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Finished with "Finishing"? Not yet.

JEFF MARTIN AND MASSIE SANTOS BALLON

As the Sequencing, Finishing and Analysis in the Future (SFAF) Meeting held in Santa Fe, New Mexico on June 1–3, 2011 came to a close, a question arose as to whether the word "Finishing" would be removed from future meeting banners.

"Certainly not," replied SFAF organizer Chris Detter, head of the Genome Science Group at Los Alamos National Laboratory (LANL), who reminded attendees that one of the common complaints resulting from the explosion of genomic sequencing is the varying levels of sequence that can impede research and applications.

It's still not cost-effective to finish every genome sequenced, he said. The price of finishing doesn't hinder sequencing; at the Meeting, the Sanger Institute announced during the Meeting its intention to sequence 10,000 genomes, many from microbes, over the next two years. However, Detter added, the inability to finish every genome shouldn't be a deterrent to finishing any genome. The near term goal should be to better utilize new sequencing and assembly technologies to find creative solutions to efficiently complete or finish most if not all genomes sequenced. An obvious longer term goal would be to end up with a complete genome as part of the initial draft sequencing process for all genomes sequenced.

continued on page 5

SFAF organizers (left to right): David Bruce, DOE JGI/LANL; Chris Detter, DOE JGI/LANL; Darren Grafham, Sanger Institute; Mike Fitzgerald, Broad Institute; Bob Fulton, Washington University; Patrick Chain, DOE JGI/LANL; Johar Ali, Ontario Institute for Cancer Research; Donna Muzny, Baylor College of Medicine; Alla Lapidus, Fox Chase Cancer Center

Lessons from Fungi on Large-Scale Production

***Aspergillus niger* (Sue Karagiosis, PNNL)**

For decades, citric acid has been produced on a commercial-scale basis with the help of the fungus *Aspergillus niger.* Outside industry, *A. niger* is also known to be involved in the global carbon cycle, and its enzymes can be used to break down plant cell walls and get at the sugars that can in turn be fermented for use as biofuels.

"*Aspergillus niger* is an industrial workhorse for enzymes and small molecules such as organic acids," said Scott Baker of the Pacific Northwest National Laboratory. "We know that this single organism is used for production of organic acids and for enzymes, and it can degrade plant cell wall matter for sugar production. For biofuels it's a highly relevant organism since it's already been scaled up, shown to be safe, and used for enzyme production. That's why it was such an important organism to further characterize through DNA sequencing."

The DOE JGI generated the 35-million base genome of *A. niger* ATCC 1015, the wild type strain that was used in research that led to the first patented citric acid

continued on page 5

Tringe Awarded $2.5M DOE Grant

Susannah Tringe

Susannah Green Tringe, head of the DOE JGI Metagenome Program, has been awarded a $2.5 million grant by the DOE Office of Science Early Career Research Program to conduct genomic studies of microbial communities (metagenomes) in restored wetlands around the San Francisco Bay-Delta region of California.

Tringe will use the five-year grant to conduct genomic-based studies on the roles microbial communities play in restored wetlands, and the communities' impact on long-term carbon sequestration. She plans to start by focusing on the restored wetlands of Twitchell Island in the Sacramento/San Joaquin Delta, an area that has a carbon sequestration rate of one kilogram per square meter per year and, which, she says, "is comparable to, if not greater than" the carbon sequestration rates achieved from tropical reforestation.

"Restoration of wetlands has the potential to remove significant amounts of carbon dioxide from the atmosphere, due to rapid accumulation of emergent vegetation and low rates of biomass decomposition in the anoxic soil," she wrote in her proposal. "Most of the long-term carbon storage takes place in the soil or sediment, yet little is known about the belowground microbial communities that are likely key determinants of the relative balance between carbon storage and atmospheric recycling."

Tringe joined the DOE JGI in 2003 as a postdoctoral fellow under Director Eddy Rubin after completing her doctoral studies at Stanford University and completing a postdoctoral fellowship at the University of New Mexico. She has served as DOE JGI Microbial Systems Group Lead and then Deputy Metagenome Program Head. She has been involved in several metagenomic studies, including the study of microbial communities in the termite hindgut, the leaf cutter ant and in the cow rumen, as well as of microbial communities in ocean dead zones.

The DOE Early Career Research Program funds principal investigators who have received their Ph.Ds within the last 10 years and are either untenured assistant professors on the tenure track, untenured associate professors on the tenure track, or full-time, nonpostdoctoral, permanent DOE national laboratory employees. The minimum award size is $150,000 per year for five years for universities and $500,000 per year for five years for DOE national laboratories. Tringe is one of 65 applicants who were awarded funding for their projects from more than 1,100 proposals received.

To see the full list of Program awardees and their proposal abstracts, go to http://science.energy.gov/early-career/

SPOTLIGHT: DOE JGI'S SPOC TEAM

Top Row (L-R): Victor Vasquez, Gigi Pang, Christine Naca, Erin Dunwell, Nancy Hammon, Miranda Harmon-Smith; Bottom Row (L-R): Steven Wilson, Susan Lucas, Richard Pope

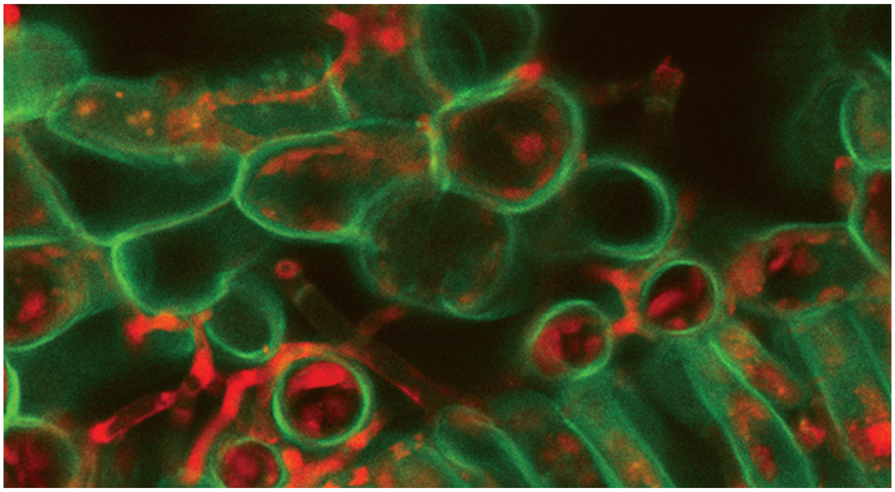
At the DOE JGI, the Strategic Planning Operations and Capabilities (SPOC) team is quietly streamlining the Institute's end-to-end processes to help shape the organization into a Genomic Foundry. The group members have several decades of experience in several DOE JGI departments such as Industrial Engineering, Operations, Production, Shipping & Receiving, Software Development, Training and Project Management and Operations.

At the helm is Susan Lucas, who previously headed the DOE JGI Production department for 10 years. "We are a global operational efficiency team," she said. "We look at how JGI as an organization can get better from managing our proposal process to our customer signoff by understanding our operations and measuring their progress."

As the newest addition to the DOE JGI Operations Department, the SPOC team's recommendations and implemented improvements are done with the help of Lean Six Sigma practices. More than 20 "quick and simple" Six Sigma projects have already been implemented, ranging from color-coding test tubes to reduce operator error when loading reagents on an instrument, to tracing contamination errors in the Illumina process back to the source, leading to zero fails and saving thousands of dollars annually.

"You'll see this team rolling up their sleeves and digging into the details, then stepping back to implement a more robust, repeatable process," Lucas said.

Fungal genomics to fend off fungal plant pathogens



Original confocal microscopy image of infected leaves from poplar cv. (Stéphane Hacquard, INRA Nancy).

Many DOE JGI projects focus on sequencing fungi to learn more about their abilities to break down organic matter and to identify enzymes involved in these pathways. Another category of fungal projects concentrates on plant pathogens which reduce crop yields and could lead to less biomass available for the production of cellulosic biofuels.

In a study published online the week of May 2, 2011 in the *Proceedings of the National Academy of Sciences*, an international team of researchers that included Fungal Genome Program head Igor Grigoriev, as well as several members from the DOE JGI, compared the genomes of two rust fungi to identify the characteristics by which these pathogens can invade their plant hosts and to develop methods of controlling the damage they can cause.

The team led by co-first author Sébastien Duplessis of the French national agricultural research institute (INRA) worked on the poplar leaf rust fungus *Melampsora larici-populina*, which was sequenced at the DOE JGI under the 2006 Community Sequencing Program. A second team led by co-first author Christina Cuomo of the Broad Institute of MIT and Harvard and Les Szabo from Agricultural Research Service USDA and University of Minnesota worked separately on the wheat and barley stem rust fungus. The groups then collaborated to conduct a comparative genomic analysis of the two rust pathogens to reveal the role they play in infecting the host plant and acquiring nutrients. This is first joint fungal genomics study for the DOE JGI and the Broad Institute.

Poplar leaf rust outbreaks weaken poplar trees, a candidate bioenergy feedstock whose genome sequence was published by the DOE JGI in 2007. Duplessis said that unlike wheat and other plants, it is difficult to estimate the economic damage resulting from poplar rust outbreaks though the most common figure indicates as much as 50 percent annual growth loss in poplar plantations following major rust epidemics. Part of the problem lies in the fungal method of attack. “For a perennial species such as poplar attacked by an obligate biotroph, the host is maintained alive and the tree is not killed,” he said.

Aside from keeping the host alive, Duplessis and his colleagues noted that these plant pathogens use a two-pronged attack where the fungi mask their proximity to the plant and then use enzymes to attach the fungal cell wall to the plant cell wall and then invade the host.

The 101-million base pair genome of *M. larici-populina*, the first tree pathogen sequenced, was made publicly available in 2008. INRA’s Francis Martin, a senior author on the study and long-time DOE JGI collaborator, said that the work means researchers now have the genomes of two fungi that interact with poplar in very different ways. Martin and his colleagues were part of the group that worked on the symbiont *Laccaria bicolor*, whose genome sequence was published in 2008. “[The *Melampsora* genome] will allow a better understanding on how a ‘bioenergy’ tree interacts with its cortege of microbial associates,” he said.

He said the researchers plan to sequence more *Melampsora* genomes to better understand the process by which the rust fungus adapts to its host and overcome the plant’s resistance. “Our paper demonstrates that the rust fungi genomes contain more than a thousand of such small effectors that likely interfere with plant perception systems and activation of defense reactions. Thus a targeted approach to disrupt the effectors entry and action might be complicated.”

Pietro Spanu, a molecular plant biologist at Imperial College London who studies a mildew that is also a fungal pathogen, said that the paper is part of a recent spate in genome publications on these fungi, and the information allows researchers to see for the first time the “remarkable convergences” in the evolution of these pathogens. “It’s like discovering that in order to fly you need wings, and each group has different types of wings.”

Spikemoss Plows New Path for Biofuels Research

In the May 5, 2011 edition of *Science Express*, a team of researchers from over 60 institutions including senior authors DOE JGI's Dan Rokhsar and Igor Grigoriev, reported the genome analysis of *Selaginella moellendorffii*, a tiny plant that helps fill in a large gap in plant evolution from unicellular algae to flowering plants. Some researchers are already employing the sequence to detail the development pathway of lignin, the woody material that helps plants stay upright, and which is challenging to remove for the production of cellulosic biofuels.

The bioenergy application of the genome sequence comes as no surprise to study first author Jody Banks, a Purdue University botanist who originally proposed that spikemoss, as the plant is more commonly known, be sequenced as part of the DOE JGI's 2005 Community Sequencing Program. "When you burn coal, you're burning *Selaginella's* ancestors," she said.


***Selaginella moellendorffii* (Jing-Ke Weng, Salk Institute)**

Banks and her colleagues used a comparative genomics approach to identify the core genes that are likely to be present in a common ancestor to land plants, looking at the genomes of *Selaginella*, the alga *Chlamydomonas*, the moss *Physcomitrella* and 14 angiosperms or flowering plants, including *Arabidopsis* and rice to identify common genes. Spikemoss stands tall like grasses, but because it diverged from flowering plants more than 400 million years ago, it doesn't have the roots and leaves like later plants.

Grigoriev noted that the *Selaginella* genome helps fill in a large gap in plant evolution from the unicellular green alga *Chlamydomonas*, sequenced at the DOE JGI and published in 2007, to flowering plants with vascular systems. "*Selaginella* occupies a phylogenetically important position for which we had no reference," he said. "On one end of the spectrum we had mosses such as *Physcomitrella*" — the first moss to have its genome sequenced and published by DOE JGI — "and on the other are angiosperms such as grasses including *Brachypodium*," whose genome was published by DOE JGI last year.

Banks said having the spikemoss genome revealed that the transition from mosses to plants with vascular systems didn't involve as many genes as going from a vascular plant that doesn't produce flowers to one that does. She also said that the *Selaginella* research community has grown up around the availability of the genome, which was made publicly available through the DOE JGI's plant portal Phytozome in 2009. One metric she cites is the number of researchers who've contributed to the *Selaginella* Genomics wiki she helps maintain, whose existence spread solely by word of mouth. "There are more than 100 co-authors now just because people are interested in the genome," she said. "There have been a large number of recent papers, all including *Selaginella* genes because it really helps the researcher understand the evolution of their favorite gene family. *Selaginella* represents a whole branch of the plant evolutionary tree that no one has sampled before, and it is really important."

To help vascular tissues to stay upright, plants rely on lignin, a polymer biofuels researchers are targeting for investigation because its rigid structure is challenging to break down, impeding their use as potential bioenergy feedstocks. Banks' colleague Clint Chapple, a co-author on the paper and a Purdue colleague, has been using the *Selaginella* genome to study the pathways by which three different types of lignin are synthesized in plants.

"What we learned is that *Selaginella* not only invented the S type of lignin independently, maybe even earlier, than angiosperms but that they go about doing it through a related but different chemical route," Chapple said. He described a recent project (funded by the National Science Foundation) in which enzymes from the lignin-synthesizing pathway in *Selaginella* were used to modify the canonical lignin-producing pathway in *Arabidopsis* to produce the polymer. Having the genome sequence offers strategic research opportunities, he said. "We've known for some time that if you alter the lignin building blocks you can improve biomass for agricultural and industrial uses."

Not Finished Yet *continued from page 1*

Steve Turner of Pacific Biosciences touched upon the issue of finishing during his update on the company's single-molecule real-time (SMRT) system. A dozen machines have been installed for testing at various organizations, including both the DOE JGI and LANL, and the longer sequence reads and shorter run times are being balanced against error rates that are higher than existing short-read technologies. Aside from discussing how to improve the error rates of the SMRT sequencers, Turner also noted that the company is working on an "auto-finishing" process that would allow researchers to get an assembly without manual intervention.

While the Pacific Biosciences team offers a potential tool for finishing, others are working on tools to incorporate PacBio reads into assemblies, the topic of one of the Meeting workshops. Many of the talks there focused on first assembling Illumina data and then piecing together the Illumina contigs using PacBio data.

One of the challenges in using the SMRT sequencers is that while the technology allows for the generation of longer sequence reads than those from Illumina or 454 sequencers, the data is riddled with errors and there is currently no software available for making corrections. Bioinformaticist Adam Phillippy of the National Biodefense Analysis and Countermeasures Center (NBACC) in Maryland used this opportunity to outline software his team has developed and plans to release shortly that uses Illumina reads to correct the SMRT sequencers' data.

The Sanger Institute's goal, for example, will eventually add another 100 terabase pairs of available sequence to the genomic data currently sitting in data centers around the world, adding to the existing bottleneck of data analysis. To help overcome this barrier, the DOE JGI's Zhong Wang gave a talk on BioPig, a collection of cloud computing tools that can be used to scale data analysis and management.

BioPig, Wang said, could act as a pipeline for dealing with large sets of data, on the order of the quarter Terabase of metagenomic data generated from the cow rumen project published in Science earlier this year, or even larger. With BioPig, researchers could look for contamination issues in large datasets and conduct gene-centric assembly of genes from metagenomes in a matter of hours. "Cloud computing shows great potential for scalable analysis on very large datasets," he concluded.

The full Meeting schedule is at http://www.lanl.gov/conferences/finishfuture/

Fungal Lessons *continued from page 1*

process, under the 2005 Community Sequencing Program. "It was thought that if we understood what makes the citric acid process so productive, then we could start to understand how to make other organic acids that could be commodity chemicals," said Baker. "We now have the tools and the foundation of knowledge to be able to ask some additional important questions that we weren't equipped with the genomic resources to answer before."

In a paper published online ahead of print May 4, 2011 in *Genome Research*, a team led by Baker compared the genome of this *A. niger* strain with one sequenced by a company in the Netherlands in 2007 that has undergone mutagenesis and selection for enzyme production.

Learning more about the genetic bases of the behaviors and abilities of these two industrially relevant fungal strains, the study authors wrote, will allow researchers to exploit their genomes towards the more efficient production of organic acids and other compounds, including biofuels.

For example, as of 2007, the global market for citric acid was estimated to be approximately $1.2 billion with more than 500,000 tons produced annually by fermentation. "Having the genetic blueprint for a citric acid-producing fungus will increase our understanding of the organism's metabolic pathways that can be fine-tuned to enhance productivity or alter its metabolism to generate other green chemicals and fuels from renewable and sustainable plant-derived sugars," said Randy Berka, Director, Novozymes, Inc., and one of the publication's authors.

By analyzing the genomes on several levels—DNA, chromosome, gene and protein—Baker and his colleagues found several hundred unique genes in each strain that are key to their predominant characteristics. For example, *A. niger* ATCC 1015 had a higher expression of traits involved in high citric acid yields. On the other hand, the induced mutant strain had more elements related to efficient enzyme production. The team also noted that the genes involved in boosting enzyme production in the induced mutant strain of *A. niger* may have come from another *Aspergillus* strain via horizontal gene transfer, which allows one organism to acquire and use genes from other organisms.

Of the 47 authors on this paper, 30 are from Europe. "This is an excellent example of international collaboration combining genome sequencing with functional genomics, transcriptomics and metabolomics, which led to a system level study and comparative analysis of two *A. niger* strains," said study co-author Igor Grigoriev, head of the DOE JGI Fungal Genomics Program.

continued on page 8

JGI IN THE NEWS

Broadening the Knowledge Base of Fungal Plant Pathogens

DAVID SHOR

An international consortium of scientists, including researchers at the DOE JGI, has published the analysis for *Mycosphaerella graminicola,* the first filamentous fungus to have its genome finished. The 39.7 Megabase genome serves as a resource to help researchers learn more about the methods plant pathogens use to attack and damage crops, including those being considered for use as feedstocks for biofuels production.

As detailed in the June 9, 2011 issue of *PLoS Genetics,* the fungal pathogen causes septoria tritici blotch in wheat, considered one of the top three more economically damaging diseases of this crop in the United States. While scientists recognized the effects of wheat leaf blotch, they didn't understand the pathogen's mode of action. The genome of *M. graminicola* was sequenced as part of the 2005 Community Sequencing Program, enabling researchers to characterize the pathway by which the fungal pathogen invades wheat and damages the plant.

Igor Grigoriev, the Fungal Genomics Program head at the DOE JGI, said "the finished genome of *Mycosphaerella graminicola* will serve as an excellent reference for analysis of other bioenergy crop pathogens that are being sequenced by the JGI." Among these pathogens is the fungus that causes poplar leaf rust, which genome was published earlier this year (see page 3). By establishing this wide base of knowledge, scientists will be better able to apply the findings from this specific genome to a larger variety of pathogens, and thus be more successful in limiting problems to important crops.

Comparative genomics of social amoebae

When food is plentiful, slime molds such as *Dictyostelium discoideum* behave as individuals, but when food is scarce, they come together to form multicellular "fruiting bodies" that look like a flower bud atop a single stalk or foot.

Studying social amoebae such as *Dictyostelium* allows researchers to learn more about multicellularity because they can exist in both single cell and multicellular states. Additionally, from a bioremediation perspective, slime molds are important candidates in cleaning up sites contaminated with chemicals and radioactive materials.

The potential bioremediation application is why the DOE JGI sequenced the genome of the slime mold *Dictyostelium purpureum. D. purpureum* is a close relative of *D. discoideum*; the two are separated by just 400 million years of evolution and share many of the same characteristics. In the February 2011 issue of *Genome Biology,* researchers including DOE JGI Fungal Program head Igor Grigoriev compared the 33-million base draft sequence of *D. purpureum* with the finished genome of the model organism *D. discoideum.* The researchers noted in the paper that the social amoebae have a highly sophisticated recognition system that allows them to distinguish same-species *Dictyostelium* from others. They also found that the "genes involved in sociality evolve more rapidly, probably due to continuous adaptation and counter-adaptation."

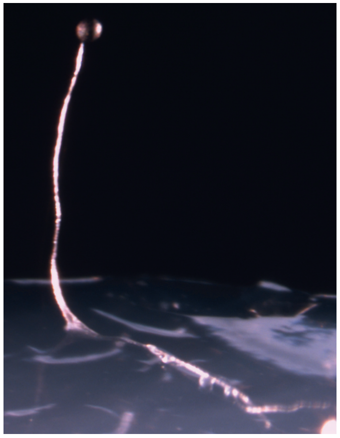
Managing mercury pollution through genomic resources

Mercury from industrial and transportation sources has been polluting aquatic environments. In order to better understand and manage mercury pollution, a team of researchers at Oak Ridge National Laboratory collaborated with scientists at DOE JGI, including Microbial Program head

Courtesy of Gert Kema, Wageningen UR

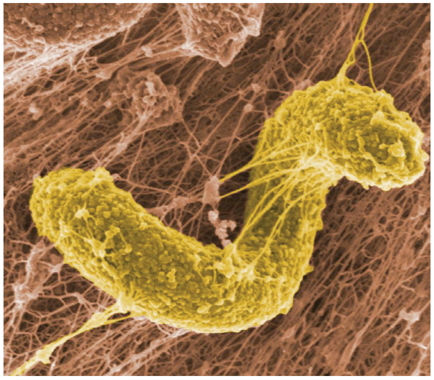
Septoria tritici blotch of wheat

Natasha Mehdiabadi, Rice University



***D. purpureum* fruiting body**

Image courtesy of PNNL via Flickr/Creative Commons



Color-enhanced photo from SEM image of sulfate-reducing *Desulfovibrio desulfuricans* in a biofilm matrix.

Tanja Woyke, and at Los Alamos National Laboratory to sequence the genome of the sulfate-reducing bacterium, *Desulfovibrio desulfuricans* strain ND132.

Isolated from Chesapeake Bay sediment, the *D. desulfuricans* strain ND132 can produce the human neurotoxin methylmercury. “What is not known are the genes or the proteins that allow these bacteria to mediate the transformation,” said ORNL’s Steven Brown.

To help answer the question of how a bacterium can convert inorganic mercury into a more toxic compound, in the April 2011 issue of the *Journal of Bacteriology,* Brown and his colleagues reported that the 3.8-million base genome of *D. desulfuricans* had been sequenced using 454 and Illumina platforms, and that candidate protein-encoding gene models were predicted using Prodigal and GenePRIMP, software developed at the DOE JGI. The genome is currently described as noncontiguous finished (there are six gaps remaining), indicating a high-quality assembly with automated and manual improvements.

Arabidopsis lyrata reference genome now available

Under the 2006 Community Sequencing Program, the DOE JGI selected *Arabidopsis lyrata,* a close relative of the model system *A. thaliana* for sequencing. By comparing their genomes and the genomes of other, related species, researchers could gain insight into the genes and pathways involved in how plants respond to disease and environmental stress.

Joshua Mayer/Flickr

Arabidopsis lyrata

In a report published online April 10, 2011 in *Nature Genetics*, a team of researchers led by collaborators Magnus Nordborg and Detlef Weigel and including DOE JGI’s Igor Grigoriev and Jeremy Schmutz at the HudsonAlpha Institute for Biotechnology, compared the sequences of *A. thaliana* and *A. lyrata.*

“An exciting opportunity to understand what drives differences in genome size over shorter time scales is offered by the genus *Arabidopsis* in the Brassicaceae family,” the researchers noted in their paper comparing the two species that diverged 10 million years ago.

Representing the research team, Nordborg also discussed the differences between these two plant genomes during the recent 6th annual DOE JGI User Meeting in a talk (http://bit.ly/IUQDkd) entitled “How to lose half your genome in 10 million years and live to tell the tale.”

Sequenced using the Sanger platform, the high-quality 207 Megabase pair reference genome of *A. lyrata* was found to be nearly twice as large as that of *A. thaliana.* The model plant also had fewer chromosomes and roughly 17 percent fewer genes compared to *A. lyrata,* leading Nordborg to refer to it as “a bare-bones genome” during his talk.

Corals learning to adapt to global climate change

The decrease in ocean pH levels and the corresponding slowdown in coral growth in recent decades have been linked to the increasing levels of carbon dioxide trapped in the atmosphere, and which are being absorbed in the ocean.

As coral reefs are the primary habitat for several marine organisms, their decline has significant impacts on the health of the marine ecosystems and ocean productivity. To better understand the contributions of corals to the global carbon cycle, one of the 2007 DOE JGI Community Sequencing Program projects led by former DOE JGI researcher Monica Medina, now at the University of California, Merced, included plans to generate a dataset of expressed sequence tags or ESTs, small portions of a genome that can be used to help identify unknown genes and chart their locations along the sequence, from the reef-building coral *Acropora palmata*.

The *A. palmata* EST dataset was used in a study published online May 25, 2011 in *PLoS ONE*, wherein a team of researchers including DOE JGI’s Erika Lindquist compared the generated data to an EST dataset of another reef-building coral to identify the proteins involved in helping corals adapt to global climate change. The comparative analysis identified several proteins evolving at an accelerated rate, such as those involved in immunity, reproduction and sensory perception.

“The category that was the most enriched with rapidly evolving proteins — cell adhesion — may also be related to symbiosis,” noted the study authors in their paper. These proteins are expected to evolve under positive selection due to the need for readjustments, e.g., due to the “arms race” between the coral and the bacterial symbionts.

Pete Faulkner, Mission:awareness/Marine Photobank

***Acropora* table coral on the Great Barrier Reef**

Roy Kaltschmidt, LBNL

The second JGI Science @ the Lesher event was held on May 9, 2011 in downtown Walnut Creek with a focus on the role of microbes in the global carbon cycle. After DOE JGI Public Affairs Manager David Gilbert (standing, left) made introductions, DOE JGI's Jonathan Eisen (center, left) discussed the importance of studying microbes, touching briefly upon the ongoing Genomic Encyclopedia of Bacteria and Archaea (GEBA) project, while postdoctoral fellow Rachel Mackelprang (center, right) reminded people about the thawing Arctic permafrost as a potent source of greenhouse gases. Finally, Terry Hazen (far right) of Lawrence Berkeley National Laboratory revisited his keynote talk at the 6th annual DOE JGI User Meeting regarding microbes and the 2010 Deepwater Horizon oil spill.

KTVU Channel 2 Health and Science Editor John Fowler (second from the left) moderated the panel discussion regarding "The Deal with Carbon: How Earth's Mighty Microbes Respond." Watch the talk online at http://bit.ly/kgaThH or check out DOE JGI's YouTube channel for videos of the two JGI Science @ the Lesher events at http://bit.ly/JGIYouTube.

On May 17, 2011, Laura Chincilla-Miranda, President of Costa Rica, visited Lawrence Berkeley National Laboratory along with her ministers of Science and Technology and Foreign Trade. They were briefed by representatives from several Laboratory divisions including Energy and Environmental Sciences, Life Sciences, Environmental Energy Technologies, the DOE JGI and the Joint BioEnergy Institute (JBEI). They then visited the Molecular Foundry and the National Center for Electron Microscopy. From left to right: Anabel Gonzalez (Costa Rica Minister of Foreign Trade), Alejandro Cruz (Costa Rica Minister of Science and Technology), Kristin Balder-Froid, Jennifer Ridgeway, Don DePaolo, Miquel Salmeron, President Laura Chinchilla Miranda, DOE JGI Director Eddy Rubin, Robert Kostecki, Mina Bissell, Hector Garcia Martin, and Rosio Alvarez.

Roy Kaltschmidt, LBNL

Fungal Lessons

continued from page 5

"Nearly a dozen additional *Aspergillus* strains that are used in industry are either being sequenced or in the queue to be at the DOE JGI," Grigoriev said. "A better understanding of genomic content and organization and how rearrangements and mutations lead to desired traits should facilitate further optimization of these strains for different bio-products."

Contact The Primer
David Gilbert, Editor / DEGilbert@lbl.gov

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