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Fungal Friends with Genomic Benefits

Unseen by the human eye, plants interact with many species of fungi and other microbes in the surrounding environment, and these exchanges can impact the plant's health and tolerance to stressors such as drought or disease, as well as the global carbon cycle.

Some of these interactions involve mycorrhizal fungi, which live in the roots of host plants and exchange sugars that plants produce by photosynthesis for mineral nutrients that fungi absorb from the soil. Recent studies indicate that mycorrhizal fungi also play a significant role in belowground carbon sequestration, which may mitigate the effects of human-caused CO_2 emissions.

To understand the basis for fungal symbiotic relationships with plants, a team from the U.S. Department of Energy Joint Genome Institute (DOE JGI),a DOE Office of Science user facility managed by Lawrence Berkeley National Laboratory, and longtime collaborators at the French National Institute for Agricultural Research (INRA) and Clark University conducted the first broad, comparative phylogenomic analysis of mycorrhizal fungi, drawing on 49 fungal genomes, 18 of which were sequenced for this study. DOE JGI Fungal Genomics Program head Grigoriev called this "first large-scale study of mycorrhizal genomics … the first step in both broader and deeper exploration of mycorrhizal diversity, their interactions with host plans, and roles in forest ecosystems using genomics tools."

In a study published ahead online February 23, 2015 in *Nature Genetics*, these researchers describe how the comparative analyses of these genomes allowed them to track the evolution of mycorrhizal fungi. The results help researchers understand how plants and fungi developed symbiotic relationships, and how the mutualistic association provides host plants with beneficial traits for environmental adaptation.

"Mycorrhizal symbioses are highly complex, but analyses of the 49 genomes indicate that they have evolved independently in many fungal lineages," said INRA's Francis Martin, one of the study's senior authors.

To understand the genetic shifts underlying the repeated origins of mycorrhizal lifestyles, the researchers focused on enzymes that degrade plant cell walls from 16 gene families associated with plant cell wall degradation. They took their cue from the first sequenced ectomycorrhizal fungus, *Laccaria bicolor* and the first sequenced arbus- *continued on page 2*

Some of the most conspicuous forest mushrooms, including the fly agaric (*Amanita muscaria*), are considered mycorrhizal fungi. (Francis Martin, INRA)

in this issue

Toward targeting sorting of microbial cells

As part of the DOE JGI's 10-Year Strategic Vision, the Emerging Technologies Opportunity Program (ETOP) was launched in 2013 to help further the genomic capabilities offered by the DOE JGI to its users. In partnership with the DOE JGI through ETOP, researchers at other institutions around the world are developing new technologies that can then be used by the DOE JGI and its users to tackle energy and environment applications.

One of these ETOP projects involves characterizing individual microbial cells by combining labeling with heavy water, Raman microspectroscopy, microfluidics and flow cytometry. Proposed by researchers at MIT and the University of Vienna, Austria, the technology could accelerate the functional characterization of genes from metagenomic sequencing experiments, one of DOE JGI's highest priorities.

The early results of this ETOP project were described in the January 13, 2015 issue of the *Proceedings of the National Academy of Sciences* by a team led by University of Vienna researchers. Working toward a universally applicable technique that would allow researchers to evaluate microbial activities at the single cell level, the team *continued on page 3*

Formerly intractable, no longer insurmountable

Genome researchers have spoken often of the challenges of sequencing plants with more than two paired sets of chromosomes (polyploidy). For example, in the case of bread wheat (*Triticum aestivum*), multiple hybridization events have led to a genome that is five times larger than that of humans and more than 80 percent of it made up of repeat sequences. To generate a whole-genome shotgun assembly of such a complex genome, researchers need to be able to assemble short reads coming off next-generation sequencing platforms and also use significant computational resources to manage the data.

Image by Takuma Kimura via Flickr CC BY-SA 2.0

In the January 31, 2015 issue of *Genome Biology*, an international team of researchers led by the DOE JGI described a strategy that employs the above criteria. Using short read sequencing technology, the team assembled over 9-billion basepairs (Gbp) of the 16 Gbp bread wheat genome using Meraculous, a whole genome assembler for next-generation sequencing data geared for large genomes, and access to the Edison supercomputer at the National Energy Research Scientific Computing Center (NERSC), another DOE user facility, saving the team days of compute time.

The team's work comes on the heels of the International Wheat Genome Sequencing Consortium's release of the bread wheat genome in *Science*. DOE JGI Chief Informatics Officer and former Plant program head Dan Rokhsar noted that he and his colleagues took part in the IWGSC effort, contributing a dense genetic map.

In the current paper, the team highlighted some of the differences between the IWGSC's sequence, and their own whole-genome shotgun draft genome assembly. They added that their whole-genome shotgun approach allowed them to anchor more than 7.1 Gbp of the genome to chromosomal locations, while only 4 Gbp is anchored in the previous reference sequence. The impact of the team's whole-genome shotgun strategy was highlighted in a separate Genome Biology article, in which the authors compared the DOE JGI's bread wheat assembly against the one released in *Science* last year.

The longer-term impact of this work is that this improved strategy for dealing with large and complex genomes (frequently characteristic of plants that, as potential biofuel feedstocks, are of major interest to DOE) will accelerate and advance the sequencing of, and exploitation of, plant genomes.

Ectomycorrhizal fungi

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cular mycorrhizal fungus *Rhizophagus irregularis* — all work done at the DOE JGI — which illuminates the origins and evolution of these enzymes, knowledge to be applied in collaboration for improving biomass breakdown for biofuels production.

Through molecular clock analyses, which combine genome-scale molecular data with fossil calibrations, the team could work backwards to estimate when saprotrophic and mutualistic lineages last shared common ancestors based on the amount of divergence.

The analyses of the fungal genomes and fossils suggested that in comparison to brown rot fungi and white rot fungi that evolved over 300 million years ago, ectomycorrhizal fungi emerged fairly recently from several species and then spread out across lineages less than 200 million years ago. The team also found that up to 40 percent of the symbiosis-induced genes were restricted to a single mycorrhizal species.

David Hibbett of Clark University, another of the study's senior authors, compared the work to a previous collaboration with the DOE JGI detailed in *Science* to trace the evolution of white rot fungi, which are capable of breaking down cellulose, hemicellulose and lignin in plants.

"Together these studies tell a story about how mushroom-forming fungi evolved a complex mechanism for breakdown of plant cell walls in 'white rot' and then cast it aside following the evolution of mycorrhizal associations, as well as the alternative decay mechanism of 'brown rot,'" Hibbett said. "The other major part of the story is that in mycorrhizal lineages there is a huge turnover in genes that are upregulated in the symbiosis- many of these have no homologs in even closely related species, suggesting that the evolution of the symbiosis is associated with massive genetic innovation."

Martin, leader of the Mycorrhizal Genomics Initiative, a DOE JGI Community Science Program project, spoke at the 10th Annual Genomics of Energy & Environment Meeting.

Emergent Ideas for Exploring Uncultivated Microbes at AAAS

Taking advantage of the broad spectrum of scientists gathered for the recent annual American Association for the Advancement of Science Annual Meeting held February 12-16, 2015 in San Jose, Calif., DOE JGI researchers and users organized a symposium on technologies that are pushing the boundaries of metagenomics.

DOE JGI Program Head Susannah Tringe moderated the panel that took place on February 13, which focused on techniques researchers could apply to learn more about the mostly-unknown bacteria, archaea and fungi that play significant roles in the biogeochemical processes create and sustain the conditions for life on Earth. These techniques augment the single-cell genomics and metagenomics strategies that the DOE JGI has contributed to advancing over the last dozen years.

Longtime collaborator Steven Hallam from the University of British Columbia (currently on sabbatical as a Visiting Scholar in the Bioengineering Department at Stanford University) focused on his Community Science Program (CSP) projects studying microbial communities in oxygen-minimum zones in northeast subarctic Pacific Ocean using a combination of single-cell genomics and metagenomics. While he and his team have been able to identify dominant organisms in these populations that play key roles in various cycles, he added that, "although we can identify the key microbial players we still know very little about how they interact with one another to solve metabolic problems in the environment." With multi-omics data produced at the JGI and new computational tools, however, his group is starting to build community-level metabolic networks.

Jennifer Pett-Ridge presenting at AAAS. (Atlantic Photo)

Jennifer Pett-Ridge of Lawrence Livermore National Laboratory followed with a talk on isotope probing approaches she's used in conjunction with several CSP projects, focused on complex microbial communities from microbial mats and soil rhizosphere. In particular, she highlighted the use of high-resolution imaging secondary ion mass spectrometry (nanoSIMS) to track the metabolic activities of single microbial cells and identify keystone organisms involved in biogeochemical cycling of carbon and nitrogen.

DOE JGI Microbial Program Head Tanja Woyke closed the session, providing the audience a glimpse into the future of function-driven single-cell genomics and underlining the benefits accrued from tapping into the Institute's resources for users. As a case in point, she highlighted a project involving researchers from the University of Vienna and MIT under the Emerging Technologies Opportunity Program (see page 1) that will provide the DOE JGI with the capability to perform Raman-activated cell sorting combined with single-cell genomics. She noted the various programs through which researchers can submit a proposal, including the CSP and the JGI-EMSL Collaborative Science Initiative, a program through which researchers can also harness the capabilities of the Environmental Molecular Sciences Laboratory, a DOE user facility at Pacific Northwest National Laboratory. Learn more about these collaborative programs at: http://jgi.doe.gov/collaborate-with-jgi/.

ETOP Project

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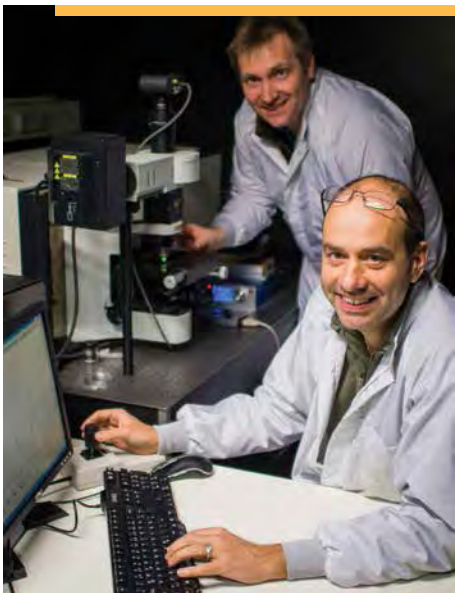
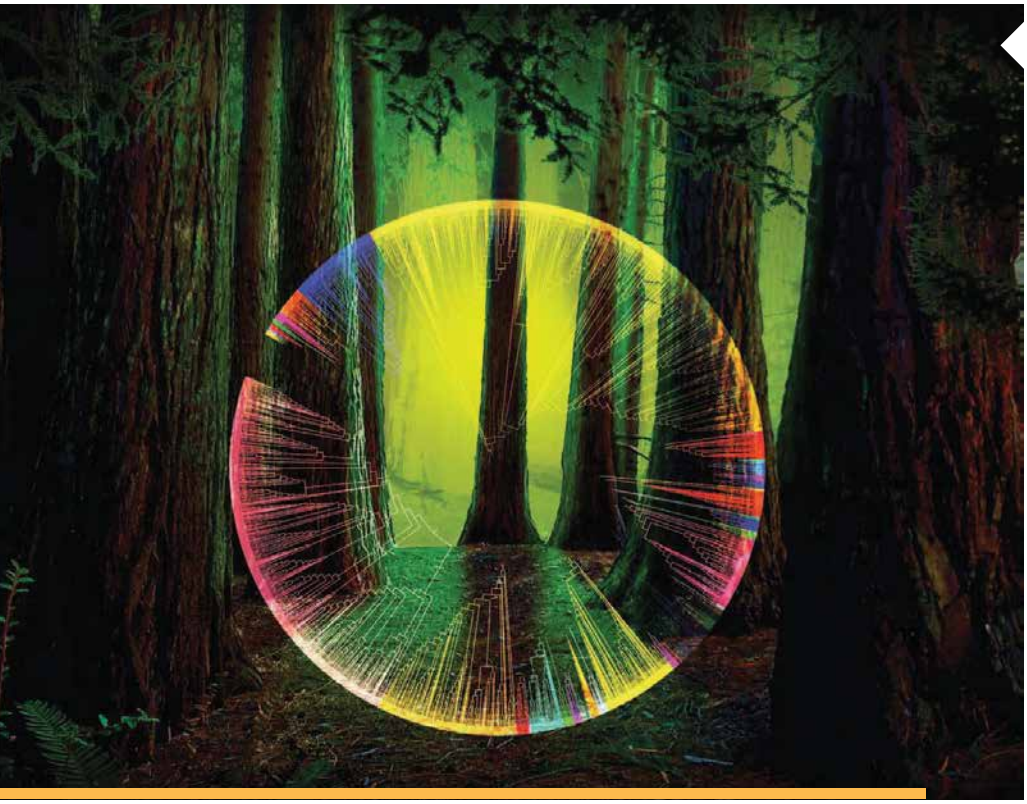
conducted proof-of-principle experiments to study te efficacy of a process that involved incorporating heavy water (deuterium) isotopes into molecules, and then using Raman spectroscopy to chemically identify the microbes.

David Berry from the University of Vienna spoke about the ETOP project during the DOE JGI 2014 Genomics of Energy & Environment Meeting. Watch his presentation at http://bit.ly/JGIUM9_Berry. The full list of selected ETOP projects can be found at http://bit.ly/JGI13ETOP.



ETOP project lead Michael Wagner (foreground) of the University of Vienna with colleague Markus Schmid at the Raman microspectrometer. (Courtesy of M. Wagner)



DOE Joint Genome Institute researchers are illuminating new branches of the tree of life by characterizing novel microbes sourced from extreme, inhospitable and isolated environments, which they expect to be preferred niches for early life, potentially sheltered from more modern microbial competitors. (Berkeley Lab-Zosia Rostomian)

"We are poised to discover new life"

"We are poised, armed with a new toolkit of powerful genomic technologies to generate and mine the increasingly large datasets to discover new life that may be strikingly different from those that we catalogued thus far," said DOE JGI Director Eddy Rubin. "Nature has been tinkering with life for at least three billion years and we now have a new set of ways to look for novel life that have so far eluded discovery."

With Microbial Program head Tanja Woyke, Rubin authored a perspective piece published November 6, 2014 in the journal *Science* on why the time is right to apply genomic technologies to discover new life on Earth. They proposed the division of microbial life on Earth into three categories: explored, unexplored, and undiscovered. The first can be grown in the laboratory. The second encompasses the uncultivated organisms from environmental samples known only by their molecular signatures. The third, the focus of the perspective, is the yet-undiscovered life that up until now has eluded detection.

"Massive-scale metagenomic sequencing of environmental DNA and RNA samples should, in principle, generate sequence data from any entity for which nucleic acids can be extracted," Rubin noted. "Analysis of these data to identify outliers to previously defined life represents a powerful means to explore the unknown."

Rubin suggested targets for the discovery of novel life including extreme, inhospitable and isolated environments that are expected to be preferred niches for early life, potentially sheltered from more modern microbial competitors. He proposed not just looking "'under the street lamp' — at environments that we have already previously studied." This would include low oxygen subsurface sites with environmental conditions predating the Great Oxidation Event that occurred about 2.3 billion years ago when the atmosphere went from very low to high oxygen concentrations. Support for the idea that isolated low-oxygen environments may be preferred niches for early life comes from observations that anaerobic niches deep within Earth's crust tend to harbor ancient branches within the domains of life.

In addition, Rubin pointed to the advent of single-cell sequencing with microfluidic and cell sorting approaches, focused specifically on cells that lack genes that match previously identified ones, as another approach in the search for completely novel organisms.

There is no lack of opportunities for exploring the planet's microbial diversity, Rubin said. "Students contemplating careers may be well served to join the legions of 21st Century cartographers, who, like the DOE JGI user community, are interpreting the coordinates generated by the tools of genomics and other advanced omics to map the metabolic potential of the planet."

Exploring the "undiscovered" classification is expected to be a boon for enriching the public data portals, Rubin said. He also noted that lurking among these difficult ones may well be the discovery of a "fourth domain" of life. To watch Rubin's talk on "microbial dark matter" at the DOE JGI's 2014 Genomics of Energy and Environment Meeting, go to http://bit.ly/JGIUM9Rubin.

The Shipworm's Strategy for Destruction

For centuries, the shipworm, a worm-like, wood-eating marine clam considered "the termite of the sea," plagued shipbuilders and engineers just as terrestrial termites vex homeowners. These bivalves ruined Christopher Columbus' 4th trip to the Caribbean in the early 1500s, instigated flooding of the Netherlands in the 18th and 19th centuries, and caused an estimated $15 million in damages to the wharves of San Francisco, California around 1920. Only when copper sheathing was introduced to naval vessels in the 18th century did the shipworm's capability for destruction slow.

For bioenergy researchers, including DOE JGI scientists, the shipworm's destructive capabilities could prove useful for the industrial production of advanced biofuels from woody plant mass. Under the DOE JGI's Community Science Program, a team led by collaborator Daniel Distel, Director of the Ocean Genome Legacy Center of New England Biolabs at Northeastern University, has focused on the shipworm *Bankia setacea* to learn more about the enzymes it utilizes to break down wood for nutrition.

In a study published November 25, 2014 in the *Proceedings of the National Academy of Sciences,* Distel and his DOE JGI colleagues — including Microbial Program Head Tanja Woyke, Metagenome Program Head Susannah Tringe, and Micro-Scale Applications Lead Rex Malmstrom — described the novel strategy by which this mollusk breaks down and digests wood.

"Most animals, including people, have beneficial bacteria in their digestive system to help them digest food and would quickly become sick and malnourished without them," Distel said. "But shipworms have no bacteria in the part of the gut where their food is digested. Instead, they house symbiotic bacteria inside specialized cells in their gills, a location far removed from the gut."

Think of shipworms as albino earthworms with an abrasive shell that allows them to burrow into wood. The wood particles that enter their mouths make their way into their stomachs, and it turns out the digestive enzymes need to make a similar trip. Through genome sequencing, proteomics, biochemistry, and microscopy, the team demonstrated that the wood-degrading enzymes produced in the gill bacterial community make the trip from the region known as the Gland of Deshayes to the gut in order to break down the mollusk's meal and convert the cellulose into sugars.

"No other animal in the world is known to rely on bacteria outside of its digestive system to produce its digestive enzymes and no other intracellular bacterium is known to produce enzymes that function in the outside world of the host," Distel said.

For the study, the team used shipworms from Puget Sound in northwestern Washington. Researchers isolated multiple bacterial endosymbionts from the gill tissues and sequenced their genomes, and also sequenced the collective "metagenome" of the gill microbial community. They also used proteomics to characterize the proteins found in the shipworm gill and cecum tissues and compare them with the bacterial genomes and metagenomes — demonstrating that the abundant digestive enzymes in the gut derive from gill endosymbionts.

The team is still pondering the reasoning behind having the wood-degrading enzymes produced away from where digestion actually takes place, but they suggested that this strategy allows the shipworm to serve as a simple model system to work out the minimal enzyme requirements for efficiently breaking down cellulose. "Because only selected wood-degrading enzymes are transported, the shipworm system naturally identifies those endosymbiont enzymes most relevant to lignocellulose deconstruction without interference from other microbial proteins," they wrote in the paper. "Thus, this work expands the known biological repertoire of bacterial endosymbionts to include digestion of food and identifies new enzymes and enzyme combinations of potential value to biomass-based industries such as cellulosic biofuel production."

The "termite of the sea" may prove useful for generating biofuels. (Dan Distel, Ocean Genome Legacy Center of New England Biolabs)

Dan Distel's presentation on "How to Eat a Wooden Ship: A Genomic View of Wood-Eating Bacterial Endosymbiosis in the Shipworm *Bankia setacea*" from the DOE JGI's 2011 Annual Genomics of Energy & Environment Meeting can be viewed at http://bit.ly/JGIUM6Distel.

Image by Wes Agresta and courtesy Argonne National Laboratory

Enhancing Microbial Pathways for Biofuel Production

Terpenes are hydrocarbons produced in microbes and plants such as conifers that act as a self-defense mechanism against pests, among other functions. Bioenergy researchers see terpenes are high-energy metabolites that could be used for producing biofuels from plant feedstocks on a commercial scale. For example, terpene production in eucalyptus is of interest to the bioenergy researchers who were part of an international consortium of researchers, including DOE JGI scientists, which described the eucalyptus genome in *Nature* last year. One side project resulting from work done there is being led by study co-author Jerry Tuskan of the DOE JGI as well as Oak Ridge National Laboratory (ORNL) and the BioEnergy Science Center (BESC), a DOE Bioenergy Research Center (BRC). Tuskan's team is working on oil gland formation in plants and expressed interest in determining the biochemical pathway of terpene production in eucalyptus leaves to develop a sustainable alternative to jet fuel.

In the January 2015 issue of *Applied and Environmental Microbiology,* DOE JGI researchers collaborated with another BRC, the Joint BioEnergy Institute (JBEI), to find ways of enhancing terpene yield in bacteria. In previous studies, JBEI researchers had reported that bisabolane, a biofuel resulting from the precursor terpene bisabolene, could serve as an alternative to diesel fuel. They wanted to find a way to improve terpene production in *E. coli* using the metabolic DXP pathway, which they consider more efficient in terms of final yield compared to the mevalonate pathway. To develop a novel route that would take C5 sugars (such as the xylose formed when hemicellulose is broken down) to terpenes, they used a directed-evolution strategy and deleted specific genes involved a key point in the pathway. The results led to their discovery of two novel routes: one that arose through spontaneous mutations; and, one found through overexpression of a selected candidate gene, for producing the terpene and candidate biofuel bisabolene.

They also noted that applying the engineering process to the DXP pathways in plants and algae "could provide a more direct link from carbon fixation (Ru5P in the Calvin cycle) to the terpene pathway."

Complete Genomes from Single Cells Still Elusive

As most of the microbes in, on, and around the plant are undiscovered or unculturable, single-cell genomics affords researchers a way to conduct environmental genomics studies without having to culture the microbes. The technology allows researchers to look at an individual microbe's function within the community and improve the process of classifying microbial genetic relationships. Already, partial microbial genomes recovered from single cells are providing researchers with metabolic information and clues about population genetics. Still, a single standard operating procedure for the process of recovering a single-cell genome from an environmental sample has yet to be developed.

Though researchers at DOE JGI have been able to successfully derive a complete genome from a single bacterial cell, this result remains the exception rather than the norm. In a perspective article published January 8, 2015 in *Frontiers in Microbiology,* a team led by Microbial Program head Tanja Woyke detailed the various challenges encountered, starting with the process of prepping the sample and isolating single cells for study. The process of isolating a single cell generally requires using fluorescence activated cell sorting (FACS), and there are cells that are too big or too small, or too attached to other cells or particles.

Once single cells have been isolated and the DNA has been extracted and amplified for sequencing, it turns out the quality of the genome recovered can vary wildly. The team conducted an experiment, generating single cell genomes of three different, Gram-negative bacteria — *Pedobacter heparinus* DSM 2366, *Escherichia coli* K12-MG1655, and *Meiothermus ruber* DSM 1279 — for which the DOE JGI already had complete genome sequences. They found that the median amount of the genome recovered for the *E. coli* strain was 93 percent, but the *M. rube*r strain was only 49 percent. The researchers posited a number of reasons for the variation, from *M. ruber* being more resistant to the process of having its cell walls broken down to extract the DNA compared to the other bacteria, to limited genome access.

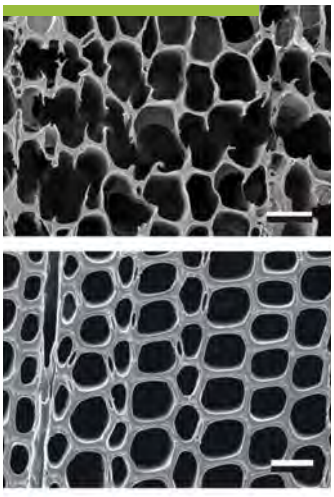
"For the time being, we will have to settle with partial genomes from a fraction of the cells contained within an environmental sample and reconstructing each cell's

genome from a complex environment still remains a dream rather than reality," the researchers concluded. "However, these partial single-cell genomes are clearly pushing microbial genomics into exciting, untapped territory, enabling the discovery of unexpected metabolic features, providing insights into population genetics, and improving the phylogeny of microbes."

How a White Rot Tackles Freshly-Cut Wood

Bioenergy researchers are probing the processes by which fungi first break down wood and leaf litter in forests and lawns, and then convert the materials into sugars. They hope to harness this information at industrial-scale settings.

DOE JGI researchers have been sequencing and analyzing two primary groups of fungi: brown rots and white rots. While both groups can break down the cellulose and hemicellulose in plant cell walls, only white rots can break down lignin as well. This difference, though seemingly slight, is the reason why one fungal genomics study in *Science* proposed that an ancestral white rot fungus may have ended the formation of coal deposits.



Scanning electron microscopy (SEM) image of pine that was substantially eroded by the white rot *P. gigantea* compared against a SEM of sound wood (bottom). Bar = 40 µm. (Image from Hori et al. *PloS Genet.* doi:10.1371/journal.pgen.1004759.g002)

Many of the white rot fungal genomes sequenced and analyzed at DOE JGI are known to break down decaying wood. In a study published December 4, 2014 in *PloS Genetics* however, a consortium including DOE JGI researchers reported on the mechanisms by which the white rot fungus *Phlebiopsis gigantea* breaks down plant cell walls and resinous components in the freshly-cut sapwood of conifers. In one aspect of the study, researchers monitored the progress of the fungus on wafers of sapwood from aspen, pine and spruce over three months and compared these results against uninoculated wafers. In another experiment, they measured the fungus' levels of gene expression in a scenario where glucose had been extracted from freshly-harvested pine wood using acetone, and a scenario where the glucose had not already been extracted from the freshly-harvested wood.

"The results advance understanding of the early and exclusive colonization of coniferous wood by *P. gigantea* and also provide a framework for developing effective wood protection strategies, improving biocontrol agents and identifying useful enzymes," the team concluded.

Water Availability and Panic Grass Variants

Switchgrass (*Panicum virgatum*) holds promise as a potential bioenergy feedstock for the DOE because it is a perennial grass that is also salt-tolerant, drought-tolerant, and thrives on marginal land. However, the plant also contains multiple copies of its genome, making it difficult for researchers to map its genetic code.

Hall's panic grass (*P. hallii)* is a smaller, close relative of switchgrass with a shorter life cycle. In a *New Phytologist* paper published September 23, 2014, a team from the University of Texas-Austin and including DOE JGI researchers utilized the genetic similarities between switchgrass and panic grass to identify traits related to the grasses' ability to thrive under various water availability conditions. The DOE JGI is sequencing this plant to develop it as a model system for genetic and genomic work.

Using two varieties of *P. hallii — var. hallii* that thrives in very dry (xeric) habitats and *var. filipes* that thrives in habitats with moderate (mesic) water levels — the team statistically mapped (through quantitative trait locus or QTL mapping) traits involved in the divergence of this species. The information lends insights into how ecotypes are formed as evolving populations of a species adapt to a particular environment.

"The same set of ecotype-differentiating traits found between xeric and mesic varieties of *P. hallii* are also involved in the divergence of upland and lowland ecotypes of the closely related bioenergy crop switchgrass," the team noted in their report. "Gaining insight into the molecular details of colocalizing QTL in these systems will be an important next step in understanding the factors constraining or facilitating adaptation and ecotypic differentiation to

The team mapped QTLs for 9 morphological traits and, in one instance, found that 5 traits including tiller and leaf size and shape as well as flowering time map to the same region. The team noted in their study that their findings suggest some traits involved in the formation of variants may evolve in tandem, while other traits evolve independently. This work will allow the association of genomic features in panic grass with its responses to water availability; given the similarity of panic grass to switchgrass, this will point researchers to those genomic regions in switchgrass that could serve as targets for further studies to learn how to exploit these regions for the improvement of switchgrass for bioenergy.

At the annual Genomic Science Meeting held February 22-25, 2015 in Tysons, Virginia, DOE Program Manager Dan Drell caught up with (left to right): DOE JGI collaborator Janet Jansson, Division Director of Biological Sciences at the Pacific Northwest National Laboratory; Metagenome Program Head Susannah Tringe; and DOE JGI collaborator Kirsten Hofmockel of Iowa State University. Jansson heads a DOE JG Community Science Program (CSP) project related to the Next-Generation Ecosystem Experiment, while Hofmockel's CSP project compares soil microbial communities from a variety of bioenergy cropping systems. Download the meeting abstract book: http://bit.ly/GSC-2015

At the International Plant and Animal Genome Conference (PAG XXIII) held January 14-18, 2015 in San Diego, California, the DOE JGI shared a booth (from left, second, third, and fourth: Ranjan Priya [ORNL], Sunita Kumari [CSHL] and Meghan Drake [ORNL]) with the DOE Knowledgebase (Kbase) and hosted a joint workshop. DOE JGI collaborators talked about their plant projects and KBase users discussed the benefits of a large-scale computational resource for comparative functional genomics and systems biology of microbes, plants and their communities. In the photo below, DOE JGI Plant Program head Jeremy Schmutz stands with KBase Plants Science Team Lead Doreen Ware and DOE Program Manager Cathy Ronning.

Congressman Mark DeSaulnier (CA-11), standing second from the right, visited the DOE JGI, located at his District's geographic center, on February 20, 2015. The Representative and his staffer Pat Joyce met with senior JGI leadership, including Operations Deputy Ray Turner (far left) and Science Deputy Jim Bristow (second from left), for an overview of JGI's contributions to characterizing plants, fungi, microbes and consortia of microbes (known as metagenomes) and their relevance to the DOE mission. Metagenome Program head Susannah Tringe (center) and postdoctoral fellow Susie Theroux (far right) the briefed the visitors on a project that has both local and global implications, studying the microbial diversity and carbon cycling in San Francisco Bay and Sacramento-San Joaquin River wetlands. Before they left, the visitors were given a tour of JGI's sequencing platforms.

Contact The Primer

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