Office of Biological and Environmental Research Biological Systems Science Division Update

Dawn Adin, Ph.D.

Acting Director, Biological Systems Science Division
Department of Energy
Office of Biological & Environmental Research

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Update on Programmatic Activities – Completed Activities (since April)

May
- ☑ FOA/Lab – Early Career panel

June
- ☑ FOA – Integrative Computational Tools panel
- ☑ FOA – Reaching a New Energy Sciences Workforce (RENEW) panel ⬅ **SC Initiative**
- ☑ FOA – Funding for Accelerated, Inclusive Research (FAIR) review ⬅ **SC Initiative**
- ☑ Lab – Biopreparedness Research Virtual Environment (BRaVE) panel ⬅ **SC Initiative**

July
- ☑ Lab – Accelerate Innovations in Emerging Technologies review ⬅ **SC Initiative**
- ☑ Lab – Energy Earthshot Research Centers (EERC) review ⬅ **SC Initiative**
- ☑ FOA – Science Foundations for Energy Earthshots (FOA) review ⬅ **SC Initiative**

Aug
- ☑ SFA Review – Secure Biosystems Design Science Focus Area (SFA) virtual panels

Sept
- ☑ Overcoming barriers in plant transformation: A focus on bioenergy crops virtual workshop

Update on Programmatic Activities – Upcoming Reviews/Activities

❑ Annual Bioenergy Research Center (BRC) Reviews – Nov, Dec, Jan, Feb

❑ LBNL-Berkeley Synchrotron Infrared Structural Biology (BSISB) Onsite Review - Nov

❑ 2024 Genomic Science PI Meeting - April 2-4: Hybrid Meeting (tentative)

❑ 2024 Enabling Capabilities PI Meeting - April 2-4: Hybrid Meeting (tentative)

❑ DOE KBase Reverse Site Visit – Spring 2024

Potential Funding Opportunities for FY 2024 (dependent on appropriations)
❑ Bioimaging Research and Approaches for the Bioeconomy and the Environment
❑ Low Dose Radiation Research
❑ Microbial Systems Biology to Enable Production of Next-Generation Biofuels and Bioproducts
❑ Early Career Research Program (ECRP)
❑ Reaching a New Energy Sciences Workforce (RENEW)
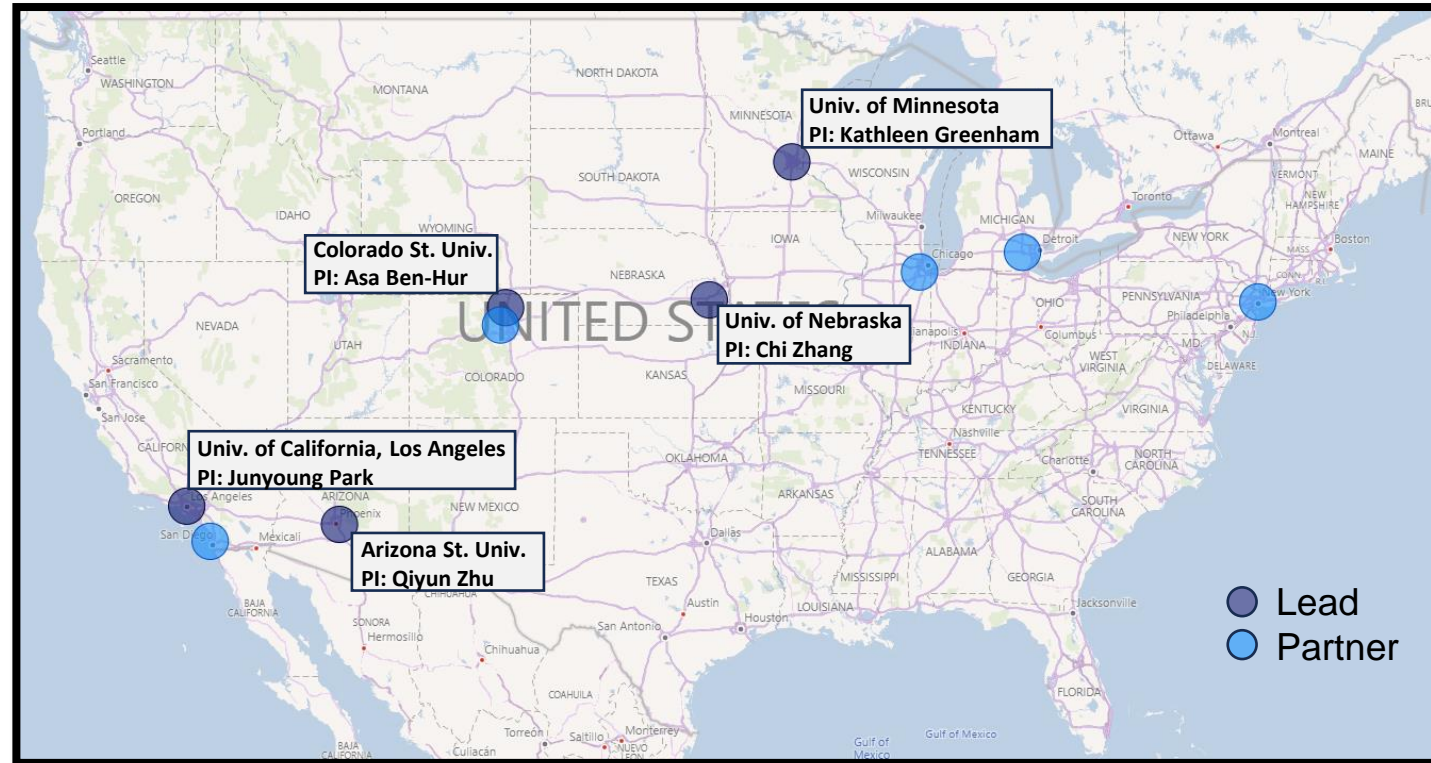❑ Funding for Accelerated, Inclusive Research (FAIR)

New – Computational Biology Awards
Integrative Computational Tools for Systems Biology DE-FOA-0002878

5 new projects

Novel computational tools or analytical approaches to integrate large, disparate data types from multiple/varied sources leading to scalable solutions for omics analysis, data mining, and knowledge extraction from complex data sets (experimental and calculated) to achieve coordinated knowledge or integration of knowledge to decipher relationships of biological systems.

> ML-based systemic flux quantitation tool to quantify metabolic fluxes within and across microbes in communities

> Deep learning framework to predict transcription factor binding and chromatin state in model plants

> Bioinformatics framework to quantify genotype-specific RNA-splicing variants in multi-omics data to identify candidate genes that influence plant adaptability to the environment

> Computational tools to explore the diversity of temporal regulation of specialized metabolites in plants

> Expand development of scikit-bio, a Python library implementing various data structures, algorithms, and metrics for bioinformatics analyses for analyzing multi-modal, multi-omic data of complex community systems

https://www.energy.gov/science/articles/department-energy-announces-47-million-research-integrative-computational-tools

https://science.osti.gov/-/media/funding/pdf/Awards-Lists/2878-BER-Comp-Bio-Awards-List.pdf

New – Computational Biology Awards

2 new projects

Enhancing Data Management across BER Facilities and Computational Resources

➤ Develop platform-agnostic bioinformatics Data Transfer System (DTS) to enable transfer of data between BER supported programs in a new and efficient way that supports FAIR data principles and data management best practices.
➤ Supports data transfers (push and pull) across all JGI resources, KBase, NMDC, EMSL, and ESS-DIVE.

Enhancing KBase Platform Data and Software Security

➤ Addresses the most pressing security concerns for the KBase platform
➤ Updates infrastructure to automate vulnerability detection and facilitate updates to guard against potential security flaws.

New – Biopreparedness Research Virtual Environment (BRaVE) Initiative Awards
Advancing DOE's distinctive capabilities to support national biopreparedness and response – LAB 23-2955

4 new projects

Innovative multi-disciplinary experimental and computational technologies to understand molecular mechanisms underlying host-pathogen interactions tow develop new approaches for disease detection and design of targeted interventions

➢ Decoding host-pathogen dynamics with 4D (epi)genomics
➢ Enhancing biopreparedness through a model system to understand the molecular mechanisms that lead to pathogenesis and disease transmission
➢ Phage Foundry: A high-throughput platform for rapid design and development of countermeasures to combat emerging drug-resistant pathogens
➢ Unlocking the molecular basis of plant-pathogen interactions to create resilient bioenergy crops
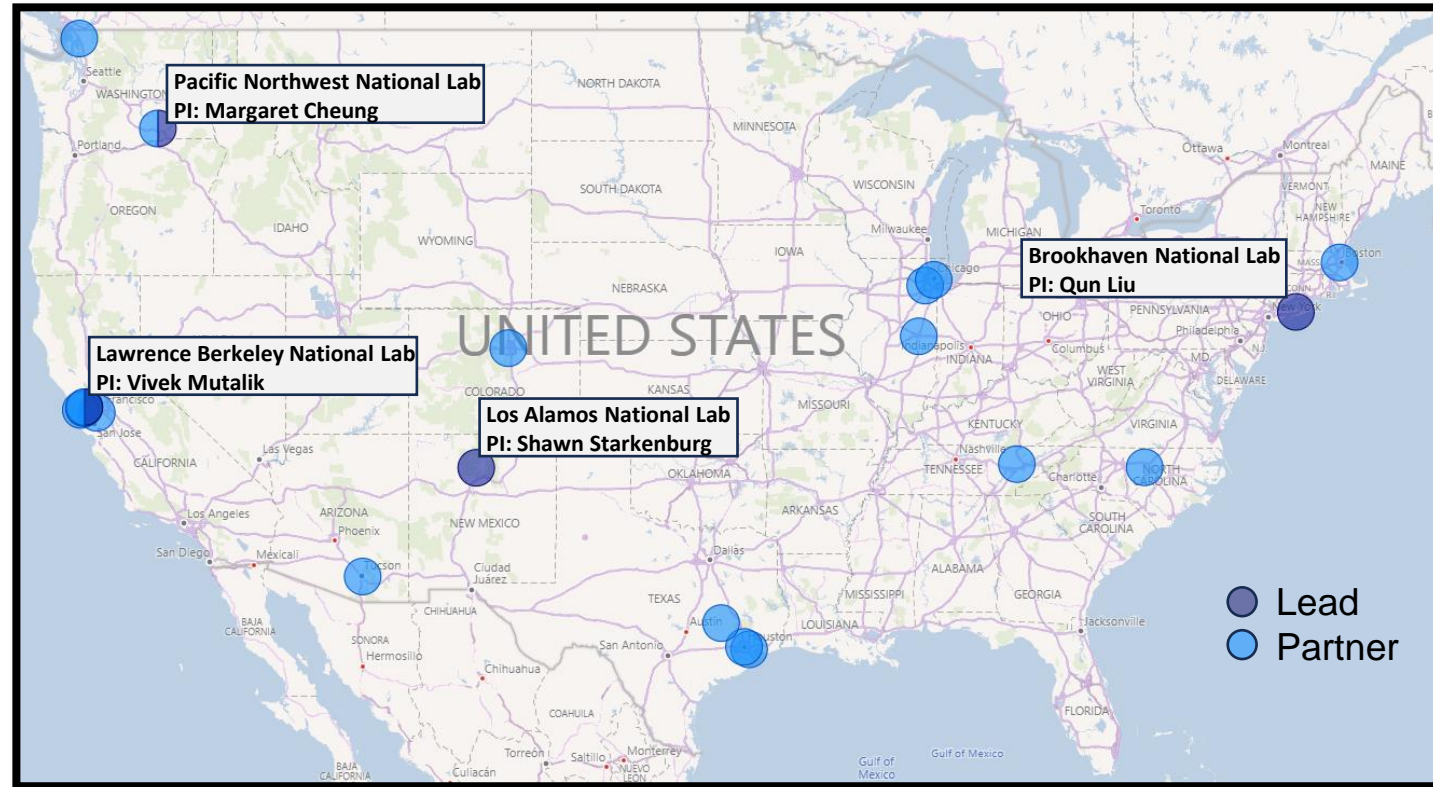
Note: Office of Science Programs supported a total of **10** awards.
Additional awards by ASCR and BES focus on developing more complete models of how epidemics spread, designing novel anti-pathogen materials, and providing innovations in DOE's user facilities.
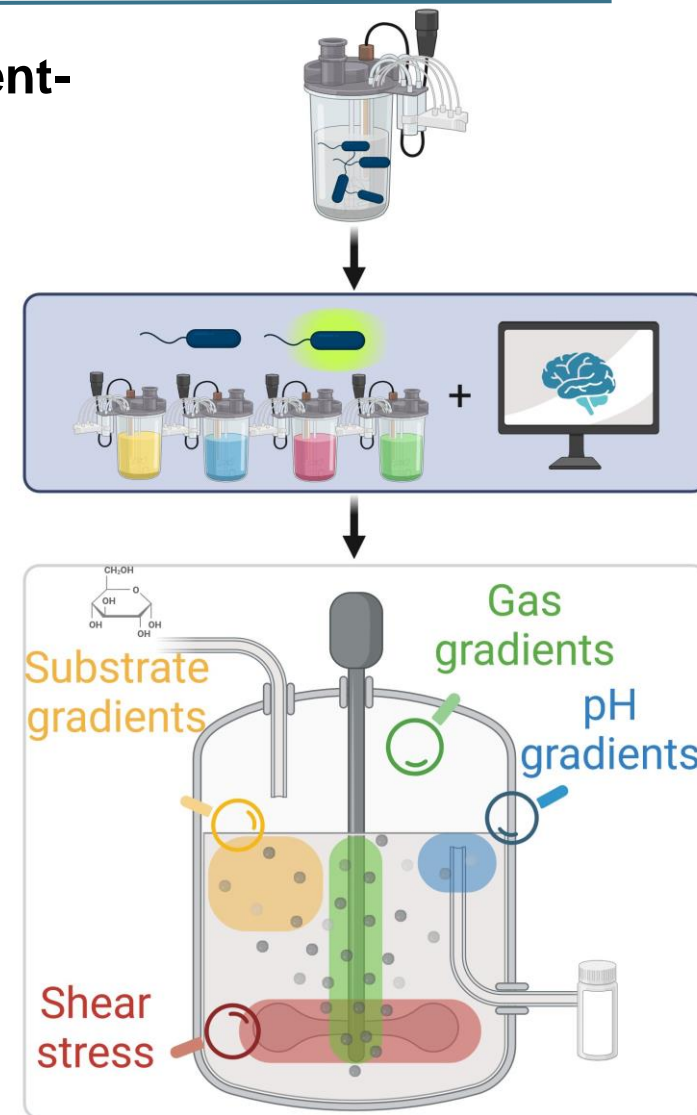
Real-time Sensing and Adaptive Computing to Elucidate Microenvironment-Induced Cell Heterogeneities and Accelerate Scalable Bioprocesses

PI: Davinia Salvachúa Rodríguez

Led by the **National Renewable Energy Laboratory (NREL)** with collaborators at PNNL, UC Davis, UC San Diego, and University of Puerto Rico, Río Piedras, this project will:

➢ Study and model microbial behavior in bioreactors to address why promising biomanufacturing processes that work well in the laboratory often fail when scaled up for mass production in industrial-size bioreactors.

➢ Combine multi-omics approaches, synthetic biology, and advanced computational modeling to understand the cell-to-cell heterogeneity that occurs in large-scale bioreactor cultures.

➢ Focus on industrial microbial hosts as proof of concept to develop a host-agnostic approach to predict the behavior of microbes within their microenvironments.

➢ Attempt to close this heterogeneity knowledge gap to address the Lab Announcement's goal of accelerating the transition from new technology discovery to commercialization.

Note: Office of Science programs supported a total of <u>**11**</u> Accelerate awards

https://www.energy.gov/science/articles/department-energy-announces-73-million-basic-research-accelerate-transition
https://science.osti.gov/-/media/funding/pdf/Awards-Lists/3010-Accelerate-Awards-List.pdf

4 new BER projects

National Laboratory projects in fundamental research to accelerate scientific breakthroughs for the Energy Earthshots Initiative.

BSSD is funding 2 EERCs in support of the Carbon Negative Shot.

➢ Engineer plants and microbes for more efficient transfer of C to soils and soil carbon storage

➢ Understand chemical and physical interactions in soils that favor long-term C storage

➢ Study the impact of enhanced rock weathering

➢ Model impact of terrestrial C storage across different scales.

➢ Leverage AI technology and automated, self-driving lab technology to optimize C-storage conditions
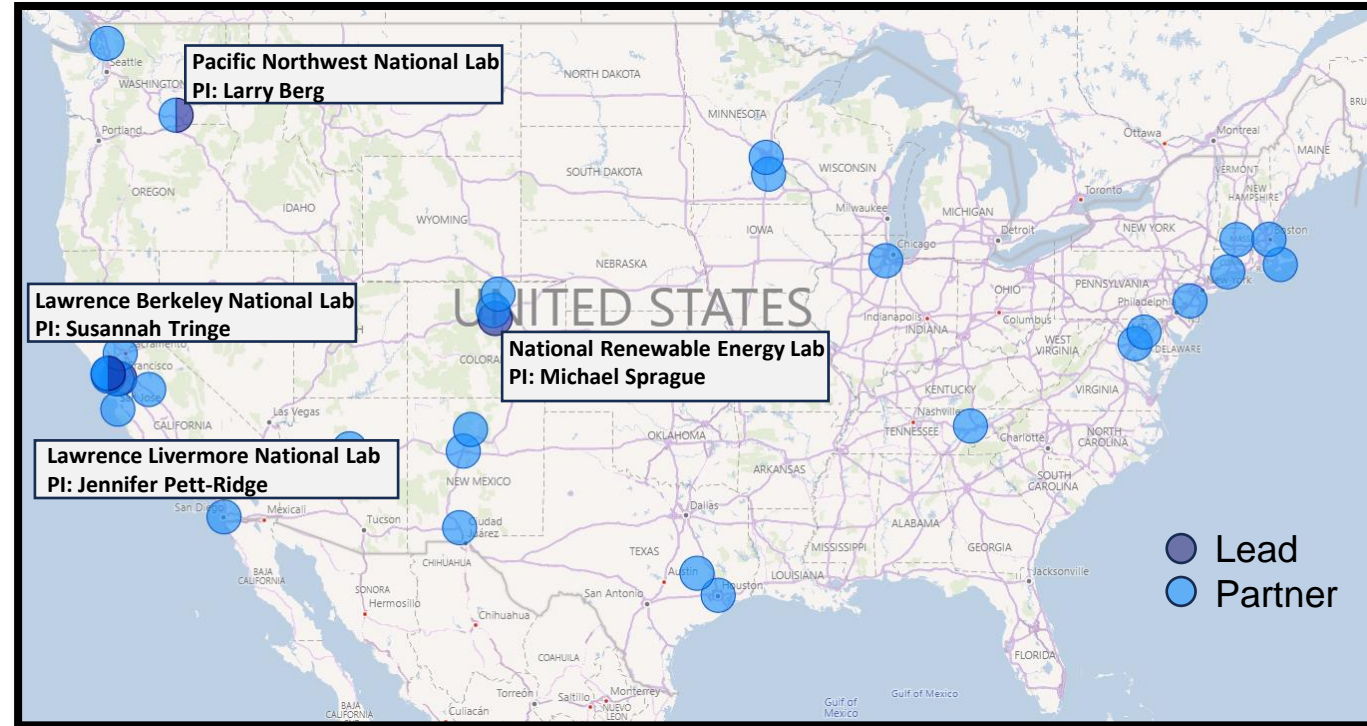
Note: Office of Science Programs supported a total of **11** awards.
EESSD leads **one** and is in support of **one more** EERC with relevance to the Floating Offshore Wind Shot.

https://www.energy.gov/science/articles/department-energy-announces-200-million-energy-earthshot-research-centers-support
https://science.osti.gov/-/media/funding/pdf/Awards-Lists/2954-Energy-Earthshot-Research-Centers-Awards-List.pdf
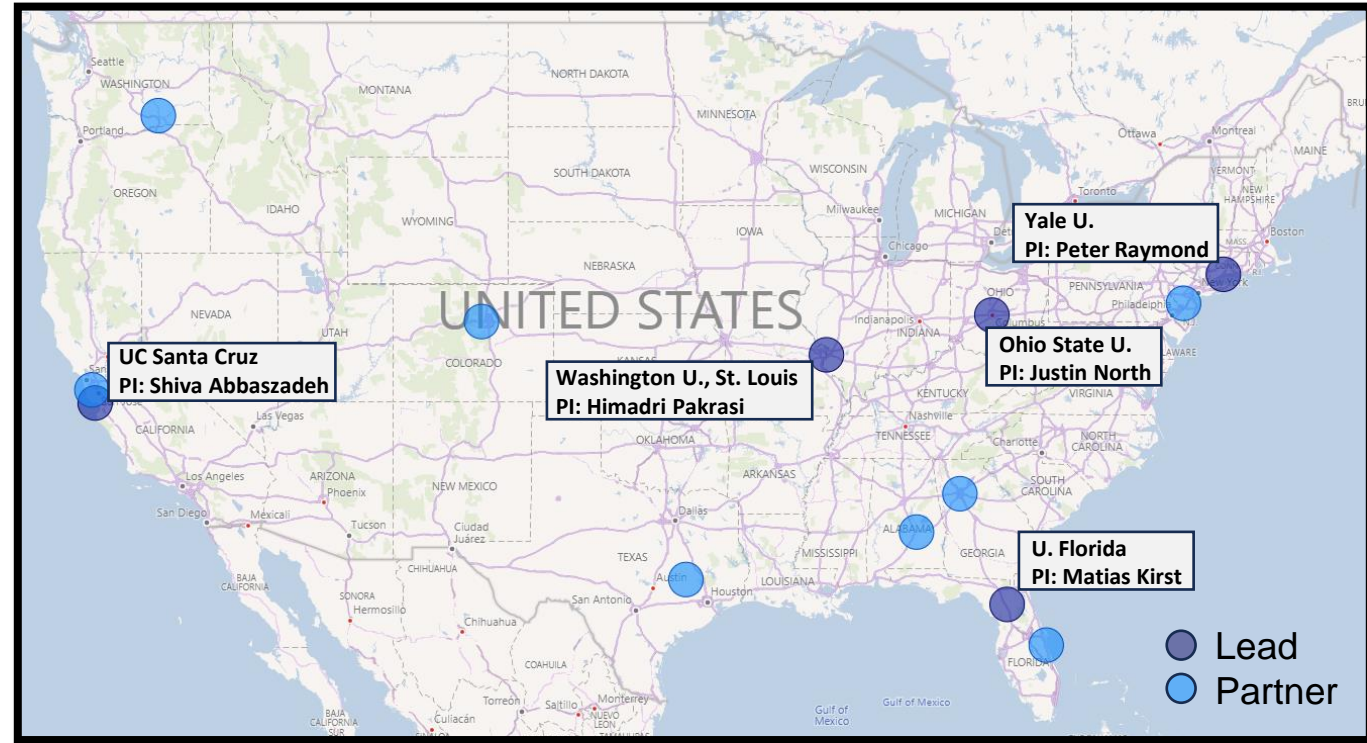
5 new BER projects

University projects to accelerate innovations toward clean energy solutions and address basic research challenges motivated by the DOE Energy Earthshot Initiative.

BSSD is funding _4_ projects in support of the Carbon Negative and Industrial Heat Shots.

- ➤ Understanding how plant roots affect soil organic carbon (SOC) accumulation
- ➤ Study the mechanisms that regulate SOC gain and loss in the rhizosphere by the action of roots, microbes, and soil structure
- ➤ Genetically engineer biopolymer synthesis in poplar roots for enhanced soil C stability
- ➤ Engineer biological propylene synthesis from lignin and CO2 to enable a carbon neutral bioeconomy
- ➤ Develop novel transporters, enzymes, and pathways in cyanobacteria to convert and secrete atmospheric nitrogen as reduced N species.

Yale U.
PI: Peter Raymond

Ohio State U.
PI: Justin North

UC Santa Cruz
PI: Shiva Abbaszadeh

Washington U., St. Louis
PI: Himadri Pakrasi

U. Florida
PI: Matias Kirst

Lead
Partner

Note: Office of Science Programs supported a total of **18** awards.
EESSD is supporting **1** project with relevance to the Carbon Negative Shot.

https://www.energy.gov/articles/doe-announces-264-million-basic-research-support-energy-earthshotstm
https://science.osti.gov/Initiatives/SCEarthshots/Foundations

New – RENEW and FAIR Initiative Awards
Complementary DEI efforts across SC and BER

Reaching a New Energy Sciences Workforce (RENEW) – DE-FOA-0002929

RENEW supports **experiential training and mentorship** across BER's portfolio at institutions historically underrepresented in science.

3 new BSSD projects

- **Ernst Cebert – Alabama A&M University**
  - Collaboration with BRC-CABBI and LBNL/JGI
  - Genetics and breeding research with C4 bioenergy crops
- **Marina Kalyuzhnaya – San Diego State University**
  - Collaboration with LBNL and PNNL
  - Impacts of nutrient availability and abiotic stresses on sustainable growth of sorghum
- **Suzanne Sindi – University of California, Merced**
  - Collaboration with LBNL/JGI
  - Using 'omics and other technologies to understand bioenergy and biosystems

Note: BER supported a total of **8** awards.

Funding for Accelerated, Inclusive Research (FAIR) – DE-FOA-0002931

FAIR **supports and enhances research** across BER's portfolio at institutions historically underrepresented in science.

2 new BSSD projects

- **Bagyalakshmi Muthan – West Virginia State University**
  - Collaboration with BNL
  - Understanding the role of duckweed transcription factors in triacylglycerol metabolism and abiotic stress tolerance in plants
- **Michael Thompson – University of California, Merced**
  - Collaboration with SLAC
  - Developing temperature-jump X-ray crystallography to study dynamic biosynthetic enzymes at synchrotrons and XFELs

Note: BER supported a total of **3** awards.

New Workshop – Overcoming barriers in plant transformation: A focus on bioenergy crops
September 18-20, 2023

Wayne Parrot, University of Georgia (Chair)

Sally Assmann, Pennsylvania State University
William Gordon-Kamm, Corteva Agroscience
Jeremy Schmutz, Hudson Alpha
Veena Veena, Danforth Plant Science Center
Margaret Young, Elizabeth City State University

Report in Spring 2024

Focus on identifying knowledge gaps and barriers in developing new tools and resources that address plant transformation of bioenergy crops.

- 3-day virtual workshop with presentations and discussion breakout sessions
- Attended by 95+ people with diverse research backgrounds and expertise representing academia, DOE National Laboratories and User Facilities, non-profit research facilities, industry, and Federal Agencies
- Included topic areas:
    - Technical and biological challenges associated with plant transformation
    - Legal and regulation issues with editing and engineering bioenergy crops
    - How to develop an inclusive community and increase the pool of future plant biologists

BSSD Science Highlights

112 JGI Publications from April 1, 2023 - September 25, 2023

Selected Highlights

➤ Rewiring metabolism of *Clostridium thermocellum* for consolidated bioprocessing of lignocellulosic biomass poplar to produce short-chain esters. *Bioresource Technology*

➤ A scaffolded and annotated reference genome of giant kelp (*Macrocystis pyrifera*). *BMC Genomics*

➤ BONCAT-FACS-Seq reveals the active fraction of a biocrust community undergoing a wet-up event. *Frontiers in Microbiology*

➤ Inference and reconstruction of the heimdallarchaeial ancestry of eukaryotes. *Nature*

➤ Identification of mobile genetic elements with geNomad. *Nature Biotechnology*

➤ Engineering a new-to-nature cascade for phosphate-dependent formate to formaldehyde conversion in vitro and in vivo. *Nature Communications*

➤ Viruses interact with hosts that span distantly related microbial domains in dense hydrothermal mats. *Nature Microbiology*

➤ JGI Plant Gene Atlas: an updateable transcriptome resource to improve functional gene descriptions across the plant kingdom. *Nucleic Acids Research*

JGI News Releases and Highlights:
• jgi.doe.gov/news-publications
• jgi.doe.gov/category/science-highlights
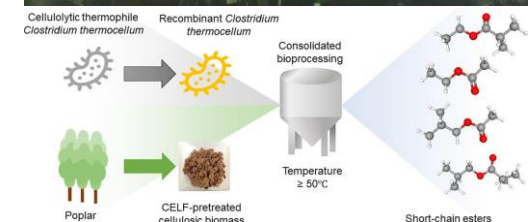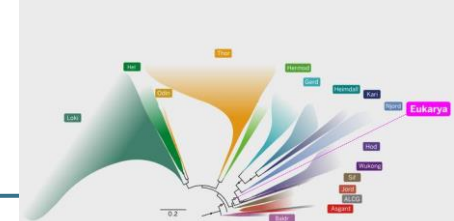
Identifying mobile genetic elements with geNomad

Background

A software tool called geNomad provides fast and precise identification and classification of viruses and plasmids, two of the most common forms of mobile genetic elements, based upon their gene content and their genetic sequences.

Approach

➢ geNomad is an annotation and classification framework combining and building on two standard techniques for identifying viruses and plasmids - marker gene-based and a neural network approach.

➢ DOE Joint Genome Institute researchers designed the algorithms and developed the software using computing resources at NERSC.

➢ JGI partnered with a team from the National Microbiome Data Collaborative to implement geNomad into the NMDC EDGE Platform.

geNomad is a tool that identifies and classifies MGEs based upon their gene content and their genetic sequences.
(Kent Leech for Berkeley Lab)

Results

In tests, geNomad processed over 2.7 trillion base pairs of sequencing data, leading to the discovery of millions of viruses and plasmids available through the IMG Virus Resource (IMG/VR) and just-launched IMG Plasmid Resource (IMG/PR) databases.

Significance/Impacts

➢ geNomad is accessible to a wide audience: can run locally or on a web application, with a command line interface option.

➢ Integration with NMDC EDGE enables geNomad to be easily incorporated into larger workflows that include other tasks.

➢ geNomad was used to build the version 4 of IMG/VR (with more than 15 Million viral genomes) and the first version of IMG/PR (with more than 700K plasmids from metagenomes and metatranscriptomes).

Camargo A.P. *et al.* Identification of mobile genetic elements with geNomad. *Nat Biotechnol* (2023). doi:10.1038/s41587-023-01953-y

Host Genetics Play a Significant Role in the Composition of Switchgrass Root Microbiomes

TEXAS — The University of Texas at Austin
MICHIGAN STATE UNIVERSITY
BERKELEY LAB
University of Missouri
HudsonAlpha INSTITUTE FOR BIOTECHNOLOGY

Objective

Investigated the root bacterial communities of switchgrass grown in native range locations to see if host genetics determined the composition of the microbiome.

Approach

➢ 1,961 samples from field sites in Texas, Missouri, and Michigan were sequenced to determine the composition of the switchgrass root microbiome.
➢ Effect of environment vs. host genetics on the composition of the root microbiome was characterized by a genome wide association study (GWAS) to identify loci in the host genome associated with the differing abundance of these microbes.

Result/Impacts

➢ Discovered switchgrass genotype determined a large portion of the plant's microbiome.
➢ Identified switchgrass genes that appear to influence microbe abundance.
➢ Variation in genes implicated in plant immunity, development, and signaling were associated with microbiome compositional differences.
➢ Found conserved set of core bacteria that were found in high abundance on roots across the native range sites. Most of these core microbes differ in abundance between host genotypes in an environmentally dependent manner.
➢ These results may help to engineer or breed switchgrass varieties that form stronger beneficial associations with their microbiomes.
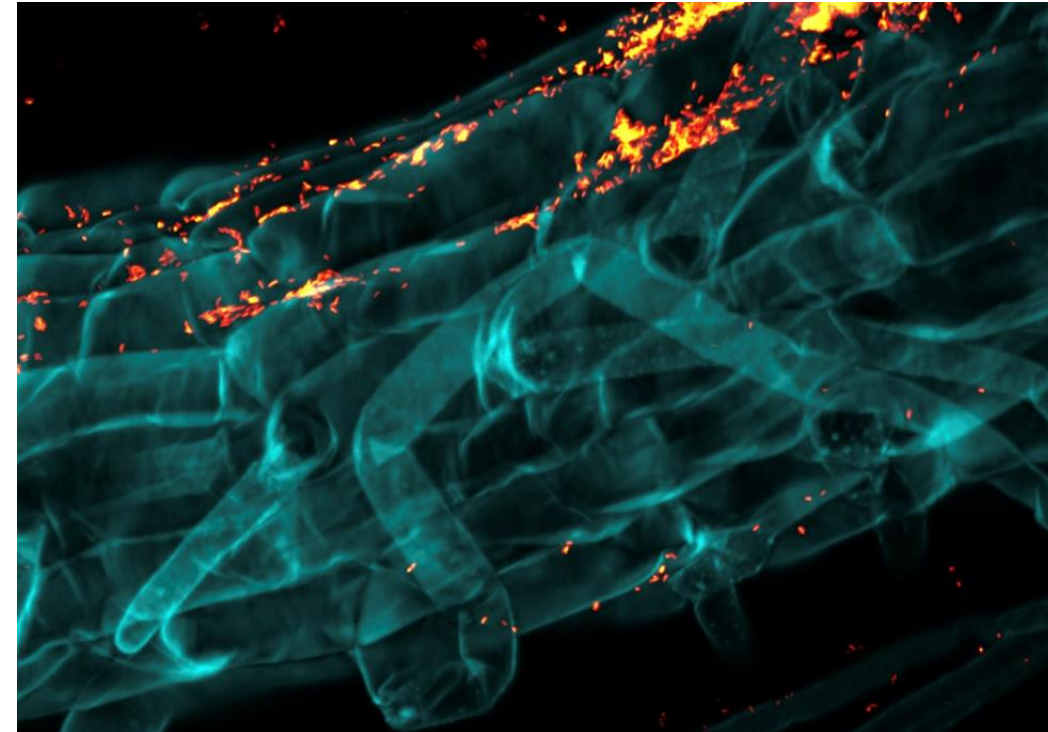
Confocal microscope image of a switchgrass root (blue) colonized by fluorescently labeled bacteria (in yellow and orange).

Published SC Highlight June 27, 2023:
https://www.energy.gov/science/ber/articles/host-genetics-play-significant-role-composition-switchgrass-root-microbiomes
Publication on OSTI: https://www.osti.gov/biblio/1970495

Imaging Shows How Inorganic-Microbe Hybrids Use Light to Turn Carbon Dioxide into Bioplastics

Objective

Visualize at the level of single cells or molecules how the microbes in semiconductor biohybrids convert solar energy to carbon dioxide to produce bioplastics and biofuels.

Approach

➤ Developed a new imaging platform that combines multi-channel fluorescence imaging with photoelectrochemical current mapping.

➤ Provides quantitative assessments of protein behaviors and a mechanistic understanding of how the electron transport occurs from the semiconductor to the bacteria cell.

➤ Assessed functional roles of two hydrogenases – one bound to the cell membrane and the other soluble in the cytoplasm.

Result/Impacts

➤ Correlated the properties of cellular proteins and showed that light-generated electrons can move directly to the bacteria with surprising efficiently.

➤ Better understand how these biohybrids function and provides insight on how they can be modified to convert energy more efficiently.

➤ Platform can be used to study other biological-inorganic systems.
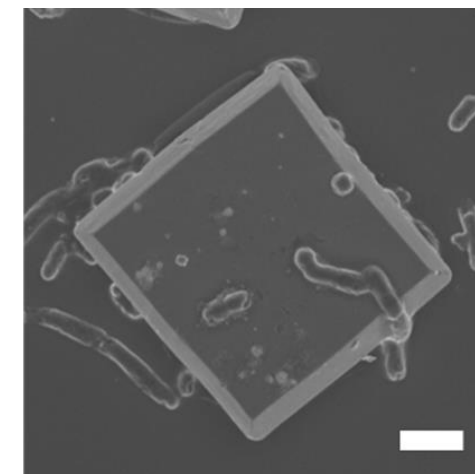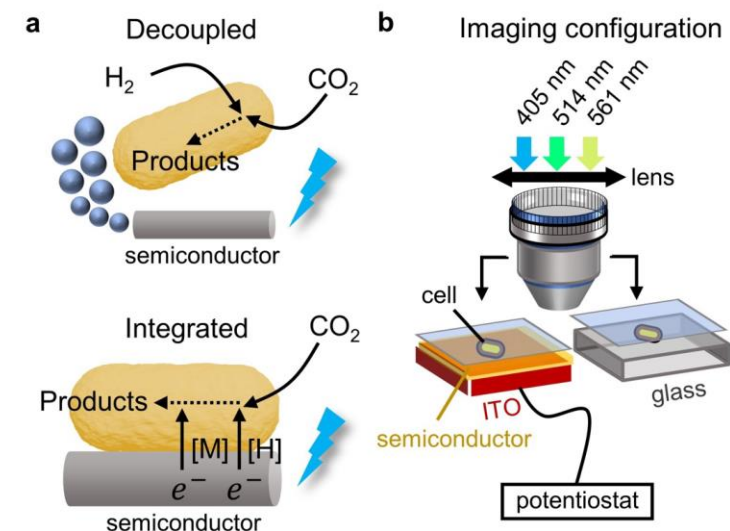
Novel Split Selectable Markers Allow for Multi-gene Transformation in Plants

Background
➢ Complex plant traits (e.g., yield) are controlled by multiple genes.
➢ Stacking multiple genes in plants is important to develop crops with desirable traits but challenging due to limited selected marker options.
➢ Gene stacking involves using one selectable marker for each gene, but selection effectiveness varies depending on the specific selectable markers used and conditions.

Approach
➢ Selectable marker genes were divided into two fragments tagged with split inteins.
➢ Two partial fragments were cloned into plasmid vectors and then co-transformed into plants.
➢ Partial selectable marker fragments were reassembled into full-length functional proteins via trans-splicing of split inteins.

Results
➢ A visible marker, RUBY, successfully reconstituted from two non-functional fragments through *Agrobacterium*-mediated leaf infiltration in tobacco.
➢ Split Hyg^R and the split Kan^R selectable marker systems established in *Arabidopsis* and *Populus* for *Agrobacterium*-mediated stable transformation, by stacking two reporter genes (eYGFPuv and RUBY).

Significance
➢ Demonstrate split–Kan^R and split–Hyg^R are effective for both *in planta* and plant tissue culture co-transformation in herbaceous and woody plants.
➢ Split selectable marker systems provides a valuable tool for gene-stacking in both herbaceous and woody plants allowing markers to be used multiple times.
➢ Technology has great potential for accelerating the improvement of plant traits.
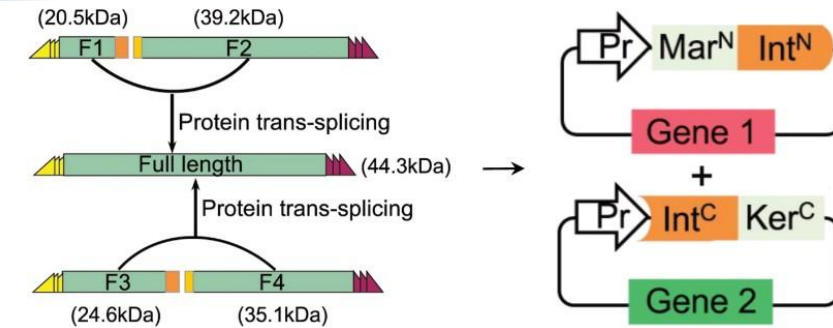
The selectable marker Hyg^R was split into two parts (F1 + F2 or F3 + F4) and cloned into two different plasmid vectors for stacking two genes (Gene 1 and Gene 2).
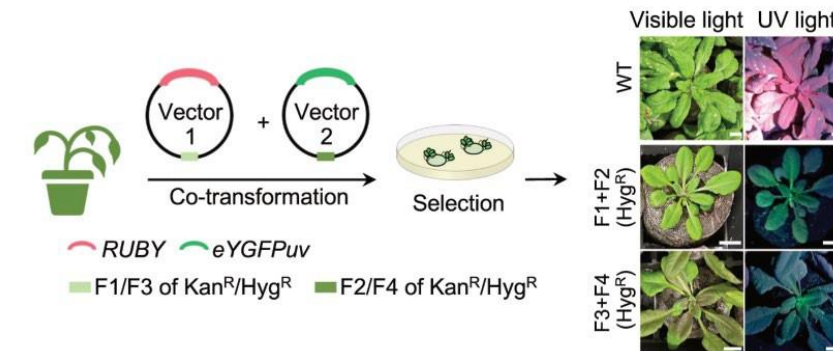
The split Hyg^R selectable marker system was used to stack two reporter genes (eYGFPuv and RUBY) in Arabidopsis. The RUBY expression shows a purple-leaf phenotype under visible light. The eYGFPuv expression shows green-leaf phenotype under UV light.

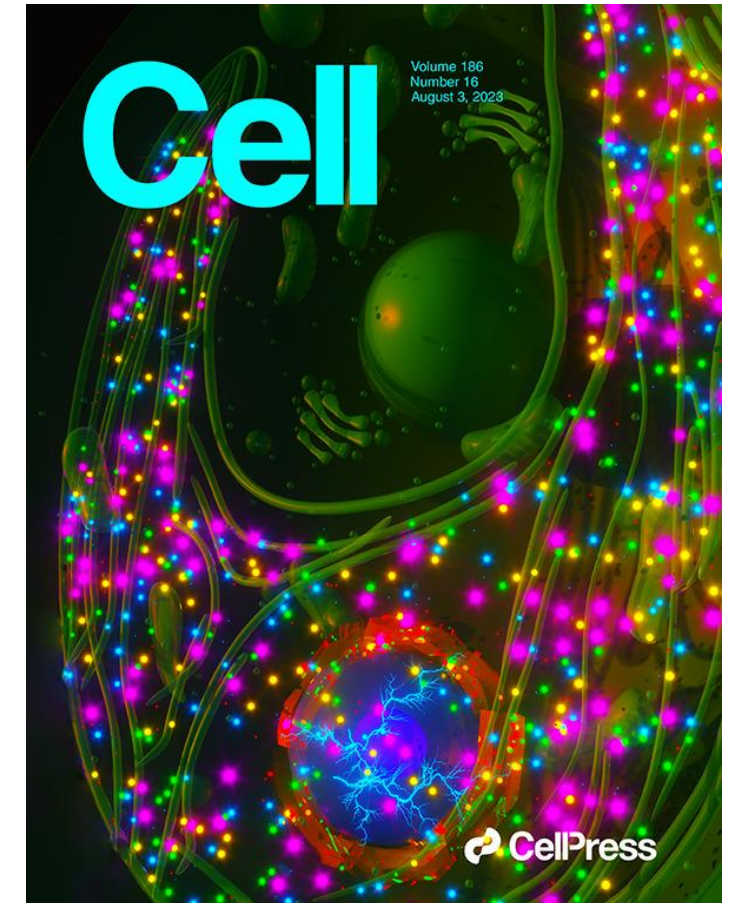# A Spatial Atlas of the Chloroplast Proteome

Objective
Use fluorescent protein tagging to build a spatial localization map of the *Chlamydomonas* chloroplast proteome.

Approach
➢ Starting with nearly 6,000 protein annotations from multiple sources, the location of 1,034 chloroplast-associated proteins was determined in *Chlamydomonas* using fluorescent tagging and confocal microscopy.
➢ Subcellular localization of proteins was mapped to 141 distinct patterns across 17 major organelles or cellular sites, and many chloroplast proteins were also found in other organelles or cellular structures.
➢ Machine learning was used to predict the location of all *Chlamydomonas* proteins.

Result/Impacts
➢ Developed a comprehensive spatial atlas of chloroplast proteins, constituting a valuable resource to help understand and manipulate photosynthesis.
➢ Discovered new chloroplast structures and brought new insights on its internal spatial organization.
➢ Identified new components of known chloroplast structures such as the chloroplast envelope, its DNA-protein complexes, fat storage microcompartments, and protein bodies involved in capturing carbon dioxide from the atmosphere.

Thank you

https://science.osti.gov/ber

https://www.energy.gov/science/ber/biological-and-environmental-research