JGI JOINT GENOME INSTITUTE
A DOE OFFICE OF SCIENCE USER FACILITY

Approved Proposals FY11

Following are the approved user proposals for fiscal year 2011.

Community Science Program (CSP) Plans

Algae

Proposer	Affiliation	Organism
Kerfeld, Cheryl	DOE JGI	Genome and Transcriptome Analyses of Two Extremely Acidophilic and One Neutrophilic Eukaryotic Algal Species with Diverse Mechanism for CO2 Acquisition
Lovejoy, Connie	Laval University, Canada	Small planktonic single celled eukaryotes from the Arctic Ocean

Plants

Proposer	Affiliation	Organism
Muehlbauer, Gary	University of Minnesota	Whole genome shotgun sequencing of the barley genome

Vogel, John	USDA-ARS	Surveying natural diversity of the model grass *Brachypodium distachyon*

Fungi

Proposer	**Affiliation**	**Organism**
de Vries, Ronald	CBS-KNAW Fungal Biodiversity Centre, the Netherlands	Comparative analysis of Aspergilli to facilitate novel strategies in fungal biotechnology
Goodwin, Stephen	Purdue University	Sequencing of pathogens and extremophiles in the Dothideomycetes
Hibbett, David S.	Clark University	Community proposal to sequence a diverse assemblage of saprotrophic Basidiomycota (Agaricomycotina)
Jeffries, Thomas	Forest Products Laboratory	Yeasts of Biotechnological, Taxonomic and Physiological Interest
Martin, Francis	INRA, France	Exploring the Genome Diversity of Mycorrhizal Fungi to Understand the Evolution and Functioning of Symbiosis in Woody Shrubs and Trees
Pisabarro, Antonio	Public University of Navarre, Spain	Comparative transcriptomics pipeline for saprophytic basidiomycota
Pringle, Anne	Harvard University	Comparative transcriptomics of closely related saprotrophic and ectomycorrhizal *Amanita* species.
Spatafora, Joseph	Oregon State University	Phylogenomics and the origin and diversification of Kingdom Fungi

Turgeon, Gillian	Cornell University	Cochliobolus: expanded and deepened
Turk, Martina	University of Ljubljana, Slovenia	The varieties of the black yeast-like fungus *Aureobasidium pullulans*: evolution and use in biotechnology

Bacteria/Archaea

Proposer	**Affiliation**	**Organism**
Bertilsson, Stefan	Uppsala University, Sweden	Genome wide diversity and population genetics in uncultured aquatic bacteria: single cell genomics of the freshwater SAR11 group and the ubiquitous Actinobacteria ac1 lineage
Chistoserdova, Ludmila	University of Washington	Genomes of fifty methylotrophs isolated from Lake Washington
Eichorst, Stephanie	Los Alamos National Laboratory	Populating the branches of the Phylum Acidobacteria with relevant soil strains
Eisen, Jonathan	DOE JGI	Continuation of the Genomic Encyclopedia of Bacteria and Archaea pilot project
Kalyuzhnaya, Marina	University of Washington	Coupling function to genomics via single-cell phenotyping and genome sequencing
Liu, Wen-Tso	University of Illinois	Single cells genomics for uncultured Archaea dominating in a terrestrial subsurface aquifer abundantly containing methane

Sievert, Stefan	Woods Hole Oceanographic Institute	Shedding Light on the Dark: Single-cell Genomics of Uncultivated Epsilonproteobacteria Inhabiting the Subseafloor Biosphere at Deep-Sea Hydrothermal Vents
Stepanauskas, Ramunas	Bigelow Laboratory for Ocean Sciences	Generating reference genomes for marine ecosystem research: Single cell sequencing of ubiquitous, uncultured bacterioplankton clades
Tsiamis, George	University of Ioannina, Greece	Unraveling the unique microbial diversity of the Etoliko lagoon in Western Greece through a single cell genomics approach

Metagenomes

Proposer	**Affiliation**	**Organism**
Bryant, Donald	Penn State University	Metagenomic and metatranscriptomic analysis of anoxygenic, chlorophototrophic microbial mat communities in Yellowstone National Park
Campbell, Barbara	University of Delaware	Metagenomic and metatranscriptomic analysis of carbon cycling in Delaware coastal waters
Dionisi, Hebe	Patagonian National Research Center, Argentina	Microbial Community Structure and Metabolic Potential of Chronically Polluted Marine Sediments from Cold Regions of the Northern and Southern Hemispheres
Distel, Dan	Ocean Genome Legacy Foundation, Center for Marine Research	The complete shipworm microbiome: a comparative genomic and metagenomic analysis of lignocellulose-degrading microbial communities from multiple species of wood-boring bivalves.

Girguis, Peter	Harvard University	[Linking mantle to microbe: a community-wide effort to ally hydrothermal vent microbial identity and ecology to geochemical cycles via metagenomics]()
Hallam, Steven	University of British Columbia, Canada	[Microbial Systems Ecology of Expanding Oxygen Minimum Zones in the Eastern Subtropical North Pacific Ocean]()
Kerfeld, Cheryl	DOE JGI	[Metagenomic Sequencing for Understanding Microbial Carbon Cycling by Biological Soil Crusts of Arid Lands]()
Macalady, Jennifer	Penn State University	[Uncultivated and novel microbial lineages in terrestrial subsurface biofilms from a sulfidic aquifer]()
McMahon, Katherine	University of Wisconsin	[High-resolution temporal and spatial dynamics of microbially-mediated carbon processing revealed though time-series metagenomics in freshwater lakes]()
Moran, Mary Ann	University of Georgia	[Transcriptional analysis of a marine bacteria-phytoplankton binary model system]()
Muyzer, Gerard	Delft University of Technology, the Netherlands	[Metagenomics of microbial communities from soda lakes and soda solonchak soils]()
Tringe, Susannah	DOE JGI	[Microbial community impact on carbon sequestration in managed wetland “carbon farming”]()