THE PRIMER

JGI
JOINT GENOME INSTITUTE
DEPARTMENT OF ENERGY

winter 2014
volume 11
issue 1


Mimulus guttatus (Image courtesy of James Gaither)

in this issue

A Barrel of Monkey Flowers — Model Plant's Genome Holds Surprising Legacy

Genomic variation is a feature of all natural populations and is vitally important in order to survive changes in their environments. Genetic variation among individuals, to which DNA recombination is an important contributor, is passed from parents to offspring and helps explain that different individuals in the population may harbor a diverse set of traits. Understanding and characterizing this variation requires both appropriate model organisms and a considerable amount of sequencing capacity, of the scale that the DOE Joint Genome Institute can handle.

Published the week of November 11, 2013, in the journal *Proceedings of the National Academy of Sciences* (PNAS) (http://bit.ly/1bmKbFI), a group of researchers led by the DOE JGI completed a draft sequence of the monkey flower *(Mimulus guttatus)* genome and identified the historic footprints of DNA recombination events that have shaped the development of this plant species over the last several hundred thousand years. By extension, these observations should inform new plant breeding strategies that could be vitally important to developing improved bioenergy plant feedstocks.

The genus *Mimulus* is commonly known as the monkey flower because of its resemblance to a scrunched up monkey face (*Mimulus* derives from the Latin term for "mime"). The flower is a near cousin to the oft-domesticated snapdragon.

Uffe Hellsten, an astrophysicist-turned computational scientist in the Plant Genomics Group at the DOE JGI and first author on the PNAS paper said that he and his colleagues traced some 400,000 events that took place within a wild population of *Mimulus*.

Recombination events in monkey flower (and plants in general, the team presumed) work the same way they do in yeast but unlike those in mammals, where hot spots are heavily influenced by the presence of binding sites for a particular recently evolved

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Community Science Program partners with EMSL for first time in 2014

For the latest round of the Community Science Program (formerly the Community Sequencing Program), the DOE JGI has joined forces with the Environmental Molecular Sciences Laboratory (EMSL) at the Pacific Northwest National Laboratory to provide complimentary scientific resources to significantly expand genomic understanding to cellular function. This new effort and program name reflect DOE JGI's vision of serving the scientific community as a next-generation genome science user facility. The inaugural round of eight accepted proposals showcases the synergy between these two DOE user facilities, in addition to 29 other CSP 2014 projects.

Five of the eight new DOE JGI-EMSL proposals focus on carbon cycling, and three relate to improvements in biofuels production. Each of these projects will tap the capabilities at both facilities to further the research in ways that would not otherwise be possible, and all should be complete within 18 months.

Two of the carbon cycling projects focus on soil microbial communities. Mary Firestone from the University of California, Berkeley, will study the plant-soil-microbial interactions of the annual grass *Avena fatua* with soil from a

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A Bacterial "Conversation" in a Cold and Salty Antarctic Lake

Sequestered in Antarctica's Vestfold Hills, Deep Lake became isolated from the ocean 3,500 years ago by the Antarctic continent rising, resulting in a saltwater ecosystem that remains liquid in extreme cold, and providing researchers a unique niche for studying the evolution of the microbes that now thrive under such conditions. Deep Lake's microscopic inhabitants are dominated by haloarchaea, microbes that require high-salt concentrations to grow and are naturally adapted to conditions — at minus 20°C — that would prove lethally cold to other organisms. In a detailed analysis (http://bit.ly/JIBhfA) published online the week of September 30, 2013, in the journal *Proceedings of the National Academy of Sciences* (PNAS), researchers have, for the first time, been able to get a complete ecological picture of the Deep Lake microbial community.

A team led by Rick Cavicchioli of the University of New South Wales, Australia, partnered with the U.S. Department of Energy Joint Genome Institute (DOE JGI) to generate sequence data from DNA isolated from individual microbes and compared them with metagenomic (microbial community) information sampled at various depths of Deep Lake.

"Understanding how haloarchaea can thrive in Deep Lake could be used to develop engineering concepts for reducing energy costs in a variety of situations, such as for cleaning up contaminated sites in permanently or seasonally cold regions," Cavicchioli said. Owing to the ability of salt-loving enzymes to function under extremes, he suggests they could also be used as catalysts for peptide synthesis and enhanced oil recovery, and can function in water-organic solvent mixtures. "These enzymes will be especially useful for transforming contaminated sites with particularly high levels of petroleum-based products," he added.

Deep Lake's extremes have rendered the microbial neighborhood rather homogeneous. Four isolates in the study represented about 72 percent of the cells in the community. Though gene exchange across species boundaries is considered infrequent, the researchers observed that haloarchaea living in the Lake's hypersaline environment practice it comparatively often, like neighbors "chewing the fat" in a small-town coffee klatch. "It's intriguing that while gene exchange is rampant, species lineages appear to be maintained by virtue of each species having a high level of specialization, enabling niche partitioning and peaceful coexistence," said Cavicchioli of their findings. "Haloarchaea are known for being 'promiscuous,' that is, prone to exchanging DNA between themselves. Our study demonstrated that this exchange occurs at a much higher level than has previously been documented in nature. They communicate, share, specialize, and coexist."

What distinguishes this "conversation" is that the haloarchaea of Deep Lake exchange the information of DNA not just between species but among distinct genera, and moreover in huge tranches, some 35,000 letters of code, with not a letter out of place.

Cavicchioli noted that "as the content being shifted around lack core genes, it speaks to these microbes' ability to be flexible and collaborative. This shuttled gene content could confer such benefits as resistance to viruses or bolstering their ability to respond to specific environmental factors. Moreover, the markers that we analyzed indicated that a high level of gene exchange occurs throughout the Deep Lake community."

"Every time we 'poke an omics stick' in there we find things we never expected," Cavicchioli said. "Each lake also has its own unique characteristics, so there is a lot more to be discovered."


Deep Lake as an expedition work site in November 2008, shown with mobile work shelters and equipment for sampling (Image courtesy of Rick Cavicchioli)

Codependence Between Plants and an Ancient Fungal Scavenger

Glomeromycota is an ancient lineage of fungi that has a symbiotic relationship with roots that goes back nearly 420 million years to the earliest plants. More than two-thirds of the world's plants depend on this soil-dwelling symbiotic fungus to survive, including critical agricultural crops such as wheat, cassava, and rice. Analysis of the *Rhizophagus irregularis* genome has revealed that this asexual fungus doesn't shuffle its genes the way researchers expected. Moreover, rather than having lost much of its metabolic genes, as observed in many mutualistic organisms, it has expanded its range of cell-to-cell communication genes and phosphorus-capturing genes.

A team led by the French National Institute for Agricultural Research (INRA) and including researchers from the Department of Energy Joint Genome Institute (DOE JGI) reported the complete genome of *R. irregularis* (formerly *Glomus intraradices*) in a paper published online November 25 in the journal *Proceedings of the National Academy of Sciences* (*PNAS* http://bit.ly/PNAS-Glomus). The fungus is a member of the Glomeromycota family, a group often called arbuscular mycorrhizal fungi (AMF).

A relic of fungal evolution, AMF diverged early on from other forms of fungus. They form dense clusters of branched structures — called arbuscules —- in root cells, much like a tight, many-fingered handhold. The arbuscules are the main route of nutrient exchange between plants and fungi. Unable to live on their own, AMF are entirely dependent on their plant hosts for the sugars they need for food.


Spores and hyphae (root-like extensions) of an AMF, *R. irregularis*, grown among carrot hairy roots. (Image courtesy of Guillaume Bécard, University of Toulouse)

But AMF are also adept at capturing phosphorus from the soil and making it available for their hosts. Phosphorus, a critical element for cellular function, is otherwise difficult to extract from the soil and is often the limiting factor for how quickly a plant grows.

Scientists theorize that the benefits these fungi provided enabled ancient plants to evolve during the Paleozoic era, about 250 to 500 million years ago. Over time, plants adapted their essentially rootless primordial form and developed deeper and stronger roots to take advantage of the nutrients that underground AMF fed them.

The research team found that the genome is among the largest fungal genomes sequenced, weighing in at 153 million base pairs (Mb). For comparison, the button mushroom (*Agaricus bisporus*), also sequenced and published by the DOE JGI, has a genome of about 30 Mb. Through several generations, portions of *R. irregularis's* genome were duplicated, invaded by repeated transposable elements, famously known as "jumping genes." Unlike many other fungi, *R. irregularis* seems to lack mechanisms that can keep these transposable elements from running amok.

Among the expanded portions of its genome, *R. irregularis* had several genes for phosphorus metabolism and communication between cells via signaling proteins. Another surprise for the research team was in the genes that govern metabolism. "Obligate parasites often have broken metabolism, missing some genes in critical metabolic pathways which make them dependent on their host," said Igor Grigoriev, lead for JGI's Fungal Genomics Program. "We did not find such genes here." *R. irregularis* has retained much of its metabolic machinery, unlike many other obligate parasitic organisms.

Teasing apart the complex relationship between soil fungi and plants is likely to have an impact on improving biofuel production from plant biomass. "Through analysis of this and other mycorrhizal genomes, we can help to better understand interactions and conditions critical for a sustainable growth of bioenergy plants, but also staple crops, a prerequisite to help feeding the world," said Francis Martin of the French National Institute for Agricultural Research (INRA) and one of the senior authors of the paper.

Watching Cyanobacteria Assemble Their "Engines"

Cyanobacteria, found in just about every ecosystem on Earth, are one of the few bacteria that can create their own energy through photosynthesis to "fix" carbon — from carbon dioxide molecules — and convert it into fuel inside miniscule compartments called carboxysomes. Two recent JGI studies focused on exploring these mysterious "black boxes" that cyanobacteria use to generate their energy.

Although cyanobacteria are often called blue-green algae, that name is a misnomer since algae have complex membrane-bound compartments called organelles — including chloroplasts — which carry out photosynthesis, while cyanobacteria, like all other bacteria, lack membrane-bound organelles. Much of their cellular machinery — including their DNA — floats in the cell's cytoplasm unconstrained by membranes. However, they do have rudimentary microcompartments where some specialized tasks happen.

Looking a lot like the multifaceted envelopes of viruses, carboxysomes are icosahedral, having about 20 triangle-shaped sides or facets. They contain copious amounts of ribulose 1,5 biphosphate carboxylase oxygenase (commonly called RuBisCo), an extremely abundant but slow enzyme required to fix carbon, inside their protein shells.

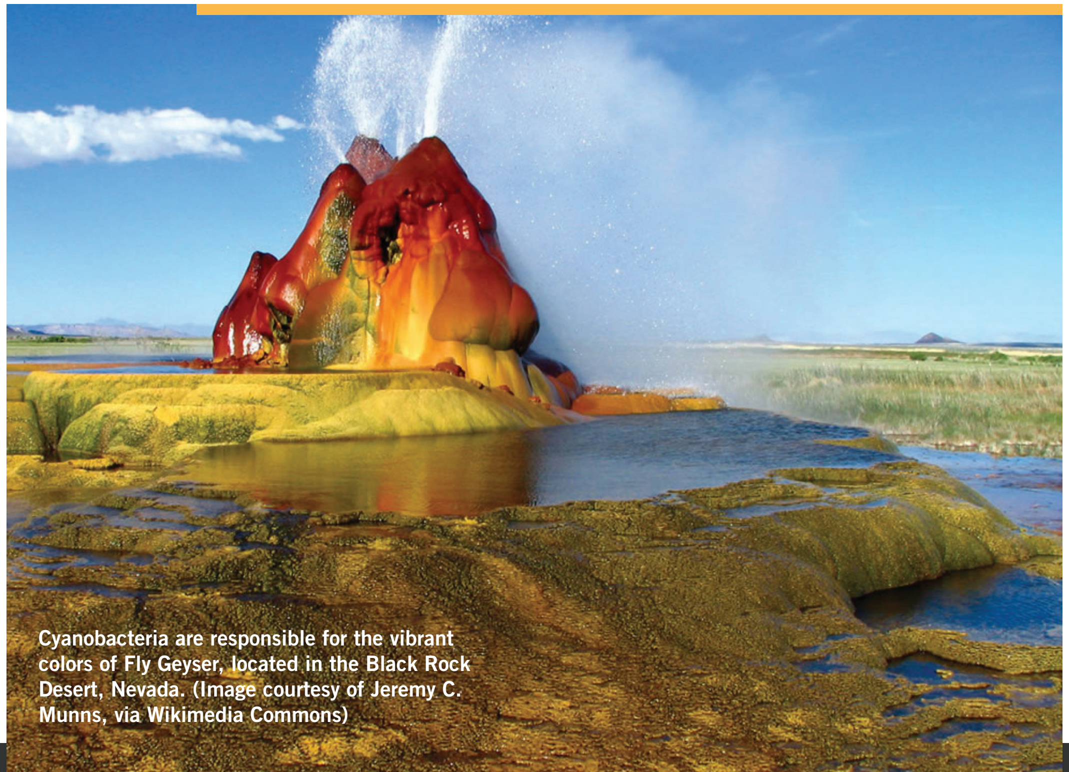
Senior author Cheryl Kerfeld, formerly with JGI and now at Michigan State University and UC Berkeley, and her team used a pioneering visualization method to make what are, in effect, movies of this complex and vital cellular machinery being assembled inside living cells. They observed that bacteria build these internal compartments in a way never seen in plant, animal, and other eukaryotic cells.

"The carboxysome, unlike eukaryotic organelles, assembles from the inside out," said Kerfeld. The findings (http://bit.ly/1c8g6hO) were published on November 21, 2013, in the journal *Cell*.

The microcompartment also helps concentrate carbon dioxide and corral it near RuBisCo, while locking out oxygen, which otherwise tends to inhibit the chemical reactions involved in carbon fixation. It's the first time scientists have been able to watch bacterial organelles as they are built by living cells. Kerfeld noted that the filming technique is a major advance over previous methods. First author Jeffrey Cameron devised a way to knock out genes responsible for creating the building blocks of carboxysomes. He then introduced fluorescent-marked versions of those building blocks and took time-lapse digital images of the bacteria as they built carboxysomes from scratch. TEM microscopy was used to get detailed images of intermediate steps in carboxysome assembly.

Previously, in partnership with Sam Deutsch of JGI and the Advanced Light Source at the Lawrence Berkeley National Laboratory, Kerfeld's team cleared up a debate among researchers about the role of a key carboxysome shell protein called Ccml, upholding the theoretical structure of carboxysomes. Other research had suggested that Ccml had a different shape than expected and didn't behave in the way scientists thought it did. The study (http://bit.ly/19YI2Sc) was published online, on August 15, 2013, in the journal *Photosynthesis Research*.

Because they are so abundant, cyanobacteria play a major role in the Earth's carbon cycle, the movement of carbon between the air, sea, and land. "A significant fraction of global carbon fixation takes place in carboxysomes," said Kerfeld. Cyanobacteria, along with plants, impact climate change by lowering the amount of carbon from the atmosphere and depositing it in organic matter in the ocean and on land. Understanding carbon fixation in cyanobacteria contributes to our understanding of how this ubiquitous organism affects the global carbon cycle.



Cyanobacteria are responsible for the vibrant colors of Fly Geyser, located in the Black Rock Desert, Nevada. (Image courtesy of Jeremy C. Munns, via Wikimedia Commons)

CSP Program

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California grassland, a model ecosystem for further exploration of the rhizosphere, the soil and microbial community around plant roots. Kirsten Hofmockel from Iowa State University will combine the DOE JGI's high-throughput sequencing capabilities and EMSL's cell-sorting technologies to conduct a large-scale comparative analysis of soil microbial communities.

Marc Libault of the University of Oklahoma and his team will study a single-cell model, the root hair cell, to advance our understanding how the soybean and sorghum transcriptome and epigenome responds to various environmental stresses.

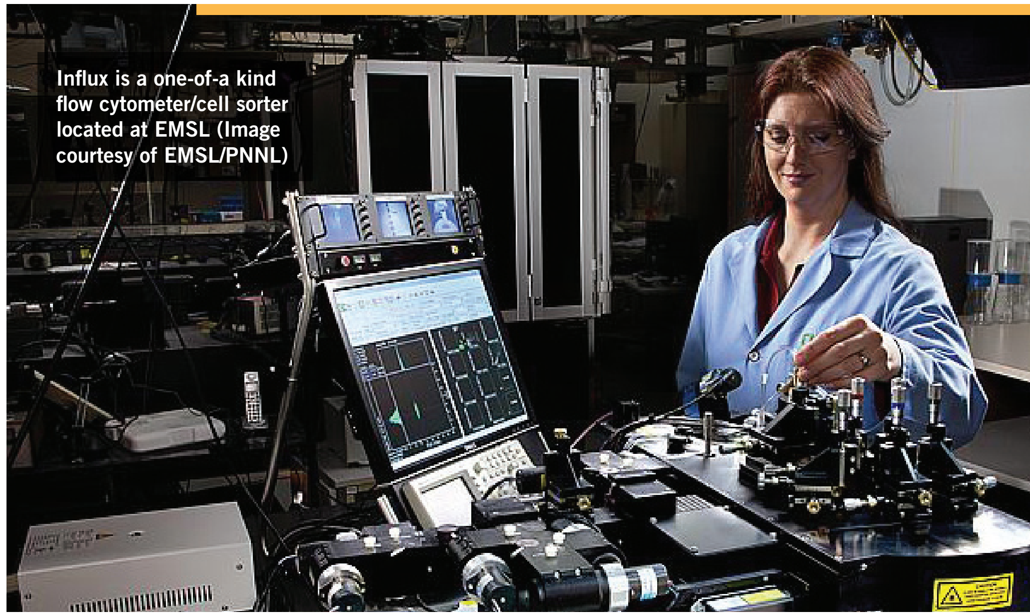
Two other carbon cycling projects involve the study of cyanobacteria. Matthias Hess at Washington State University – Tri-Cities will build on the DOE JGI's pioneering work in filling the gaps in the tree of life through the Genomic Encyclopedia of Bacteria and Archaea (GEBA) pilot project (http://www.jgi.doe.gov/programs/GEBA/) and a recent spin-off focused specifically on cyanobacteria (http://1.usa.gov/19CXINp) to better understand photosynthetic microbial communities and their central role in carbon and nitrogen cycling. Philip Weyman of the J. Craig Venter Institute will study the interactions between the *Pleurocarpous* feathery moss and cyanobacteria found in boreal forests. Since these ecosystems are enormous carbon sinks, their health and productivity is of vital importance to monitoring and moderating future increases in CO_2.

Colleen Hansel at the Woods Hole Oceanographic Institution will focus on a family of wood-degrading fungi known as Ascomycetes, which include molds and mildews.

Three projects focus on fungi's role in improving biofuel production. Steve Harris from the University of Nebraska-Lincoln will build upon previous DOE JGI sequencing of the industrially important filamentous fungi *Aspergillus niger* and *Trichoderma reesei*. Michelle O'Malley from the University of California, Santa Barbara, builds from a previous DOE JGI project, one that characterized the microbial communities in the cow rumen. In this new proposal, however, the researchers will target anaerobic fungi in communities isolated from large herbivores (elephant, giraffe, goat, horses, and sheep) that are involved in breaking down plant biomass.

Finally, Harold Kistler from the U.S. Department of Agriculture – Agricultural Research Service will focus on finding ways to efficiently and abundantly produce compounds known as terpenoids in filamentous fungi in order to evaluate them as renewable biofuels.

To learn more about the 2014 Community Science Program, visit http://1.usa.gov/17vfQri.

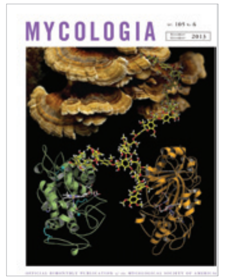


Influx is a one-of-a kind flow cytometer/cell sorter located at EMSL (Image courtesy of EMSL/PNNL)

CSP 2014 Projects Announced

The U.S. Department of Energy Joint Genome Institute (DOE JGI) 2014 Community Science Program portfolio seeks to parse functional information extracted from complex ecosystems to address urgent energy and environmental challenges. These massive, data-intensive undertakings require interdisciplinary approaches. Twenty-nine proposals, in addition to the eight that will rely on joint expertise of JGI and the Environmental Molecular Sciences Laboratory (EMSL) at the Pacific Northwest National Laboratory, have been selected to be carried out entirely at DOE JGI.

All 37 projects selected by an external review panel out of 123 full proposals reflect the emphasis on collaboration between researchers and the potential of further expanding research communities working on these topics. The full list of projects that make up the CSP 2014 portfolio may be found at http://bit.ly/CSP14-list. For more information about both CSP calls for proposals, go to http://www.jgi.doe.gov/CSP/index.html



Fungus family dynamics

The Polyporales family of fungi is a diverse group, mostly made up of wood-rotters. As such, they are important to the global carbon cycle. Many members of this group are highly efficient at decaying lignin (part of the tough cell wall that protects plant cells). But understanding the evolutionary relationships between different species and genera in this group has been challenging.

In a paper (http://bit.ly/1dTRKqy) published in the November/December 2013 issue of *Mycologia* as part of a special section on Polyporales, researchers compared both methods. The team, led by Manfred Binder of Clarke University, used the 10 available whole genomes of Polyporales members and compared them to all known genes from this family. This analysis yielded new details about the evolutionary relationships between species, which they detailed in several phylogenetic trees of several clades.

Bioremediator bacteria's DNA "light switch"

DNA methylation is a common signaling tool cells use to tell genes if they should be "on" or "off." However, its role is poorly understood for the vast majority of prokaryotes. *Shewanella* bacteria grow naturally almost everywhere and play key roles in global carbon and nitrogen cycles. They are also major microbial players in cleaning up environments contaminated with toxic metals and radioactive waste.

In a study (http://bit.ly/1fqzMwZ) published ahead of print online on August 30, 2013 in the *Journal of Bacteriology*, DOE JGI researchers used next-generation sequencers from Pacific Biosciences to gain insights into the role of DNA methylation. The team's results indicated that DNA methylation regulates a number of processes in *S. oneidensis* MR-1, including genome replication and DNA mismatch repair.

Mexican sheoak root bacteria degrading enzymes

Micromonospora are a soil and water-dwelling bacteria that have been eyed for their potential in biofuel processing because of their ability to break down cell walls. Some species have even been found in the rumen of cattle and termite guts. In 2005, *Micromonospora* sp. L5 was found growing in the root nodules of *Casuarina equisetifolia* in Irapuato, Mexico. It was subsequently shown to be capable of fixing nitrogen. In a paper (http://bit.ly/18YOJE9) published online September 26 in the journal *Genome Announcements*, researchers, led by Anne Hirsch of UCLA, isolated and sequenced the complete genome of a species of *Micromonospora*. Genes the researchers identified include several enzymes that degrade cell walls. However, they did not find any genes similar to the nif gene, which is responsible for nitrogen fixation in other bacteria and cyanobacteria species.

Trees of the genus *Casuarina* can tolerate highly saline soil and air pollutants such as sulfur dioxide and nitrogen dioxide. They are also important as nitrogen-fixing plants and fuel crop.

Microbial mat communities withstand big salinity swing

Hot Lake, a remote lake in Washington State near the Canadian border, is home to seasonal microbial mat communities — multi-layered sheets of bacteria and archaea — that are relatively stable in the summer, but disintegrate over the winter. Snowmelt and rain replenish the water every spring, but the microbial mat communities weather a tenfold increase in salinity over the summer months as the water evaporates.

The researchers found that, surprisingly, the composition of the microbial communities didn't change much in response to drastic changes in salinity. The composition of the microorganisms seemed to respond more to changes in available light than changes in salinity.

The study (http://bit.ly/J8U5nx), published November 13, 2013, in the journal *Frontiers in Microbiology* was part of a Community Sequencing Project that was started in 2012, led by James Fredrickson of the Pacific Northwest National Laboratory.

Novel metabolites discovered with combination of profiling and genomics

Researchers examined 10 diverse cyanobacteria species, detecting 264 different secondary metabolites (compounds produced during normal cellular metabolism not directly involved in cell growth) that may play an important role in interactions outside the cell and the genes linked to those molecules. More than half of the molecules were previously unknown. The results (http://bit.ly/1erVYuc) were published September 30 in the journal, *Marine Drugs*.

The team found betaines in nine of the 10 cyanobacteria studied. Another surprising finding was that one of the cyanobacteria, *Microcoleus vaginatus*, produced a series of unusual sugar polymers. *M. vaginatus* lives in soil crusts, soils in arid climates held together by organic material and microorganisms. The researchers are planning next to study how cyanobacteria metabolites contribute to the food web around them and are used by neighboring organisms.

Image courtesy of Kyle T. Ramirez, via Wikimedia Commons

Beetle gut microbial enzymes for biomass breakdown

The Asian longhorned beetle *(Anoplophora glabripennis)* (http://1.usa.gov/1kZB57h) is an invasive species first discovered in the United States in 1996. The microbial community in the beetle's midgut is capable of breaking down the lignin, cellulose, and hemicellulose in wood to acquire needed nutrients, but little is known about the processes involved. In a study (http://bit.ly/1cfgexw) published September 2, 2013, in the journal *PLOS ONE*, researchers compared the metagenome assembly from the wood beetles to annotated assemblies in the DOE JGI's IMG/M database.

The findings revealed that the beetle's midgut contained a community dominated by aerobes. The team, led by John E. Carlson of Pennsylvania State University, identified several genera of fungi and bacteria in the assembly; many of the microbes have been associated with the breakdown of lignocellulose, hemicellulose, and other similar compounds. The metagenome assembly also led to the identification of candidate genes for a variety of functions, including lignin-degrading enzymes, cellulases, xylose utilization, and fermentation as well as for nitrogen and nutrient acquisition.

Gulf of Mexico microbial diversity dive

DOE Joint Genome Institute researchers have been involved in several studies of the effects of the Deepwater Horizon oil spill on the Gulf of Mexico microbial communities.

In a study (http://bit.ly/JIGZ11) published online on August 1, 2013, in *The ISME Journal*, the researchers, led by Mary Ann Moran of the University of Georgia, once again reviewed the microbial populations in the Gulf of Mexico, this time focusing on the expressed genetic information of an ecosystem or metatranscriptomes for those species in the bathypelagic zone, some 1,000 meters to 4,000 meters underwater where no sunlight penetrates.

The findings confirmed that the diversity of microbes and their functional roles in the waters has decreased since the oil spill. However, the team also found that some microbial populations did not appear to be affected by the events that took place three years ago, as their numbers remain similar both before and after the April 2010 explosion. The findings suggest that the original microbial community might be restored.

Chloroflexi's role in aquifer sediments

Microorganisms in aquifer sediments are responsible for subterranean carbon turnover as well as degrading organic contaminants and can heavily impact the quality of underground drinking water (http://1.usa.gov/18Vaoew). Bacteria of the phylum Chloroflexi are responsible for a substantial amount of the microbial population in sediments. However, these microbes are poorly understood, as only six of about 30 Chloroflexi classes have been sequenced.

In a study published August 5, 2013, in *Microbiome* (http://bit.ly/1gJuyQV), researchers were able to reconstruct

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Monkey Flower

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protein (PRDM9). The DOE JGI approach achieved an unprecedented resolution by exploiting the presence of a large number of "SNPs" (single nucleotide polymorphisms), which are single nucleotide (a letter of the genetic code) changes between the DNA sequences of different individuals. On average, monkey flower has one change every 35 letters. This is in stark contrast to human genomes, where only about one in 1,000 nucleotides differ. These SNPs can provide genomic signposts to precisely locate past recombination events so that they can be correlated with heritable differences between individuals. Understanding these correlations in *Mimulus guttatus* will shed light onto the biology of other plants, including bioenergy crops.

"This high resolution allows us to find that hot and cold spots vary within a few hundred or thousand bases," Hellsten said. Cold spots appear to have very little recombination, and are inherited as unshuffled blocks from parents, while hot spots display a spectrum of "temperatures," ranging from "lukewarm," which are common in the genome, to increasingly hotter in less common regions. The team also found that recombination events much more commonly occur close to the beginning of genes.

"The DOE JGI *Mimulus* reference genome provides a valuable service to the research community because it enables the identification of the genes and other important features of the genome structure, such as regulatory and repeated elements, that might contribute to its evolutionary and ecological diversity," said John Willis, a longtime DOE JGI collaborator from Duke University and co-author of the PNAS paper. "Now that *Mimulus* is officially published as a reference genome, we should see an avalanche of publications from other research groups capitalizing on the genomic infrastructure that we have provided," he said.

The *Mimulus guttatus* draft genome is publicly available at the DOE Joint Genome Institute's plant data repository, Phytozome: http://www.phytozome.net/mimulus.php. ⁘

DOE JGI Highlights

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three near-complete Chloroflexi genomes from the metagenomic data collected at the Integrated Field-Scale Subsurface Research Challenge Site (IFRC) in Colorado as part of a DOE JGI Community Sequencing Program project led by collaborator Jill Banfield of UC Berkeley. Metabolic analyses revealed that Chloroflexi can break down plant mass, play roles in subsurface carbon and nitrogen cycles, and can adapt to changing oxygen levels. These traits, the researchers noted, were likely to apply to Chloroflexi in other sediment environments. ⁘

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GENOMICS OF ENERGY AND ENVIRONMENT

Meeting

March 18-20
2014

Walnut Creek
CALIFORNIA

Topics: Microbial genomics, fungal genomics, metagenomics, and plant genomics; genome editing, natural products, pathway engineering, synthetic biology, high-throughput functional genomics, and societal impact of technological advances. State-of-the-art presentations by invited speakers as well as short talks selected from poster abstracts.

In addition, tutorials on genomic informatics, data management, and new genomic technologies.

Keynotes

Annalee Newitz, *io9*
Steve Quake, *Stanford University*

Other Confirmed Speakers

Martin Ackermann, *ETH Zurich*
Luke Alphey, *Oxitec*
Mary Berbee, *University of British Columbia*
Nicole Dubilier, *Max Planck Institute for Marine Microbiology*
Katrina Edwards, *University of Southern California*
Michael Fischbach, *University of California, San Francisco*
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