Approved Proposals FY16

Following are the approved user proposals for fiscal year 2016 including CSP, CSP Small-Scale, Synthesis, and FICUS projects.

FY 2016 Community Science Program (CSP) Plans

PI	Affiliation	Project Description
Catcheside, David	Flinders University (Australia)	Acquisition of the sequestrate (truffle like) habit by basidiomycete macrofungi
Cooper, Elizabeth	Clemson University	Comparative transcriptomics of sweet and grain sorghum to understand the mechanism and timing of sugar accumulation in an important bioenergy crop
de Vries, Ronald	CBS-KNAW Fungal Biodiversity Centre (Netherlands)	Dissecting the different approaches of ascomycete fungi to degrade plant biomass
DeLong, Ed	University of Hawaii at Manoa	Going long and going deep: Comprehensive open ocean community single cell genome sequencing at the model open ocean time series study site, station ALOHA
Dollhofer, Veronika	Bavarian State Research Center for Agriculture (Germany)	Anaerobic fungi and assessment of their potential for biogas production

Duplessis, Sebastien	INRA (France)	Sequencing a reference genome for *Phakopsora pachyrhizi*, the fungal pathogen responsible for the Asian Soybean Rust
Francis, Christopher	Stanford University	Metagenomic characterization of nitrogen-cycling microbial communities impacting uranium release in the Upper Colorado River Basin
Hamelin, Richard	University of British Columbia (Canada)	Pathobiome of bioenergy trees
Hibbett, David	Clark University	Comparative and functional genomics of shiitake mushrooms: an international collaboration to resolve evolutionary relationships, substrate specificity, growth profiles, and routes to domestication in the amphi-Pacific genus *Lentinula*
Juenger, Tom	University of Texas at Austin	Exploring natural genetic diversity in switchgrass (*Panicum virgatum*) and its microbiome
Kalyuzhnaya, Marina	University of Washington	Systems level insights into methane cycling in arid and semi-arid ecosystems via community metagenomics and metatranscriptomics
Lorito, Matteo	University of Naples (Italy)	Supporting the development of microbial probiotics for grasses useful in sustainable bioenergy production
Martin, Francis	INRA (France)	1KFG: Deep sequencing of ecologically-relevant Dikarya
Mayali, Xavier	Lawrence Livermore National Laboratory	Influence of phycosphere-associated bacteria on microalgal biofuel production

McMahon, Katherine	University of Wisconsin-Madison	Diel cycles of gene expression in oligotrophic, dystrophic, and eutrophic lakes to identify new gene functions and dissect carbon cycling metabolisms
Merchant, Sabeeha	University of California, Los Angeles	Comparative genomics and expression profiling of snow algae *Chlamydomonas cribrum* and *Chloromonas nivalis*
Niyogi, Kris	University of California, Berkeley	Functional genomics of photosynthesis in *Chlamydomonas*, JGI's flagship alga
O'Malley, Michelle	University of California, Santa Barbara	Genomic basis for syntrophic interactions between anaerobic gut fungi and methanogenic archaea
Pires, J. Chris	University of Missouri-Columbia	Investigating the diversity of mycorrhizal fungi to understand the evolution and function of symbiosis with orchids
Plett, Jonathan	University of Western Sydney (Australia)	Exploring the genomic basis for the global diversification by the ectomycorrhizal genus *Pisolithus*
Poland, Jesse	Kansas State University	The Intermediate Wheatgrass Genome: A resource for understanding mechanisms of perenniality and accelerating the development of perennial crops
Rappe, Michael	University of Hawaii at Manoa	Metagenomics of viral and microbial communities inhabiting warm, anoxic fluids of the sediment-buried deep ocean crust
Schachtman, Daniel	University of Nebraska	Systems analysis of the physiological and molecular mechanisms of Sorghum nitrogen use efficiency, water use efficiency and interactions with the soil microbiome

Spatafora, Joey	Oregon State University	Genomics of the early diverging lineages of fungi and their transition to terrestrial, plant-based ecologies
Umen, James	Donald Danforth Plant Science Center	Single cell and population dynamics of chromatin across the diurnal cycle in the model alga *Chlamydomonas*
Walsh, David	Concordia University (Canada)	Microbial metagenomics of carbon cycling communities in northern aquatic ecosystems
Wrighton, Kelly	Ohio State University	Life in the extreme deep terrestrial subsurface: microbial metabolism before and after shale gas extraction

Small-Scale Proposals

Proposer	**Affiliation**	**Project Description**
Beman, J Michael	University of California, Merced	Metagenomics of methane production and oxidation in high altitude lakes of Yosemite National Park
Chistoserdova, Ludmila	University of Washington	Understanding methane cycling through manipulation of synthetic methane-oxidizing communities
Cullings, Ken	NASA Ames	Extreme endosymbiosis: An investigation into a unique fungal microbiome found in geothermal ecosystems in Yellowstone National Park and New Zealand
DeAngelis, Kristen	University of Massachusetts, Amherst	Expanding genomic diversity of terrestrial bacteria: linking genes to metabolism in the

		slower-growing members of forest soil bacterial communities
Kostka, Joel	Georgia Institute of Technology	The role of the Sphagnum microbiome in carbon and nutrient cycling in peatlands
McMahon, Katherine	University of Wisconsin-Madison	Reference genomes for abundant freshwater taxa – *Actinobacteria* and *Verrucomicrobia* phase 2
Meredith, Laura	Stanford University	Microbial, chemical, and physical drivers of COS fluxes and 18O-CO2 exchange rates in soils
Miller, Christopher	University of Colorado, Denver	Developing a systems-level understanding of biotic and abiotic controls on microbial methane cycling in freshwater wetlands
Redmond, Molly	University of North Carolina, Charlotte	Metagenomic sequencing of methane-oxidizing mesocosms from the Gulf of Mexico and Hudson Canyon
Rich, Jeremy	Brown University	Metagenomic sequencing of an uncultivated bacterial phylum in marine sediments amended with organic carbon and nitrate
Saito, Mak	Woods Hole Oceanographic Institution	Characterizing *Synechococcus* dominated populations from the Costa Rica dome and surrounding waters
Shade, Ashley	Michigan State University	Response and recovery of surface soil microbial communities to an ongoing underground coalmine fire
Simister, Rachel	University of British Columbia	Linking microbial genomic capacity to geochemical process in the deep terrestrial biosphere

Slonczewski, Joan	Kenyon College	Cyanobacterial communities of Antarctic Lake Fryxell liftoff mats and glacier meltwater
Tolar, Bradley	Stanford University	Monitoring the transcriptional response of a representative low-salinity ammonia-oxidizing thaumarchaeote to shifts in environmental conditions
Walsh, Davi	Concordia University	Metagenomics of western Arctic Ocean microbial communities
Wilkins, Michael	Ohio State University	Seasonal sulfur cycling as a control on methane flux in carbon-rich prairie pothole sediment ecosystems
Wrighton, Kelly	Ohio State University	Identifying key genomes and metabolisms responsible for near-surface methane cycling in freshwater wetlands

Synthesis Proposals

Proposer	Affiliation	Project Description
Chang, Jui-Jen	Biodiversity Research Center,Academia Sinica	Designer Operons-A biomimic approach to the regulation of an enzyme cocktail for an artificial enzyme complex
Chen, Brandon	Genomatica, Inc.	Engineering efficient methanol utilization for renewable chemicals
McCourt, Peter	University of Toronto	Exploring the perception landscape of the strigolactone receptor

Prather, Kristala	Massachusetts Institute of Technology	Combinatorial assembly, screening and functional characterization of a recombinant glucaric acid pathway in *S. cerevisiae*
Shen, Ben	The Scripps Research institute	Construction of bacterial artificial chromosome (BAC) vector libraries for comparative genomics, elucidation of gene functions and heterologous expression of targeted genes
Smanski, Mike	University of Minnesota	Towards a mechanistic understanding of disease suppressive soils: Refactoring natural product gene clusters
Wang, Clay	University of Southern California	Identification of fungal secondary metabolites with novel structures
Zimmer, Jochen	University of Virginia	Synthesis of cellulose synthase genes implicated in primary and secondary plant cell wall formation for structural and functional analyses of plant cellulose biosynthesis

FY 2016 Facilities Integrating Collaboration for User Science (FICUS) JGI-EMSL Plans

Proposer	**Affiliation**	**Project Description**
Bell-Pedersen, Deborah	Texas A&M University	Specialized Ribosomes: A New Frontier in Gene Regulation
Cardon, Zoe	Marine Biological Laboratory	3D Reality Check: Developing Structural Support for Predicting Microbial Function and Interpreting Microbial “Omics” Data

Doty, Sharon	University of Washington	Nitrogen fixation in *Populus*: Identification and localization of the key diazotrophs in planta
Duhaime, Melissa	University of Michigan	Building the phage-host-environment interaction data to scale from genes-to-ecosystems: Towards predictive modeling of wild microbial and viral community dynamics
Eastwood, Dan	Swansea University (UK)	Genomes to dynamic decay communities: Understanding fungal interactions during early decomposition events in natural lignocellulosic substrate
Neumann, Rebecca	University of Washington	A Rhizosphere-Scale Investigation of the Relationship Between Plant Productivity and Methane Emissions from Wetlands
Orphan, Victoria	California Institute of Technology	Fluorescence-based cell sorting and targeted proteomic analysis of active methane-oxidizing syntrophic consortia from environmental samples
Pan, Chongle	Oak Ridge National Laboratory	Integrated Omics Analyses of a *Populus* Pedigree for Crop Improvement