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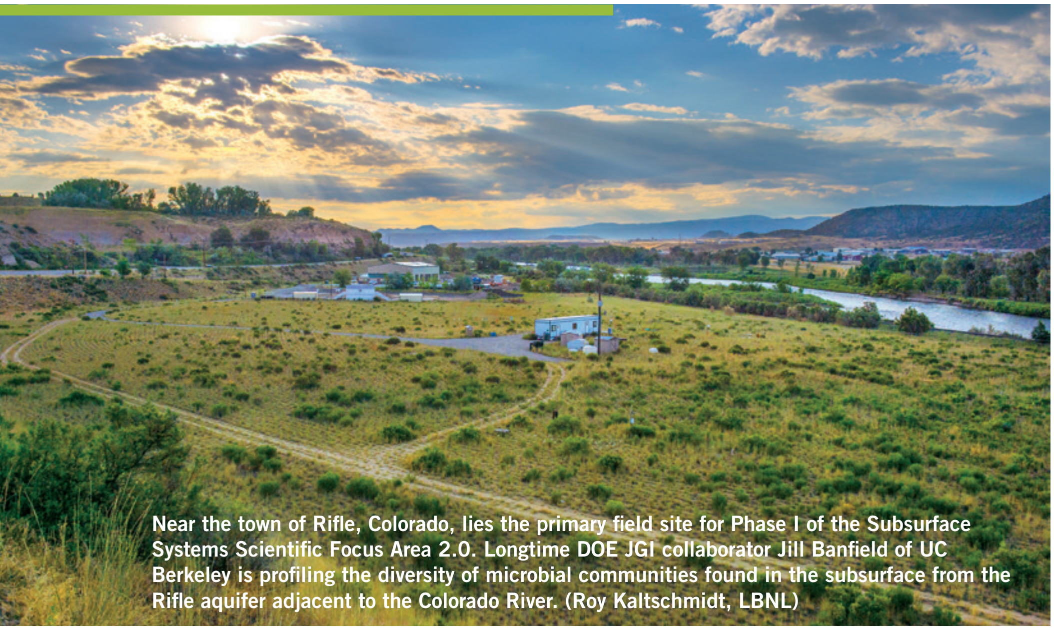
Delving Deeper into Earth's Data Mine:

2015 Community Science Program Portfolio Selected



Near the town of Rifle, Colorado, lies the primary field site for Phase I of the Subsurface Systems Scientific Focus Area 2.0. Longtime DOE JGI collaborator Jill Banfield of UC Berkeley is profiling the diversity of microbial communities found in the subsurface from the Rifle aquifer adjacent to the Colorado River. (Roy Kaltschmidt, LBNL)

The 32 projects selected for the 2015 Community Science Program (CSP) of the U.S. Department of Energy Joint Genome Institute (DOE JGI), a DOE Office of Science user facility, highlight diverse environments where DOE mission-relevant science can be extracted. These habitats range from sampling Antarctic lakes to Caribbean waters, and from plant root micro-ecosystems, to the subsurface underneath the water table in forested watersheds.

"These projects catalyze JGI's strategic shift in emphasis from solving an organism's genome sequence to facilitating an understanding of what this information enables organisms to do," said Jim Bristow, the DOE JGI Science Deputy who oversees the CSP. "To accomplish this, the projects selected combine DNA sequencing with large-scale experimental and computational capabilities, and in some cases include JGI's new capability to write DNA in addition to reading it. These projects will expand research communities, and help to meet the DOE JGI imperative to translate sequence to function and ultimately into solutions for major energy and environmental problems."

Among the CSP 2015 projects selected is one from Regina Lamendella of Juniata College, who will investigate how microbial communities in Marcellus shale, the country's largest shale gas field, respond to hydraulic fracturing and natural gas extraction. For example, as fracking uses chemicals, researchers are interested in how the microbial communities can break down environmental contaminants, and how they respond to the release of methane during oil extraction operations.

Some 1,500 miles south from those gas extraction sites, Monica Medina-Munoz of Penn State University will study the effect of thermal stress on the Caribbean coral *Orbicella faveolata* and

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DOE JGI, EMSL Select 2015 Collaborative Science Projects

The DOE JGI and the Environmental Molecular Sciences Laboratory (EMSL) accepted 12 projects submitted during the 2014 call for Collaborative Science Initiative proposals. The selected researchers will have access to the capabilities of both user facilities. They will also be able to generate datasets unique to these two facilities—beyond what could be generated by either facility by itself.

These projects fall within the second collaborative call by EMSL and the DOE JGI since the first in winter 2013. The collaborative call represents a unique

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The interaction between aspens, ectomycorrhizal fungi and plant growth promoting bacteria is the focus of a selected proposal from Jonathan Cumming of West Virginia University. (Image by Roy Kaltschmidt, LBNL)

Evidence of Selection on Poplar Genomes

To develop climate change simulations, researchers consider factors such as how plant ranges might shift, and how factors such as temperature, water availability, and light levels might come into play. Forests creeping steadily north and becoming established in the thawing Arctic is just one of the predicted effects of rising global temperatures.

A recent study published in the October 2014 print issue of *Nature Genetics* offers a more in-depth, population-based approach to identifying such mechanisms for adaptation, and describes a method that could be harnessed for developing more accurate predictive climate change models. For the U.S. Department of Energy, which is developing biomass crops for biofuels production, this knowledge could determine which genetic blueprints of a biomass crop may thrive better than others in certain environments. The team led by Gerald Tuskan of Oak Ridge National Laboratory and the DOE JGI and Stephen DiFazio of West Virginia University used a combination of genome-wide selection scans and analyses to understand the processes involved in shaping the genetic variation of natural poplar (*Populus trichocarpa*) populations.

As part of this long-term study, the team took samples from 1,100 poplar trees growing in wild populations in California, Oregon, Washington and British Columbia. They then clonally propagated (through cuttings) these trees in three plantations in California and Oregon. For their analyses, they pared the group down to 544 unrelated individuals whose genotypes could be accurately determined so as to characterize the genetic basis for variation in adaptation. The shift from an approach focused on single candidate genes to the large-scale computational approach analyzing all of them is made possible by the availability of the poplar genome, which was published in the journal *Science* in 2006 by the DOE JGI.

"This is the first time that deep genomics resources have ever been applied to an ecological question, in this case: 'What does selection do at the genome level?'" said Tuskan. "In the past, people looked at adaptation to factors such as temperature and light levels, and they examined variation in those genes as they vary across environmental gradients. There was a preconceived notion and a very narrow view of what was causing the response. Here, we took five major approaches, applied them blindly to the whole genome, and let the analysis show us where the fingerprints of selection are and what genes fall under those fingerprints."

Given the importance of poplar trees, not just for their role in the ecosystem, for instance, in capturing carbon, but also for their economic importance in fields ranging from timber to bioenergy, study first author Luke Evans of West Virginia University noted that the ability to have plantations of poplars through vegetative propagation is a significant tree-breeding tool for picking the appropriate stocks for the task. "If you know every base in a genome, you can skip whole generations and use genomic information to predict how well an individual will do," he said. "Plantations serve as the initial tests where you can take that genomic information and calibrate those predictions. With those reference points, you can scale everything."

Watch a video of Tuskan talking about poplar plantations and the importance of understanding genetic selection at http://bit.ly/Tuskan14fingerprints. Research made possible by the availability of the poplar genome has been presented at the DOE JGI Annual Genomics of Energy & Environment Meeting and can be viewed from http://usermeeting.jgi.doe.gov/past-meetings/.

Read the full story about the current study at http://jgi.doe.gov/signatures-selection-inscribed-poplar-genomes/.

Close-up of a poplar leaf bud. The team identified hundreds of genomic regions that contribute to adaptive traits for wild populations of poplars, such as how regional temperatures can affect the timing of spring bud flush and fall bud set. (DOE JGI)

Virus-Host Interactions in An Oxygen-Starved Inlet

Multicellular life needs dissolved oxygen in the water to thrive. In certain coastal areas, extreme oxygen-starvation produces “dead zones” that decimate marine fisheries and destroy food web structure. There are currently more than 500 oxygen minimum zones (OMZs) worldwide, encompassing roughly eight percent of ocean volume that is considered oxygen-starved. Microbial community metabolism in these oxygen-starved waters directly impacts nutrient and energy conversion processes, including the production and consumption of the greenhouse gases carbon dioxide, methane, and nitrous oxide.

In collaboration with the DOE JGI, University of British Columbia researcher Steven Hallam has been studying a microbial community dominated by SUP05 in a currently uncultivated group of microorganisms that thrive in the most oxygen-starved regions of the water column. Recent studies in British Columbia’s Saanich Inlet estimated that SUP05 bacteria could be responsible for as much as five percent of global primary productivity, making them key players in ocean carbon cycling.

In a study published online August 29, 2014 in the journal *eLife*, Hallam teamed up with another DOE JGI collaborator, Matt Sullivan of the University of Arizona, to investigate marine viruses infecting SUP05 to better understand how viral infection influences the bacteria’s ecology and metabolic potential.

In the study, the team collected several thousand individual bacterial cells from three depths spanning the Saanich Inlet oxygen gradient. Nearly 130 SUP05 single amplified genomes (SAGs) were recovered, sequenced, assembled, and annotated. Forty-two of the sequenced SUP05 SAGs were found to contain a total of 69 viruses representing five new genera.

“There’s a lot of microbial community sequence data out there, but it’s a lot harder to get the viral sequence data,” said Sullivan. “What we’ve done is leverage the microbial datasets being generated for microbial ecology and automate the process to be able to see the viruses in that data.”

Hallam noted that through the CSP program, his lab has been able to generate 340 human genome equivalents of time-resolved microbial, metagenome, and metatranscriptome data from OMZs. “That’s the largest data set in existence specifically focused on OMZs,” Hallam said.

Read the full story at http://jgi.doe.gov/decoding-virus-host-interactions-in-oxygen-starved-ocean/.

Saanich Inlet, a seasonally anoxic fjord on the coast of Vancouver Island in British Columbia, Canada, is a natural laboratory for studying OMZs. (Ocean Networks Canada via Flickr, CC BY-NC-SA 2.0)

Tagging Marine Viruses

The sheer volume of cyanobacteria in the oceans makes them major players in the global carbon cycle and responsible for as much as a third of the carbon fixed. However, marine viruses, up to 100 million of which can be found per 1 mL of seawater, outnumber them.

In another project with the DOE JGI, marine virologist Matt Sullivan set out to learn more about viral diversity and the viruses that are capable of drastically decreasing cyanobacterial populations, thus affecting the global regulation of biogeochemical cycles. They conducted a population-scale survey of cyanophages isolated from a single sample of water collected in Monterey Bay, Calif. using a game-changing new technique and the results appeared in the September 11, 2014 print edition of *Nature*.

“I often joke that viruses are only as interesting as their microbial hosts,” said Sullivan, “which makes cyanophages pretty important. Not only do they affect marine photosynthesis through mortality of cyanobacteria, but these viruses also encode photosynthesis genes — decade-old finding made in collaboration with JGI — that means cyanophages help drive global biogeochemical cycles that are crucial for running all kinds of energy conversions on the planet. The challenge for us, if we wanted to develop predictive capacity, was to develop a method that allowed us to simultaneously examine thousands (or more) of wild cyanobacterial viruses from the millions of non-cyanobacterial viruses in seawater — this would get us beyond learning about them one at a time.”

Sullivan’s team used a technique known as viral tagging, in which viruses and so-called “host bait” are stained with a fluorescent dye to find out with which hosts the phages associate. After screening for

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A project from Stanford University's Kabir Peay focuses on how fungal communities in animal feces decompose organic matter. His project has a stated end goal of developing a model system that emulates the ecosystem at Point Reyes National Seashore, where Tule elk are the largest native herbivores. (Matt Knoth via Flickr CC BY-NC-ND 2.0)

Brachypodium mutant with curly leaves and stems. A team led by USDA-ARS researchers will develop a genome-wide collection of several thousand mutants of the model grass *Brachypodium distachyon* to help domesticate the grasses that are being considered as candidate bioenergy feedstocks. (Richard Sibout, INRA)

the metabolic contribution of its coral host *Symbiodinium*. The calcium carbonate in coral reefs acts as carbon sinks, but reef health depends on microbial communities. If the photosynthetic symbionts are removed from the coral host, for example, the corals can die and calcification rates decrease. Understanding how to maintain stability in the coral-microbiome community can provide information on the coral's contribution to the global ocean carbon cycle.

Longtime DOE JGI collaborator Jill Banfield of the University of California (UC), Berkeley is profiling the diversity of microbial communities found in the subsurface from the Rifle aquifer adjacent to the Colorado River. The subsurface is a massive, yet poorly understood, repository of organic carbon as well as greenhouse gases. Another research question, based on having the microbial populations close to both the water table and the river, is how they impact carbon, nitrogen and sulfur cycles. Her project is part of the first coordinated attempt to quantify the metabolic potential of an entire subsurface ecosystem under the aegis of the Lawrence Berkeley National Laboratory's Subsurface Biogeochemistry Scientific Focus Area.

Banfield also successfully competed for a second CSP project to characterize the tree-root microbial interactions that occur below the soil mantle in the unsaturated zone or vadose zone, which extends into unweathered bedrock.

Several fungal projects were selected for the 2015 CSP portfolio. Among these projects is one from Timothy James of University of Michigan, who will explore the so-called "dark matter fungi"— those not represented in culture collections. By sequencing several dozen species of unculturable zoosporic fungi from freshwater, soils and animal feces, he and his colleagues hope to develop a kingdom-wide fungal phylogenetic framework.

Along similar lines is a project from Christian Wurzbacher of The Leibniz Institute of Freshwater Ecology and Inland Fisheries or IGB in Germany. His proposal involves characterizing fungi from the deep sea to peatlands to freshwater streams to understand the potentially novel adaptations that are necessary to thrive in their aquatic environments. The genomic information would provide information on their metabolic capabilities for breaking down cellulose, lignin and other plant cell wall components, and animal polymers such as keratin and chitin.

Many of the selected projects focus on DOE JGI Flagship Plant Genomes, with most centered on the poplar (*Populus trichocarpa*). Some projects focus on learning more about the interactions between the poplar tree and its fungal, non-pathogenic symbionts or endophytes. Other projects focus on candidate bioenergy grasses with gene expression studies of miscanthus and sorghum to understand how these plants recycle nutrients, and of the transcripts in switchgrass to find the variations associated with desirable biofuel traits such as increased biomass and responses to drought and salinity stressors.

Another group of projects focuses on better understanding how microbial communities in peatlands respond to rising temperatures. For example, Kathleen Treseder of UC Irvine will study genes involved in sensitivity to higher temperatures in fungi from a warming experiment in an Alaskan boreal forest. The team's plan is to fold the genomic information gained into a trait-based ecosystem model called DEMENT to predict carbon dioxide emissions under global warming. In contrast, Hinsby Cadillo-Quiroz at Arizona State University will conduct a study of the microbial communities in the Amazon peatlands to understand their roles in both emitting greenhouse gases and in storing and cycling carbon. The peatlands are hotspots of soil organic carbon accumulation, and in the tropical regions, they are estimated to hold between 11 percent and 14 percent, or nearly 90 gigatons, of the global carbon stored in soils.

The CSP 2015 projects were selected by an external review panel from 76 full proposals received that resulted from 85 letters of intent submitted. The total allocation for the CSP 2015 portfolio is expected to exceed 60 terabases (Tb) — or the equivalent of 20,000 human genomes of plant, fungal and microbial genome sequences. The full list of projects may be found at http://jgi.doe.gov/our-projects/csp-plans/fy-2015-csp-plans/.

Previous CSP projects and other DOE JGI collabora-

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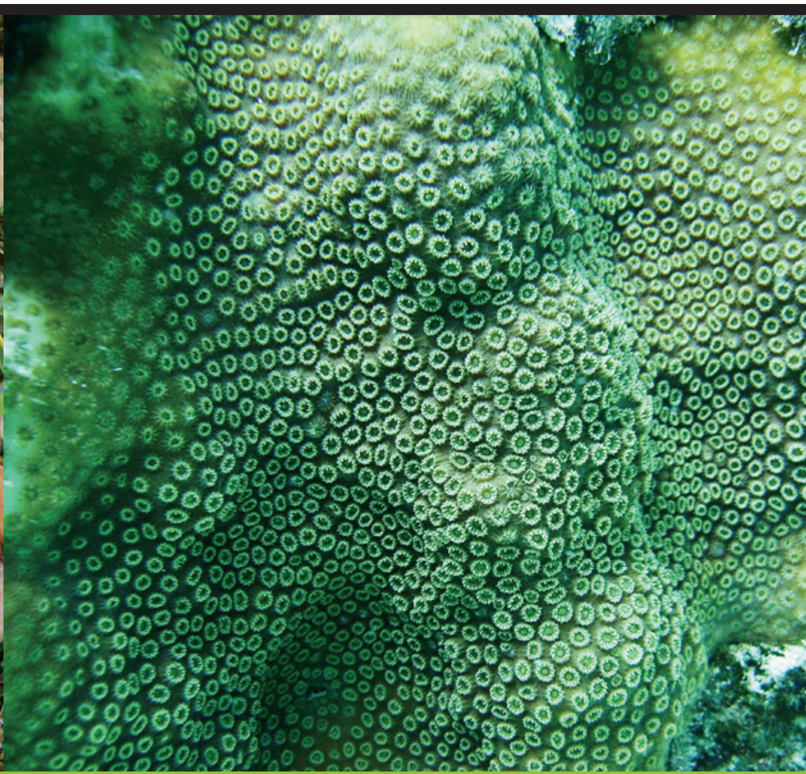
Jose Maria Barrasa of Spain's University of Alcala proposed a focused study of *Agaricales* fungi. Shown here are representative lifestyles in *Agaricales*. Images A and B depict leaf litter degrading species growing in forest (*Lepista nuda*) and meadow (*Agrocybe pediades*) habitats, respectively. Image C is of a wood decaying species (*Gymnopilus junonius*). Image D is of a buried wood decaying species (*Gymnopus fusipes*). (Jose Maria Barrasa, Universidad de Alcala)



Coral reefs are threatened tropical marine ecosystems whose fundamental unit is the reef building coral. The calcium carbonate in coral reefs acts as carbon sinks, but reef health depends on microbial communities. Monica Medina-Munoz of Penn State University will study the effect of thermal stress on the Caribbean coral *Orbicella faveolata* or boulder coral and its holobiont microbiome. This is a close-up view of boulder coral polyps. (Image courtesy of The Ohio State University.)

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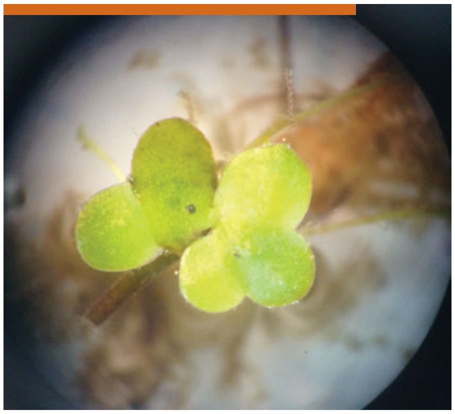
opportunity for researchers to combine the power of genomics and molecular characterization in one research project to help advance the missions of the Department of Energy's Office of Biological and Environmental Research (BER). BER, which is within DOE's Office of Science, stewards both EMSL and the DOE JGI, and both user facilities play critical roles in supporting DOE's energy, environment and basic research missions.

"These approved projects represent an excellent cross-section of research in biogeochemistry, carbon cycling and biofuel/bioproduct production," said Scott Baker, EMSL's Science Theme Lead for the Biosystem Dynamics and Design. "It's very exciting to continue our collaboration with JGI and I look forward to the insights and impact these projects will produce."

Researchers submitted a total of 31 proposals during the call. The 12 approved projects will kick off in fiscal year 2015 and run for up to 18 months.

Learn more about the accepted projects at http://jgi.doe.gov/jgi-emsl-announce-2015-collaborative-science-projects/.

A DOE JGI-EMSL Collaborative Science Program project proposed by Byron Crump of Oregon State University looks at the effects of sunlight on the metabolic rates of microbes responding to thawing permafrost. This image of coastal erosion reveals the extent of ice-rich permafrost underlying active layer on the Arctic Coastal Plain in the Teshekpuk Lake Special Area of the National Petroleum Reserve in Alaska. (Brandt Meixell, USGS via Flickr, CC BY-2.0)



One of the selected 2015 DOE JGI-EMSL projects comes from Sarah Lebeis at the University of Tennessee. She is interested in studying the effects of bacteria co-cultivation on health of duckweed (*Lemna minor*) strains. For example, duckweed treated with bacteria has been shown to have a higher chlorophyll content compared to untreated duckweed. (Jon Sullivan via Flickr, CC BY-NC 2.0)

Tagging Marine Viruses

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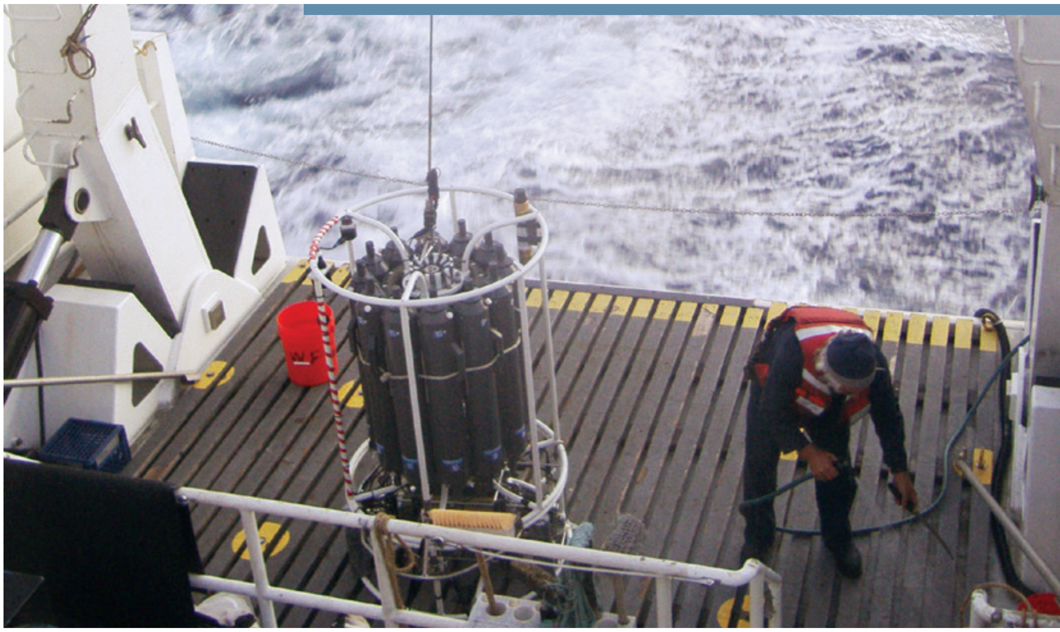
cyanophages that were tagged as being associated with a single *Synechococcus* strain, samples of the viral community metagenomes were sent to the DOE JGI for sequencing as part of a Community Science Program project proposed by Sullivan.

The novel finding here isn't the number of viruses, but rather the structured nature of the populations," Sullivan said. "With these discrete populations in a complex natural community and the genome sequence information linked to each population, we are generating hypotheses on what might be driving particular population-host interactions and the abundances of particular populations—that's viral ecology.

Learn more about the viral tagging method at http://jgi.doe.gov/dyeing-learn-marine-viruses/

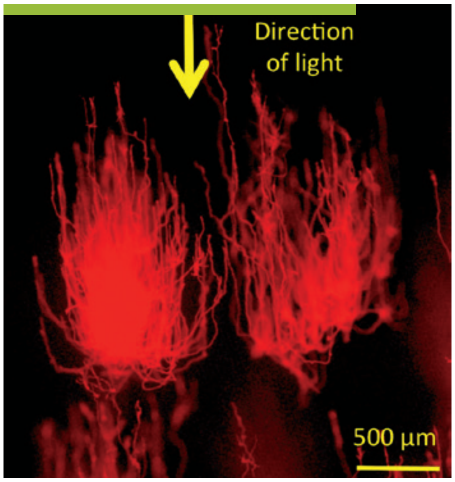


The CTD instrument was used to measure salinity, temperature, and depth, as well as collect samples for microbial and viral analysis on the back of the R/V Western Flyer. The Sullivan lab's sampling trip to Monterey Bay, Calif. was made possible by MBARI's Alex Worden and the CANON initiative. (Li Deng, University of Arizona)

Science Highlights

Far-Red Light Makes Far-Reaching Algal Changes

Marine cyanobacteria such as *Prochlorococcus* and *Synechococcus* are known to be responsible for more than a quarter of the net primary productivity in oceans, but terrestrial cyanobacteria also contribute significantly to global photosynthesis. In a study published online August 21, 2014 in the *Science Express* edition of *Science*, a team led by Penn State University's Don Bryant, a longtime DOE JGI collaborator, has found a strain of cyanobacteria in hot springs that utilizes wavelengths of sunlight that neither humans nor cyanobacteria can see to conduct photosynthesis. Known as JSC-1, the strain of *Leptolyngbya* cyanobacteria isolated from a floating microbial mat at LaDuke hot spring near Yellowstone National Park in Montana was sequenced as part of a DOE JGI Community Sequencing Program project.

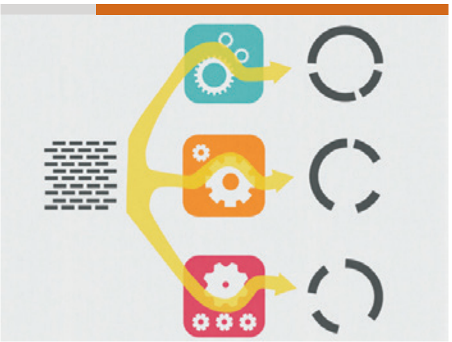


Fluorescence image of microcolonies of the *Leptolyngbya* sp. strain of cyanobacteria cells (JSC-1) collected from a hot spring near Yellowstone National Park. The image shows that the cells grow towards the light provided from above only. (Image courtesy of Bryant Lab)

To convert sunlight into energy-rich compounds, cyanobacteria primarily rely on three complexes known as Photosystem I (PS I), Photosystem II (PS II), and phycobilisomes (PBS). The team found that JSC-1 demonstrates what is called Complementary Chromatic Acclimation, in which the cyanobacteria changes color in response to the color of the light in order to maximize its photosynthetic yield. As part of the study, they grew JSC-1 under white fluorescent light, green-filtered fluorescent light, red-filtered fluorescent light, far-red light, and two wavelengths that simulate the solar irradiance reaching Earth's surface. They found that when JSC-1 shifts from growing under white light to growing under far-red light, more than 40 percent of its genome responds by making changes to boost photosynthetic efficiency. Most of the core proteins of PS I and PS II are replaced, and there are structural changes to PBS core substructures. The team referred to this response as "Far-Red Light Photoacclimation" or FaRLiP.

"This enhanced photosynthetic performance in [far-red light] would be ecologically significant … for example, in mats, stromatolites, cyanobacterial blooms, or in the shade of plants," the team reported. "FaRLiP should also benefit organisms living in sandy soils, because far-red light penetrates deeper than visible wavelengths.… Thus, FaRLiP could have a significant impact on cyanobacterial photosynthesis in soil crusts."

Automating Genome Assembler Selection



DOE JGI bioinformaticist Michael Barton has been developing a public repository of genome assemblers called nucleotid.es to help the DOE JGI team select a genome assembler for sequencing projects in process. "A lot of assemblers are being produced in the bioinformatics community, and instead of reading subjective papers with assemblers, you can test the assemblers for yourself," Barton said, "with the added benefit of having reproducible research so that anyone can produce the results." Learn more at http://jgi.doe.gov/automating-selection-process-genome-assembler/.

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tions are highlighted in some of the DOE JGI Annual User Meeting talks that can be seen at http://usermeeting.jgi.doe.gov/past-speakers/. The 10th Annual Genomics of Energy and Environment Meeting will be held March 24-26, 2015 in Walnut Creek, Calif. Registration will open the first week of November at http://usermeeting.jgi.doe.gov/.

The DOE JGI Community Science Program also accepts proposals for smaller-scale microbial, resequencing and DNA synthesis projects and reviews them twice a year. The CSP advances projects that harness DOE JGI's capability in massive-scale DNA sequencing, analysis and synthesis in support of the DOE missions in alternative energy, global carbon cycling, and biogeochemistry.

A Visit from the Bangladesh Agriculture Minister

On September 3, 2014, Matia Chowdhury, Honorable Minister of Agriculture of the People's Republic of Bangladesh, visited the DOE JGI to explore possible collaborations in the area of plant genomics. Ms. Chowdhury was joined by Maqsudul Alam, Professor and Chair of the Department of Microbiology, University of Hawaii and Principal Investigator of the Basic and Applied Research on Jute Project, and by Monjurul Alam, Senior Program Manager of National Jute Genome Project. Jute is the plant that is used to make burlap and is one of the most affordable natural fibers and is second only to cotton in the amount produced. Bangladesh and India account for about 95 percent of the world jute production. The delegation is in the process of developing the Bangladesh Agri-Genome Center and met with DOE JGI leadership to learn about emerging genomic science and technologies, and about the lessons that the DOE JGI has learned over its 15-year history. The Bangladeshi contingent was organized and joined by Los Alamos National Laboratory researchers and former DOE JGI staff Chris Detter and David Bruce.

In the foreground (left to right), DOE JGI's Sequencing Platforms Team lead Chris Daum shows off the Pacific Biosciences SMRT cell technology to Monjurul Alam, Senior Program Manager of National Jute Genome Project, Ms. Matia Chowdhury, Honorable Minister of Agriculture of the People's Republic of Bangladesh and Maqsudul Alam, Principal Investigator of the Basic and Applied Research on Jute Project. In the background, Bangladeshi-DOE JGI visit organizers David Bruce (left) and Chris Detter of Los Alamos National Laboratory.

Scientific Achievement Awards for DOE JGI Staff

Among the 2014 recipients of the Lawrence Berkeley National Laboratory Director's Award for Exceptional Achievement are the DOE JGI's Tanja Woyke and Axel Visel.

Woyke is the Microbial Program Head while Visel is the Science Lead of Strategic Planning. Both were individually recognized in the Scientific category for "significant scientific or technical contribution leading to important progress in an area of research or toward completion of a project." All of the awardees were recognized at a ceremony held on September 29, 2014.

We invite you to join us at the

10TH ANNUAL

DOE Joint Genome Institute Genomics of Energy & Environment Meeting

March 24-26, 2015 in Walnut Creek, CA
Registration opens November 6 at
usermeeting.jgi.doe.gov

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