

Eucalyptus Tapped for Next Tree Genome Project Through CSP

The JGI Community Sequencing Program (CSP) is contributing to an ambitious international effort to decode the genome of Eucalyptus, one of the world's most valuable fiber and paper-producing trees—with the goal to maximize its potential in the burgeoning bioenergy market and for capturing excess atmospheric carbon.

The scientific effort to characterize the Eucalyptus genome, uniting some two

dozen institutions worldwide, is led by Alexander Myburg of the University of Pretoria (South Africa), with co-leads Dario Grattapaglia, of EMBRAPA and Catholic University of Brasilia (Brazil), and Jerry Tuskan of Oak Ridge National Laboratory—JGI's Laboratory Science Program lead. The 600-million-nucleotide tree genome was selected as one of JGI's CSP FY2008 major allocations.

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NEW BIOENERGY RESEARCH CENTERS MEET AT JGI

BY BRUCE BALFOUR

On August 30 and 31, leaders from the three new DOE Bioenergy Research Centers met for the first time at JGI in Walnut Creek.

Arriving from the Great Lakes Bioenergy Research Center (GLBRC), the BioEnergy Science Center (BESC), and the Joint BioEnergy Institute (JBEI), they came to hear about JGI's expertise, talk about their research plans, look for collaboration opportunities, and offer a preview of the sequencing capacity they'll need over the next few years.

An integral part of the \$375 million initiative launched by Energy Secretary Bodman in June, each BRC combines the efforts of national labs, universities, and private industry working with national user facilities such as JGI, making the collaborations in these centers

unusually complex for DOE-funded projects. DOE program manager Patrick Glynn characterized the relationship between the vertically integrated BRCs as "competition/collaboration" where they're all working toward the same goals to increase the rate of discovery. Participants welcomed this approach.

"As scientists in this field, we have successfully competed and collaborated for years, so I don't foresee any problems," said Wolf Frommer, Stanford professor and Vice President of Feedstocks at JBEI.

JGI Director Eddy Rubin kicked off the session with encouraging words about JGI's history of increasing speed, efficiency, and sequencing capacity while continually lowering costs. He predicted an even more dramatic trajectory for sequencing-by-synthesis technologies currently being vetted.

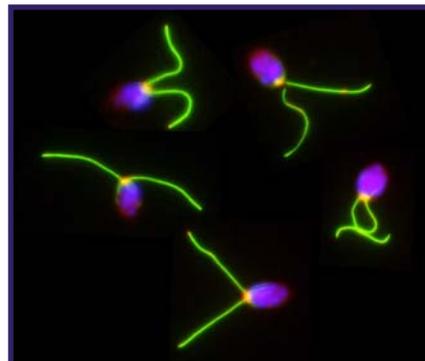
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Chlamy Genome Catalogs Carbon Capture Role as Ancient Cousin of Plants and Animals

The genome analysis of a tiny green alga has uncovered hundreds of genes that are uniquely associated with carbon dioxide capture and generation of biomass. Among the *(cont. on page 15)*



Chlamy in synchronized swim

JGI FACES

NICK EVERSON

Finance & Materials Manager

Nick comes to us via LLNL, where he was the lead resource manager for the Biosciences and Biotechnology Division. Prior to LLNL, he also worked at Intel Corporation in Santa Clara as a financial analyst and in the US Navy as a submarine electrician. Nick



Nick Everson

has a BS in Business Administration from UC Berkeley's Haas School of Business, and is returning to Haas this fall to pursue his MBA in the Evening & Weekend MBA program. Nick lives with his wife, Janet, and two children, Declan and Annabelle, in Hayward and enjoys golfing, basketball, and spending quality time with his family.

YAKOV GOLDER

Informatics Department Head

Yakov joined JGI in April 2007 and oversees the Genome Data Systems, IMG, Genome Assembly, Genome Annotation, Comparative Genomics, Production Informatics, Infrastructure, and Systems Administration. Yakov received his B.S. in Computer Science from the City College of New York (CUNY) and M.S. in Computer Science from New York Institute of Technology. He has more than 20 years of technical leadership experience at established corporations and startups in the delivery of complex, high-performance software applications, including social networking, workflow management, investment management, customer relationship management (CRM), and health care. Prior to JGI, Yakov served as Vice President of Technology at CNET Networks, where he oversaw the engineering organization in the online community division. There he

was responsible for the high-performance photo-sharing web site www.webshots.com, which boasted over 1B page views monthly. Prior to CNET, Yakov worked at eBay where he was responsible for two critical areas of eBay's complex web infrastructure: application data persistence and messaging. Yakov's significant experience in designing and building enterprise class software systems for both the private and public sector, builds upon previous involvement in development of both software as a service web sites and more traditional software product development in the engineering, industrial automation and online communities markets. Yakov also brings a wealth of knowledge to JGI in the application of established and emerging development patterns & practices, a solid grasp of applying agile methods, and experience in building and coaching high-performance project teams. Yakov is married to former LBNL scientist Elina Golder-Novoselsky and lives in Walnut Creek. He enjoys traveling, good food (Elina does the gourmet cooking), table tennis and chess.



Yakov Golder

CHERYL R. KUSKE

LANL JGI Center Director & Group Leader

Cheryl received her BS and MS degrees from North Carolina State University in horticulture & plant pathology, respectively. Through her MS thesis and 3 years working in the agrichemicals industry, she studied soilborne fungal and nematode pathogens of plants. She obtained her PhD degree in plant pathology and molecular biology from UC Davis in 1989, where she studied non-cultured bacterial plant pathogens now known as phytoplas-



Cheryl Kuske

mas. She received Director's Funded and Alexander Hollaender Postdoctoral research fellowships at LANL, and conducted her postdoctoral research on biochemical and molecular characterization of enzymes involved in heavy metal accumulation and resistance in plants. Cheryl's research over the past 14 years has focused on development and use of molecular methods to study soil, water and aerosol microbial communities. Her research program has been dual track with applications to DOE missions and to biothreat security. Cheryl received LANL's Distinguished Patent Award in 2004 for development of bacterial biosensors, and the LANL Fellow's Prize for Research for her contributions to environmental microbiology and biosecurity in 2006. She joined the JGI in June of 2007 as the LANL JGI Center Director. Cheryl and her husband Larry have 2 children, age 8 and 10. The family enjoys outdoor activities, including skiing, whitewater sports, hiking and bicycling.

CHRIS WATCHMAKER

Principal Human Resources Generalist



Chris Watchmaker

Chris joins JGI after spending the past three and one-half years at LBNL in the Operations HR area. Prior to coming to the Lab, Chris worked in Human Resources at Applied Biosystems. He has over twenty years of HR experience in biotech, the staffing

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Meet the JGI Project Management Office

The JGI Project Management Office (PMO) was established to better handle the organization, tracking, and flow of sequencing projects through the JGI sequencing pipeline. Led by David Bruce, the PMO consists of a team of three other project managers: Lynne Goodwin, Kerrie Barry, and Christa Pennacchio, each of whom specializes in plant, microbial, or environmental projects. Also working closely with the PMO are scientist Susannah Tringe and production manager Tijana Glavina del Rio.



David Bruce and Lynne Goodwin

The JGI Global Project Tracking System (GPTS) database is the project manager's primary resource for tracking and communicating project progress through the sequencing process. The PMO is involved in a project from the moment a proposal is approved to the close-out of the research.

A project manager (PM) is assigned to oversee the progression of each project throughout the pipeline steps, and to facilitate communication between the JGI functional groups and the PI to ensure the research goals set forth by the proposal are being met in a timely fashion.

Once all the documentation is in place, the PM works with the PI to approve and ship samples for sequencing by the JGI. Once samples are received, the PM's focus shifts to the production line. PMs help navigate a



Kerrie Barry

project through the various phases of production sequencing by providing the functional group leads with information about the project, helping the PI resolve problems, and tracking the project in a global project tracking database.

Project managers face several challenges in helping a PI achieve the research goals set forth in a proposal. The most common problem is obtaining appropriate starting material. Often, collaborating labs have difficulty obtaining sufficient DNA, or DNA of sufficiently high quality, for the desired amount of sequencing. In such cases, the PMO directs the scien-



Christa Pennacchio

tists to protocols that have worked for other groups, or in some cases puts them in touch with JGI scientists who offer advice.

ERT Hosts Cribbing Workshop



From left to right: Nancy Hammon, Catherine Adam, Mike Houston (local Community Emergency Response Team (CERT) member), Sam Pitluck, and Kristen Taylor demonstrate cribbing technique in the lot beside the JGI warehouse.

In September, the JGI Emergency Response Team (ERT) learned a technique called "cribbing" that will allow them to safely extricate victims trapped under heavy debris. This technique enables a small team to lift as much as 12 tons! First, the debris must be stabilized so it will not shift and potentially increase injuries to the victim. Once the debris has been stabilized, the cribbing team removes all small pieces of debris. Any remaining heavy or large debris will then be lifted off of the victim by using a fulcrum and lever to raise the heavy object off of the victim a few inches while the team builds up the box cribs under each corner. This procedure is repeated until the victim is free of the debris and can be pulled to safety.

To learn this and other techniques that you can use in an emergency situation, consider sitting in on some of the ERT classes, or even joining the team. For more information, please contact Wendy Schackwitz (WSSchackwitz@lbl.gov).

AWARDS & NEW HIRES

JGI PROMOTIONS

Mansi Chovatia

Research Associate
Sequencing/Cloning Technology

Victor Kunin

Bioinformaticist Project Scientist
Microbial Ecology

Nikos Kyrpides

Computational Biologist Staff Scientist
Genome Biology

Natalia Ivanova

Computational Biologist Scientist
Genome Biology

Kostas Mavrommatis

Bioinformaticist Research Scientist
Genome Biology

AWARDS

OPA AWARD:

IMG/M Team: Natalia Ivanova and Nikos Kyrpides

Developing the IMG/M system and metagenomic data analysis and contributing to advancing JGI's leadership in the field of metagenomics in support of the DOE mission for alternative energy production, global carbon cycling, and bioremediation.

Rolling QC Team: Harris Shapiro, Jasmy Pangilinan and Joel Martin
Contributions towards the success of the JGI's Rolling QC Project.

Individual Award: Rob Egan

Accomplishment in successfully restoring the data management system in a remarkably short period of time.

SPOT Awards:

Property Inventory Team: Ron McKeever & Mark Jacintho

Outstanding performance in successfully completing the LBNL Wall-to-Wall Inventory in an efficient and customer-service focused manner.

Rolling QC Team: Alex Copeland, Rob Egan, Jeff Froula, Ed Kirton, Michael Zhang

Exceptional team effort leading to the success of the Rolling QC project, thereby improving the accuracy and efficiency of the JGI's sequencing work.

JGI NEW EMPLOYEES

Crystal Wright

Research Associate
Programs/Genetic Analysis

Natasha Zvenigorodsky

Research Associate
Programs/Sequencing Technology

Kanwar Singh

Sr. Research Associate
Programs/Sequencing Technology

Marcel Huntemann

Software Developer 1
Programs/Phylogenomics

John Schiappacasse

Financial Analyst 3
Operations

Nick Everson

Finance & Materials Manager
Operations

Andrew Allison

Research Technician
Sequencing

Laura Sandor

Research Technician
Sequencing

Bejaine Bayot

Research Technician
Sequencing

Peter Williams

Computer Scientist
Informatics

Igor Shabalov

Software Developer 4
Informatics

Cristina Albers

HR Assistant III
Human Resources

Mathew Dunford

Systems Administrator 3
Systems Administration

Matthias Hess

Computational Bio PD Fellow
Genetic Analysis

Christa Pennacchio

Sr. Scientific Engr. Assoc.
CSP

Margie Lozano

Administrative Assistant III
Operations

Anna Engelbrektson

Research Assoc
Microbial Biology

Anthony Kosky

Group Lead
Web Engineering

Eric Greenwade

Computer Scientist
Genome Data Systems

Simon Minovitsky

Software Developer 3
Genome Annotation Portal Group

JGI Post-Doc Wins T-Shirt Contest for 30th Anniversary LBNL Runaround

The winner of this year's Lawrence Berkeley National Laboratory "Runaround" t-shirt design contest is Parag Vaishampayan, JGI post-doc. Vaishampayan said his design was inspired by the bioenergy programs at

the Lab and JGI. The Runaround took place Friday, Oct. 19. T-shirts were be given to all participants and volunteers. The results can be found at: <http://www.lbl.gov/today/2007/Oct/22-Mon/10-22-07.html>



Winner Parag Vaishampayan

LANL HOSTS FACE METAGENOMICS WORKSHOP

BY CHERYL KUSKE

The Department of Energy Office of Science has been studying the responses of terrestrial ecosystems to elevated carbon dioxide and ozone using free-air carbon dioxide enrichment (FACE) and open top chamber (OTC) experimental field sites. After 10-12 years of operation, the six FACE and OTC site experiments will be coming to completion, offering an excellent opportunity to determine the effects of long-term elevated CO₂ on below-ground plant parameters and soil microbial communities. We now have a unique opportunity to conduct disruptive sampling of the soils in the sites, which opens the door to a variety of below-ground studies to correlate to the extensive datasets on plant performance and other ecological parameters. In August, Cheryl Kuske and David Bruce of the LANL JGI hosted a small workshop at DOE in Germantown with the goal of developing a science

and implementation plan, based on metagenomic technology, to assess the climate change responses of the below-ground microbial communities in the DOE terrestrial ecosystem FACE and OTC sites.

The workshop was attended by scientists from the FACE sites, representatives from the JGI, and DOE program managers. Workshop participants came to consensus on major research questions that could be addressed using genomics, especially those that would span all six ecosystems under investigation, and discussed several approaches to using genomic and metagenomic technologies that could be applied to these research questions. We began to outline a four-tier research and sequencing strategy that will become the basis of a written roadmap and strategic plan. This initiative would use JGI's substantial sequencing capability to address a significant DOE mission in terrestrial ecosystem climate change response. This research area requires a comparative



ORNL Open Top Chamber (OTC) field site

genomics approach to define responses linked to the climate change parameters in the very complex soil system. In addition to providing information on below-ground microbial responses to long-term climate change, this initiative will potentially push current sequencing technologies and enable research, technology, and analytical advances that could be applicable to other ecosystems.

MegaBACEs Go Bye-Bye

BY CHRIS DAUM

On August 2, the JGI Production Genomics Facility witnessed the end of a sequencing era. Thirty-six MegaBACE 4500 sequencers were loaded with plates and processed their final sequencing runs. For the last eight years, three generations of MegaBACE DNA sequence analysis platforms have been an indispensable component of the JGI production sequencing line. During their long run, 480,000 sample plates were loaded, generating more than 62 billion high-quality bases. The MegaBACE platform has

been phased out to allow for the integration of next-generation technologies.

With the inception of the capillary-based MegaBACE 1000 platform in late 1999, significant advances were made over the industry standard slab gel instruments of the time, particularly in the areas of automation, workflow, and operation. The 84 MB1000 instruments in use at the JGI went on to play a crucial role in the Human Genome Project.

With the launch of the updated MegaBACE 4000 platform in late 2001, a new standard for high-

throughput sequencing was set, with its 384-capillary array system accelerating the sequencing analysis process. The JGI adopted this updated platform in early 2002 and used 21 MB4000 instruments as a principal sequencing platform until December 2004. With the advent of the MegaBACE 4500 platform in early 2003, the paradigm of high-throughput DNA sequencing was poised to shift forward once again. Development work and onsite testing of the new MegaBACE platform began at the JGI in February 2003 in collaboration with GE HealthCare (formerly

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Dinoroseobacter shibae Jamboree in Germany

BY IRENE WAGNER-DÖBLER, HELMHOLTZ-CENTRE FOR INFECTION RESEARCH, BRAUNSCHWEIG, GERMANY; IWD@GBF.DE

Dinoroseobacter shibae is a member of the Roseobacter group, a phylogenetic lineage within the Alphaproteobacteria, which is abundant in the ocean. It was isolated from toxic dinoflagellate cells, eukaryotic unicellular photosynthetic algae that are responsible for “red tides” resulting in paralytic shellfish poisoning. *Dinoroseobacter shibae* itself is able to conduct a special type of bacterial photosynthesis, called aerobic anoxygenic photosynthesis, and has a complex quorum-sensing system that presumably helps the organism to control its interaction with the host.

After JGI and its collaborators had sequenced the genome, an annotation Jamboree was held in Braunschweig, Germany, from September 10-14, to unravel the genetic adaptations of *D. shibae* to its habitat as they are reflected in the genome. The hosting institute, Helmholtz-Center for Infection Research (HZI), provided the necessary facilities: A



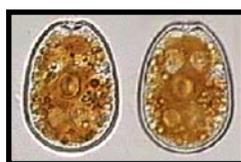
Irene Wagner-Döbler

room for working with 30 high-speed Internet connections, a meeting room for daily seminars, and unlimited fuel for the scientists (coffee and cookies). The 28 participants included professors of microbiology and PhD students from the universities of Braunschweig, Göttingen and Oldenburg, and microbiologists from the German Culture Collection (DSMZ).

Thanks to a grant from the Volkswagen Foundation, JGI Genome Biology Program head Nikos Kyrpides was able to participate and provide two talks about IMG (http://img.jgi.doe.gov/), a kick-off presentation on the first day, and a general talk for the whole HZI at the end of the Jamboree.

He demonstrated IMG's latest features, provided access to specialized software, answered questions, and contributed significantly to the success of the Jamboree.

Five days of full-time work on the genome was a special experience for all.



Prorocentrum lima, a toxic dinoflagellate, from which *Dinoroseobacter shibae* was isolated.

Some had never mined a genome before in such a way, and were excited about the easy access IMG provides, and about the overwhelming amount of information presented. The fundamentals of biochemistry and physiology, known only to experienced professors, proved to be of invaluable importance. The interdisciplinary nature of the gathering was also important: Pathways identified by biochemists were given possible adaptive significance by ecologists. All enjoyed the possibility to interact closely and directly, across the keyboard or over coffee—not to forget good friendly talks in the evening over beer, which helped bring the group together. The Jamboree provided the outline of possible key stories for the genome paper. These are now being completed by the contributing scientists, together with the manual annotation of the genome, with the aim of having the manuscript ready by December.

LATEST JGI ANNOTATION JAMBOREES

Daphnia, Bloomington, IN, July 7-9, 2007

Volvox, JGI, Aug 6-10, 2007

<http://conferences.cgb.indiana.edu/daphnia2007/index.html>

Aureococcus, Southampton, NY, Oct 3-5, 2007
www.aureococcus.org

Eukaryote Annotation report:

15 new eukaryotes were annotated in FY07,

6 genomes were updated

7 currently in annotation

18 Genome Portals were publicly released

Annotated Eukaryotes FY2007

	Annotated	Public	Published
<i>Pichia stipitis</i>	●	●	●
<i>Ostreococcus lucimarinus</i>	●	●	●
<i>Nematostella vectensis</i>	●	●	●
<i>Chlamydomonas reinhardtii</i>	●	●	■
<i>Physcomitrella patens</i>	●	●	○
<i>Laccaria bicolor</i>	●	●	○
<i>Branchiostoma floridae</i>	●	●	○
<i>Monosiga brevicollis</i>	●	●	○
<i>Trichoderma reesei</i> , finished	●	●	○
<i>Naegleria gruberi</i>	●	●	○
<i>Thalassiosira pseudonana</i> , finished	●	●	○
<i>Phaeodactylum tricornutum</i> , finished	●	●	○
<i>Sporobolomyces roseus</i>	●	●	○
<i>Nectria haematococca</i> MPVI, finished	●	●	○
<i>Phycomyces blakesleeana</i>	●	●	○
<i>Daphnia pulex</i>	●	●	○
<i>Postia placenta</i>	●	●	○
<i>Volvox carteri</i>	●	●	○
<i>Lottia gigantea</i>	●	●	
<i>Mycosphaerella fijiensis</i>	●	●	
<i>Micromonas pusilla</i> CCMP1545	●		
<i>Capitella</i> sp. I	●	●	
<i>Aureococcus anophagefferens</i>	●	●	
<i>Helobdella robusta</i>	●	●	
<i>Trichoplax adhaerens</i>	●	●	○
<i>Trichoderma virens</i>	●	●	
<i>Phytophthora capsici</i>	●		
<i>Micromonas pusilla</i> NOUM17, finished	●		
<i>Micromonas pusilla</i> CCMP1545, improved	■		
<i>Emiliana huxleyi</i>	■		
<i>Selaginella moellendorffii</i>	■		
<i>Sorghum bicolor</i>	○		
<i>Batrachochytrium dendrobatidis</i> JAM81	○		
<i>Chlorella</i> sp. NC64A	○		
<i>Ostreococcus</i> RCC809	○		
<i>Trichoderma atroviride</i>	○		

●— done during FY07

●— prior to FY07

■— October 2007

○— in progress

Rock Star Educator Spends Summer at JGI

BY RANDY MONROE

My summer at JGI began before the school year ended, working with Phil Hugenholtz's Microbial Ecology team comprised of Phil, Falk Warnecke, Suzan Yilmaz, Julita Madejska, Hector Garcia Martin, and Victor Kunin.

It was, and still is, a fantastic opportunity to be involved with cutting-edge science that allows the integration of laboratory skill sets for the middle-school level. This unique opportunity began a year ago, with the idea of learning about our local metagenomic resource with a goal to design and introduce a program for the Foothill students. I was presented with the task of finding a relatively little known group of bacteria called OP11.

Approximately 10 years ago, Phil discovered some novel thermophilic (a type of extremophile that likes temperatures above 45C) bacteria in Yellowstone National Park, in a hot spring called Obsidian Pool near the Mud Pots in the southeastern side of the park. He named one group of these thermophiles OP11. Since its discovery, OP11 and many related organisms have grown into an entirely previously unknown major bacterial lineage. This lineage has never been cultured and reproduced in the laboratory, nor has it ever been seen under a microscope, but DNA analysis has shown it to be quite abundant in a variety of locations, including the extreme environments of hot springs and hydrothermal vents, in the teeth of people with periodontal disease, and in several other habitats lacking oxygen (anaerobic).

My challenge was to find the critter and get a picture of it! After some initial training in DNA extraction, PCR, and elec-

trophoresis gels, I was to go to Yellowstone and obtain some fresh samples. I coordinated the journey with one of Phil's long-time colleagues, veteran Yellowstone sampler John Spear from the Colorado School of Mines who studied under microbe guru Norman Pace, now at University of Colorado, Boulder.

In Yellowstone, we sampled at Obsidian Pool (78C), OP Prime Pool (56C), and the new mud vent we deemed OP Mud Vent (85C), Sperm Pool (56C), Octopus Pool (88C and 50C edge), Norris Geyser Basin, and Mammoth, and had those samples shipped to JGI.

Upon returning to JGI, Phil wanted to organize a local sampling expedition. I arranged a day trip for Phil, Falk, Suzan and I to visit the East Bay Municipal Utility



Randy Monroe (right) with his mentor JGI Microbial Ecology Program Head Phil Hugenholtz

District's Wastewater Facility near the San Francisco-Oakland Bay Bridge and obtain some samples from two anaerobic digesters. We then headed to East Bay Regional Park in Hayward to the salt ponds, and to the South Bay city of Alviso to Don Edwards National Wildlife Refuge to obtain some truly remarkable smelling anaerobic organisms.



Randy Monroe samples the South Bay salt flats

Back in the lab, I am ultimately going to perform Fluorescence In Situ Hybridization (FISH) to view and photograph one of these remarkable organisms and learn more from those images.

How does all of this tie together? Well, in 1978 my stepfather, Jim Christy, discovered Pluto's moon Charon, naming it after my mother, Charlene. In January 2006, we were invited to NASA's Cape Canaveral for the launch of the New Horizons probe headed to Pluto and the Kuiper Belt on a Lockheed Martin Atlas V rocket. As an educator on the New Horizons Team, I also had the opportunity to work at Lockheed Martin last summer in missile defense studying Infrared Technologies. IR technologies are an important tool in studying hydrothermal vent systems. It is possible that life began on primordial Earth in such vents. If other locations, such as Europa, a moon of Jupiter, have vent systems, there may also be life there, too. It is quite possible that OP11 is living elsewhere in the solar system. Wouldn't it be grand to find it?

Randy Monroe is a 6th grade earth science teacher at Foothill Middle School in Walnut Creek, CA. In addition to his work as an educator, Randy Monroe is the front man for premier Van Halen tribute band, Hot for Teacher: <http://www.hftrocks.com/>. His summer experience was sponsored by Lawrence Livermore National Laboratory's Edward Teller Education Center (ETEC): <http://etec.ucdavis.edu>. In addition, Randy received support from the Industry Initiatives for Science and Math Education (IISME): <http://www.iisme.org/>

JGI Secures Long-Term Lease on PGF

JGI has secured a five-year extension on its lease with an option for an additional five years. The University of California Regents have signed off on a deal with landlord Hall Equities Group that will ensure JGI's long-term presence in the community of Walnut Creek, situated halfway between its parent facilities, Lawrence Berkeley and Lawrence Livermore National Laboratories. The new lease enables DOE JGI to expand the current facility on its Walnut Creek campus to include a vacant 18,000-square-foot building, which will be renovated and opened in early in 2008. This addition will serve to consolidate administrative and informatics staff and feature a new education out-

reach laboratory, bringing JGI's total footprint to 80,000 square feet.

"We are delighted to be able to extend our stay here in Walnut Creek," said JGI Director Eddy Rubin. "We have grown considerably over the last ten years as we have transitioned from determining the DNA code for the human genome to a national user facility for the DNA sequencing of many different important organisms. Our goal is to sustain our leadership in providing the information that will advance the nation's interests in developing renewable sources of clean energy, tracking the fate of carbon in our atmosphere, and restoring our environment."

"Walnut Creek is proud to be home

to one of the world's leading DNA sequencing centers in JGI," said Susan Rainey, Mayor of the City of Walnut Creek, California. "In our very own backyard, we can lay claim to having a world-class scientific resource—one first involved in sequencing the human genome, then the first tree genome, and now characterizing other plants and microbes that will play a major role in improving our energy future. In addition, JGI researchers are serving to inspire the next generation of scientists and engineers through the thousands of local high school students who have toured the facility over the years. We look forward to building on this productive community partnership for at least the next decade."

DSMZ Connection Jumpstarts GEBA

Early this year, JGI launched the Genomic Encyclopedia of Bacteria and Archaea (GEBA) project, aimed at systematically filling in the gaps in sequencing along the bacterial and archaeal branches of the tree of life. To test the feasibility of the GEBA approach, JGI has since undertaken a pilot project in collaboration with the German Collection of Microorganisms and Cell Cultures, DSMZ, to sequence 100 bacterial and archaeal genomes based on the phylogenetic positions of organisms.

DSMZ (<http://www.dsmz.de/>) is a non-profit research institution with the mission to do "science for service and service for science." DSMZ is one of Europe's leading suppliers of cultures and biological materials to customers and collaborators worldwide. The organism selection process for the pilot project is based on a combination of objective analysis of the rRNA tree of life and consultation with a scientific advisory board. All genome sequence data will be released to the community through the JGI Web site and

Genbank. In recent months, the relationship between JGI and DSMZ has taken off well beyond expectations.

"The start of this collaboration was easy because of the long-term links between some of the key players involved, including myself and Erko Stackebrandt at DSMZ, and Jonathan Eisen, Phil Hugenholtz and Nikos Kyrpides at JGI,"



DSMZ bacterial collection in Germany (Courtesy picture-alliance/dpa)

said Hans-Peter Klenk, Head of the Department of Microbiology at DSMZ. "We knew from the very beginning that there is a serious mutu-

al interest in this project and that we can trust our partners to make this project a success."

Genomic DNA is now routinely being shipped from Germany to Walnut Creek. Four microbes from the initial batch have

been finished in draft form, 20 more are in production, and 53 in the queue. "The exchange of DNA and information is very promising and bodes well for the timely completion of the pilot, with the benefits extending well beyond," said Klenk.

"The GEBA project perfectly fits to our vision for the future of microbial taxonomy and the collection of type strains in general. With the continued decrease in costs for genome sequencing and analysis, we predict that in only a few years, novel type strains will be accessed into strain collections only after their genome sequence has been revealed and analyzed."

In addition, JGI is acquiring samples from sources closer to home, from the American Type Culture Collection (ATCC). ATCC (<http://www.atcc.org/>) is a private, nonprofit resource dedicated to the collection, preservation and distribution of authentic cultures of living microorganisms, viruses, DNA probes, plants, and human and animal cells.

Klenk said that the worldwide scientific community will benefit **(cont. on next page)**

NEW TRACKING SYSTEM ROLLED OUT

BY PAT KALE

Members of the JGI Informatics Department, led by Yakov Golder, are hard at work creating a better way for JGI managers, staff and collaborators to monitor the progress of genomic projects as they make their way through the PGF and partner institutions. From the time a proposal is submitted through any of the JGI proposal-based programs, until the time that the final data set is submitted to NCBI, a system of software applications and databases will track the progress of all work performed on a collaborator's behalf. The goal is to make the JGI as transparent to collaborators as possible.

The Global Project Tracking System (GPTS) will form the backbone of this ambitious software system. It will provide the database, software interfaces, and status tracking coordination that will enable the production informatics department staff to build useful applications. This software will enable JGI staff and collaborators to inquire about the status of any genome, and answer such questions as: Has the

collaborator submitted the information required by the JGI before DNA is shipped? Has the Project Management Office (PMO) completed the user agreement? Has sequencing commenced? Has the trace data been submitted to NCBI? David Pletcher, who leads the Production Informatics group, is in charge of GPTS phase 1.

The goal of GPTS phase 1 is to deliver the basic functionality of its predecessor system in a form that has been redesigned for better performance and improved scalability. The PMO can expect to have forms to manage proposals, user agreements, PMO projects, contacts, accounts, and samples. In addition, search, summary reports, and data export to Excel spreadsheets will be provided. Two related software development efforts are in progress in David's group. The sample tube entry form, created by Duncan Scott, will replace the whole genome tracking spreadsheet currently maintained by Eileen Dalin. The plate tracking tools, created by Khela Baskett, will improve the ability of the production sequencing staff to schedule and track plates. GPTS phase 1 was rolled out at the

end of September 2007.

Since the release, data cleanup and application fine-tuning efforts are underway to correct any incomplete or bad data, check and update contact and cost-accounting information, apply new conventions for controlled vocabularies, fix minor bugs, and train additional users.

In parallel with GPTS phase 1, several other software development efforts are in the works. They will feed data into GPTS, and report data from GPTS to the PMO and collaborators. The Collaborator Status Reporter, which provides collaborators with at-a-glance status information, will be released with GPTS phase 1. The Required Information application will automate the process of submitting, reviewing and accepting sample information prior to the shipment of DNA. Look for this application to be completed before the end of the year. Follow-on projects include a contact management system, a LIMS for the Cloning Technology group, and a Web portal for the PMO. These projects are the responsibility of the Web Team (Joni Fazo, Rene Perrier, Annette Greiner), led by Pat Kale.

DSMZ Connection

cont. from page 8

from the GEBA pilot project by gaining access to a much better balanced database for microbial genomes.

"The phylogenetically diverse genomes analyzed within the GEBA pilot project will provide urgently needed anchors for the improved annotation of data coming out of the many ongoing metagenome projects. In addition, DSMZ will provide easy and affordable access to biological material, cultures as well as DNA, of all GEBA pilot project strains to the world-wide scientific

community—without any strings attached.

"Moreover, participation in the GEBA pilot project provides an excellent opportunity to train our staff and the next generation of genomicists."

"Hans-Peter is one of the pioneers of microbial genomics, said GEBA godfather Jonathan Eisen. "He was the first author on the second archaeal genome to be published and he has been a leader in microbial evolution studies for some 20 years. It is an honor to work with him on such an important topic."

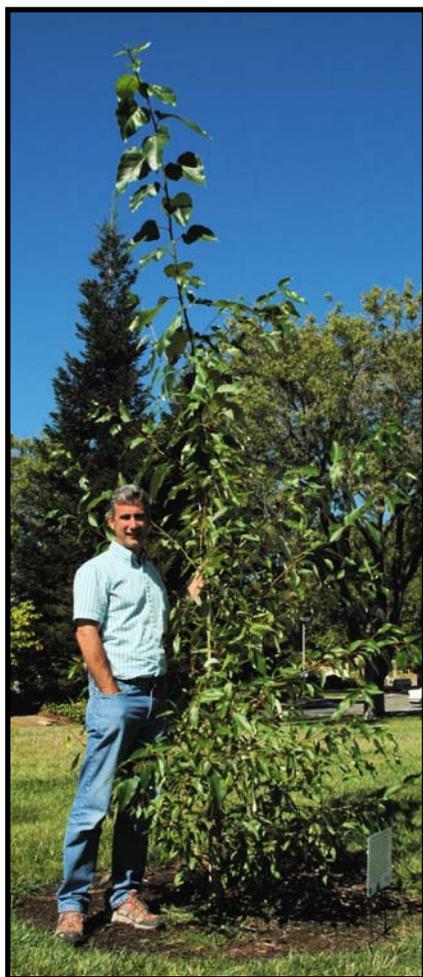
"I view the entire project as a triumph of cutting-edge science from two government institutions with perfect complementarity, forming an international partnership for the benefit of the entire community," said Nikos Kyrpides, JGI Genome Biology Program head.

JGI, DSMZ and others involved are pursuing possible options for funding a continuation of GEBA beyond the pilot phase to sequence hundreds, and perhaps even thousands, of microbial genomes.

Poplar Watch

BY JERRY TUSKAN

Populus trichocarpa is a species that has indeterminate growth, which means that as long as the conditions are right, it will keep putting out new leaves and elongating its stem. That's an unusual trait. Most plants grow in a determinate manner—they have a set number of cell divisions and that's it. In the case of perennial plants, the extent of determinate growth is determined by the condi-



Jerry Tuskan and his poplar friend

tions of the previous year. The plant retains a metabolic signal of how much to grow the subsequent year. In the case of perennials, which can't afford to invest too many resources in a drought year or a cold-interrupted growing season, it's a way of predicting what the next year is going to be like.

Poplars, on the other hand, will keep growing until water, nitrogen, and/or nutrients become limited, or daylight shortens, and to some degree, cold weather sets in. However, because it does not have as many cold receptors, if you keep giving it nitrogen and water, it will grow right into the early frost period in the fall.

For bioenergy applications, we are seeking to harness these traits, because the more of the growing season that a plant can capture, the more biomass they put on. One of the objectives is to maximize how long the leaves are displayed to the sun. Some researchers are selecting for photoperiod response because plants can perceive when the days start getting shorter and in response they start setting buds. Typically, more southern sources of plant material set bud later, requiring a much shorter day to cause them to set bud. So, in short-rotation biomass farms, we can use that trait to maximize the amount of biomass.

The other change occurring this time of year is the secondary thickening of the cell walls within the xylem. With each primary cell division, cell wall forms. In trees, a secondary cell wall is formed that becomes the woody part of its architecture, i.e., the stem. There are three layers of cells (S1, S2, S3) required to construct mature xylem cells. Lignification is the final step in the maturation process. In September, as the growing season begins to

decline, and because of the poplar's indeterminate habit, most of the cells formed late in the season will not actually mature that season. Secondary thickening and secondary cell wall formation is arrested and lignification continues next season.

Because of the relationship between indeterminate growth and lignification, if you take a core from a poplar tree you won't see annual rings like a redwood or a pine.

As a tree ceases to grow late in the season, there is a spike of lignification. This process has implications for bioenergy. Lignin is not convertible to sugar because it's polyphenolic and impedes the invasion of microbes and their cell wall degrading enzymes. Among our goals is to minimize the lignin, to the extent possible, and still have the plant cells and tissue remain healthy. So, elucidating the process of cell wall formation during dormancy, and what triggers that maturation process and the deposition of lignin, will help us tailor plants for our energy crop domestication project.

Over the next five years, we hope to tease apart some of this complexity to better our understanding of the molecular mechanisms behind cell wall formation, lignification, and indeterminate growth.

JGI Poplar Virtual Yard (Meter)

Stick: 192 inches (16 feet) as of Oct 10, 2007, representing a 3.5x growth spurt in less than 13 months since the ceremonial planting.

Jerry Tuskan, Oak Ridge National Laboratory, is the JGI Laboratory Science Program Lead

JGI Hosts Undergraduate Educators for Microbial Genome Annotation Workshop

On October 18 and 19, JGI's Undergraduate Research Program convened the first Workshop in Microbial Genome Annotation. Nineteen educators from 14 institutions participated, representing a diverse cross-section of research universities, state and liberal arts colleges. The goal of the workshop was to provide the tools and ideas for advancing genomics and bioinformatics across undergraduate curricula.

Cheryl Kerfeld, JGI's Education Program head, presented a survey of current bioinformatics tools and strategies for integrating annotation across the life sciences curriculum, including algorithms for gene calling, pathway annotation, and characterization of hypothetical protein function.

The participants subdivided into work-



Front to back, left to right; Front row: Cheryl Bailey, University of Nebraska-Lincoln; Kelynne Reed, Austin College; Sharyn Freyermuth, University of Missouri; Ferda Soyer, Izmir Institute of Technology (Turkey); Zhaohui Xu, Bowling Green State University. Second row: Kathleen Scott, University of South Florida; Sabine Heinhorst, University of Southern Mississippi; Cheryl Kerfeld, JGI; Tuajuanda Jordan, HHMI; Jay Lennon, Michigan State University. Back row: Daniela Bartels, ANL; Brad Goodner, Hiram college; Erin Sanders-Lorenz, UCLA; Christopher Kvaal, Saint Cloud State University; Mitrick Johns, Northern Illinois University; Folker Meyer, ANL; Jayna Ditty, University of St. Thomas; Tobias Paczian, ANL. Stuart Gordon, Hiram College, not pictured.

JGI's Stanman Tops NorCal

Greg Stanley, the Joint Genome Institute's facilities manager, won the NorCal Top Comp Association Championship in late September with his 409 c.i. Chevy small block-powered dragster. The event took place at Famoso Raceway near Bakersfield.



ing groups based on their teaching interests—biochemistry, microbiology, molecular genetics, and those planning to develop bioinformatics courses—to explore curriculum options that they will implement at their respective institutions in the winter-spring term of 2008.

The educators were sent back to their institutions with homework—to engage their classes in collectively annotating (assigning biological function to the sequence of) the microbe *Ammonifex degensii*—a heat-loving bug of geothermal origin. Folker Meyer and his team at Argonne National Laboratory are working

closely with Kerfeld in developing the platform of bioinformatics tools that the students will use to complete their assignment.

“We had an extraordinarily productive short time together,” said Kerfeld. “I am optimistic that when we reconvene at JGI next June, they'll all be primed to discuss their results and be in a position to begin drafting a paper.”

Kerfeld said that the participants will complete a survey conducted by the Oak Ridge Institute for Science and Education (ORISE), which will serve as starting material for an evaluation *(cont. on page 14)*

Len Pennacchio Receives Presidential Award

Len Pennacchio—JGI Genetic Analysis Program Head and Senior Staff Scientist in the Genomics Division at Lawrence Berkeley National Laboratory—is the recipient of The Presidential Early Career Award for Scientists and Engineers (PECASE) for his significant contributions to the generation and interpretation of the human genome sequence. Specifically, he is being honored for his systematically assigning gene regulatory function to the human genome through the coupling of vertebrate comparative genomics and large-scale studies in mice, using a world-class and unique mouse resource that he established.

“Len is extraordinarily capable at getting things done,” said JGI Director Eddy Rubin. “I think that we’ll be seeing more great

accomplishments coming from Len’s contributions.”

The Presidential Early Career Award for Scientists and Engineers was created to honor and support the extraordinary achievements of young professionals at the outset of their independent research careers in the fields of science and technology. The Presidential Award embodies the high priority placed by the government on maintaining the scientific leadership position of the United States by producing outstanding scientists and engineers who will broadly advance science and the missions important to the participating federal agencies.

Pennacchio and the other 2006 PECASE recipients were honored in an award ceremony in Washington, DC at the Presidential Hall

of the Dwight D. Eisenhower Executive Office Building on November 1, 2007. Each award recipient receives a plaque, a citation from the President, and \$50,000 per year for five years to support their research.



Pennacchio (left) receiving the PECASE plaque from DOE Deputy Undersecretary Clay Sell in the Washington DC ceremony on Nov 1

JGI Triathlete—Mission Accomplished!

BY MEGAN KENNEDY

My triathlon went much better than anticipated. I finished in 3:03:38—much better than my 3:20 estimate. All worries of seals and sharks were gone in the chaos of a mass swim start. After the pack spread out, I had a good swim. The spectators saw a pod of dolphins swim by—a good sign that

there weren’t any sharks in the area. One of the most impressive and inspiring parts of the race was watching the founder of the Challenged Athletes Foundation use crutches in the soft sand to get



Megan Kennedy bikes

into the water, then crutch his way out and around the swimmers’ half way point and go



Megan Kennedy runs

pace. The run was the toughest part, having pushed myself during the swim and bike portions. The cheering from my teammates, coaches, and family kept me going.

Thank you for the donations to the Leukemia and Lymphoma Society. 1.4 million dollars were raised by Pacific Grove Team in Training triathletes. To date, 800 million dollars have been raised for blood cancer research!

back into the water.

I had a strong bike ride and was so focused on not drafting that I hardly had any time to enjoy the beautiful scenery. I’ll have to go back and bike it at a more leisurely

pace. The run was the toughest part, having pushed myself during the swim and bike portions. The cheering from my teammates, coaches, and family kept me going.

Thank you!
Megan

Megan Kennedy, JGI Sequencing Department staffer, writes about the Triathlon at Pacific Grove on September 8, which entailed a 0.9-mile swim through kelp beds, 24.8-mile bike ride and a 6.2-mile run.

Megan exceeded her contribution goal, collecting \$3,550 on behalf of the Leukemia and Lymphoma Society.

PS: For those who asked how to sign up for races, check out active.com and onourmarkevents.com. Active also provides links to local sports teams.

There’s still time to help the Leukemia & Lymphoma Society fight cancer and support patients. <http://www.active.com/donate/tntgsf/mckennedy>

Eucalyptus

cont. from page 1

The project will also be supported by ArborGen, LLC, a South Carolina-based forestry biotechnology company. ArborGen will provide access to their collection of Eucalyptus sequences and will work to enable transformation of the model *E. grandis* clone that will be the source of the genomic sequence.

“Sequencing the Eucalyptus genome will help us overcome many of the major obstacles toward achieving a sustainable energy future,” said Myburg. “Embedded in this information is the molecular circuit map for superior growth and adaptation in woody plants that can be optimized for biomass production. Its unique evolutionary history, keystone ecological status, and adaptation to marginal environments make Eucalyptus the focus of choice for expanding our knowledge of the evolution and adaptive biology of all perennial plants.”

The genus Eucalyptus, comprised of over 700 different species, includes some of the fastest growing woody plants in the world and, at approximately 18 million hectares in 90 countries, it is one of the most widely planted genus’ of plantation forest trees in the world.

“The Eucalyptus genome will provide a window into the tree’s metabolic pathways, shedding light on such traits as cold tolerance, osmotic potential, membrane integrity, and other agronomic features,” said co-lead Tuskan. “As the genus is amenable to genetic transformation, it can serve as a validation platform for candidate gene expression studies—helping us to expand Eucalyptus’ range and exploit its potential as a bioenergy plantation crop.”

“This monumental project will enable improved breeding strategies for cellulosic ethanol feedstocks and contribute to environmentally sound improvements in productivity for the global forestry industry,” said project collaborator Maud Hinchee, Chief Technical Officer of ArborGen. “This

effort will help us advance our goals of producing renewable high-value biomass from a smaller environmental footprint.”

A considerable amount of carbon is already tied up in Eucalyptus biomass. Coupled with the emerging economic incentives for carbon sequestration, Eucalyptus is a prime candidate for increased efforts to remove carbon from the atmosphere. “In countries such as Brazil, Eucalyptus is used as a source of renewable energy for high-quality steel production in a way that reduces the net production of greenhouse gases. Eucalyptus is capable of sequestering carbon at rate of 10 tons of carbon/hectare/year and has a positive net carbon balance even when it is used to generate energy from charcoal or for pulp and paper production. Furthermore, plantation forestry of Eucalyptus plays a crucial role in reducing the pressure on tropical forests and associated biodiversity,” said project co-lead Grattapaglia.



Maximizing Eucalyptus

Recent Notable JGI-Enabled Publications

Genome-Wide Experimental Determination of Barriers to Horizontal Gene Transfer

<http://www.scienceonline.org/cgi/content/abstract/1147112>

Science Express Reports 18 October 2007 [DOI: 10.1126/science.1147112]

Rotem Sorek, Yiwen Zhu, Christopher J. Creevey, M. Pilar Francino, Peer Bork, Edward M. Rubin

A JGI survey identified genes that kill the bacteria employed in the sequencing process and throw a microbial wrench in the works. It also offers a possible strategy for the discovery of new antibiotics.

Sea Anemone Genome Reveals Ancestral Eumetazoan Gene Repertoire and Genomic Organization

<http://www.sciencemag.org/cgi/content/abstract/317/5834/86>

Science 6 July 2007: Vol. 317. no. 5834, pp. 86 – 94, DOI: 10.1126/science.1139158

Nicholas H. Putnam, Mansi Srivastava, Uffe Hellsten, Bill Dirks, Jarrod Chapman, Asaf Salamov, Astrid Terry, Harris Shapiro, Erika Lindquist, Vladimir V. Kapitonov, Jerzy Jurka, Grigory Genikhovich, Igor V. Grigoriev, Susan M. Lucas, Robert E. Steele, John R. Finnerty, Ulrich Technau, Mark Q. Martindale, Daniel S. Rokhsar

Sea anemones are seemingly primitive animals that, along with corals, jellyfish, and hydras, constitute the oldest eumetazoan phylum, the Cnidaria. Here, we report a comparative analysis of the draft genome of an emerging cnidarian model, the starlet sea anemone *Nematostella vectensis*. The sea anemone genome is complex, with a gene repertoire, exon-intron structure, and large-scale gene linkage more similar to vertebrates than to flies or nematodes, implying that the genome of the eumetazoan ancestor was similarly complex.

Genome sequencing reveals complex secondary metabolome in the marine actinomycete *Salinispora tropica*

<http://www.pnas.org/cgi/content/abstract/104/25/10376>

PNAS | June 19, 2007 | vol. 104 | no. 25 | 10376-10381

Daniel W. Udway, Lisa Zeigler, Ratnakar N. Asolkar, Vasanth Singan, Alla Lapidus, William Fenical, Paul R. Jensen, and Bradley S. Moore

Our analysis shows that *S. tropica* dedicates a large percentage of its genome (approx 9.9%) to natural product assembly, which is greater than previous *Streptomyces* genome sequences as well as other natural product-producing actinomycetes.

Bioenergy Centers

cont. from page 1

question from DOE Office of Biological and Environmental Research's Dan Drell about whether it would be useful for the BRCs to do any in-house sequencing, Jay Keasling noted that JBEI has no plans to buy sequencers or to try and duplicate the expertise available at JGI.

Each of the three BRC directors gave an overview of their plans for the next five years. Jay Keasling discussed the organization of JBEI and initial feedstock targets of *Arabidopsis* and rice. Martin Keller described the BESC structure and their goal to overcome biomass recalcitrance for improving biomass processing. Tim Donohue of GLBRC talked about plans for conversion of biomass into energy products while also studying economic and environmental sustainability of the biomass-to-biofuel pipeline.

During the lunch break, JGI Sequencing Department Head Susan

Lucas led a group through a tour of the sequencing line, ending up at the 454 and Illumina sequencers for a detailed discussion of new techniques.

To highlight the array of expertise



available at JGI, Jim Bristow spoke after lunch about project management; Paul Richardson discussed microbial sequencing and IMG; Susannah Tringe explained eDNA, metagenomics, and

IMG/M. Tringe also pointed out that the rate-limiting step in sequencing metagenomes is in getting good-quality genomic DNA samples. Jerry Tuskan talked about his eucalyptus project and the JGI plant program. The last talk of the first day was by Len Pennachio, who explained resequencing and compared the relative advantages of the Sanger, 454, and Illumina processes.

"JGI's activities are on a critical path for all of the Centers," said Glynn.

"This is our number one priority," said JGI Deputy Director Jim Bristow. "JGI can commit to getting the Center's highest priority projects done. What rules at the end of the day, is getting high quality DNA through the door."

The participants acknowledged that this was an important first step in a process to identify, refine, and prioritize bioenergy-relevant sequencing targets that JGI will seek to accommodate in the production queue in the coming years.

Undergraduate Educators

cont. from page 11

of the workshop. The Howard Hughes Medical Institute (HHMI) senior program officer for science education, Tuajuanda Jordan, participated in the workshop as an observer.

"This workshop really serves as a model for stretching our resources to bring together scientists and educators," said Jordan. "This is a trend we are seeing, something that HHMI is doing as well. The tools developed by Argonne are helping to bring these communities together. This is the prevailing model for science education in this country—and I think it's terrific."

"What this means to a faculty member trying to innovate science education: I don't have to go it alone," said Cheryl Bailey, Ph.D., Assistant Professor,

Department of Biochemistry, University Nebraska-Lincoln. "We can see how this works across many institutions to help those in the future incorporate this type of learning at their institution. The backing by JGI gives us the credibility to make changes in our science courses; the workshop was a true collaborative effort with input and feedback working on all levels of the project. It is truly a wonderful way to innovate science education and serves to both develop faculty members and the students they engage."

The American Society for Microbiology (ASM) has a long-standing commitment to undergraduate education. In their Committee on Undergraduate Education's strategic plan, released earlier this year,

they cited their interest in supporting and assessing pilot projects, including the JGI's, to involve undergraduate students in genomic research and those initiatives that leverage undergraduate teaching fellowships and undergraduate genomic research programs to attract underrepresented populations.

Said ASM Education Department Director, Amy Chang, "I am encouraged by the reports of JGI's first microbial annotation workshop for undergraduate educators. Their objective is consistent with our interests in building a network of educators and providing access to the pertinent tools to create opportunities those students interested in pursuing careers in microbial genomics and bioinformatics."

Chlamy Genome

cont. from page 1

15,000-plus genes revealed in the study are those that encode the structure and function of the specialized organelle that houses the photosynthetic apparatus, the chloroplast, which is responsible for converting light to chemical energy. The genome also provides a glimpse back through time to the last common ancestor of plants and animals. The project, led by JGI; the University of California, Los Angeles; and the Carnegie Institution, and including contributions from over 100 international collaborators, is featured in the Oct. 12 edition of the journal *Science* (*Science* 318, 245 (2007); DOI: 10.1126/science.1143609).

The single-celled alga *Chlamydomonas reinhardtii*, while less than a thousandth of an inch in diameter, or about one-fiftieth the size of a grain of salt, is packed with many ancient and informative surprises. Affectionately known to its large research community as “Chlamy,” the alga is a powerful model system for the study of photosynthesis and cell motility. The genes that encode the alga’s “flagella,” which propel it much like a human sperm tail, were also cataloged in this

study. Defects in these genes are associated with a growing list of human diseases.

“The Chlamy genome is like a green time capsule that affords a view into the complex core machinery that gave rise to today’s energy-capturing and oxygen-producing chloroplasts,” said Daniel Rokhsar, DOE JGI Computational Biology Program head, who co-led the effort with DOE JGI Computational Scientist Simon Prochnik, Arthur Grossman of the Carnegie Institution and Stanford University, and Sabeeha Merchant of UCLA.

“DOE JGI’s particular interest in Chlamy centers on its keen ability to efficiently capture and convert sunlight into energy, and its role in managing the global pool of carbon,” said Rokhsar. The sequence analysis presents a comprehensive set of genes—the molecular and biochemical instructions—required for these capabilities. Rokhsar said that with these data now publicly available, new strategies for biology-based solar energy capture, carbon assimilation, and detoxification of soils by employing algae to remove heavy metal contaminants will begin to surface. The analysis will also

shed light on the capabilities of related algae that can produce biodiesel and biocrude as alternatives to fossil fuels.

The results will also help researchers figure out the construction of chloroplasts, which house the machinery inside plant and algal cells that serve as “solar panels,” absorbing sunlight and coupling carbon dioxide and water to produce the starting materials—sugars—that fuel all other metabolic processes. These pathways, described in the DNA sequence, represent opportunities for improving efficiencies for this conversion process and ultimately biofuels production.

Other DOE JGI authors on the Chlamy *Science* paper include Astrid Terry, Asaf Salamov, Erika Lindquist, Harris Shapiro, Susan Lucas; Jane Grimwood and Jeremy Schmutz at the Stanford Human Genome Center; and the *Chlamydomonas* Annotation Team led by Igor Grigoriev and including Peter Brokstein, Inna Dubchak, David Goodstein, Leila Hornick, Wayne Huang, Jinal Jhaveri, Yigong Lou, Diego Martinez, Abby Ngau, Bobby Otilar, Alexander Poliakov, Aaron Porter, Lukasz Szajkowski, Gregory Werner, and Kemin Zhou.

JGI Faces

cont. from page 2

industry, public accounting and HR consulting. Chris has a BA in English from UC Davis and a MA in Higher Education Administration/Labor & Industrial Relations from Michigan State University. Chris lives here in Walnut Creek with his wife, Cindy, and two sons, Robert and Michael. He enjoys sports (including coaching youth teams), cooking and spending time with family. By the way, Chris is an avid baseball and Cal football fan.

CHRISTA PENNACCHIO

Senior Project Manager

Christa is a new member of the JGI Project Management Office, supporting ESTs and new technologies. Prior to that, she worked as a Biomedical Scientist at LLNL, initially mapping and characterizing chromosome 19 genes as part of the Human Genome Project, and most recently

managing the I.M.A.G.E. Consortium, a collaborative gene discovery effort that has produced over 10M publicly available cDNA clones. Christa received her BS in Biology from Saint Mary’s College. She lives in Oakland with her husband Len and son Alex, and enjoys gardening, cooking/eating and reading.

MegaBACEs

cont. from page 5

Amersham). During this assessment period, the MB4500 system went through several modifications, reagent reformulations, and software changes. By July 2003, three official release versions of the MB4500s were installed for proof-of-principle sequencing validation tests. The decision was made to upgrade all



MegaBACE 4500 poses with Chris Daum

MB4000s to the new MB4500 platform and, by early 2005, the JGI was operating 36 of these instruments full time, with their new solid-state laser system offering longer read lengths.

On September 6, the machines

were wheeled out of Building 100, wrapped in plastic, fork-lifted onto trucks and transported to LBNL's 904 warehouse where the excess process has begun. The former MegaBACE laboratory will be retrofitted to accommodate new sequencing technology instruments and procedures that are currently being developed and integrated into the JGI Production Sequencing Pipeline. The first of these will be the Roche (454) Genome Sequencer platform.

Anyone interested in obtaining a piece of history and using the MegaBACE 4500, contact LBNL Property Management's Cindy Lytle, (510) 486-6569, CJLytle@lbl.gov or Dave McFann (510) 486-6769, DJMcFann@lbl.gov.

DOE offers a unique donation program called the Energy-Related Laboratory Equipment (ERLE) Grant Program, where any nonprofit, educational institution of higher learning—such as a university, college, junior college, technical institute, museum, or hospital—is eligible to apply. The applicant must be located in the US and interested in establishing or upgrading energy-oriented educational programs in the life sciences, physical and environmental sciences, or in engineering. For additional information: <http://erle.osti.gov/erle/>.

Hold the Date

March 26-28, 2008
JGI User Meeting

Community Sequencing Program

Sequencing Plans for 2008

JGI's current list of major allocations for the Community Sequencing Program can be seen on our website at:

<http://www.jgi.doe.gov/sequencing/cspseqplans2008.html>

CSP Bioenergy Call

Letters of Intent due
January 21, 2008

Forms and information for electronic submission will be posted soon on the JGI website.

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