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DOE JOINT GENOME INSTITUTE
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Phytozome Gets Juiced Up

The first two citrus genome sequences have been added to the publicly available database Phytozome, a project of the DOE JGI and the Center for Integrative Genomes. In an announcement made by Fred Gmitter, Jr., head of the International Citrus Genomics Consortium and a citrus geneticist at the University of Florida, on January 15 during the Plant and Animal Genome (PAG) XIX conference in San Diego, Calif., the annotated sequences of sweet orange (*Citrus sinensis*) and the Clementine mandarin (*Citrus clementina*) join two dozen other plant genomes, many of which were sequenced at the DOE JGI. [To see the list of other DOE JGI-related presentations during PAG XIX, go to page 5.]

"Citrus is the most economically significant and widely grown fruit crop in the world," said Gmitter, who added that in the United States alone, the citrus industry is worth $20 billion annually. "However, these industries are under attack by several plant pathogens that debilitate the trees and are highly contagious, stimulating very significant investment of grower dollars in research to seek solutions."

Grown in more than 100 nations, the *C. sinensis* genome was the first collaboration between the DOE JGI and the University of Florida, born out of a 2004 proposal from the ICGC and the U.S. National Citrus Genomics Steering Committee. The sequence was generated at the University of Florida Interdisciplinary Center for Biotechnology Research and Roche 454 Life Sciences, using 454 technologies. In addition, DOE JGI had previously produced some Sanger sequence in an interagency pilot project. The data are expected to assist geneticists and breeders focused on improving one of the world's most important fruit crops.

Image by Scott Bauer, USDA

THE PLANT PAGES

Check out page 5 for DOE JGI-relevant talks at the Plant and Animal Genome (PAG) XIX Conference

January 15-19, 2011
San Diego, California

The *Cucumis sativis* (cucumber) genome, sequenced by Roche with 454 technology, can be found in Phytozome.net.

A second citrus genome project was begun in 2007, once again involving the DOE JGI and the ICGC. A sample of the haploid Clementine was provided by Spain's Instituto Valenciano de Investigaciones agrarias (IVIA) and the plant's sequencewas generated at the DOE JGI, France's Genoscope and Italy's Instituto di Genomica Applicata (IGA) and then assembled at the HudsonAlpha Institute for Biotechnology by a team led by Jeremy Schmutz before being annotated at the Walnut Creek, Calif.-based Institute. Spain's LifeSequencing also contributed 454-derived Clementine transcriptome and genome sequences to the project. DOE JGI Plant Genomics Program lead Dan Rokhsar noted that Schmutz and the international sequencing colleagues are working on a chromosome-scale assembly that is expected to be made available later this year.

"Citrus is a diverse genus, but we know very little about how sequence variation gives rise to phenotypic differences," said Gmitter, who noted that the availability of these two citrus genomes only marks the beginning of citrus genomics (see more information on page 3). "We haven't yet done a deep comparison of the two sequences, but once undertaken this will be a critical first step to better understand inter- and intra-species variation in citrus. As more plant genomes find their way to Phytozome, it is becoming more widely recognized as a first source for genome researchers looking to exploit genome sequences in their research."

continued on page 4

Growing Interest in the "Go To" Site for Plant Genomics

Jeff Dangl is the John N. Couch Professor of Biology at the University of North Carolina at Chapel Hill and a member of the DOE JGI's Scientific Advisory Committee. In 2009 Dangl received the American Society of Plant Biologists' Stephen Hales Prize in recognition of "his role in developing the concepts and elucidating the fundamental mechanisms that govern plant-pathogen interactions" and was recognized by the International Society for Molecular Plant-Microbe Interactions for his pioneering research.

The Dangl Lab employs the model plant species *Arabidopsis thaliana* to identify the sequence information necessary for plants to mount a resistance reaction against phytopathogenic bacteria and fungi. *A. thaliana* was one of the first plant genomes made available on the web portal Phytozome, and Dangl took a few minutes away from his research to discuss how the genome's accessibility benefits his lab and other researchers around the world.

For the community of plant biologists, are there knowledge gaps that the DOE JGI's plant sequencing projects have begun to address?

A: Many! JGI is the "go to" site for plant genomics, mostly because the project portfolio is so broad. The DOE JGI sequencing efforts, driven by the Community Sequencing Program (CSP) and by in-house bioenergy needs, have resulted in genomes and genomics analysis tools that span from lower plants like moss to highly complex bioenergy species like poplar.

How has your lab's research been advanced by access to and use of Phytozome?

A: We have used Phytozome to analyze several plant protein families that are of interest to our group. We use fairly typical features, like the construction of evolutionary trees, and alignment tools to understand structure-function relationships that we can then use to construct and test mutants.

Image courtesy of Jeff Dangl

Where do you see the DOE JGI's contributions taking plant biology and, more specific to your interests in plant cell structure and virulence factors, in the future?

A: I hope that the DOE JGI continues to be the place where the breadth of plant genomics can be experimentally approached. Unlike "animal genomics," which is essentially all about human health, we humans use a diversity of plants for a diversity of purposes and it's therefore necessary to actually build a tool kit for plants across that breadth. The DOE JGI has been a leader in that effort. I hope that the DOE JGI will be able to "add value" to their genomes by developing new informatics-based tools with which to assemble "next gen" sequencing projects and with which to understand genotype to phenotype correlation, from mRNA expression atlases in various species to understanding and exploitation of natural variation within important species.

Anything else that you would care to add?

A: My own personal interest is to bring the power of reductive genetics and genomics to bear on understanding how plants and microbes form stable mutualistic and symbiotic relationships in the complex environments of the rhizosphere (the soil region where plant-microbe interactions take place) and phyllosphere (the total above-ground plant surfaces). To this end, I hope that the plant genomics and metagenomics groups at the DOE JGI start to have overlapping interests that will propel the definition of plant-associated metagenomes to as high a level of understanding as currently emerging in the studies of human microbiomes.

Revisit Dangl's talk on a "Plant Genomics Roadmap" from the 2009 DOE JGI User Meeting at http://bit.ly/dXKVTM

POLISHING SEQUENCE QUALITY

After sequencing and assembling a draft genome, the data is improved by repeat resolution, gap closure and polishing.

One DOE JGI tool that resolves base calling errors from sequences run on the 454 platform by aligning Illumina read data to the draft assembly is known as Polisher. Developed by Stephan Trong and his colleagues in the Finishing group, the software looks at Illumina data to correct consensus errors and supports correctly called bases that might be considered "below standard quality."

The software requires the Arachne genome assembler developed by the Broad Institute and the graphical assembly viewer Consed. The Fasta sequence of the draft is aligned to Illumina reads using Arachne and the regions where 70 percent of the Illumina coverage disagree with the sequence are targeted. Corrections such as insertions and deletions are made in these low quality regions are made after they've been verified with the Illumina data.

The Polisher software is freely available to interested academic parties. Contact degilbert@lbl.gov.

Orange You Glad?

Citrus geneticist Fred Gmitter, head of the International Citrus Genome Consortium, answers five questions regarding the genomic collaborations between the ICGC and the DOE JGI released in January 2011 on Phytozome and announced during the PAG XIX Conference.

What were the DOE JGI's contributions to the sweet orange genome project and the Clementine project?

A: The pilot for the sweet orange genome started as a DOE JGI Community Sequencing Program (CSP) project. Several years later, Roche 454 Life Sciences and the University of Florida (UF) teamed up to produce deep coverage of this diploid with 454 sequence, funded in part by the Florida Citrus Production Research Advisory Council (FCPRAC), a citrus industry organization that funds research with grower self-taxed funds. The assembly and annotation of this outbred genome was done by scientists from Roche, the University of Florida, Georgia Institute of Technology and the DOE JGI.

In parallel, the ICGC had been formed in 2003 to secure funding to produce a reference genome for citrus, and selected a haploid Clementine mandarin tree as the ideal substrate for sequencing to avoid problems associated with assembling heterozygous genomes. The ICGC met for several years at the DOE JGI in Walnut Creek, and later at Genoscope, to plan strategy and coordinate activities to produce this haploid genome sequence. In the last year and a half, sequencing began in earnest, led by Genoscope in France, the Istituto di Genomica Applicata (IGA) in Italy, and the DOE JGI in the US, including both Walnut Creek and HudsonAlpha campuses. This was the last major Sanger sequencing project at the DOE JGI, and the resulting sequence assembly is of extremely high quality. It will serve as the citrus reference genome for the analysis of sequence variation in a host of applications.

What is the benefit of having the information available on JGI's Phytozome portal?

A: Phytozome is becoming more widely recognized as a first source for genome researchers looking to exploit genome sequences in their research. Citrus is in the malvid clade along with cotton, papaya, brassicas (broccoli, Chinese cabbage, cauliflower, canola), and *Arabidopsis*. So it is in a critical position for comparative analysis to identify core conserved genes and genetic elements on the one hand, and to study novel and/or rapidly changing genomic features that are more variable on the other hand.

What do researchers get out of having two citrus genomes available?

A: Citrus is a diverse genus, but we know very little about how sequence variation gives rise to phenotypic differences. Even the hybrid origin and diversification of the sweet orange is mysterious and shrouded in antiquity, in the same way that domesticated dog breeds are. The higher quality, Sanger-based haploid Clementine genome will serve as the foundation for efforts now beginning to take place that will explore further the genetic and allelic diversity within citrus and its wild relatives. Although the two projects aren't directly comparable because sweet orange is a rather heterozygous diploid and the Clementine DNA source is haploid, we also get to compare and contrast different strategies for genome sequencing.

How does the taxpaying public benefit?

A: The U.S. Department of Energy supported the citrus pilot; the rest of the work at the DOE JGI was paid for by other sources, notably the Florida citrus industry (FCPRAC) and the Brazilian government. So, the expertise in plant genomics that has built up with DOE funding over the years, and the capacity for high-throughput sequencing, was harnessed for the citrus project but it didn't take funds from our bioenergy related work.


Courtesy of Fred Gmitter

ICGC head Fred Gmitter

Citrus is the most economically significant and widely grown fruit crop in the world, and likewise in the US. The most serious threat is a disease known as Huanglongbing (HLB, or "citrus greening"), which threatens potential extermination of the citrus industries in the US and Brazil. It is the grave danger posed by HLB that has stimulated very significant investment of grower dollars in research to seek solutions. At the center of the research agenda has been these sequencing efforts, to provide tools for the broad range of citrus research projects aimed at mitigating the HLB threat through improved diagnostic technologies, understanding the underlying genetic basis for symptom development in highly susceptible and more tolerant citrus accessions, and devising genetic strategies for resistance and possible therapy.

What's next?

A: With the ever increasing efficiency and decreasing cost of sequencing technologies, many other citrus genomes of economic, scientific, or regional significance will be explored to understand and to utilize the genetic diversity within the gene pool, not only to improve disease resistance, but also to address the full gamut of opportunities to improve tolerance of environmental stress, productivity, and the nutritive and human-health promoting properties of this most important fruit crop.

Developed as a centralized web portal for comparative plant genomics, Phytozome.net provides the scientific community with access to a rapidly growing number of plant genomes, as well as tools for visualizing and analyzing the information. The portal presents gene clusters that represent modern descendants of ancestral gene sets, constructed at 10 key phylogenetic nodes that can be used to access clade-specific relationships. Where possible, each gene has been annotated with PFAM, KOG, KEGG, and PANTHER assignments, and publicly available annotations from RefSeq, UniProt, TAIR, JGI are hyperlinked and searchable.

Not counting the citrus genomes, the genomes most recently added to Phytozome are of the Colorado blue columbine (*Aquilegia coerulea*), foxtail millet (*Setaria italica*) and the green alga *Volvox carteri*, which appeared in *Science* over the summer. Annotation updates for the first tree sequenced (*Populus trichocarpa*), cassava, *Chlamydomonas* and *Physcomitrella* were also made available in the November 2010 release.

More than half of the genomes available on Phytozome were predominantly sequenced at the DOE JGI in line with the U.S. Department of Energy missions of bioenergy and environmental applications. Plants considered as candidate feedstocks for biofuel production such as poplar and *Sorghum bicolor* — the second-most prevalent possible biofuels crops in the United States — are being studied to learn more about how plants convert solar energy to chemical energy. Other plants such as the alga *Chlamydomonas* and the monkeyflower *Mimulus guttatus* are being studied for their ability to sequester carbon and to understand how they cope with toxic pollutants in soils, respectively.

Right: Papaya image by Peggy Greb, USDA; Cassava image courtesy of Neil Palmer/CIAT; Peach image courtesy of Clemson University; Foxtail millet image by Wayne Dixon Photography

Colorado blue columbine

The plant genomes currently available on Phytozome (http://phytozome.net/) are:

Organism	**common name**
Aquilegia coerulea	Colorado blue columbine
Arabidopsis lyrata	Lyre-leaved rock cress
Arabidopsis thaliana	Thale cress
Brachypodium distachyon	Purple false brome
Carica papaya	Papaya →
Chlamydomonas reinhardtii	Green algae
Citrus clementina	Sweet orange
Citrus sinensis	Clementine mandarin
Cucumis sativus	Cucumber
Glycine max	Soybean
Manihot esculenta	Cassava →
Medicago truncatula	Barrel medic
Mimulus guttatus	Monkey flower →
Oryza sativa	Rice
Phycomitrella patens	Moss
Populus trichocarpa	Poplar
Prunus persica	Peach →
Ricinus communis	Castor bean
Selaginella moellendorffii	Spikemoss
Setaria italica	Foxtail millet →
Sorghum bicolor	Sweet Sorghum
Vitis vinifera	Grape
Volvox carteri	Volvox
Zea mays	Maize

DOE JGI at PAG XIX (January 15-19, 2011) The full agenda is online at http://bit.ly/gCMMjR

Saturday, 15 January 2011		
8:00 am - 12:30 pm	**Fruit and Nut Crops Workshop**	**San Diego Room**
8:25 am	**Ignazio Verde,** Instituto di Genomica Applicata, Udine, Italy *Whole Genome Resequencing Reveals a Reduced Nucleotide Variability in Peach*	
10:20 am - 12:30 pm	**Speciation Genomics Workshop**	**Pacific Salon 1**
11:40 am	**John Willis,** Duke University *Genetic basis of reproductive isolation in* Mimulus	
1:30 pm - 3:40 pm	**Barley Workshop**	**San Diego Room**
	Gary Muehlbauer, Department of Agronomy and Plant Genetics, University of Minnesota *Sequencing the barley genome in 2011*	
1:30 pm - 3:40 pm	**Citrus Genomic Workshop**	**Royal Palm Salon 5 & 6**
	Fred G. Gmitter Jr., Citrus Research and Education Center, University of Florida-IFAS *The Haploid Mandarin And Diploid Sweet Orange Genome Sequences*	
3:50 pm - 6:00 pm	**Bioenergy Grass Genomics Workshop**	**Pacific Salon 4 & 5**
5:20 pm	**Andrew H. Paterson,** University of Georgia *Comparative genomics of* Sorghum, Saccharum, *and* Miscanthus	
3:50 pm - 6:00 pm	**Non-Seed Plants Workshop**	**Sunrise Room**
4:20 pm	**John Archibald,** Dalhousie University *The genomes of nucleomorph-bearers*	
5:00 pm	**Andrew C. Cuming,** University of Leeds *The* Physcomitrella *genome: the flagship resource for comparative plant genomics*	
Sunday, 16 January 2011		
8:00 am - 6:00 pm	**Forest Trees Workshop**	**Sunrise Room**
8:10 am	**Gerald Tuskan,** Oak Ridge National Laboratory *Assembly and Annotation of the Eucalyptus Genome Sequence*	
3:40 pm	**Jeff Dean,** University of Georgia *The* Pinus taeda *BAC Browser*	
1:30 pm - 6:00 pm	**Cacao Genome Sequencing & Cacao Breeders Workshop**	**Pacific Salon 6 & 7**
2:00 pm	**Jeremy Schmutz,** HudsonAlpha Institute for Biotechnology *Sequencing And Assembly Of The Cacao Genome*	
3:50 pm - 6:00 pm	**International Cotton Genome Initiative (ICGI) Workshop**	**Pacific Salon 3**
4:55 pm	**Andrew Paterson,** University of Georgia, Plant Genome Mapping Laboratory *Update on the* Gossypium raimondii *genome sequence*	
Tuesday, 18 January 2011		
10:20 pm - 12:30 pm	**Brachypodium Genomics Workshop**	**Pacific Salon 2**
11:20 am	**John Sedbrook,** Illinois State University and Great Lakes Bioenergy Research Center *Manipulating lignin composition and structure in* Brachypodium distachyon *to improve plant biomass for biofuels*	
10:20 am - 12:30 pm	**Cassava Workshop**	**Sunrise Room**
10:30 am	**Claude Fauquet,** Danforth Center *Strategic Priorities of the Global Cassava Partnership for the 21st Century (GCP21) for Cassava Improvement*	
11:30 am	**Simon Prochnik,** DOE Joint Genome Institute *Cassava genome annotation improvements and analysis of protein families*	
3:50 pm - 6:00 pm	**Perennial Grasses Workshop**	**Pacific Salon 2**
4:30 pm	**Pamela Ronald,** University of California, Davis *Overview of the switchgrass genome sequencing project*	
5:30 pm	**Kankshita Swaminathan,** University of Illinois, Urbana-Champaign *Genomic biology of miscanthus*	
Wednesday, 19 January 2011		
10:20 am - 12:30 pm	**Sorghum and Millets Workshop**	**Royal Palm Salon 1, 2, & 3**
11:00 am	**Dr. Jeff Bennetzen,** Department of Genetics, University of Georgia, Athens *Sequence analysis of foxtail millet and its close relatives*	

JGI IN THE NEWS

DOE's Magellan Cloud Recognized at SC10


Roy Kaltschmidt, LBNL

Magellan, the U.S. Department of Energy's cloud computing project, received the "Best Use of High Performance Computing (HPC)" Award during the international supercomputing conference SC10 held in New Orleans, La. on November 13-19, 2010. The award was one of those determined by an online vote as part of the HPCWire Reader's Choice Awards and are annually handed out during the conference focused on high performance computing, networking, storage, and data analysis.

The award was received by representatives from Argonne National Laboratory and Lawrence Berkeley National Laboratory as the Magellan system is housed at the Argonne Leadership Computing Facility (ALCF) in Illinois and the National Energy Research Scientific Computing (NERSC) Center in California.

The DOE JGI was one of the early users of the NERSC-based Magellan system when the Institute found itself in need of increased computing resources last spring. Within three days, a team of NERSC, DOE JGI and DOE Energy Science Network staff had deployed a dedicated nine gigabyte virtual circuit that provided Institute collaborators worldwide with increased computational capacity without changing their workflows.

For more information, see the original Argonne news release at http://bit.ly/b3N2m4

Flagship Microbial Genome Program Project: 100 Rhizobium Genomes


Bob Bjork, USDA

Agricultural productivity is heavily dependant on nitrogen, and so the symbiotic interactions between nitrogen-fixing bacteria and crops are of interest to researchers around the world. A recently launched project at the DOE JGI focuses on sequencing 100 different strains of these bacteria to better understand the relationships between the microbes and plants.

"The value here (in addition to the obvious scientific value)," said Metagenome Program lead Nikos Kyrpides, "is that we formed a partnership with a consortium of 50+ scientists coordinated by Wayne Reeve of Australia's Murdoch University, which will be sending the samples — we're expecting the first samples — and will help us in the analysis."

Rhizobial bacteria are found in the soil and interact with legumes such as peas and clover at the root nodules. The bacteria fix atmospheric nitrogen inside the nodules and contribute nearly two-thirds of the nitrogen used in agricultural production.

The team plans to look at rhizobial genomes collected from distinct geographical regions. Reeve noted that this project is the first large-scale attempt to understand the genetics involved in the plant-bacteria interactions.

"I consider this project one of the flagship projects," said Microbial Genome Program lead Tanja Woyke, who also noted that the data could eventually be linked to the Rhizosphere Grand Challenge.

A Genome for Methane Studies

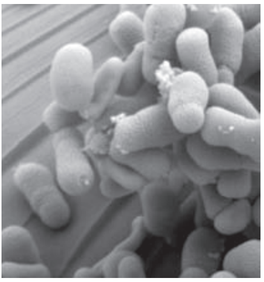


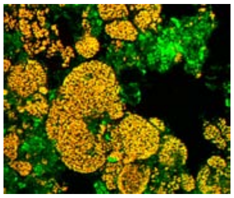
Image courtesy of Ezra Kulczycki

Though methane is 21 times more potent than carbon dioxide, it is considered the second most important greenhouse gas. To better understand the bacteria involved in the global methane cycle, the DOE JGI sequenced, assembled and annotated the genome of *Methylosinus trichosporium* OB3b, which was published online October 15, 2010 in the *Journal of Bacteriology*. The methanotroph, as methane-oxidizing bacteria are called, could help reduce levels of atmospheric methane and was selected as a DOE JGI Community Sequencing Program (CSP) project in 2008.

Led by DOE JGI collaborator Lisa Stein from the University of Alberta, the 4.8-million base pair draft genome was sequenced using Roche 454 and Illumina machines. Aside from genes involved in methane oxidation, genes involved in nitrogen fixation and ammonia transport were also identified.

Originally isolated in 1970, the bacterium has been extensively studied to identify and characterize several key enzymes involved in methane oxidation. For example, one enzyme is crucial to *M. trichosporium's* ability to use copper in order to efficiently oxidize methane, a mechanism that significantly impacts global methane oxidation patterns.

Unpredictable MDA Biases in Metagenomic Analyses



Multiple displacement amplification (MDA) is a technique often applied to genomic studies of low-biomass environments that are limited by the amount of DNA available. One problem with using the method in single cell genomic studies however has been amplification bias that impacts quantitative analyses.

In a paper published in the December 2010 issue of *Nature Methods*, former DOE JGI researcher Phil Hugenholtz teamed with Susan Yilmaz and Martin Allgaier to find out if similar amplification biases were detected in studying microbial communities. MDA was first performed on environmental DNA samples extracted from garden compost, activated sludge and termite hindgut, and biases were assessed using high-throughput small-subunit rRNA gene amplicon pyrosequencing.

The team found that anywhere from three and 28 percent of the taxa detected in the samples were skewed, with relative abundance numbers unpredictably increased or reduced.

"We find that not only does MDA introduce significant and reproducible biases in population relative abundance, different MDA protocols introduce opposing skews in many populations making it impossible to predict introduced bias for a given microbial community. This essentially precludes quantitative comparative analyses of metagenomic datasets using MDA," noted Hugenholtz.

A Salt-Loving Microbe's Sequence

Considered the saltiest body of water capable of supporting life, the Great Salt Lake in the state of Utah is the third saltiest body of water on earth and contains petroleum seeps, heavy metals and high sulfur concentrations. One Great Salt Lake microbe whose genome has been sequenced by the DOE JGI is *Methanohalophilus mahii.* The project was led by DOE JGI's Nikos Kyrpides and Hans-Peter Klenk of the Geman Collection of Microorganisms and Cell Cultures (DSMZ) and the article appeared online December 2010 in the journal *Archaea*.

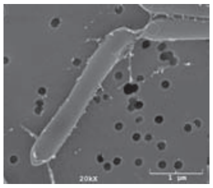
Image by Chris Allen

***M. mahii* was isolated from the Great Salt Lake in Utah.**

The two million base pair genome is the first representative of its genus that is a salt-loving microbe capable of using reduced one-carbon compounds. Kyrpides and his colleagues identified genes using Oak Ridge National Laboratory's Prodigal genome annotation pipeline and the DOE JGI's GenePRIMP manual curation pipeline, before conducting manual functional annotation using the DOE JGI's Integrated Microbial Genomes Expert Review (IMG-ER) platform. Comparing *M. mahii's* genome with those of other known methanogenic microbial genomes allows researchers to study the genomic adaptations of methanogens to marine and freshwater environments.

The U.S. Department of Energy's interest in sequencing the microbes found in the Great Salt Lake lies in identifying adaptations to the harsh environment which could be used to chemically fix sulfur and carbon and detoxify pollutants. Additionally, sequencing the microbial biodiversity found here expands the DOE JGI's ongoing Genome Encyclopedia of Bacteria and Archaea (GEBA) project.

Clostridia Bacterial Genomes Sequenced for Biofuel Production



Courtesy of C. Hemme

The DOE JGI has been sequencing the genomes of several bacteria and archaea to harness their capabilities in breaking down cellulose and hemicellulose, which make up the largest component of plant biomass, and the most difficult to cost-effectively break down for commercial biofuel production. Many microbes that can break down biomass do so with the help of enzyme complexes known as cellulosomes, and researchers hope to identify more of these enzymes with the help of the DNA sequences generated.

In a paper published online October 1, 2010 in the *Journal of Bacteriology,* several DOE JGI researchers including Director Eddy Rubin report that 20 species of the bacteria *Clostridia* have been sequenced at the Institute using Sanger, 454 and Solexa (Illumina) methods. Due to assembly and finishing issues, seven of the 20 genomes, including the heavily-studied thermophile *C. thermocellum,* are left as high-quality permanent draft genomes.

Of the remaining 13 bacterial species, nine of the genomes have been finished, including *C. cellulolyticum,* which was isolated from decayed grass compost and can ferment plant materials to produce ethanol and hydrogen for use as alternative energy sources. Three of the *Clostridia* genomes are still being sequenced and the other three genomes are in queue to be sequenced. In keeping with Director Rubin's goals of providing users with services beyond sequencing, all draft genomes were annotated through the DOE JGI-ORNL annotation pipeline and then analyzed using the DOE JGI Integrated Microbial Genomes data management system.

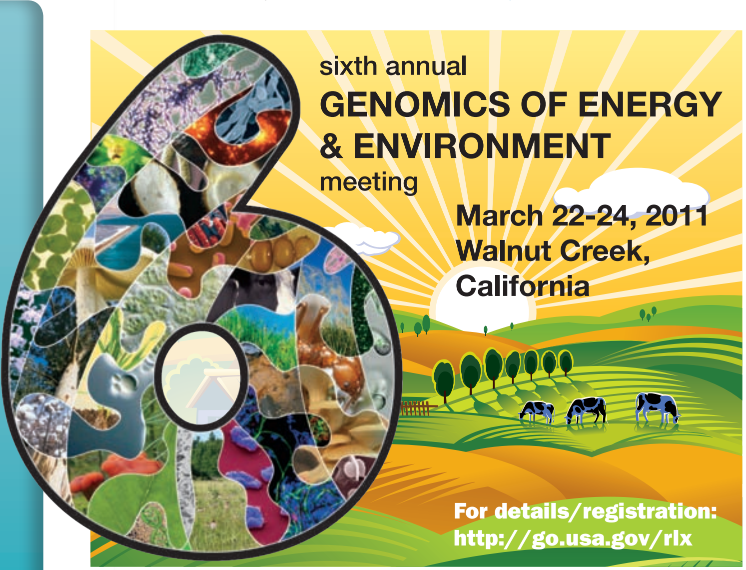
Sanger Shutdown

In October, the DOE JGI retired the last of the sequencers that used the tried-and-true Sanger sequencing technology in a ceremony with words from DOE JGI Director Eddy Rubin (left) and Production head Susan Lucas (right). The workhorse of the Institute for a decade, the machines were instrumental in sequencing human chromosomes 5, 16 and 19, which made up the DOE JGI's 11 percent contribution to the Human Genome Project.

The DOE JGI started incorporating next-generation Roche 454 and Illumina sequencers in 2007, and now relies solely on these technologies, which have helped ramp up the Institute's sequencing capacity from megabases to terabases. DOE JGI's Damon Tighe created a video tribute to Sanger, which can be viewed on the Institute's YouTube channel at http://bit.ly/bAwVS8.

How Do You Say "Energy Genomics" in Mandarin Chinese?

Find out on the DOE JGI's YouTube channel and on youku.com. The Energy Genomics video created in collaboration with the Ex'pression College for Digital Arts earlier this year has been translated and captioned in Mandarin Chinese by DOE JGI's Hui Sun, Mingkun Li and Zhong Wang. Check it out on the Institute's YouTube channel at http://bit.ly/fW2XAz. For those outside the United States, the video is also available on youku.com at http://bit.ly/cPVnhi.



sixth annual
GENOMICS OF ENERGY & ENVIRONMENT
meeting

March 22-24, 2011
Walnut Creek, California

For details/registration:
http://go.usa.gov/rlx

Fuelled by Agave

DOE JGI's Axel Visel (pictured left in front of *Agave franzosinii* at the Ruth Bancroft Garden in Walnut Creek) and Stephen Gross (right) will collaborate with June Simpson (Cinvestav, Mexico, center) to study the transcriptome of *Agave tequilana*, a candidate biofuel feedstock for semi-arid climates. This project is funded by an LDRD (Laboratory Directed Research and Development) grant and part of Lawrence Berkeley National Laboratory's Carbon Cycle 2.0 initiative, an interdisciplinary effort aimed at integrating research activities across divisions with the mission to deliver creative solutions toward a carbon-neutral energy future.

A Collaborative Effort

Alex Worden (right) of the Monterey Bay Aquarium Research Institute turned the DOE JGI Scientific Advisory Committee meeting held December 2010 into a family affair, bringing her newborn and husband Rudolf Gausling. Helena Jill Gausling-Worden was born November 1 and weighed 8 lbs, 6 oz.

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