Approved Proposals FY21

Following are the approved user proposals for CSP, FICUS JGI-EMSL-NEON, CSP Functional Genomics and CSP New Investigator calls.

Community Science Program

Proposer	Affiliation	Proposal Description
Bahram, Mohammad	Swedish University of Agricultural Sciences (Sweden)	Evolution of Nutritional Modes of Ceratobasidiaceae (Basidiomycota, Fungi)
Bhattacharya, Debashish	Rutgers University	Extreme Solutions to Extreme Problems: Studies of Life at the Edge Using Cyanidiophyceae Red Algae
Chopra, Ratan	University of Minnesota	Pennycress – A Solution for Global Food Security, Renewable Energy and Ecosystem Benefits
Cosgrove, Daniel	Pennsylvania State University	Synthesizing Microbial Expansins with Unusual Activities

D'Agostino, Paul	Technische Universität Dresden (Germany)	Expanding Genomic Knowledge of Unexplored Symbiotic and Terrestrial Cyanobacteria
Hammond, Ming	University of Utah	High-Throughput Functional Discovery of Bacterial Sensory-Enzymes
Hanschen, Erik	University of Arizona	A Genomic Approach to Understanding Mechanism and Consequences of Life Cycle Evolution in Green Algae to Understand Reproduction in Biofuel and Feedstock Relevant Algae
Harkess, Alex	Auburn University	The Brassicales Genome Initiative
Hatzenpichler, Roland	Montana State University	Taxonomic, Genomic, Metabolic, and Functional Heterogeneity in Yellowstone Geothermal Features
Hurley, Amanda	Wisconsin Institute for Discovery	Novel Secondary Metabolite-Producing Bacteria for Plant Disease Control
Larkin-Swartout, Alyse	University of California, Irvine	Detecting Nutrient Limitation and Coastal Biogeochemical Responses to El Nino Using Microbial Eco-Genomic Biomarkers

Looney, Brian	Duke University	Metatranscriptomic Study of Ectomycorrhizal Fungal Communities of Populus Across a Diversity Gradient
Lopes dos Santos, Adriana	Nanyang Technological University (Singapore)	New Green Genes
Ma, Li-Jun	University of Massachusetts Amherst	Genome Dynamics, Chromosomal Rearrangements and Potential Functional Impacts in *Fusarium*, A Genus of Endophytic, Plant Pathogenic and Saprophytic Fungi
McDaniel, Stuart	University of Florida	The Metabolic Basis of Bryophyte-Microorganism Interactions
McKay, John	Colorado State University	Enabling Reverse Genetics in the Oil Seed Crop *Camelina sativa* Through Mutant Population Sequencing
Mock, Thomas	University of East Anglia (United Kingdom)	100 Diatom Genomes Project
Moran, Mary Ann	University of Georgia	Temperature Effects on Metabolite-Mediated Autotroph-Heterotroph Carbon Transfer

Nuccio, Erin	Lawrence Livermore National Laboratory	Deeply Rooted: Using Metagenomics and Isotope-Assisted Metagenomics to Determine How Switchgrass Alters Subsoil Carbon Sequestration
Ozias-Akins, Peggy	University of Georgia	Sequencing of Apomictic Relatives of Switchgrass for Apomixis Gene Discovery and Comparative Genomics
Schuppenhauer, Michael	Lawrence Berkeley National Laboratory	SMARTFARM Metagenome Analysis of Carbon and Nitrogen Cycling in Commercial Bioenergy Crop Soils
Shen, Ben	The Scripps Research institute	Large-Scale Genome Sequencing for Establishing a Natural Products Genomics Resource Center
Slotkin, R. Keith	Donald Danforth Plant Science Center	Transcript Annotations of Repetitive Elements Enable Investigation of Previously Inaccessible Dark Matter Regions of Complex Bioenergy Plant Genomes
Spietz, Rachel	Montana State University	Impacts of Viral Infections Upon Microbial Carbon Cycling in the Samail Ophiolite

White III, Richard	University of North Carolina at Charlotte	Elucidating the Role Of Bacteriophage Lifestyle Strategy in Microbially-Mediated Perennial Rhizosphere Nitrogen Transformations
Willis, John	Duke University	Genomic Resources for Mimulus, a Powerful Plant System for Analyses of Environmental Adaptations
Wommack, Eric	University of Delaware	Deducing Gene to Function Linkages Within Virioplankton Populations Through the Lens of Ecosystem Gradients

FY 2021 Facilities Integrating Collaboration for User Science (FICUS) JGI-EMSL Proposals

Proposer	Affiliation	Proposal Description
Bailey, Vanessa	Pacific Northwest National Laboratory	Characterization of simplified soil communities with high and low carbon use efficiency across differing moisture treatments
Bhatnagar, Jennifer	Boston University	Plant-mycorrhizal-decomposer interactions under climate change: the role of shifting plant carbon allocation

Blanchard, Jeff	University of Massachusetts, Amherst	Integrative analysis of multi-omic data across NEON eco-climatic regions
Glass, N. Louise	University of California, Berkeley	Nuclear cooperation, sharing of public goods and coordination of plant biomass utilization: probing functions unique to multinucleate syncytial fungi
Hatzenpichler, Roland	Montana State University	Ecophysiology, inter-domain interactions, and biogeochemical impact of an aerobic methane-producing freshwater bacterium
Heyduk, Karolina	University of Hawaii	Characterizing the molecular and metabolic regulation of drought-tolerant CAM photosynthesis
Mouser, Paula	University of New Hampshire	Membrane adaptations in response to environmental and engineered perturbations: Implications on attachment and carbon cycling in the deep terrestrial subsurface
Selbmann, Laura	University of Tuscia (Italy)	Metabolic processes and trophic interactions in Antarctic cryptoendolithic communities
Swaminathan, Kankshita	HudsonAlpha Institute for Biotechnology	Characterization of self-incompatibility in the bioenergy grass Miscanthus
Ziels, Ryan	University of British Columbia (Canada)	Resolving carbon fluxes within microbial communities inhabiting full-scale bioenergy facilities

CSP Functional Genomics

Proposer	Affiliation	Proposal Description
Alper, Hal	University of Texas at Austin	Accessing an expanded transport-ome through a transporter protein library
Geddes, Barney	North Dakota State University	Synthetic symbiotic gene clusters for engineering designer rhizobium-legume symbioses
Henrissat, Bernard	Technical University of Denmark	Large scale functional exploration of the Carbohydrate-Active Enzymes sequence space
Lowe-Power, Tiffany	University of California, Davis	Synthesis and functional analysis of type VI secreted secretion (T6SS) genes from plant symbiotic bacteria
Mahadevan, Radhakrishnan	University of Toronto	Transcription Factor Biosensor Libraries for Community Use in Metabolic Engineering
Mueller, Alex	LanzaTech, Inc.	Cell-free combinatorial assessment of the genomic landscape of gas-fermenting Clostridium autoethanogenum for use in biosynthetic design
Narayan, Alison	University of Michigan	Profiling chemical function across sequence space
Nayak, Dipti	University of California, Berkeley	Functional Characterization of Energy Conservation Pathways in Methanogenic Archaea within the Methanosarcina Genus
Robinson, Serina	Eawag Swiss Federal Institute of Aquatic	Functional characterization of metagenomic hydrolases from stream biofilms enabling access to alternative organic carbon pools

	Science and Technology	
Woolston, Ben	Northeastern University	Development of a Robust Genome Engineering Toolbox for the Model Acetogen Eubacterium limosum

CSP New Investigator

Proposer	Affiliation	Proposal Description
Carey, Sarah	Auburn University	Transcriptomic analyses of the high-seed oil halophyte *Batis maritima*
Evans, Rebecca	Washington State University	Metagenomes of the developing soils of Mount St Helens responding to nitrogen deposition and invasive species and the impact on soil carbon storage and cycling
Fairbanks, Dawson	University of Arizona	Determining seasonal trait based microbial responses to moisture pulse events in the Jemez River Basin Critical Zone
Fernandes, Vanessa	The University of New Mexico	Unraveling the genomes of novel genera in the *Microcoleus steenstrupii* complex to understand climate change responses in biocrusts
Fulweiler, Robinson	Boston University	Relating microbial community function to methane emissions in temperate seagrass meadows

Garrigues Cubells, Sandra	Westerdijk Fungal Biodiversity Institute (Netherlands)	Study of the functional conservation and diversity of fungal transcriptional regulators involved in plant biomass degradation.
Geddes, Barney	North Dakota State University	Elucidating the genetic determinants of rhizobial effectiveness at symbiotic nitrogen fixation
Ghimire, Sabita	Miami University	High ammonium toxicity in ammonia-oxidizing bacteria
Glassman, Sydney	University of California, Riverside	Using metagenomics to elucidate microbial mechanisms of altered carbon and nitrogen cycling post-fire in southern California Chaparral
Igwe, Alexandria	University of Miami	Local adaptation of nitrogen-fixing bacteria, *Microvirga*, to high-stress serpentine soils
Jackrel, Sara	University of California, San Diego	Bacterial drivers of the Home-Field Advantage and the role of locally accelerated litter decomposition in the carbon cycle
Leisner, Courtney	Auburn University	Genomic regulation of plant biomass and nutrient responses to elevated atmospheric carbon dioxide levels in soybean
Lopez Pozo, Marina	University of Colorado at Boulder	Influence of rhizosphere microbes on duckweed transcriptome under elevated CO2

McGonigle, Julia	Bigelow Laboratory for Ocean Sciences	Linking Genomes to Phenomes in Extremophilic Microorganisms with Advanced Single Cell Approaches
Prenni, Jessica	Colorado State University	Investigating the Relationship Between Cover Crop Species Diversity, the Composition and Function of the Soil Microbiome, and Soil Health
Sandaa, Ruth-Anne	University of Bergen (Norway)	Metatranscriptomic analysis of the different steps in a marine giant virus-algae infection
Sillo, Fabiano	Institute for Sustainable Plant Protection, National Research Council (Italy)	Mining ectomycorrhizal genomes and transcriptomes: from pan-genome to adaptive evolution in a climate change scenario
Su, Wei Wen	University of Hawaii at Manoa	RNA-seq analysis of *Yarrowia lipolytica* to decipher synthesis of acetyl-CoA derived oleochemicals from waste lipid feedstock for biomanufacturing of biofuels and bioproducts
Vimercati, Lara	University of Colorado at Boulder	Transcriptomic studies of the polyextremophilic yeast *Naganishia friedmannii* exposed to freeze-thaw stress
Xie, Meng	Brookhaven National Laboratory	Exploring transcriptional responses to iron bioavailability in *Populus*