Approved Proposals FY15

Following are the approved user proposals for fiscal year 2015 including CSP and JGI-EMSL Collaborative Science Initiative projects.

FY 2015 Community Science Program (CSP) Plans

Proposer	Affiliation	Project Description
Baliga, Nitin	Institute of Systems Biology	Genome-wide analysis of chromatin accessibility and miRNA-mediated transcriptional regulation of lipid accumulation in *Chlamydomonas reinhardtii*
Banfield, Jill	University of California, Berkeley	Genome-resolved metagenomic analysis of microbial function in the subsurface
Banfield, Jill	University of California, Berkeley	Tree-driven diel microbial carbon dynamics in the vadose zone
Barrasa, Jose Maria	University of Alcala (Spain)	Study of the lignocellulolytic machinery in saprobic wood and leaf litter degrading Agaricales
Busby, Posy	University of Washington	Mechanisms of interaction in the foliar fungal microbiome of *Populus trichocarpa*

Cadillo-Quiroz, Hinsby	Arizona State University	Microbial composition and metagenomic functional potential across tropical peatlands: comparative evaluation and modeling of C decomposition to greenhouse gases
Campbell, Barbara	Clemson University	Biogeochemical cycling links between terrestrial and marine systems
Cavicchioli, Rick	University of New South Wales (Australia)	Seasonal variation in Antarctic microbial communities: ecology, stability and susceptibility to ecosystem change
Chistoserdova, Ludmila	University of Washington	Methane oxidation as a community function: defining partnerships and strategies through sequencing metagenomes and metatranscriptomes of laboratory manipulated microcosms
DiFazio, Steven	West Virginia University	Sex determination in the Salicaceae
Frank, Carolin	University of California, Merced	Diazotrophic aboveground endophytes in native pines, poplar and willow
Fredrickson, Jim	PNNL	Spatio-temporal functional profiling in model microbial communities
Hallam, Steven	University of British Columbia (Canada)	Microbial engines driving organic matter transformations in the dark

		ocean: an integrated biological and chemical perspective
James, Timothy	University of Michigan	Revealing the ecological function of uncultured fungal dark matter in freshwater ecosystems using single cell genomics
Klassen, Jonathan	University of Connecticut	Metagenomic mining of natural product diversity and understanding its contribution to ecosystem function in the cellulolytic fungus-growing ant symbiosis
Klenk, Hans-Peter; Goker, Markus	University of Newcastle (UK); DSMZ (Germany)	Exploiting the genomes of the Actinobacteria: plant growth promoters and producers of natural products and energy relevant enzymes united in a taxonomically unresolved phylum
Lamendella, Regina	Juniata College	Systems biology approach to fracking for environmental monitoring
Laudencia-Chingcuanco, Debbie	USDA-ARS	Creating a genome-wide sequence-indexed collection of grass mutants
Liu, Wen-Tso	University of Illinois	Shedding light on the anaerobic wastewater treatment “black-box” in anthropogenic carbon cycling: exploring the uncharted ecological function of uncultured microbial taxa through next-generation sequencing technology

Loper, Joyce	USDA-ARS	Exploring the genomic diversity of the *Pseudomonas fluorescens* group
Medina-Munoz, Monica	Penn State University	How do coral hosts communicate with their associated microbial community?
Peay, Kabir	Stanford University	Coprophilous fungi as a model system for understanding the metagenomics of carbon cycling in microbial eukaryote communities
Simon, Holly	Oregon Health & Science University	A systems approach to evaluate physical constraints and microbial controls on fluxes of nutrients and energy in a coastal ecosystem
Sorek, Rotem	Weizmann Institute of Science (Israel)	Comparative genomics of a single organism: In search of acquired immunity in trees
Swaminathan, Kankshita	University of Illinois	Understanding variance in allele specific expression in the polyploid Saccharinae
Thon, Michael	University of Salamanca (Spain)	Evolution and adaptation of carbohydrate utilization in the *Colletotrichum acutatum* species complex
Treseder, Kathleen	University of California, Irvine	Genomes and transcriptomes of decomposer fungi responding to warming in Alaskan boreal forest

Wildermuth, Mary	University of California, Berkeley	Comparative genomics of powdery mildews and associated host plants
Wosten, Han	Utrecht University (Netherlands)	Functional genomics of lignocellulose degradation by Agaricomycete fungi
Wurzbacher, Christian	IGB (Germany)	Whole genome sequencing of aquatic fungi responsible for the degradation of recalcitrant substrates in liquid environments
Young, Erica	University of Wisconsin	Metagenome and metatranscriptome of complex algal communities growing in wastewater: Bioremediation, nutrient transformation, carbon sequestration
Zhang, Baohong	East Carolina University	*Panicum virgatum* small RNA sequencing to identify gene expression changes related to biofuel traits

JGI-EMSL Facilities Integrating Collaborations for User Science (FICUS) Plans

Proposer	Affiliation	Project Description
Colwell, Frederick	Oregon State University	Integrated Biogeochemical Modeling of Microbial Consortia Mediating Anaerobic Oxidation of Methane in Dynamic Methane Hydrate-bearing Sediments

Crump, Byron	Oregon State University	Decoding DOM Degradation: How Does Carbon Source and Sunlight Exposure Alter Microbial Metabolism and Expression of Genome-Encoded Metabolic Degradation of Permafrost Organic Matter?
Cumming, Jonathan	West Virginia University	Mapping the Metabolism of Nutrient and Carbon Exchange in the Plant-Microbe Symbiosis
de Vries, Ronald	CBS-KNAW Fungal Biodiversity Centre	Dissecting Intraspecies Diversity in Fungal Wood Decay
DiChristina, Thomas	Georgia Institute of Technology	Sensing External Metals by Outer Membrane Beta-Barrel Proteins
Lebeis, Sarah	University of Tennessee	Uncovering the Composition and Function of the Aquatic Microbiome for Duckweeds
Luthey-Schulten, Zaida	University of Illinois at Urbana-Champaign	Quantifying Differential Expression and Identifying Bottlenecks in Methanogenic Pathways
Magnuson, Jon	Pacific Northwest National Laboratory	Elucidating the Influences of Engineered N-glycosylation Motifs in Bacterial Biomass Hydrolyzing Enzymes upon Heterologous and Native Gene Expression, Secretion and Degradation in *Aspergillus niger*
Rich, Virginia	University of Arizona	Systems-level Insights into Carbon Transformations in Thawing Permafrost by Parallel High-resolution Organic Matter and Microbial Community Characterizations
Stegen, James	Pacific Northwest	Coupling Microbial Communities to Carbon and Contaminant Biogeochemistry in the Groundwater-Surface Water Interaction Zone

	National Laboratory	
Vilgalys, Rytas	Duke University	Integrated Genomic/Transcriptomic/Secretomic Study of Plant-Fungal Interactions Between Pines and Their Symbiotic Ectomycorrhizal Fungi in the Mushroom Genus *Suillus*
Wrighton, Kelly	The Ohio State University	Microbial Controls on Biogeochemical Cycling in Deep Subsurface Shale Carbon Reservoirs