

Oysters to sunflowers: genomics of the 5th DOE JGI User Meeting

BY MASSIE SANTOS BALLON

The 5th Annual DOE Joint Genome Institute “Genomics of Energy & Environment” User Meeting started off on a provocative note: the first speaker, Dennis Hedgecock of the University of Southern California, compared eating an oyster to “kissing the sea on the lips.” Given the meeting’s focus on genomics for energy and the environment, Hedgecock was quick to note that Pacific oysters can annually sequester the amount of carbon equivalent to that produced by the African nation of Cameroon

during the same period. He said researchers are interested in finding ways to boost the oyster’s ability to capture carbon just as biofuels researchers are interested in using the idea of hybrid vigor to boost biomass production in energy crops.

Over 430 researchers converged on the Walnut Creek Marriott on March 24-26, 2010 to hear how genome sequencing can be applied to a number of DOE-relevant missions. These include the development of cellulosic biofuels and understanding and maintaining important biological and geo-

logical processes, such as the carbon and nitrogen cycles, for the environment.

The first day of the session featured several projects that had resulted in significant publications over the past year.

Following Hedgecock, Steven Hallam from the University of British Columbia talked about oxygen minimum zones and how the genomes of microorganisms in these regions are informing researchers about the effects of climate change on the global carbon and nitrogen cycles. Alexandra Worden from the Monterey Bay Aquarium Research Institute *cont. on page 2*



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DOE JGI takes home 2nd Ergo Cup



The DOE JGI now has a matched pair of Ergo Cups after winning at the 13th Annual Applied Ergonomics Conference held March 22-25 in San Antonio, Texas. On hand to accept the award were (left to right): Christine Naca, Melanie Alexandre, Nicole Shapiro, Megan Kennedy, Angela Tarver, Bridget Swift, and Marty Pollard.

The DOE JGI’s winning entry, “Empowering Employees in Ergonomics,” was for the Ergonomic Program Improvement Initiatives category and highlighted key elements of DOE JGI’s employee-led activities and safety culture such as “potty training” to provide safety information in high-traffic areas and employee-led safety walk-

throughs. “This award is arguably the most prestigious recognition in applying ergonomics and extremely relevant to reducing MSD injuries,” said Andrew S. Imada, President of the International Ergonomics Association. “To win this award twice in such a short interval is truly remarkable.”

The DOE JGI previously won the 2007 Ergo Cup for its entry to the Team-driven Workplace Solutions category. The Shake ‘N Plate instrument was designed to ease upper body fatigue for employees working on the Sanger sequencing production line that were manually processing 22 cm x 22 cm plates of bacterial cultures.

Genomics of Energy & Environment

cont. from page 1



Meeting attendees listen to JBEI's Jay Keasling deliver the opening keynote. (All 2010 DOE JGI User Meeting photos taken by Roy Kaltschmidt, LBNL)

described how tiny microorganisms such as *Ostreococcus* and *Micromonas* play a major role in the global carbon cycle. Gary Stacey, associate director of the National Center for Soybean Biotechnology at the University of Missouri, noted that the complete soybean genome released in January had already proven “a catalyst for rapid progress.” And Francis Martin from the French institute INRA described the evolution of mycorrhizal symbiosis using the genomes of *Laccaria bicolor* and the Perigord black truffle *Tuber melanosporin*, a delicacy that was featured in the March 28 issue of *Nature*.

Christina Cuomo of the Broad Institute then talked about amphibians in crisis due in part to pollution, pesticides and climate change. And as the day drew to an end, the DOE JGI took the opportunity to premiere a short “Energy Genomics” video (see <http://www.youtube.com/user/JointGenomeInstitute>) done in collaboration with the Ex'pression College for Digital Arts. The animated project explains how sequencing genomes of plants, fungi, microbes and metagenomes can impact the quest to produce cellulosic biofuels.



“This is a state of knowledge talk; we're still in discovery phase.”

*Steve Hallam,
University of British Columbia*

Finally, Jay Keasling, director of the Joint Bioenergy Institute, closed the first day's session with a keynote address (see page



“We do what most people do when we don't have data: we make simulations. It matches our data perfectly...”

*Forest Rohwer,
San Diego State University*

4) on synthetic biology to develop biofuels.

The recurring theme of the second day was the development of biofuels, from feedstock production to the challenges faced in bringing the product to market. Monsanto's Steve Knapp led off the morning with a talk on woody sunflowers. Several researchers from the Energy Biosciences Institute — Evan DeLucia, Madhu Khanna and Steve Moose — discussed the various challenges (see page 6) associated with developing and producing biofuel feedstocks, considering the



“While we have a lot of promiscuous mutants, they have a lot of interesting features.”

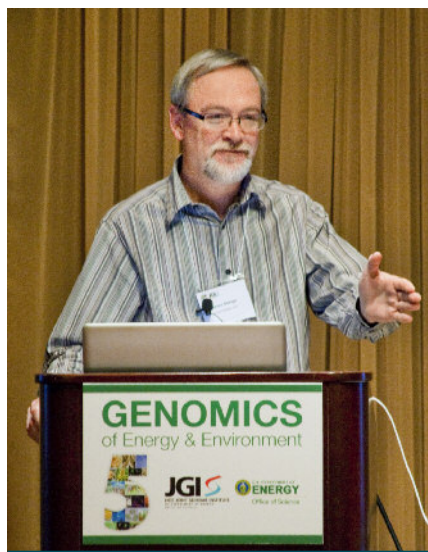
Joseph Noel, Salk Institute

potential ecological impact, technical requirements and policy and regulatory issues. In the midst of this discussion, Roger Pennell from Ceres delivered the day’s keynote lecture (see page 5) on how genes and genomics can improve energy crops. Finally, Steve Savage of Cirrus wrapped up the day with a look at whether criteria such as carbon and water footprints, pesticide use and biodiversity impact should be considered in defining metrics for developing biomass-based energy.

Interspersed between the biofuel discussions were talks ranging from Duke University’s Tom Mitchell-Olds on the importance of conducting field studies in pristine environments and the scarcity of such sites to San Diego State University’s

Forest Rohwer on ocean viral metagenomics (see page 8). Victoria Orphan from CalTech spoke on sulfate-reducing bacteria and deep-sea nitrogen fixation while Detlef Wiegel from the Max Planck Institute referenced a 2005 DOE JGI Community Sequencing Project on sequencing relatives of the model plant *Arabidopsis thaliana* while using analogies involving cars, German engineering and small, heavily-armored shrimp.

The first two days of the User Meeting concluded with poster sessions primarily



“I don’t know right now what metrics will be used, but I can’t imagine there won’t be one.”

Steve Savage, Cirrus Partners

featuring projects with DOE-relevant missions that had been selected for the Community Sequencing Program. The second day’s poster session was held at the DOE JGI campus and provided the meeting attendees with an opportunity to see the

user facility in person. As DOE JGI director Eddy Rubin noted during his opening remarks, people typically send DNA samples for sequencing through the mail. During his own presentation (see page 6) on microbial communities in cow rumen, Rubin showed a photo of a DOE JGI researcher elbow-deep in a cow’s stomach and noted, “This is the nature of the JGI. We don’t do ocean cruises.”

The last day of the DOE JGI User Meeting featured a variety of sequencing techniques and applications. The DOE JGI’s Tanja Woyke started off the morning with a look at single cell sequencing and was followed by Concordia University’s Adrian Tsang on thermophilic fungi to help break down lignocellulose for biofuels production. The Salk Institute’s Joseph Noel then gave a brief talk on chemodiversity in nature.

“There is no more fitting end to this meeting than having Rita Colwell talk on ‘Solving problems with sequences’,” said DOE JGI’s Len Pennacchio as he introduced the final keynote speaker. Colwell, announced as the 2010 Stockholm Water Prize recipient earlier in the week, closed the User Meeting with a talk about her decades of research on cholera. She spoke (see page 4) of the techniques applied to her work, ranging from simple, low-cost water purification methods, to sequencing the genome of the disease-causing bacterium *Vibrio cholerae* to better understand the disease-causing microorganism and finally to the use of bioinformatics and global tracking systems to monitor the spread of these microorganisms in the oceans through conditions such as various weather patterns and climate change.

The 6th Annual DOE JGI User Meeting is scheduled for March 21-25, 2011. Videos of the 2010 User Meeting are posted on the DOE JGI’s SciVee channel: <http://www.scivee.tv/node/17188>.

User Meeting Keynotes

Yes we can – engineer fuel-producing microbes

BY LYNN YARRIS

Borrowing from President Obama's inspirational "Yes we can!" theme, Jay Keasling, CEO of the Joint BioEnergy Institute (JBEI), assured User Meeting attendees that microbes can be engineered to produce next generation biofuels. Through the tools of synthetic biology, he said, microbes can and are being developed in order to efficiently convert lignocellulosic biomass into replacement fuels for gasoline, diesel and jet engines.

Delivering a keynote address before a capacity crowd in the main ballroom of the Marriott hotel in Walnut Creek, Keasling, one of the world's premier synthetic biology scientists, compared the engineering of fuel-producing microbes to building a computer or synthesizing styrene.

"Each of these activities requires a

knowledge base, off-the-shelf components, a system and an idea," he said.

In the case of biofuels, the first step was the idea, sparked by the need for sustainable transportation fuels and national energy independence, and international concerns about carbon emissions. Such fuels, sometimes dubbed "grassoline," could replace gasoline on a gallon-for-gallon basis and would be carbon-neutral, meaning they would not add to the atmospheric carbon levels that are exacerbating global climate change.

Furthermore, Keasling said, a system for producing advanced biofuels is already in place in the form of the microbial central metabolism system. This system can be tapped to produce advanced biofuels derived from isoprenoids, fatty acids and various alcohols.

Off-the-shelf components, however, are a work in progress, Keasling said. Through the genomics research at DOE JGI and the synthetic biology research at JBEI, the biological "parts" needed for advanced biofuels synthesis are being developed. This effort should get a major lift with the start of "BIOFAB," which stands for the International Open Facility Advancing Biotechnology. The goal of BIOFAB, which will be operated at JBEI, is to produce thousands of free, standardized DNA parts that will be made available to academic or biotech laboratories.

The knowledge base that provides the information critical to characterizing parts and processes, making standard connections, creating independent devices, and designing, creating and debugging models is another work in progress, Keasling said. Again the on-going research efforts at DOE JGI and JBEI are playing a big role.

In his keynote address, Keasling also stressed the need for a "systems biology" approach that can speed the development of advanced biofuels. This systemic

approach calls for the integration of information from a multitude of different experiments on the assumption that in a system such as an advanced biofuel, every individual component of the system wields a certain degree of influence.

"Can we consolidate all the system components for production of an advanced biofuel into a bioprocessing microbe?" Keasling asked rhetorically before answering: "Yes, we can!"

Lynn Yarris is a senior science writer at Lawrence Berkeley National Laboratory.

Colwell's cholera crusade

BY CASEY ZAGLIN

Days before the User Meeting, the 2010 Stockholm Water Prize went to Dr. Rita Colwell from the University of Maryland for her work on cholera. So no one was surprised when Colwell described her extensive work on the disease in her keynote address: "Solving Problems with Sequences."

Colwell depicted cholera as "a global infectious disease that does not carry a passport." The source of the disease, the two chromosome, waterborne bacteria *Vibrio cholerae*, travels in warmer waters and is especially infectious to children living where water quality is poor, such as Malaysia, India, Zimbabwe and Bangladesh. Colwell said that in 2007, over 150,000 cases of cholera were reported by several countries.

However, cholera is not only isolated to less developed countries. The disease crossed U.S. borders as recently as 1999 in Chesapeake Bay, Md. Any location that has the proper conditions for *V. cholerae* to survive is where you can find cholera, Colwell said.

"Whoever wishes to pursue the science of medicine must first investigate the seasons of the year and what occurs



"I like to say ethanol is better for drinking than for driving."

Jay Keasling



“When one tugs at a single thing in nature, he finds it hitched to the rest of the universe.”

Rita Colwell quoting John Muir

in them,” Colwell quoted fourth century BC physician Hippocrates. Applied to the study of cholera, she said the key to understanding where cholera cases would occur next was to first understand the environment *V. cholerae* lives in.

Through her studies, Colwell and her colleagues were able to link cholera episodes with ocean temperatures and plankton blooms. By mapping global water temperatures and weather patterns using satellite tracking systems, Colwell was able to predict hot spots for cholera outbreaks. She also help developed the Chesapeake Bay Forecast System, which predicts the probability of where to find *V. cholerae* in an area based on the water temperature and water quality.

Environmental monitors in place, Colwell reasoned that deciphering *V. cholerae*'s genome would allow researchers to understand the bacterium better. After sequencing over 20 bacterial strains with help from Los Alamos National Laboratory, the genetic codes established a lineage of the pathogens that can carry cholera. The researchers were able to track the bacteria's

evolutionary changes around the world given the genomic and biogeological data.

Colwell ended her talk by sharing her future plans for the *V. cholerae* genome. She believes that the most beneficial aspect of sequencing *V. cholerae*'s genome is to create a DNA-based vaccine that works at the genetic level, rather than a surface based vaccine. Because of the constant “genomic drift” and “genomic shift” in cholera strains like in the flu, surface vaccines have little effect, whereas a DNA vaccine might have more success.

Ceres engineering energy crops

BY JANELLE WEAVER

Solving the world's energy problems will rely on joint efforts between universities, national labs and companies. Ceres is a biotechnology company located in Thousand Oaks, Calif. that uses cutting-edge genomic techniques to improve energy crops, such as switchgrass, sorghum, *Miscanthus* and woody crops.

Researchers at Ceres are identifying genes that enhance key traits in energy crops. So far, their promising research shows that DNA function in one crop plant stays conserved across different crop species. This will greatly facilitate the translation of their research discoveries into bioenergy and agricultural practices.

More than 10 years ago, Roger Pennell, Vice President of Trait Development at Ceres, began to sequence DNA in energy crops. “The key question 10 years ago was: How do you find genes that will enhance key traits in agriculture,” said Pennell, who presented his work at the User Meeting. “At that time, there was no whole-genome sequence.” Now he has helped create extensive DNA libraries and annotated genomes that allow for comparisons across species, including rice, soybean and *Arabidopsis*.

Once Pennell and his team assembled DNA libraries, they set out to test key genes

for enhancing crop traits. They tested 12,000 genes in *Arabidopsis* in more than 40 screens and about 900 genes in rice. One thousand genes seemed promising for bioenergy applications. In their screens, they identified genes that were related to growth in low levels of nitrogen, flowering time, and more. They went on to identify drought and biomass genes in rice and test them out in fields in China. And they tested drought genes in switchgrass in fields in Arizona. These discoveries will allow Pennell's team to develop a range of plants that resist stress and produce high yields.



“The key question 10 years ago was: how do we find genes that will enhance key traits in agriculture?”

Roger Pennell

Ceres will continue to identify genes that are important for bioenergy applications, Pennell said in his keynote address. The company hopes to develop a line of dedicated energy crops that will reduce reliance on fossil fuels.

Janelle Weaver is a graduate student in the UC Santa Cruz Science Communication program.

Paving the road to biofuels

BY RON KOLB

Four principal investigators studying biofuels in the Energy Biosciences Institute (EBI) brought their messages of possibilities and potential to genomics researchers at the User Meeting. In addition to hearing what genetic profiling can do to assist in the production of biofuels, the attendees also heard about the political and social influences that will help shape the new field.

DOE JGI Director Eddy Rubin provided the most tangible evidence of the Meeting's overall theme. He and his EBI research team are seeking keys to a biofuels revolution in the rumen of cows. "We are looking at organisms and environ-

ments that are capable of breaking down biomass," he said.

"The cow rumen system is easily accessible, and you can insert and remove different substrates (from the cow's stomach)."

From the deconstruction of switchgrass, a prospective biofuel feedstock, researchers extracted the DNA from the rumen, looked at its chemical composition and studied the microbes found there – bacteria that could be responsible for the digestion and, thus, provide clues to the enzymes at work in such deconstruction of cellulose and other plant products.

"Can we identify the organisms?" he asked rhetorically. "Can we withdraw full-length genes and show how they work, and then assemble genomes with metagenomic data?" After a discussion of their collection and analysis of gigabases of data and their identification of a few hundred cellulolytic enzymes, Rubin expressed confidence that novel cellulases that will increase the rate of biomass deconstruction — a key step on the road to develop-

EBI Energy Farm (Brian Staffer for the Institute for Genomic Biology/University of Illinois)

ing effective and economical biofuels — will be found.

Steve Moose is addressing the challenge from another angle. The plant geneticist from the University of Illinois at Urbana-Champaign is leading an EBI effort to understand the genetic basis — and ultimately improve the crop growth — of the leading candidate feedstock for cellulosic ethanol, *Miscanthus*. A fast-growing, broadly productive tall grass, *Miscanthus* has the qualities of being able to thrive in



U of Illinois/EBI plant geneticist Steve Moose



DOE JGI Director Eddy Rubin

Trawling deep metagenomic data is a successful strategy to add to the diversity of enzymes with desired activities

difficult environments, virtually without fertilizer, while restoring carbon to the earth. And it is not a food crop.

"We want to build a *Miscanthus* genetic linkage map," Moose said, indicating that the grass' roots may be found in ancient strains in Japan. "The JGI has loaded *Miscanthus* data into sequence data viewers and are generating maps. We learned a lot about *Miscanthus* in a very short time, and we are moving toward genes we can trace."

Using comparative genomics, Moose said he will use the completed genomes of

sorghum and other grasses to help identify the relevant *Miscanthus* genes. A perennial grass whose reproduction is rhizome-based, *Miscanthus* is a relatively unknown hybrid that could be bred for genetic diversity and traits like resistance to pathogens. Moose's genetic maps will provide the schematics for such modifications.

"Twenty-first century crop improvement will be driven by genomics," Moose predicted, and the roomful of DOE JGI users at the Walnut Creek Marriott had no doubts about it.

They may have been less sure about the somewhat cautious words of social scientists Madhu Khanna and Evan DeLucia, both leading EBI programs at the University of Illinois. Khanna told them about the roles that technology and policy will play in the future of second-generation biofuel feedstocks. The challenges — economic, social and environmental — are as daunting as the technical ones.

"In economics, biofuels have to compete with oil on the market, and feedstocks have to offer a return to farmers that is comparable to conventional crops," said the agricultural economist. "There are concerns of food vs. fuel, and if biofuels raise food prices, how much are we willing to accept? And in the environment, we need to be friendlier than oil, but with land use



U of Illinois/EBI agricultural economist
Madhu Khanna



U of Illinois/EBI plant ecologist
Evan DeLucia

that doesn't impact on biodiversity, water use and greenhouse gas emissions."

And, she added, it will all be guided by the policies that countries put into place. Incentives will influence the development of certain feedstocks, and controls will dictate emissions and other life cycle requirements. Khanna and her EBI colleagues are working to identify those impacts and suggest ways to maximize sustainability and responsibility.

With little experience in biofuel feedstocks on which to base their analysis, scientists are turning to the corn ethanol industry to leverage experience there. "Improving energy efficiency, developing labor-saving technology, and achieving economies of scale are all realized in the corn curve," Khanna said, but quickly noted that corn is not being looked upon as a long-term biofuel option given its competition as a food crop.

"Long-run sustainability depends on yields — competition for land, as well as use of marginal solids — plus attributes like energy intensity and water use, and policy incentives that differentiate among biofuels based upon environmental benefits," she concluded.

Her Illinois colleague, plant ecologist Evan DeLucia, is also studying sustainability as it pertains to biofuel's impacts on the land and atmosphere. His topic title

included both words "promise" and "challenge," indicating that things won't be as simple as just planting feedstock crops.

Citing the last two decades during which production of crops such as corn and soybeans doubled, DeLucia said it "wasn't a bloodless green revolution. The nitrogen application alone was enormous. We are farming as much as we can, but it comes at great ecological cost." The drainage of Midwestern farm irrigation, laden with damaging plant nitrates, into the polluted Mississippi River is just one consequence, he said.

At the EBI Energy Farm, 320 acres of experimental fields at the University of Illinois, DeLucia's team has planted side-by-side plots of various feedstocks, monitoring things like carbon in the air and earth, nitrogen flux and water use. "The objective is to close the biogeochemical gap of carbon, nitrogen and water, figure out the physiological fluxes, and determine the feasibility of sustainability on the landscape," he told them.

Miscanthus has shown positive results in tests and is likely to do even more to reduce carbon in the atmosphere and sink it into the ground as the crops are established, according to the team's early analysis. In older stands, "even in the first seven or eight years, the perennials (like *Miscanthus*) are rebuilding soil carbon," he said, noting that corn generally depletes the soil of its carbon while leaching nitrates that lead to greenhouse gases emissions.

The DeLucia group is gathering data, building models and projecting outcomes from a variety of scenarios. And he says as long as lawmakers await research results like his before rushing into irrational policymaking, "We have the potential to diversify our fuels with lignocellulosic feedstocks, and to redirect the agricultural system to optimize for food and fuel production."

Ron Kolb is Communications Manager at the Energy Biosciences Institute.

Charting ocean communities

BY JANELLE WEAVER

The combined activity of the oceans' organisms is equivalent to all the fossil fuel energy on the planet. Ten million viruses and hundreds of thousands of microbes lurk in each milliliter of seawater. Understanding the diversity of viruses and microorganisms in the ocean may lead to important insights about harnessing energy from oceans.

Forest Rohwer of San Diego State University is unraveling the mysteries of microscopic predators using metagenomics — a technique he uses to sequence the DNA of all viral communities in the ocean. Viruses are the most common marine predators, yet about 80 percent of viral

DNA remains unknown.

“Viruses represent the largest region of unexplored sequence space on earth,” said Rohwer, who presented his work at the User Meeting.

By using metagenomics, Rohwer can reconstruct the diversity of viral and microbial communities across different environments, such as freshwater ponds and salterns, areas used for salt-making. Each ecosystem has unique viral and microbial communities and distinct DNA signatures. But the abundances within main categories of microbes and viruses, and the organisms that dominate remain stable across time. Though the global communities remain sta-

ble, the relative abundances of different populations cycle over time. “There’s a rapid turnover of genotypes in all ecosystems,” Rohwer said.

The way that global categories remain constant, but individuals and strains change, matches the evolutionary model called the Red Queen’s Hypothesis. “Predators and prey run from each other to stay in the same place,” Rohwer said of the model. “They change so they don’t die.”

Though Rohwer is not a bona fide DOE JGI user (yet), his insights into the genomics of the oceans’ organisms may one day lead to practical uses for solving the world’s energy problems.



DOE JGI’s Matthew Zane describes the Illumina sequencing platform to (left to right): 2010 Stockholm Water Prize recipient and User Meeting keynote speaker Rita Colwell, OBER Program Manager Dan Drell, OBER/DOE Computational Biology and Bioinformatics Program Manager Susan Gregurick, and South Dakota State University associate professor Ruanbao Zhou.



DOE JGI’s Matthias Hess talks about the cow rumen project with Arthur Katz of the DOE Office of Biological & Environmental Research.



DOE JGI’s Wendy Schackwitz explains the process of analysis for resequencing projects using the Illumina platform.



DOE JGI’s Damon Tighe discusses the application of single cell genomics to the CSP 2009 hoatzin project.

The Battle for the Biofuels Market

BY CASEY ZAGLIN

The possibility of biofuels displacing petroleum products in the transportation fuels market has got companies of all sizes competing to develop and produce commercially-viable biofuels. In one corner, small biofuel companies that specialize in producing one type of biofuel are trying to get their names and products into the transportation fuels market. In the other corner, well-established "Big Oil" corporations are branching out into the biofuels industry as one of their many side projects.

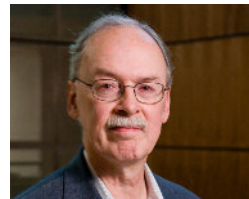
The Bringing Biofuels to Market panel at the University of California, Berkeley's Energy Symposium on March 4, 2010 focused on these two main types of biofuel producers and the challenges both sides face.

The panel was moderated by Chris Somerville, Director of the Energy Biosciences Institute at UC Berkeley. Representing the smaller biofuel companies were

David Walther, Engineering Director for Cobalt Biofuels, a developer of technologies in the commercial production of biobutanol, and Tyler Painter, Chief Financial Officer for Solazyme, a renewable oil company using algal biotechnology. Representing the larger corporations was Steve Pietsch, Process Technology Advisor for BP.

Walther and Painter discussed their companies' struggles to conform to the transportation fuels market set up by larger corporations. They explained that companies of their size try to do what big companies like BP do but cheaper, and they do this by focusing on specific markets and products.

One challenge small companies face is conforming to the environmental regulations of the fuels market. While Walther and Painter both agreed that small-scale companies need to consider regulatory issues, Walther also commented that "environ-



**EBI Director
Chris Somerville**
(Photo: Brian
Staffer)

mental regulations are the responsibility of the product owner, not of the producer." In contrast, Pietsch explained that since BP has been around long enough that it can sell the lowest cost product at the largest scale, it's been relatively easy for them to be able to get ahead in testing its biofuel products to meet the necessary regulations even though the biofuels market isn't the company's main focus.

Held at the Martin Luther King Jr. Student Union on the UC Berkeley campus, the symposium was organized by the Berkeley Energy & Resources Collaborative and featured a total of 12 panels that explored how policy, technology, and business practices could shape global energy issues.

BY MASSIE SANTOS BALLON

Water resources are much in demand as climate change and a burgeoning world population take their toll on an aging infrastructure. A report from the U.S. Geological Survey showed that water withdrawals in 2007 were almost equivalent to reservoir capacity, and a 2009 report from the American Society of Civil Engineers estimated that as much as seven billion gallons of clean drinking water is lost each day through leaking pipes.

Despite these figures, no one seems to know how much water is really available since the same resource can be counted multiple times when used by a power plant or irrigating agricultural fields.

During the 4th Annual UC Berkeley Energy Symposium held on campus March 4,

panelists representing scientists, engineers and policy makers gathered to discuss the challenges in meeting long-term water demand and how to account for and allocate the water.

As more people turn to growing feedstock crops for cleaner, sustainable biofuels, concerns also mount over the corresponding increase in water demand. For example, a report released earlier this year by engineers at the University of Virginia noted that algae production uses more water than bioenergy crops such as switchgrass and corn.

UC Berkeley economist Michael Hanemann argued that the biggest resource stressor is neither the changing climate nor the ongoing shift in transportation energy sources but rather the growing population. He said California could have as many as 75 million people living in the

state by the end of the century, and to meet the needs of the population as well as of agriculture and industry, he predicted that future water use will be heavily reliant on desalination processes and re-use.

Matthew Heberger, a water resources engineer who now works for the Pacific Institute noted that part of the problem lies in human behavior. For example, he said, federal standards have required that new toilets cannot use more than 1.6 gallons per flush since 1994, but only 40 percent of California's toilets meet these low-flow requirements. Water companies need to do their part in making customers more aware of the natural resource as a commodity, he said, teaching them how to conserve water at home and implementing strategies such as tiered pricing rates.

A video of the water panel is on the UC Berkeley Energy Symposium's website at <http://berc.berkeley.edu/videos-2010#water>.

Accounting
for every
drop

N • O • T • A • B • L • E • P • U • B • L • I • C • A • T • I • O • N • S

Small wild grass completes genome triad

The genome of a wild grass from the Mediterranean is assisting researchers in studying the more complex genomes of its more economically important relatives wheat and barley. In the February 11 edition of the journal *Nature*, the International *Brachypodium* Initiative, a consortium that includes researchers from the DOE Joint Genome Institute (JGI), presented the complete sequence of *Brachypodium distachyon*.

"*Brachypodium* has a lot of qualities that make it easy to work with in the lab," said DOE JGI collaborator John Vogel of the U.S. Department of Agriculture (USDA) Agricultural Research Service (ARS). "We're using it as a model for bioenergy crops, things like switchgrass and *Miscanthus* are perennial grasses which have the potential to provide a lot of our nation's fuel, but the process of converting that grass into fuel is far from optimized."

Also known as purple false brome, "Brachy," as the research community refers to this plant, belongs one of the three main grass subfamilies and its genome is just 272 million nucleotides in size, much smaller than the genomes of wheat and barley, which have several billion nucleotides each. Rice belongs to a second subfamily while sorghum, switchgrass and *Miscanthus* are part of the third group. As part of the effort spearheaded by Vogel, DOE JGI researcher Jeremy Schmutz at the HudsonAlpha Institute of Biotechnology in Alabama, Dan Rokhsar of the DOE JGI, David Garvin of the USDA-ARS and University of Minnesota, Todd Mockler of Oregon State University and Michael Bevan of the John Innes Centre in the United Kingdom, representatives of the three most economically important grass subfamilies — *Brachypodium*, sorghum and rice — were compared for the



***Brachypodium distachyon* is the first wild grass to be sequenced. (Roy Kaltschmidt, LBNL)**

first time to determine their evolutionary relationships.

"By having the sequences of 3 representatives we can see how genomes have changed through evolutionary time," said Vogel.

Rokhsar, head of DOE JGI's Plant Genomics Program, added that the wild grass's genome is also useful for studying the changes wrought by the domestication of other grasses to produce varieties better suited to human needs. Studying *Brachypodium*'s genome, he said, could provide insight into the origin of genetic traits and pre-existing variations.

By manually annotating the *Brachypodium* genome, Vogel and his colleagues identified the structures and possible functions of nearly 2,800 of the grass' more than 25,500 predicted genes. The *Brachypodium* genome is also expected to be of use in identifying genetic traits of agronomic interest in wheat and barley.

"Since *Brachypodium* has the traits required to serve as a functional model system—small size, short lifecycle, self fertility, simple growth requirements, small genome and can be efficiently transformed

or genetically altered—it can be used to more rapidly gain the knowledge about basic grass biology necessary to develop superior grass crops," said Vogel. "This is especially important in the context of developing grasses as biofuel crops because the crops themselves (e.g. switchgrass and *Miscanthus*) are difficult experimental subjects due to their large size, long lifecycle and complex genetics."

For more information about the institutions participating in the International *Brachypodium* Initiative, go to <http://www.brachypodium.org/>.

A video of Vogel discussing the *Brachypodium* genome project can be viewed on SciVee: <http://www.scivee.tv/node/16140> and on YouTube: <http://www.youtube.com/watch?v=KyQk9xKzw5c>.

Muddy origins for eukaryotic cell ancestors

Half a century ago, researchers took a mud sample from the grove of eucalyptus trees behind the Life Sciences building at the University of California, Berkeley and isolated a single-cell organism. Now the genome of this common soil organism *Naegleria gruberi* is being used by biolo-



The free-swimming form of *Naegleria*, with two flagella. The organism is stained to reveal the nucleus, in blue. (Lillian Fritz-Laylin/UC Berkeley)

gists to study how organisms transitioned from single-celled prokaryotes to eukaryotes.

In the March 5 issue of the journal *Cell*, a team of researchers from the DOE Joint Genome Institute, UC Berkeley, and several other institutions in the United States and United Kingdom published the *Naegleria* sequence and an analysis of the 41 million base genome.

"In a sense, analyzing the *Naegleria* genome shows us what it would be like to be on this planet more than a billion years ago, and what kind of organisms were around then and what they might have looked like," said Simon Prochnik, a DOE JGI bioinformaticist and coauthor of the *Cell* paper.

Prochnik and his colleagues compared the *Naegleria* genome to the genomes of 16 other eukaryotes, identifying what they believe is a core set of roughly 4,000 genes that may have been part of the first, most primitive eukaryotes.

Naegleria is one of the rare organisms that can alter forms. When stressed, it shifts from amoeba to flagellate and swims around using two sperm-like tails. If the environmental conditions aren't ideal, it hibernates as a hard cyst. Prochnik said the *Naegleria* genome contains nearly 16,000 protein-coding genes that help the organism switch forms.

Naegleria's genome also revealed that the organism has the metabolic flexibility to thrive in muddy soils with lower oxygen levels, possibly producing hydrogen as a byproduct in such cases. "Any kind of system that can make hydrogen has potential interest from a bioenergy point of view," said Prochnik, adding that the organism could be used to understand how hydrogen production in other organisms could be harnessed as an energy source.

Lillian Fritz-Laylin, a UC Berkeley graduate student and the first author of the *Cell* paper, said that the *Naegleria* genome will not only be of use to the community of biologists studying the organism, it will also help in understanding the evolution

of more complicated organisms.

"By comparing diverse organisms like *Naegleria* from all over the family tree of eukaryotes we can begin to understand where we come from," she said.

A video of Lillian Fritz-Laylin of UC Berkeley and Simon Prochnik of the DOE Joint Genome Institute can be viewed at the DOE JGI's SciVee channel: www.scivee.tv/node/16393. A HD version is also available on the DOE JGI's YouTube channel: http://www.youtube.com/user/JointGenomeInstitute#p/u/5/jF-PUUJf_A8

Second cnidarian genome sequenced

A freshwater polyp that has been used by scientists for over three centuries to study asexual budding, tissue regeneration and stem cell biology has been



Hydra in a Newport Beach, Calif., stream.
(Peter J. Bryant, UC Irvine)

sequenced by an international research team including scientists from the DOE JGI, the University of California, Irvine and the J. Craig Venter Institute.

Jarrod Chapman of the DOE JGI is the first author of the draft genome of *Hydra magnipapillata*, which was published in the March 25 issue of *Nature*. In the same report, the team also published the genome of a *Curvibacter* bacterium associated with the *Hydra* they had sequenced during the project.

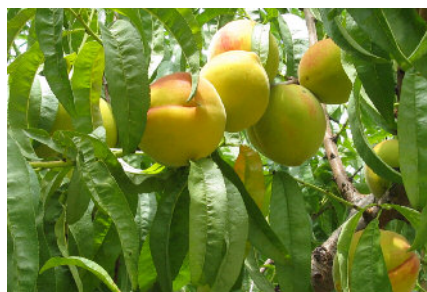
Only one other cnidarian had been sequenced prior to the *Hydra*. In 2007, researchers from the DOE JGI and UC Berkeley announced the publication of the genome of sea anemone *Nematostella*

vectensis. In comparing the two cnidarian genomes, the researchers noted that the *Hydra*'s genome sequence is approximately twice as large as that of the sea anemone.

Tasty model genome to help bioenergy crops

In 2007, the International Peach Genome Initiative was born from a pledge made by the DOE JGI at the Plant and Animal Genome conference to sequence the stone fruit. Three years later, the high quality draft genome for peach — the first member of the *Rosaceae* family, which also includes fruits such as apples, strawberries and cherries, to have its genome sequenced — was made publicly available online April 1, ahead of peer-reviewed publication.

The peach genome was sequenced by the DOE JGI in part to identify genes that control dormancy in perennials. Peaches have an "evergreen" locus that is also found in poplars and researchers hope to use that information to alter the tree's growing cycle so that these crops can accumulate more biomass annually com-



Lovell peaches from the Clemson University tree used to sequence the peach genome.
(Clemson University)

pared to control crops that lie dormant during the winter months.

For more details about the project, visit the Genome Database for Rosaceae at <http://www.rosaceae.org/peach/genome>. The peach genome information can be accessed on Phytozome at <http://www.phytozome.org/peach>.

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The DOE JGI collaborated with Emeryville, Calif.-based Ex'pression College for Digital Arts to create a short video on the DOE JGI's role in developing sustainable clean energy. View it on YouTube (<http://bit.ly/a7Rk38>), the DOE JGI homepage and several other sites.



Faced with repetitive, detail-oriented tasks, employees at the DOE JGI started a grassroots movement to improve communication and involvement in ergonomics and safety. The result was the DOE JGI's 2010 Ergo Cup victory. For more information about the ergonomic initiatives at the DOE JGI, contact Melanie Alexandre at MMAlexandre@lbl.gov.



The SFAF meeting focuses on laboratory methods and computational tools including new sequencing technologies that are used to help sequence, assemble, and finish genomes. For more information, contact Chris Detter at cdetter@lanl.gov or go to <http://www.lanl.gov/finishinginthefuture/>

Reserve the dates now.

The DOE JGI's 6th Annual User Meeting will take place March 21-25, 2011.

The DOE JGI's social media presence is expanding. Follow us on:

Twitter:

http://twitter.com/doe_jgi

Facebook:

<http://www.facebook.com/JointGenomeInstitute>

YouTube:

<http://www.youtube.com/user/JointGenomeInstitute>

SciVee:

<http://www.scivee.tv/user/7476>

Flickr:

http://www.flickr.com/photos/doe_jgi/

Find out where our research has been featured lately through JGI in the News:

<http://jginews.blogspot.com/>



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