DOE JOINT GENOME INSTITUTE
US DEPARTMENT OF ENERGY
OFFICE OF SCIENCE

the PRIMER

Spring 2008 Volume 5 Issue 1

JGI Expands Campus, Dedicates Building Under New Lease Extension

On Wednesday, February 27, during a shining interval between rain showers, the JGI dedicated a newly renovated 18,000 square-foot building at its Production Genomics Facility (PGF) in Walnut Creek. The ceremony entailed a ribbon-cutting by the latest robot to be introduced into the industrial-scale DNA sequencing line at the PGF, the new BenchCel Microplate Handling System, adapted for the occasion by JGI technicians George Mercado and Don Miller.

The new addition to the campus has enabled the JGI to consolidate approximately 80 administrative and informatics staff and includes a new research laboratory, bringing the total footprint of the facilities to 80,000 square feet.

The building to be dedicated is part of a new five-year lease extension between the University of California Regents and its landlord, Hall Equities Group, ensuring the JGI's long-term presence in the community of Walnut Creek, situated halfway between its parent facilities, Lawrence Berkeley and Lawrence Livermore National Laboratories.

"Here's a DNA molecule you can see without a microscope!" said helix sculptor Jeff Brees.

From the left, JGI's Operations Manager, Ray Turner; JGI Director Eddy Rubin; Congresswoman Ellen Tauscher's Field Representative Erik Ridley; and Walnut Creek City Council member Susan McNulty Rainey, all of whom spoke at the dedication.

JGI PGF now 80,000 SQF

Mechanisms of Plant-Fungi Symbiosis Characterized by JGI, Collaborators

Plants gained their ancestral toehold on dry land with considerable help from their fungal friends. Now, millennia later, that partnership is being exploited as a strategy to bolster biomass production for next-generation biofuels. The genetic mechanism of this kind of symbiosis, which contributes to the delicate ecological balance in healthy forests, also provides insights into plant health that may enable more efficient carbon sequestration and enhanced phytoremediation—using plants to clean up environmental contaminants. These prospects stem from the genome analysis of the symbiotic fungus *Laccaria bicolor,* generated by JGI and collaborators from INRA, the National Institute for Agricultural Research in Nancy, France, and published March 6 in the journal *Nature* (452, 88–92, DOI: 10.1038/nature06556). This international team effort also involved contributions from 16 institutions, including Oak Ridge National Laboratory; Ghent University, Belgium; Lund University, Sweden; Göttingen University, Germany; CNRS-Aix-Marseille University, France; Nancy University, France; and the University of Alabama, Huntsville.

Trees' ability to generate large amounts of biomass or store carbon is underpinned by their interactions with soil microbes known as mycorrhizal fungi, which excel at procuring necessary, but scarce, nutrients such as phosphate and nitrogen. When *Laccaria bicolor* establishes a partnership with plant roots, a mycorrhizal root is created. The fungus within the root is protected from competition with other soil microbes

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JGI DELIVERS FIRST MOSS GENOME

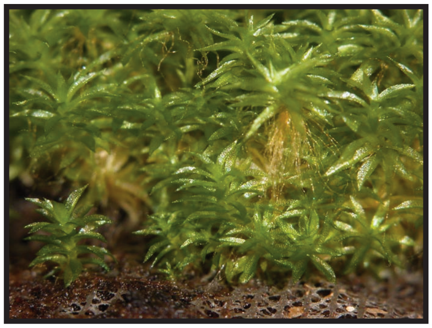
Messages from nearly a half-billion years ago, conveyed via the inventory of genes sequenced from a present-day moss, provide clues about the earliest colonization of dry land by plants. The JGI was among the leaders of an international effort uniting more than 40 institutions to complete the first genome sequencing project of a nonvascular land plant, the moss *Physcomitrella patens*. The team's insights into the code that enabled this seminal emergence and dominance of land by plants are published in the January 4 edition of the journal *Science* (Vol. 319, No. 5859, pp. 64–69 DOI: 10.1126/science.1150646).

The moss genome project, originally proposed by Brent Mishler of the University of California, Berkeley, and Ralph Quatrano of Washington University in St. Louis (WUSTL), was enabled through the JGI's Community Sequencing Program (CSP). Other project leaders include DOE JGI's Jeffrey Boore, David Cove, and Andrew Cuming of the University of Leeds (United Kingdom), Mitsuyasu Hasebe and Tomoaki Nishiyama of the National Institute for Basic Biology (Japan), and Ralf Reski of the University of Freiburg (Germany) with his associate Stefan Rensing, the paper's first author.

"*Physcomitrella* is to flowering plants what the fruit fly is to humans; that is, in the same way that the fly and mouse have informed animal biology, the genome of this moss will advance our exploration of plant genes and their functions and utility," said Eddy Rubin, DOE JGI Director. "Traits such as those that allow plants to survive and thrive on dry land will be useful in the selection and optimization of crops that may be domesticated for biomass-to-biofuels strategies."

Physcomitrella, with a genome of just under 500 million nucleotides and possessing nearly 36,000 genes (about 50 percent more than are thought to be in the human genome), is the first bryophyte to be sequenced. Bryophytes are nonvascular land plants that lack specialized tissues (phloem or xylem) for circulating fluids. Rather, they possess specialized tissues for internal transport. They neither flower nor produce seeds, but reproduce via spores.

"The availability of the *Physcomitrella* genome is expected to create important new opportunities for understanding the molecular mechanisms involved in plant cell wall synthesis and assembly," said Chris Somerville, Director of the Energy Biosciences Institute (EBI), the partnership between Lawrence Berkeley National Laboratory, UC Berkeley, the University of Illinois at Urbana-Champaign, and the global energy company BP. "The ease with which genes can be experimentally modified in *Physcomitrella* will facilitate a wide range of studies of the cell wall, the principal component of terrestrial biomass. Additionally, the moss has fewer cell types than higher plants and has a much more rapid lifecycle, which also greatly facilitates experimental studies of cell walls. Thus, the completion of the genome is an important step forward in facilitating basic research concerning the development of cellulosic biofuels."



A rolling stone gathers no *Physcomitrella patens.*

"There is a clear connection with this work and the intensifying interest in the global carbon cycle," said Mishler, a UC Berkeley professor in the Department of Integrative Biology and Director of the University and Jepson Herbaria. "The moss system is proving quite useful for studies of photosynthesis, among many other processes."

For more on *Physcomitrella*, see: http://www.jgi.doe.gov/News/news_12_13_07.html

Laccaria

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and gains preferential access to carbohydrates within the plant. Thus, the mutualistic relationship is established.

Laccaria bicolor occurs frequently in the birch, fir, and pine forests of North America and is a common symbiont of *Populus trichocarpa,* the poplar tree whose genome was determined by the JGI in 2006. The analysis of the 65-million-base *Laccaria* genome, the largest fungal genome sequenced to date, yielded 20,000 predicted protein-encoding genes, almost as many as in the human genome. In sifting through these data, researchers have discovered many unexpected features, including an arsenal of small secreted proteins (SSPs), several of which are only expressed in tissues associated with symbiosis. The most prominent SSP accumulates in the extending hyphae, the tips of the fungus that colonize the roots of the host plant.

Francis Martin, the *Nature* study's lead author, said that the genome exploration led the team to the discovery that *Laccaria* lacks the enzymes involved in degradation of the carbohydrate polymers of plant cell walls but maintains the ability to degrade nonplant cell walls—which may account for

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Applied Ergonomics

Revisiting the site of the JGI's 2007 Ergo Cup victory, a team of eight Sequencing Department and LBNL Engineering Division staff participated in the Institute for Industrial Engineers' (IIE) 11th Applied Ergonomics Conference in Orlando, Florida, held March 10–13. Once again, the JGI was chosen as one of the finalists to compete for the Ergo Cup Award, recognizing excellence in ergonomic engineering design and teamwork solutions. Such companies as GM, Boeing, Toyota and other industry giants from all over the world displayed their ergonomic interventions at the conference, where a panel of judges and the conference attendees can learn about the process and the company.

This year, the JGI had entries in two categories: the Team-Driven Workplace Solutions and Engineering and Ergonomist-Driven Workplace Solutions. In the Team-Driven category, the "Base Off" project is a small hand tool that reduces the ergonomic risk to lab workers in separating the lids from the bases that hold the sample plates used in ABI 3730 sequencers. The "It's A Peeling" project for the Engineering & Ergonomist Driven category is an automated plate-peeling machine designed in-house by Mark West and Charlie Reiter in the Engineering Division, with the assistance of the JGI Instrumentation Group. The instrument automates a high-risk manual task on the production line, peeling heat seals off sample plates.

Conference participants included Christine Naca, Simon Roberts, Martin Pollard, Gerald Ilog, Megan Kennedy, Michael Pintor, and Bridget Swift, all from the JGI's Sequencing Department, and Mark West from LBNL Engineering.

"Although the JGI did not win an Ergo Cup this year, it was a valuable learning experience and an opportunity

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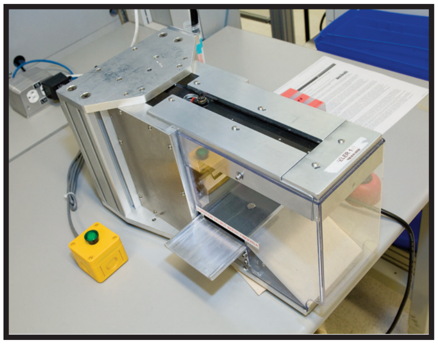
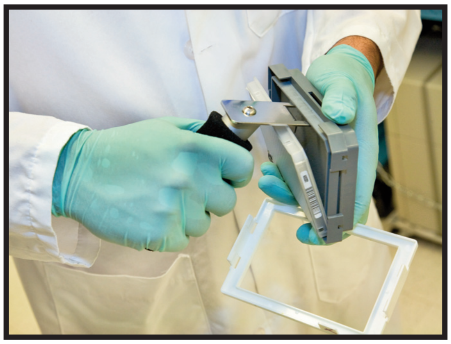
From left to right: Michael Pintor, Christine Naca, Bridget Swift, and Simon Roberts



"Base Off"



"It's A Peeling"

JGI Releases Soybean Genome Assembly To Enable Worldwide Bioenergy Research Efforts

A preliminary assembly and annotation of the soybean genome, *Glycine max,* has been made available to the greater scientific community by the JGI, to enable bioenergy research.

The announcement was made by Eddy Rubin, JGI Director, during his keynote remarks January 15 at the Plant and Animal Genome XVI Conference in San Diego. The preliminary data can be accessed at http://www.phytozome.net/soybean.

The soybean genome project was initiated through the DOE JGI Community Sequencing Program (CSP) by a consortium led by the DOE JGI's Dan Rokhsar, Stanford University's Jeremy Schmutz, Gary Stacey of the University of Missouri-Columbia, Randy Shoemaker of Iowa State University, and Scott Jackson of Purdue University, with support from the U.S. Department of Agriculture and the National Science Foundation.

The current assembly (representing 7.23x coverage), gene, set, and browser are collectively referred to as "Glyma0."

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Laccaria

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Laccaria's protective capacity. These observations point towards the dual life of mycorrhizal fungi like *Laccaria,* and its ability to grow in soil fending off pathogens and using decaying organic matter while serving as a custodian of living plant roots.

The JGI *Laccaria* effort was led by Genome Annotation Group Leader Igor Grigoriev. In his remarks to the JGI All-Hands gathering on February 27, Grigoriev echoed an analogy coined by his collaborator Francis Martin. "*Laccaria* is like Janus, the mythological caretaker of gates, doors and hallways; beginnings and endings. Janus, with his two faces looking in opposite directions, is ever-aware of opportunity."

Other JGI authors include Andrea Aerts, Erika Lindquist, Asaf Salamov, Harris Shapiro, Peter Brokstein, Chris Detter (Los Alamos National Laboratory), the DOE JGI Production Genomics Facility sequencing team led by Susan Lucas, and partners at the Stanford Human Genome Center, Jane Grimwood and Jeremy Schmutz, and Jerry Tuskan at ORNL. For more of the *Laccaria* story, see: http://www.jgi.doe.gov/News/news_3_5_08.html

FINISHING IN THE FUTURE

May 28–30, 2008
Santa Fe, New Mexico

"Finishing in the Future" is a meeting dedicated to bringing together experts in the field of genomic finishing—including representatives from the industries that serve this specialized scientific community. The meeting focuses on laboratory methods and computational tools used to help sequence, assemble, and finish genomes, including new sequencing technologies. Talks include an entire day devoted to the expanding field of metagenomics.

KEYNOTE SPEAKERS

Sydney Brenner, 2002 Nobel Prize Winner for Medicine, Founder of the Molecular Sciences Institute, and Senior Distinguished Fellow of the Crick-Jacobs Center, Salk Institute

Bruce Birren, Director of the Microbial Sequencing Center and Co-Director of the Genome Sequencing and Analysis Program, Broad Institute

Deanna Church, Coordinator for the Mouse and Human Genome Resources and Trace Archive, National Center for Biotechnology Information (NCBI)

Registration is limited to 120; please register soon if you plan to attend. To register, submit an abstract, or obtain more information as it becomes available please visit our Web site, http://www.lanl.gov/finishinginthefuture/

No registration fee is required.

If you have any questions, or would like further information, please contact Chris Detter at (505) 667-1326 or cdetter@lanl.gov.

Ergonomics

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to share the JGI approaches to applying ergonomics to real-world situations," said Simon Roberts, JGI Instrumentation Supervisor. "We had a very enthusiastic response from the hundreds of conference attendees that visited our two booths," added Marty Pollard, Instrumentation Group Leader.

"It was great to see that JGI's employee-empowered ergonomics program is on the forefront and runs as strong as many other well-known and successful companies," said industrial engineer Christine Naca, the JGI's Production Ergonomics Lead.

Soybean

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Glyma0 is a preliminary release, based on a partial dataset. This is expected to be replaced with an improved, chromosome-scale "Glyma1" version by the end of 2008. Early users of this data are encouraged to track their favorite genes by saving local copies of the DNA sequences of these loci, and not by identifier or sequence coordinate, as these will change in future versions.

The DOE JGI's interest in sequencing the soybean stems from its role as a principal source of biodiesel, a renewable, alternative fuel with the highest energy content of any alternative fuel.