University**
Connecting Nitrogen Transformations Mediated by the Rhizosphere
Microbiome to Perennial Cropping System Productivity in Marginal Lands
- 2:55-3:20 pm **Erin Nuccio – Lawrence Livermore National Laboratory (LLNL) (for Mary Firestone - University of California, Berkeley)**
Establishment to Senescence: Plant-Microbe and Microbe-Microbe
Interactions Mediate Switchgrass Sustainability
- 3:20-3:45 pm **Peggy Lemaux – University of California, Berkeley**
Lessons from the Field: How Sorghum and its Microbiome Respond to
Drought
- 3:45-4:00 pm **Break**
- 4:00-4:05 pm **Ana Alonso – University of North Texas**
Functional Analysis of Candidate Genes Involved in Oil Storage and Stability
in Pennycress
- 4:05-4:10 pm **Clint Chapple – Purdue University**
Coupling Metabolic Source Isotopic Pair Labeling and Genome Wide
Association for Metabolite and Gene Annotation in Plants
- 4:10-4:15 pm **José Dinneny – Stanford University**
Discovering Innovations in Stress Tolerance Through Comparative Gene
Regulatory Network Analysis and Cell-Type Specific Expression Maps
- 4:15-4:20 pm **Andrea Eveland – Donald Danforth Plant Science Center**
Elucidating the Molecular Mechanisms Underlying Drought Resilience in
Sorghum

- 4:20-4:25 pm **Brian Fox – University of Wisconsin, Madison**
Creation of an Acyltransferase Toolbox for Plant Biomass Engineering
- 4:25-4:30 pm **Lianyong Wang (for Martin Jonikas) – Princeton University**
Transforming Our Understanding of Chloroplast-associated Genes through Comprehensive Characterization of Protein Localizations and Protein-protein Interactions
- 4:30-4:35 pm **Yasuo Yoshikuni – Lawrence Berkeley National Laboratory (LBNL) (for Hiroshi Maeda - University of Wisconsin, Madison)**
Constructing the Nitrogen Flux Maps (NFM) of Plants
- 4:35-4:40 pm **Sue Rhee – Carnegie Institution of Washington**
High-throughput Determination of a Subcellular Metabolic Network Map of Plants
- 4:40-4:45 pm **James Schnable – University of Nebraska, Lincoln**
GCM: (T)rait, (G)ene, and (C)rop Growth (M)odel Directed Targeted Gene Characterization in Sorghum
- 4:45-4:50 pm **Gail Taylor – University of California, Davis**
Combining genome-wide association studies and expression quantitative trait nucleotide mapping with molecular and genetic validations to identify transcriptional networks regulating drought tolerance
- 4:50-4:55 pm **James Umen – Donald Danforth Plant Science Center**
Deep Green: Structural and Functional Genomic Characterization of Conserved Unannotated Green Lineage Proteins
- 4:55-5:00 pm **Kranthi Varala – Purdue University**
InferNet: Gene Function Inference by Leveraging Large, Organ-specific Expression Datasets and Validation of Non-redundant Regulators
- 5:00 **Adjourn**

5:00-7:00 pm **POSTER SESSION B**

Location: Lobby outside Columbia Ballroom (Terrace Level)

Wednesday, February 26th

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

8:30-9:50 am **DOE 2019 EARLY CAREER RESEARCH AWARDS**

Location: Columbia Ballroom (Terrace Level)

Moderator: Pablo Rabinowicz

Session Description: The 2019 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:

8:30-8:50 am **Kristin Burnum-Johnson – Pacific Northwest National Laboratory (PNNL)**
Spatiotemporal Mapping of Lignocellulose Decomposition by a Naturally Evolved Fungal Garden Microbial Consortium

8:50-9:10 am **Davinia Salvachúa Rodríguez – National Renewable Energy Laboratory (NREL)**
Elucidating Aromatic Catabolic Pathways in White-Rot Fungi during Lignin Decay

9:10-9:30 am **Josh Michener – Oak Ridge National Laboratory (ORNL)**
Systems metabolic Engineering of *Novosphingobium aromaticivorans* for Lignin Valorization

9:30-9:50 am **Kevin Solomon – Purdue University**
Genetic Tools to Optimize Lignocellulose Conversion in Anaerobic Fungi and Interrogate Their Genomes

9:50-11:10 am **PLENARY SESSION 4: EMERGING TECHNOLOGIES**

Spectrum Across BER Science

Location: Columbia Ballroom (Terrace Level)

Moderator: Shing Kwok

Session Description: BER funds science and its related technologies covering various depths of study - from field scale (UAV phenotyping) to atomic scale (micro electron diffraction imaging). This session will provide an overview of some of the emerging technologies that are being used by various scientists in BER funded research projects.

Speakers:

9:50-10:10 am **Daniel Schachtman – University of Nebraska, Lincoln**

Developing Tools to Phenotype Key Energy *Sorghum* Traits Related to Enhanced Nitrogen and water use Efficiency Under Field Conditions

10:10-10:30 am **Ivan Baxter – Donald Danforth Plant Science Center**
Leveraging High-Throughput and Tightly Controlled Environments to Understand the Physiological and Genetic Mechanisms Underlying Water-use Efficiency in C4 Grasses

10:30-10:50 am **Peter Weber – Lawrence Livermore National Laboratory (LLNL)**
New Insights into Microbial Function and Interactions Using Stable Isotope Probing and NanoSIMS

10:50-11:10 am **Jose Rodriguez – University of California, Los Angeles**
New Approaches in Electron Diffraction for Visualizing Macromolecules with Atomic Detail

11:10 am **CLOSE-OUT AND ADJOURNMENT**