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The Future of Sequencing: Revisiting Kansas

BY MASSIE SANTOS BALLON

The Sequencing, Finishing, Analysis in the Future Meeting first convened in Santa Fe, New Mexico five years ago. Back then, the conference title was much shorter, and the crowd in attendance much smaller.

The 2006 Meeting primarily focused on genome finishing technologies and how new sequencing technologies would impact them. Over the years, the Meeting's focus has moved from simply genome finishing to how next generation sequencing technologies have affected genomics overall in assembly, finishing, annotation and analysis.

Claire Fraser-Liggett summarized the current state of genomic research succinctly in her opening keynote of the 5th annual meeting held June 2-4, 2010: "We're not in Kansas anymore, and yet we are."

Addressing a record crowd of 250 attendees, Fraser-Liggett discussed current sequencing technologies and applications while revisiting issues raised long before the first SFAF meeting ever convened, and these questions were echoed by other researchers over the course of the Meeting.

For example, Fraser-Liggett noted that the importance of finishing a genome is still being debated years after it was originally raised.

"Is genome finishing feasible? We're back in Kansas revisiting the same issues we had 15 years ago," she said. [For a discussion of finishing, see sidebar *cont. on page 4*

SFAF organizers (left to right): Chris Detter, DOE JGI/LANL; Donna Muzny, Baylor College of Medicine; Jessica Hostetler, J. Craig Venter Institute; Mike Fitzgerald, Broad Institute; Johar Ali, Ontario Institute for Cancer Research; Darren Grafham, Sanger Institute; David Bruce, LANL; Patrick Chain, DOE JGI/LANL. Not pictured: Alla Lapidus, DOE JGI and Bob Fulton, Washington University.

also in this issue

Photo by Armin Hallman, University of Bielefeld, Germany

Tracking Algal Complexity

The U.S. Department of Energy has been pursuing a diversified approach toward developing carbon-neutral transportation fuels. One contribution that may inform biofuels research is reported in the July 9 issue of *Science*, where researchers led by the DOE Joint Genome Institute (JGI) and Salk Institute present the full genome of *Volvox carteri,* a multicellular alga.

"What's particularly intriguing about *Volvox* is that it has learned how to selectively turn down photosynthesis or channel it to support another cell type," said DOE JGI collaborator and co-first author Jim Umen at the Salk Institute. "While we don't yet understand this trait well, it could factor into how photosynthetic organisms can be engineered to do what we want, such as make biofuels or other products, rather than what they typically do, which is grow and make more copies of themselves."

The *Volvox* genome was compared with that of its close relative, the unicellular alga *Chlamydomonas reinhardtii,* whose genome was made available three years ago by the DOE JGI. What the team found, according to DOE JGI bioinformaticist and co-first author Simon Prochnik, is "an astonishing lack of innovation" in the *Volvox* genome when compared with *Chlamydomonas*. "This really changed the notion of how complicated it is to become multicellular," he said. "The notion that 'if you're small, you're *cont. on page 8*

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Stinkbird Guts Promise Cleaner Fuel Future

BY NICHOLAS WRIGHT

The Amazon's hoatzin is a crested bird with a blue face, red eyes and a cow's stomach. Better yet, it is surrounded by the scent of manure. Postdoctoral researcher Filipa Godoy-Vitorino thinks the hoatzin seems "like a Dr. Seuss bird." Regardless of what it looks or smells like, this strange bird could provide bioenergy researchers with novel enzymes that can break down plant biomass for use in making cellulosic biofuels.

Godoy-Vitorino managed to stumble upon this incredible bird without being led by Dr. Seuss' Lorax. Instead she was immediately drawn into the prospect when it was described to her by microbial ecologist Maria Gloria Dominguez-Bello at the University of Puerto Rico, where she did her Ph.D work.

At the core of the hoatzin's digestive processes is its crop, an organ analogous to the cow's rumen, and the only one of its kind thus far found in a bird. Unlike other birds, the folivorous hoatzin eats mostly young leaves. Its crop, about the size of a tennis ball, is huge for the gut of a bird.

In a manner similar to the rumen, the continuously fermenting crop delays passage of the digesting contents, allowing for the fiber and dietary protein to be solubilized by microorganisms so the main protein intake by the host is a result of the lysis of crop bacterial cells by the gastric lysozyme of the bird's acidic stomach. Digestive fermentation allows the hoatzin to be a unique browsing bird and therefore, the crop harbors an impressive portfolio of previously uncharacterized microbes, which could contain novel enzymes (in particular through transcriptomics) that degrade plant cell walls.

The prospective novel cellulolytic enzymes may become useful for bioenergy production from waste biomass, a strategic focus of the U.S. Department of Energy. Godoy-Vitorino's Ph.D. work on the characterization of the crop bacterial biota through 16S cloning and PhyloChip found novel cellulolytic-like bacterial lineages. Based on these findings, in 2008 Dominguez-Bello proposed that the DOE JGI sequence the hoatzin foregut contents under the Community Sequencing Program (CSP).

Filipa Godoy-Vitorino studies the only known folivorous bird — the hoatzin.

To study the hoatzin, Godoy-Vitorino traveled to Venezuela, where collaborating scientists from the Venezuelan Institute of Scientific Research (IVIC) and experts in the hoatzin physiology helped her track down the birds. The hoatzin make their nests relatively close to the ground along rivers; they're short distance flyers due to their heavy stomach and chicks dive into the water to avoid predators, returning to the nests with the help of their wing claws. Thus far, Godoy-Vitorino, now an NSF postdoctoral fellow hosted by Phil Hugenholtz* and more recently Susannah Tringe's group at the DOE JGI, has had samples from 16 birds — both chicks and adults — sequenced using the Roche 454 platform, generating about 125 million base pairs so far. The aim of the 454 pyrotags (used for sequencing 16S rRNA genes) is to profile the microbiota in the fiber and epithelial fractions of the crop previous to select samples for metagenomics analyses based on community stability and presence of potential fiber-degrading species.

Photo by M.G. Dominguez-Bello, University of Puerto Rico

The project promises to provide information about cellulose biodegradation unique to the hoatzin's gut, highlighting mechanisms not found in the cow's gut. "The hoatzin's dietary leaves have biochemical compounds (secondary metabolites), which are very toxic to the host. So these microbes are capable of degrading these phytotoxins. Since cows don't eat these different types of leaves and are restricted to grasses we believe that there must be a really unique community that is able to degrade these toxic compounds," said Godoy-Vitorino.

Comparisons between the microbial diversity and metagenomic data from the hoatzin crop to those of ruminants (including the cow) and other bird guts could be of great interest to population biologists, and will improve the understanding about the extent to which microbial communities are shaped by hosts, as well as by organ function and substrates. After the publication of this preliminary community structure data, Godoy-Vitorino said, the metagenome is next, as they look to provide a more conclusive picture of the overall function of the gut.

**Hugenholtz is now Professor and Director of the Australian Center for Ecogenomics at the University of Queensland (Australia).*

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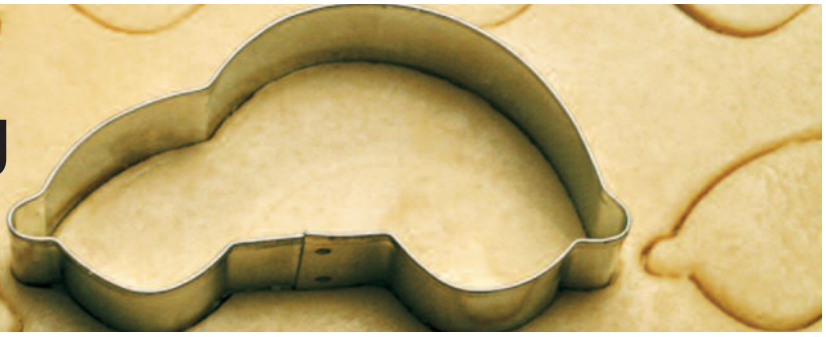
Standardizing biomass



BY MASSIE SANTOS BALLON

The California Biomass Collaborative's Seventh Annual Forum made it clear: California has a lot of biomass waiting to be converted, and these aren't just agricultural residues.

For example, according to the Central Valley Water Quality Control Board, California's Central Valley has 1.6 million cows that each produce 112 lbs of manure a day. According to CalRecycle, the state agency in charge of recycling and waste reduction, of the more than 20 million tons of organic matter produced by the state of California, less than two million tons are being used for bioenergy while 15 million tons currently go to landfills. Also, the state's forestry and fire protection division has estimated that there are roughly 10 million dry tons of forest and wood manufacturing residues that can be harvested from the 33 million acres of state forests.

As the California Energy Commission's Jim McKinney noted, however, these biomass resources have to be harvested and used in a manner that meets state and federal quality standards for air, water, and carbon dioxide emissions.

"Compliance with the law does not equal sustainability," McKinney said, defining the term as meeting present needs without impacting the ability of future generations to do so. "Can we get more energy-producing materials out of California while doing less environmental damage?"

Held on May 10-11, 2010 at the University of California, Davis, the talks focused on the challenges of sustainably extracting biomass from a variety of sources to make cellulosic ethanol a viable competitor against petroleum.

Many of the talks concerned standards to ensure that the biomass is processed in a manner that does not adversely impact the environment and can be used by the biofuel production facilities. But while most of the discussion featured standards that would be imposed on groups and industries, one of the presentations featured a voluntary standard being drafted by the Council on Sustainable Biomass Production, a nonprofit organization composed of academics, biotech researchers and representatives from the petroleum industry.

The voluntary standard adheres to existing regulations such as the federal Renewable Fuels Standard and includes requirements to monitor soil nutrient and water quality levels, avoid introducing potentially invasive biofuel feedstock crops and conduct periodic lifecycle assessments to check the emissions from producing and processing production-ready biomass from only field and forest sources.

Council member John Heissenbuttel, who spoke at the Forum, said the standard originally focused solely on biomass crops such as switchgrass but was amended quickly as the group realized that agricultural and forest residues would be the primary start-up sources of biomass. He explained the decision to have landowners opt in to the certification process — and the goal is to have most growers do so — was based on his decades of experience in the forestry industry.

In California, he said, the state forest practice laws were avoided because so much land is under a voluntary sustainability standard. "The state determined there was no need to regulate," Heissenbuttel said, "which saves money. If you can regulate yourself, save the state money and avoid the cookie cutter approach."

Another advantage of opting in would be driven by market preference. Heissenbuttel cited the case of a winegrowers collective that developed their own grape-producing standards in the Lodi region; their product is exclusively sourced and used by some wineries in the Napa Valley.

The draft standard has been posted on the Council's website since late 2009 and is currently being tested in several states, including Kansas, Nebraska, Iowa, Missouri, Tennessee and Pennsylvania. A second round of testing and standard redrafting is scheduled for next year, with the final version of the standard to be released late 2012, timed to the planting season. Among the draft revisions that need to be made by the Council is a decision on which lifecycle assessment model to base their standard on. At the moment, Heissenbuttel said, the group is considering all models.

A video of Heissenbuttel discussing the draft standard can be viewed at http://bit.ly/9nEe4q. Videos and slides of the talks are available online at http://biomass.ucdavis.edu/f2010.html.

SFAF Meeting *cont. from page 1*

on next page.]

Answering Fraser-Liggett's question in his keynote address on the second day, Chad Nussbaum, co-director of the Genome Sequencing and Analysis program at the Broad Institute, pointed out that the quality of the consensus data being generated these days "is really good now, better than finished genomes 10-15 years ago."

"Capillary electrophoresis is not dead; it just changed what it does."

–Michael Rhodes, Life Technologies

The continuing advances in sequencing technologies and the resulting drop in associated costs was the basis of another common talking point: the fate of large genome centers in an era where sequencing is affordable and accessible to all.

"This is the third time I've heard 'death of the genome center'," remarked Michael Rhodes of Life Technologies who also countered the idea that tried-and-true Sanger sequencing — and therefore the technology used for this process — has fallen by the wayside.

His comments echoed those made earlier by Jim Bristow, Deputy Director of Programs at the DOE JGI. Bristow pointed out that one advantage large genome centers have is that they are better equipped to manage and store the large amounts of sequencing data being generated than a small university lab.

"If you've got $1 million lying around you can get these next generation sequencers and produce as much sequence as the JGI," he quipped. He also noted that large genome centers have the post-sequencing capabilities required to tackle assembly and annotation, while also developing tools for comparative analysis.

Among the tools that need to be developed, said DOE JGI Genome Biology Program head Nikos Kyrpides, are standards for microbial genomics and metagenomics, as well as updating the standards for sequencing genomes. Kyrpides gave a talk on the future of microbial genomics before coming back on the last day to fill as the closing keynote speaker, where he noted that having a variety of sequencing technologies that can perform a myriad of applications continues to raise new challenges.

"Thanks to sequencing technologies our lives as bioinformaticians are becoming increasingly more difficult as we need to come up with different processes to adapt," he said. "Am I complaining? No."

The final day of the meeting revisited Fraser-Liggett's remarks that while sequencing techniques and technologies have advanced, making researchers more comfortable with conducting metagenomic analyses, the study of microbial communities is being advanced at the cost of the ability to study separate populations.

Metagenomics pioneer Jill Banfield of the University of California, Berkeley led off the discussion of studying individual microbial populations, including those considered unculturable, and referenced the need for better tools for manual curation and analysis to scale up the approach.

"NASA has been studying the stars. We know there are more microbes on Earth than stars in the universe and it's time to turn a microscope on Earth."

– Nikos Kyrpides, DOE JGI

Banfield called for high throughput sequencing to shift the perspective of metagenomics from treating the community as a single population to studying separate populations in a community. One reason for doing so, she said, is that closely related strains can be ecologically distinct and have different functions within an ecosystem.

The process recently (see page 6) allowed her group to recover genomes from ARMAN — short for Archaeal

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Richmond Mine Acidophilic Nanoorganisms — organisms "we didn't even know existed" isolated during her pioneering collaboration with the DOE JGI to sequence acid mine drainage microbial communities.

The metagenomics approach was later compared with that of single cell genomics, starting with DOE JGI's Tanja Woyke, who described a collaboration with former University of Arizona collaborator Nancy Moran (recently tapped as Yale's inaugural William H. Fleming, M.D. '57 Professor of Ecology and Evolutionary Biology) to isolate, sequence and finish a bacterial genome using a single cell (see page 7).

Woyke said the accuracy of the single cell *Sulcia* genome recovered by her team was compared against the genome recovered using a metagenomic approach. She noted that single cell techniques still face several challenges, among them contamination issues, uneven amplification of the genome and the time it currently takes to complete a project.

"Reducing the cost of sequencing doesn't reduce the cost of finishing."

– Karen Davenport, LANL

Wrapping up the session, single cell genomics pioneer Roger Lasken of the J. Craig Venter Institute delivered the final talk of the meeting, which not only compared the two sequencing approaches but also posed the possibility of combining the two techniques.

Videos of talks from the Meeting are available on the DOE JGI's SciVee channel at http://www.scivee.tv/node/18827

The Finishing Touch

Advances in sequencing technology have provided researchers with a variety of potential applications and projects, but they've also extended the debate over finishing a genome.

Finishing refers to the process in which contiguous segments of DNA sequence are linked to one another and the assemblies are verified. The process results in a high quality genome sequence made available to the scientific community. However, noted DOE JGI Finishing/Genome Assembly Group Lead Alla Lapidus, finishing a genome requires significant investments in terms of time and money to develop the software tools and cultivate the skills needed to work on the project.

"Finishing takes time, anywhere from two months to two years," Lapidus said. "Drafts can be obtained very quickly."

Given the commitment involved, some researchers choose to stick with draft genomes.

This is fine if the gene or pathway of interest is covered in the draft sequence, Lapidus noted, but sometimes that may not be the case. For example, she said, draft sequences generated by the Sanger sequencing method cover as much as 99.8 percent of the genome. In comparison, Lapidus estimated that sequence generated by Illumina machines would need hundreds-fold coverage in order to provide equivalent genetic information.

"In terms of quality, a finished genome can serve any purpose," she said. Her comments were echoed by a Microbial Genome and Metagenome (MG-M) programs advisory committee of external scientists representing sectors such as the Bioenergy Research Centers, single cell genomics, microbial ecology and high-performance computing who were convened by Microbial Genomics Program head Tanja Woyke at the recent 5th DOE JGI User Meeting.

Woyke said the decision to finish a genome is best made at the outset. The problem with revisiting a draft genome several years after it is made available, she said, is that the sequencing and finishing technologies may have changed dramatically and the researcher may find it more cost-effective instead to sequence the genome all over again to produce a nearly base-perfect sequence.

After seven years in Walnut Creek, Alla Lapidus has accepted the position of Lead Bioinformatician for the Institute of Personalized Medicine (IPM) and an Associate Professor at the Fox Chase Cancer Center (FCCC) in Philadelphia. Lapidus will start there August 1 and after that can be reached at Alla.Lapidus@fccc.edu.

The MG-M advisory committee's top recommendation was "to maintain the current resource allocation to microbial genome finishing." As the DOE JGI moves forward, Woyke said one of the goals is to continue to finish 150 microbial genomes per year, but to also produce high-quality draft genomes to meet community needs.

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DOE JGI Leads First Amphibian Genome Publication

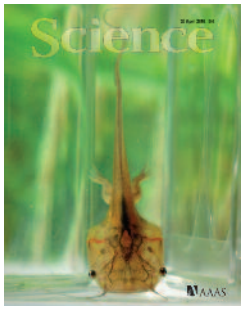

Photo by Siwei Zhang, Jingjing Li, Enrique Amaya/Univ. of Manchester (UK), Courtesy of Science

A late-stage *Xenopus tropicalis* tadpole, with emerging hindlimbs.

The genome of Western clawed frog *Xenopus tropicalis,* a native of subSaharan Africa, was reported by DOE JGI researchers and appeared on the cover of the April 30, 2010 issue of *Science*.

The project was led by DOE JGI Plant Genome Program and Computational Genomics head Dan Rokhsar, UC Berkeley professor of molecular and cell biology Richard Harland, and DOE JGI bioinformaticist Uffe Hellsten, as well as 46 other scientists from 24 institutions.

While the research could help scientists better understand the factors causing the vast die-off of amphibians around the planet, scientists are also excited about having a new tool to understand how genes work at the most basic level. The *Xenopus tropicalis* genome is composed of more than 1.7 billion chemical bases across 10 chromosomes.

"The availability of the *Xenopus* genome also opens up the possibility of studying the effect of endocrine disruptors at the molecular and genomic level," said DOE JGI bioinformaticist and study first author Uffe Hellsten. "When you look at segments of the *Xenopus* genome, you literally are looking at structures that are 360 million years old and were part of the genome of the last common ancestor of all birds, frogs, dinosaurs and mammals that ever roamed the earth."

For more information, see the U.C. Berkeley news release: http://berkeley.edu/news/media/releases/2010/04/29_xenopus_genome.shtml

Sequencing the Smallest Known Life

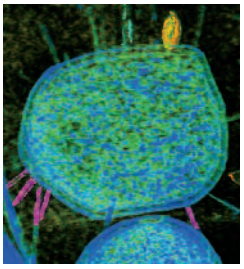

Photo by Luis R. Comolli & Cristina E. Siegerist, LBNL

In the depths of a former copper mine in Northern California dwell what may be the smallest, most stripped-down forms of life ever discovered. As reported in the April 26, 2010 issue of *Proceedings of the National Academy of Sciences,* the microbes, members of the domain of one-celled creatures called *Archaea*, are smaller than all other known microorganisms. The only potential exception is a microbe that can survive solely as a parasite attached to the outside of other cells.

The copper mine microbes are about as large as the largest viruses, which can replicate only in living organisms but are not considered to be living. Their genomes, sequenced at the DOE JGI, are among the smallest ever reported at only a million base pairs. Researchers led by DOE JGI collaborator Jill Banfield named them ARMAN for archaeal Richmond Mine acidophilic nanoorganisms.

"ARMAN are among the smallest microbes we know of that, if not free-living, are at least not permanently obliged to be a parasite or symbiont," noted co-author Luis R. Comolli, a microscopist at Lawrence Berkeley National Laboratory (LBNL). Banfield's group first described the ARMAN microbes four years ago, after identifying the organisms in acidic pools in the Richmond Mine in Iron Mountain, Calif.

The team's continued analysis has revealed amazing organization within the mine drainage biofilm communities that grow on solutions with the acidity of battery acid. The new data will help the researchers further explore the community of organisms in the mine and determine how they are able to live in such harsh conditions.

A Tool for Genome Quality

DOE JGI software developer Amrita Pati

More than a thousand microbial genomes have been sequenced in the past 15 years, and the number is expected to reach 10,000 within the next two years as scientists study their roles in tasks ranging from bioenergy to health to environmental cleanup. However, the establishment of genomic standards has lagged behind the technological advances that have made the sequencing process faster and cheaper. As a result, the DNA sequences being released have had varying levels of quality, impacting researchers' ability to reliably use the information.

To assist in checking the quality of the microbial DNA sequences generated, the DOE JGI developed a quality control tool known as the Gene PRediction IMprovement Pipeline or GenePRIMP, which was described in a paper published in the June issue of *Nature Methods.*

First author Amrita Pati, a software developer in the DOE JGI's Genome Biology Program, noted that GenePRIMP double-checks the gene boundaries, gene annotations and unannotated intergenic regions in genome sequences after the finishing process, regardless of the software originally used. She also said that the program identifies gene-calling errors such as potentially incorrect gene start and end positions, large overlaps between genes, fragmented genes and missed genes. The end result, noted senior author Nikos Kyrpides, head of the DOE JGI Genome Biology Program, is a more standardized output that allows researchers to conduct comparative analyses of genomes with greater ease.

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Cataloging the Human Microbiome Project

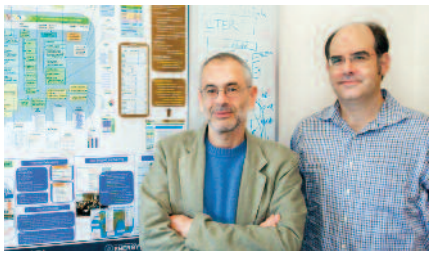

Photo by Roy Kaltschmidt, LBNL

A human being is actually a "supraorganism": a collection of human cells and microorganisms that interact with each other. To better understand the full complement of microorganisms populating the human body, in 2008 the National Institute of Health (NIH) launched the Human Microbiome Project (HMP).

The project goal is to sequence the genomes of 1,000 or more of these microbial species and assemble the information in a project reference catalog. This catalog is housed at the HMP Data Acquisition and Coordination Center (DACC), created and maintained by researchers at the DOE JGI and Lawrence Berkeley National Laboratory and supported by the NIH.

"The HMP project catalog is a unique worldwide resource," said Nikos Kyrpides (above right), head of the Genome Biology and Metagenomics Programs for the DOE JGI and the co-principal investigator of the DACC along with Victor Markowitz (above left), the Chief Informatics Officer and Associate Director at the DOE JGI. "It has a central role in the HMP, not only in maintaining the list and status of over 1,400 individual human microbiome projects, but also as a data managements system for the metadata associated with these projects."

Systems such as GenePRIMP (Gene PRediction IMprovement Pipeline) (see description on previous page), GOLD (Genomes On-Line Database) and IMG/M (Integrated Microbial Genomics with Microbiome Samples) developed by Kyrpides and Markowitz have provided the backbone for the HMP catalog.

"As the HMP moves forward, these resources will provide support for the annotation and analysis of HMP datasets, in particular via the metagenome annotation pipeline at JGI and a HMP specific version of the IMG/M system," Markowitz said.

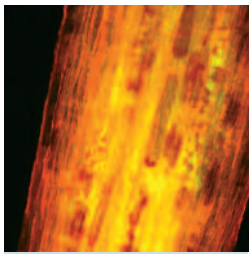

Photo by Brookhaven National Laboratory

Certain Bacteria Help Tree Growth

Despite the negative connotation, some invasive bacteria actually help plants thrive. Scientists at Brookhaven National Laboratory published the genome of one such microbe on May 13, 2010 in *PLoS Genetics*. Their work also identified a wide range of genes that help explain the symbiotic relationship between these bacteria and plants.

The Brookhaven team found *Enterobacter* (sp. 638) in the roots of poplar trees and previous studies by DOE JGI collaborator Daniel (Niels) van der Lelie and his colleagues have shown that this bacterium increases poplar growth by as much as 40 percent.

"Poplar is a model species for biofuel production, in part because of its ability to grow on marginal soils unsuitable for food crops," said van der Lelie, who leads Brookhaven's microbial ecology research program.

Combining work done at the DOE JGI, Brookhaven and the University of South Carolina, the scientists were able to identify a complete set of genes that help the bacteria *Enterobacter* (sp. 638) aid poplar growth. The studies also revealed remearkable interactions between the microbe and the tree that both survive and thrive. The work could move growth-promoting bacteria one step closer to being useful for improving biofuel feedstocks and improving agricultural crop production.

JGI Reports First Whole Uncultured Genome

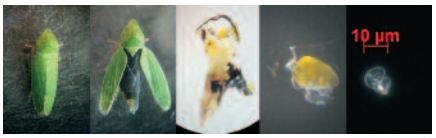

Photo by Damon Tighe, DOE JGI

In the April 23, 2010 edition of *PLoS ONE,* a team of DOE JGI researchers led by Tanja Woyke reported the first closed and finished genome derived from an uncultured bacterial cell. The team extracted a single cell from the bacteria *Sulcia muelleri* DMIN that reside in the gut of a wild sharpshooter bug caught in Berkeley, Calif. and used it to generate a 243,933 bp genome using 454 and Illumina technologies.

"Most of the microbial genomes sequenced to date are derived from organisms cultured in the laboratory," said DOE JGI Director Eddy Rubin. "We estimate that roughly 99.9 percent of the microbes that exist on this planet currently elude standard culturing methods. The power of single cell genomics is that it offers us the ability to sort out one cell from a complex environmental sample, liberate the DNA from that cell, and enzymatically produce millions of copies of that genome so that we have enough DNA to sequence it and characterize its metabolic potential."

To verify the accuracy of the single cell genome, the team used metagenomics to independently reconstruct a nearly identical *Sulcia* genome. "While the current single cell approach leaves room for improvement with respect to the elimination of exogenous DNA contamination and reduction of the amplification bias, this study represents a proof-of-principle for the reconstruction of high quality, finished single cell genomes from uncultured, environmental species," Woyke and her colleagues concluded.

Sharpshooters are considered to be important species of insect vectors for Pierce's disease (affecting wine grape production) and alfalfa dwarf diseases in the Central Valley of California.

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Marc Lepage, Special Advisor for Climate Change and Energy to the Canadian government (right), remembers shovelling earth over the 54-inch poplar sapling in front of the DOE JGI after the first tree genome was published in the journal *Science* in September 2006. Four years later, he returned to the DOE JGI to find a tree measuring 25 feet 6 inches tall with a girth of 13 inches at the base.

Lepage revisited the DOE JGI on June 23 with Geoff Munro, Chief Scientist and Assistant Deputy Minister of the Innovation and Energy Technology Sector at Natural Resources Canada (second from left) and Diana Zandberg of the Political/Economic Relations and Public Affairs division at the San Francisco, Calif. –based Consulate General of Canada (center). The trio met with Deputy Director of Programs Jim Bristow, Genetic Analysis and Genomic Technologies Head Len Pennacchio (left), Fungal Genomics Head Igor Grigoriev (second from right) and Plant Genomics Program Head Dan Rokhsar.

Volvox *cont. from page 1*

simple' is starting to unravel. The more unicellular organisms we sequence, the more we see this."

David Kirk, professor emeritus at Washington University of St. Louis and a study co-author, predicted that the community working on *Volvox* will grow significantly over the next five years due to the availability of the genome. "The work that I've been interested in all my life, which is understanding the origin of multicellularity in this group has only just begun with the sequence of the genome," said Kirk, who is known as "the grandfather of *Volvox* biology." "Now the answers are going to be much more readily accessible. I sort of wish I had been born later so I could participate, but I'm going to be on the sidelines cheering."

Finishing Touch *cont. from page 5*

The finishing selection process, she said, will be based on a number of criteria, including relevance to the DOE missions, the organism's location on the Tree of Life and the degree of difficulty.

"You can finish everything, but is it cost-effective or not?" Lapidus asked.

For many researchers, the answer is, "Yes." In their report, the committee noted that "finished genomes provide indispensable reference material." Lapidus commented that one of the reasons the DOE JGI stands out from other sequencing centers is the facility's commitment to finishing microbial genomes.

"No one's producing as many finished microbial genomes as we are," she said.

GOT HIGHLIGHTS?

Has your research benefitted from genomic information from the DOE JGI (e.g., a paper in press based on the data)? If so, contact Public Affairs Manager David Gilbert at degilbert@lbl.gov. Every week the DOE JGI highlights current publications from researchers and collaborators that were made possible by the genomic data generated, and shares that information with the Department of Energy. In return for submissions, researchers will receive a set of educational flash cards featuring some of the DOE JGI's sequencing projects.

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