

As the global population grows toward 10 billion people, Evan DeLucia, director of the Center for Advanced Bioenergy and Bioproducts Innovation (CABBI), a DOE Bioenergy Research Center at the University of Illinois Urbana-Champaign, asked attendees to rethink agriculture from an ecosystem perspective and manage the farmland that we have, while also removing CO₂ from the atmosphere.

Thinking Outside the Cell for Functional Genomics

“JGI’s strategic direction is to translate genomic information into functional understanding,” said Nigel Mouncey, Director of the U.S. Department of Energy (DOE) Joint Genome Institute (JGI), a DOE Office of Science User Facility at Lawrence Berkeley National Laboratory. “Today, the scale and cost of DNA sequencing have afforded the generation of an unprecedented level of gene and genome information for which relatively little is known regarding function. Thus, there is a critical need to rapidly, and at scale, assign validated function of genes, pathways and genomes.”

JGI has developed capabilities such as single-cell genomics, synthetic biology, and metabolomics to move beyond generating a DNA sequence to understanding gene functions for a myriad of applica-

tions. JGI’s Emerging Technologies Opportunity Program (ETOP) has worked toward bringing in new technologies developed at other institutions, making them available to JGI users. The ETOP aligns with JGI’s transition over the past two decades from a high-throughput genome sequencing center to a national user facility that provides researchers around the world with access to sequencing and computational analysis capabilities on projects relevant to the DOE missions of energy and environmental challenges.

Led by Hal Alper of the University of Texas at Austin and Michael Jewett of Northwestern University, the latest approved ETOP proposal aims to develop an optimized cell-free platform that will enable researchers to speed up the “build” and “test” portions of the design-build-test-analyze *continued on page 2*

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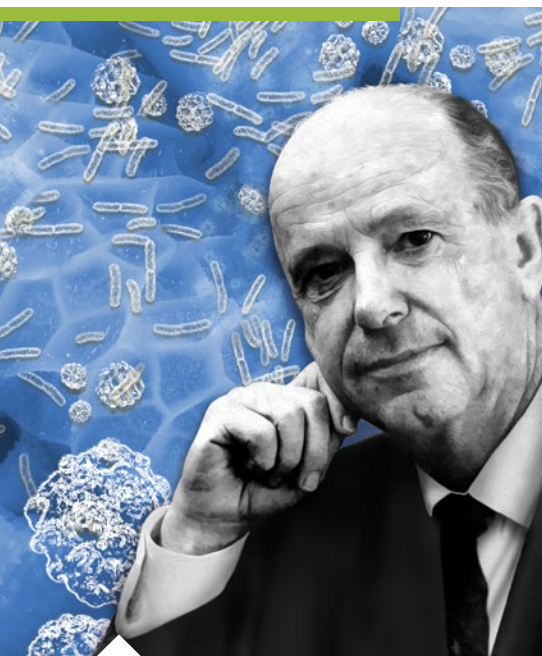
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Functional and Reproducible: Annual Meeting Keynote Highlights

Before introducing the opening keynote to the 13th Annual Genomics of Energy & Environment Meeting on March 14, 2018, JGI Director Nigel Mouncey told the audience the meeting hashtag **#JGI2018** was already trending on Twitter. It was an auspicious start to the largest annual meeting held by the JGI, with overarching themes of tools and techniques researchers are using to mine genomic information and answer questions about an organism’s metabolic structures and functions to develop solutions to energy and environmental challenges.

The first to define approaches to the macroscale and microscale perspectives of their work was MacArthur Fellow Victoria Orphan of Caltech, whose opening keynote provided an overview of the ecosystems biology approach her group is taking to link uncultivated microorganisms to biogeochemical processes. Orphan described several approaches her lab is taking to better understand the relationship *continued on page 3*

The Hungate Catalog: References for the Rumen Microbiome



The Hungate catalog is named for Robert Hungate, the microbiologist who invented the widely-used method of cultivating strictly anaerobic bacteria that now bears his name. (Image of Robert Hungate from Special Collections, University of California Library, Davis; composite image by Rekha Seshadri, JGI; and Zosia Rostomian, Berkeley Lab Creative Services).

Rumen microbes play a vital role in allowing ruminant livestock to break down the food they eat, and produce milk, meat and wool which help support the livelihoods and food security of over a billion people worldwide. The process, however, is also the single largest human-influenced source of the greenhouse gas methane, with these animals releasing approximately 138 million U.S. short tons of methane into the atmosphere each year.

Understanding the diversity and function of the rumen microbiome is a critical step toward developing technologies and practices that support efficient global food production from ruminants while mitigating methane emissions. Additionally, there is considerable interest in

identifying biotechnologically relevant enzymes for the conversion of plant feedstocks to biofuel and bioproducts.

As reported March 19, 2018, in *Nature Biotechnology*, an international team led by William (Bill) Kelly, formerly at AgResearch New Zealand's Grasslands Research Centre, and JGI scientists presented a reference catalog of rumen microbial genomes and isolates cultivated and sequenced from the Hungate1000 collection. The work, noted Kelly, is the culmination of a JGI Community Science Program (CSP) 2012 proposal that originated at a 2011 meeting of rumen microbiologists. At the beginning of the project, there were only reference genomes for 14 rumen bacteria and one rumen methanogen. The Hungate catalog now contains a total of 501 genomes—410 newly generated from this study, plus an additional 91 already publicly available from other studies.

"JGI is a world leader in conducting, enabling, and democratizing sequence-based research—and one of the few places that does science at this large scale," said Rekha Seshadri, JGI computational biologist and co-first author of the paper. The genome sequencing and analysis component of the project used resources of the National Energy Research Scientific Computing Center (NERSC), which is supported by the DOE Office of Science.

"This project is a great example of how science can progress rapidly if we do things together," added study co-first author Sinead Leahy, now with the New Zealand Agricultural Greenhouse Gas Research Centre.

Conceived as a community resource, the Hungate catalog encompasses 75 percent of genus-level taxa reported from the rumen and all 410 genomes sequenced in the study can be downloaded. The researchers were able to assign individual mi-

crobes to the major metabolic pathways involved in rumen function, and reported that in total, the catalog of genomes encode nearly 33,000 degradative Carbohydrate-Active Enzymes which can break down plant cell walls. **Full story at jgi.doe.gov/reference-catalog-for-rumen-microbiome.**

Thinking Outside the Cell

continued from page 1

cycles in synthetic biology. Cell-free systems have been used successfully for expression of individual proteins for decades, but more recent applications have focused on enzyme screening, metabolic pathway design and prototyping and immune system characterization.

"What we're trying to develop is a generic platform that's pathway-agnostic, a seamless pipeline from DNA design to prototype," said Alper. "It's a tool for both discovery and understanding, but always a way to speed up cell engineering."

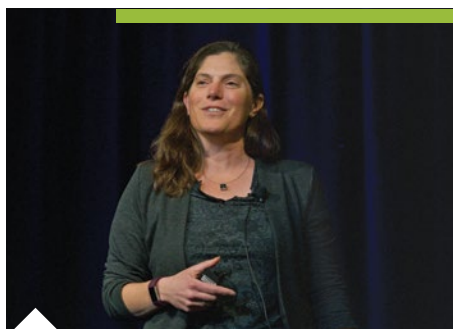
The cell-free systems approach outlined in the proposal starts by lysing pre-optimized cells from selected strains, and then working with the lysates from these strains to express genes and pathways of interest which can be mixed in cocktails of varying ratios for easily and rapidly characterizing novel and improved pathways.

Jewett added that the cell-free systems framework wasn't even possible two years ago.

"We hope to draw in researchers from the broader community that can leverage these new tools within the JGI," he added. **Read the full story at jgi.doe.gov/freedom-flexibility-etop-thinking-outside-the-cell-for-functional-genomics.**

Annual Meeting Keynotes

continued from page 1



Victoria Orphan

between the global methane budget and anaerobic oxidizers of methane (AOM), organisms in seep sediments that make a living oxidizing methane coupled to sulfur reduction. “We’re interested in breadth of genomic and ecological diversity, niche differentiation and metabolic drivers of AOM syntrophy,” she told the crowd at the Hilton Union Square in San Francisco, Calif.

To link organisms in their environments to their biogeochemical processes, she noted, “We really need a variety of different techniques. There’s no one single formula that works for an ecosystem.” In applying different techniques, she hopes the technological advances will allow researchers to bridge the different scales involved to both understand how ecosystems are working, and forecast or model how ecosystems will respond to potential changes in the future.

She also reminded the attendees to always keep in mind that the labels attached to unknown microbes can minimize their true diversity, and their roles in regulating the planet’s biogeochemical processes. “With no cultured representatives, it’s easy to get lost in the simplicity of placeholder names when there’s a lot more diversity hidden within.” **Watch her talk at bit.ly/JGI2018Orphan.**

To some extent, simplicity is desired in synthetic biology, but one can’t just knock out pathways whose



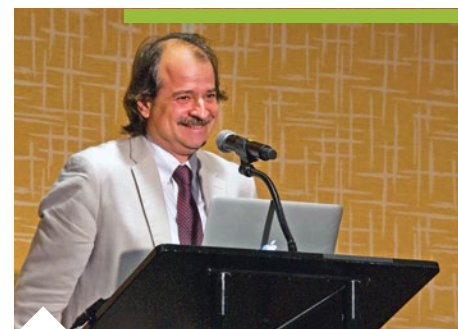
Nigel Mouncey, Kristala Prather, Susannah Tringe

unwanted end products are necessary for cell growth, said keynote speaker Kristala Prather, a professor of chemical engineering at the Massachusetts Institute of Technology (MIT). So the challenge of synthetic biology is navigating that complex network to maximize productivity while minimizing unwanted byproducts and unnecessary growth. The flagship project in Prather’s lab has been engineering microorganisms like *E. coli* and yeast to synthesize glucaric acid, considered by the DOE to be a top “value added chemical from biomass.” Although the compound is found naturally in fruit and vegetables, there is no known microbial pathway to produce it.

Prather’s starting point was a reference glucaric acid synthesis pathway from citrus, with a dozen or so steps. The goal was to maximize productivity. With no lack of sequence data, she added, “the question is how do we get through all the data we have” to identify potential proteins of interest when predictions from function annotation can lead you astray? The Sisyphean task of sorting through massive amounts of sequence data ultimately led to a collaboration with the JGI through a CSP proposal.

Watch her talk at bit.ly/JGI2018-Prather.

The final keynote address was a bracing reality check on the issue of reproducibility—or, rather, the lack



John Ioannidis

thereof—that plagues the scientific research enterprise delivered by John Ioannidis of the Stanford School of Medicine and co-director of the Meta-Research Innovation Center at Stanford (METRICS). In recent years, there’s been growing concern about this topic, reflected in an increasing number of conversations and publications across all 22 major scientific disciplines. There’s no real consensus about what “reproducible research” means, but there are at least three broad aspects, with the shared goal of enhancing trust in scientific findings.

When you do have replications, Ioannidis said, you can put all the data together and perform meta-analysis to try to assess whether they show consistency—but also whether there’s some hint of biases that might be affecting similar studies on the same question. Solutions can be thought of at each step in the scientific investigation process, but for any of these to work, however, Ioannidis stressed the need to find ways to incentivize adoption. One approach is to re-engineer the rewards system. “There’s nothing wrong with publishing papers, *per se*,” he said, “however we also need to find ways to reward scientists who score higher on quality, who share more openly, and whose work is more reproducible and has more translational impact when it is applied.” **Watch his talk at bit.ly/JGI2018Ioannidis.**

Highlights from the 2018 JGI Genomics of Energy & Environment Meeting



Merce Montoliu Nerin talked about fungi.

Lipids from Sedimentary Rocks

You can't get blood from a stone, but, as **Amy Banta** explained, you can get lipids from sedimentary rocks—and gain insight into the ancient organisms that made them. Cyclic triterpenoids, a class of lipids produced by both eukaryotes and bacteria, can be preserved for millions of years, becoming molecular fossils. But when there's a fossil lipid that has no known corollary in modern record, said Banta, a research scientist in Paula Welander's lab at Stanford University, "we don't know how to interpret what we find." In order to expand the known cyclic triterpenoid biosynthetic capability of bacteria, Welander's lab has partnered with the JGI DNA Synthesis Program to analyze putative novel triterpenoid cyclases encoded in freshwater, marine, and terrestrial metagenomes.

Diversity and Inclusion: Going Beyond Gender and Race

It's human nature for people to be most comfortable among peers who are more like themselves than not, **Sheena Becker** acknowledged, addressing the necessity of, and strategies for, increasing diversity and inclusion. Lead microbiologist at Corteva Agriscience, DowDuPont's

agriculture division, Becker cited a McKinsey study that found gender and ethnic diversity in leadership increases earnings. What's more, she said, employee diversity yields more diverse solutions; companies perform better, and there's less employee turnover. "So why do we work so hard to expand our sphere of knowledge for science," she asked, "but not our sphere of knowledge for people?" Recounting her own career trajectory to illustrate her point, she challenged the audience to start treating personal interactions as they would scientific questions.

Engineering Microbial Communities for Form and Function

"As biological engineers, we try to get our bugs of interest to do more tasks," said **Cynthia Collins** of Rensselaer Polytechnic Institute, "but it's better if we can divide the load among multiple organisms." Division of labor among different strains or species within microbial communities reduces the metabolic load on individuals and allows you to take advantage of their different capabilities, Collins noted. It also provides the flexibility of a modular platform: "I'm interested in thinking of microbes as modules for different applications," she said. For example, cellulose can be broken down using enzymes to turn waste materials into simple sugars, but production schemes are limited by the cost of enzyme purification.

Non-Conventional Yeasts for Biotechnical Applications

"Biotechnical applications start with problems or opportunities *and* markets," said **Tom Jeffries**, founder and president of Xylome, noting that the U.S. beer and wine fermentation

industries—both of which rely on *Saccharomyces cerevisiae*—total about \$108 billion and \$60 billion in annual sales, respectively. In comparison, he continued, the potential cellulosic ethanol industry is about \$100 billion per year. Xylome's non-conventional yeasts make enzymes that can break down stillage organics and convert them to high-value fish oil or palm oil substitutes. A comparative genomic analysis of yeasts done with the JGI showed wider genetic diversity than expected, which could lead to other yeasts being harnessed for biotechnological applications.

The Social Life of Bacteria

Andrzej Joachimiak, director of the Advanced Photon Source Structural Biology Center and the Midwest Center for Structural Genomics, reminded attendees there's still plenty you can learn from protein structure that you can't from sequence alone. "You have a gene, you have a sequence, we can make a protein," he said while talking about the national user facility's capabilities at Argonne National Laboratory. To underscore this point, Joachimiak looked at bacterial toxin-anti-toxin immunity systems, and specifically contact-dependent



Han Wosten revisited his JGI collaboration to sequence the fungus *Schizophyllum commune*.

growth inhibition (CDI), a phenomenon defined by delivery of protein toxin to the cytoplasm of neighbor bacteria upon contact—which he referred to as “toxin on a stick.” CDI systems are found in more than 80 different bacterial species, representing more than 30 sequence-divergent families, with commensurate diversity of toxin activity and inactivation strategies. His bottom line, said Joachimiak: “Biology rests on macromolecular structures: conceptually, functionally, and mechanistically.”

Engineering Wheat for Take-all Resistance

The fungal pathogen *Gaeumannomyces graminis* var. *tritici* infects the roots of grass and cereal plants, causing devastating “take-all disease,” which is responsible for up to \$480 million of wheat crop yield losses per year. *Avena strigosa*, known as the bristle or black oat, on the other hand, is pretty resistant to take-all, thanks to antimicrobial defense compounds called avenacins. One solution to mitigate losses due to take-all would be to use oat as a rotation crop with wheat, but farmers aren’t willing to do that due to the income difference, noted **Aymeric Leveau**, a postdoctoral scientist in Anne Osbourn’s lab at the John Innes Centre in England. “So, we need to engineer wheat to be resistant,” he said, by building an avenacin biosynthetic pathway in that plant.

Assessing Soil Microbial Responses to Land Use Change

In a wide-ranging talk that took the audience from the island of Manhattan to Southeast Asia, **Krista McGuire** of the University of Oregon presented work on microbial responses to two key types of land use change: urbanization and agriculture. Her talk ranged from the impact of green infrastructure in New York City,

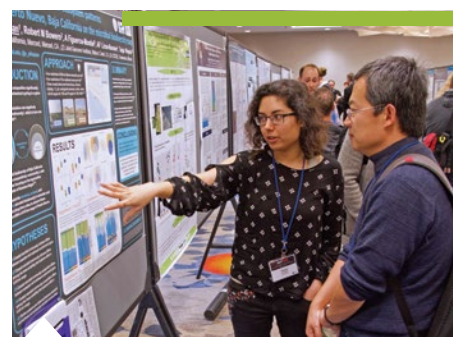
studied using fungal ecology, to the effects of land use and the ecology of ectomycorrhizal associations in old-growth tropical rainforest, oil palm plantation, and regenerating forests.

From Single Nuclei to Whole Fungal Genome Assemblies

“When you don’t have the tools, you have to make the tools,” said doctoral scientist **Mercè Montoliu Nerin** of a method developed in Anna Rosling’s lab at Sweden’s Uppsala University to obtain genomic data from single nuclei of arbuscular mycorrhizal fungi. The method, adapted from single cell genomics, involves extraction and selection of individual spores, which are then crushed, and the nuclei stained and isolated using Fluorescence-Activated Cell Sorting. Individual nuclei are then amplified to obtain enough DNA for nanopore sequencing. Montoliu Nerin presented preliminary results from the 117-megabase genome assembly of *Claroideoglossum claroideum*, quick annotation of which revealed classes of transposable elements involved in horizontal gene transfer. “Maybe they [arbuscular mycorrhizal fungi] are not only exchanging nutrients with [host] plants, but also DNA,” she mused.

Metabolite Production in Algal-Associated Bacteria

“Most of the interesting questions in science don’t end with a ‘Eureka!’ but rather end with a ‘Huh,’” noted Lawrence Livermore National Laboratory research scientist **Ty Samo** as he pondered the results showing how a growth stimulating auxin released by bacteria might interface with the diatom *Phaeodactylum tricoratum*. One of the challenges of creating robust and resilient algae for sustainable fuels is understanding how algae communicate with and are affected by the microbes surrounding them.



JGI’s Zhong Wang listens to UC Merced graduate student Sabah Ul-Hasan, who had a 2015 JGI/UC Merced fellowship.

Tools for Yeast Engineering

The yeast *Yarrowia lipolytica* is a promising host for engineered pathways for the renewable production of lipid-based fuels and chemicals. **Ian Wheeldon** and his colleagues at the University of California, Riverside are working to facilitate the rapid development of new *Y. lipolytica* strains. They first had to identify a standardized set of sites for pathway engineering, then demonstrate the sites’ usefulness. They then created both CRISPR activation (CRISPRa) and interference (CRISPRi) systems to precisely and predictably upregulate or knockdown target gene expression, respectively. These CRISPR-Cas9 based tools are the impetus for a new joint project with the JGI DNA Synthesis Program.

Selected Meeting videos are on the JGI’s Youtube channel at <http://bit.ly/JGI2018videos>.



Algal researcher Susan Brawley highlighted efforts of her JGI collaborators.

Viral Omics: At the Tip of the Iceberg



Eric Delwart of Blood Systems Research Institute (BSRI) poses a question considered by (left to right): Bonnie Hurwitz, University of Arizona; Xutao Deng, BSRI; VEGA co-organizer Phil Hugenholtz, Director of the Australian Centre for Ecogenomics at the University of Queensland; and, Nikos Kyrpides, JGI Prokaryote Super Program Head and lead organizer of the VEGA Symposium.

More than 150 people attended the first ever Viral EcoGenomics and Applications (VEGA) Symposium held during the JGI's 13th Annual Genomics of Energy & Environment Meeting in San Francisco, Calif.

The symposium opened with a keynote delivered by NCBI bioinformatician Eugene Koonin, who immediately declared viruses are the most abundant organisms, and by extension, the most important. In a talk that covered nearly all known viral groups and from his experience working on viral genomes, he talked about the increasing importance of mining metagenomic data to uncover the Earth's viral diversity, and how horizontal virus transfer is a major driver of virus evolution. "If you discover a novel virus these days," he advised, "search the metagenomic data carefully and you will probably discover a diverse and exciting new family."

As an example, he recounted the discovery of a single bacteriophage genome—crAssphage—that was abundant in the human virome (a bacteriophage commonly found in human fecal samples), but most of its genes had no known homologs and even its host had been unknown until researchers mined metagenomics data. That single phage genome, Koonin said, led to the identification of a novel family of bacteriophages that include hundreds of diverse genomes.

During his discussion of giant viruses, Koonin referenced using the 2017 Science paper he co-authored with JGI Microbial Program head Tanja Woyke and her team to consider the notion of a fourth domain of life. (**Review that work at jgi.doe.gov/discovered-novel-group-of-giant-viruses**).

"It's very clear that we are dealing with the tip of the proverbial iceberg

fishing out viral genes from general metagenomic data," he said. **Watch his talk at bit.ly/JGI2018KooninVEGA.**

Marilyn Roossinck of Penn State University ended the first day of the symposium with a keynote addressing plant viruses, even as she reminded everyone that viruses are not always pathogens. She talked about an ongoing project to inventory plant virus biodiversity, admitting, "We know every host, and I won't finish this before I retire," before sending out a call for others to carry on the work.

Addressing the disconnect between the high percentage of persistent plant viruses in the environment and the disproportionately low level of research on these groups, she talked about sampling nearly 700 plants in tallgrass prairies, from which a third were found to carry partitiroviruses. Her team questioned whether or not these viruses protect the plants from acute infections. In experiments involving jalapeño cultivars, they found virus infections could influence aphid feeding in a complex virus-plant-insect interaction network.

In another story, she talked about what she thinks is the oldest known virus, now known as *Zea mays* Chrysovirus 1, found when deep sequencing ancient corn. The viral sequence appears to have changed just 3 percent in the past thousand years. **Watch her talk at bit.ly/JGI2018RoossinckVEGA.**

Joe DeRisi, co-director of the Chan Zuckerberg Hub and also a professor at the University of California, San Francisco, used his keynote address to discuss the applications of identifying viruses. His first case study described identifying the rubella virus in the eyes of a male patient who had suffered from recurring uveitis for over half his life. Step by step, DeRisi established a plausible correlation between the viral infection and the fact that only the women in the patient's home country are vaccinated

against rubella as children. He used medical cases to describe how doctors at UCSF can now order metagenomics sequencing tests to provide an unbiased assessment of infectious diseases to help with diagnoses and subsequently, treatment. One advantage of the university hospital setting, he noted, is “a rigor and thoroughness that you don’t see in startup, with nothing hidden because we are talking about people’s lives.”

In another case, this time involving non-humans, he talked about identifying a new picornavirus seen in several bird species that causes avian keratin disorder, which causes beak overgrowth and impacts the bird’s ability to feed. Despite the original perception that only certain species are infected, he described finding the virus present not just in corvids but in raptors and now in other birds as well. **Watch his talk at bit.ly/JGI2018DeRisiVEGA.**

Among the notable talks during the Symposium was one by Siobain Duffy of Rutgers University, who covered the only group of viruses Koonin didn’t mention in his keynote – circular single-stranded DNA viruses called CRESS viruses that are pathogens and can significantly limit crop produc-



Marilyn J. Roossinck

tion. (“Because I knew [of your talk]!” Koonin retorted.) She said the known families of CRESS DNA viruses have doubled between 2011 and 2017, “and we know host range is wider than previously thought.” Reminding the crowd that most of the known viral diversity are known only by their sequences, her lab has focused on developing tools to classify novel CRESS DNA viruses and she described a few applications.

Promoting the current status and future development of publicly accessible viral databases, there were also brief presentations about JGI’s IMG/VR from David Paez-Espino and Simon Roux, and an evolving DataDic-er-based virus variation interface from



Joe DeRisi

NCBI’s Rodney Brister. “For better or worse NCBI is at the center of the data universe,” Brister said. “What can we do to make it better to find and retrieve virus data on NCBI?”

A longtime collaborator, David Mead of Varigen previously partnered with the JGI to identify thermostable enzymes from DNA sequences extracted from thermophilic environments that could be developed for industrial applications. At the VEGA Symposium, he spoke about the search for new enzymes that could be harnessed for various biotechnological applications by looking for new viruses. As an example, he spoke of the challenge in culturing and cultivating the abundant Aquificae bacteria found in hyperthermophilic geothermal environments. Searching for genes of interest, his team started with the sequence of a functional DNA polymerase that had been isolated from viral metagenomic data collected at Octopus Springs in Yellowstone National Park. From the metagenomic data, they were able to assemble the Octopus Spring OS3173 virus. Additionally, a database search for homologs of the OS3173 DNA polymerase revealed sequence variants from 12 springs in Yellowstone and other locations.

Selected VEGA Symposium videos from the Annual Meeting are on the JGI’s Youtube channel at <http://bit.ly/JGI2018videos>.



Eugene Koonin

**THE 14TH ANNUAL
Genomics of Energy &
Environment Meeting**

Hilton Union Square | San Francisco, California

HOSTED BY THE
U.S. Department of Energy
Joint Genome Institute

Watch this site! usermeeting.jgi.doe.gov

For speaker/session ideas, contact Susannah Tringe:
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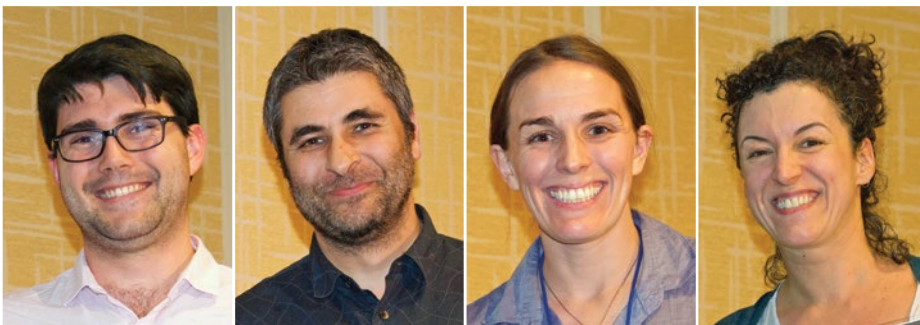
**Visualizing Microbial Interactions
and Decomposition at the Microscale**



“One of the amazing things about microbial ecology is it really highlights the awesome power of large numbers,” said **Kriti Sharma**, a graduate

student in Elizabeth Shank's lab at the University of North Carolina, Chapel Hill. A bacterium's size, for instance, constrains what it can

ingest, and as a result, microbes sometimes have to act extracellularly, and *collectively*, for their own survival. To study microbial decomposition of organic matter in soil, the Shank lab has developed a transparent soil-like microcosm based on Nafion, a synthetic fluoropolymer that becomes optically clear when wet. They've also established a multi-modal 3D imaging platform to dynamically visualize the assembly and activity of microbial communities in this soil-like environment.



Prior to John Ioannidis' keynote, JGI Director Nigel Mouncey announced the winners of the first-ever poster competition. Left to Right: UC Berkeley's Benjamin Adler (Best Student Poster); LLNL's Xavier Mayali (Best Outside-the-Box Poster); UC Davis' Christy Grettenberger (Best Postdoc Poster); and, University of Massachusetts Amherst's Kristen De Angelis (Best PI Poster).”

Register Now!

**IMG Workshop at
ASM Microbe 2018**

June 7, 2018, Atlanta, GA

<http://bit.ly/IMGatASMMicrobe2018>

Stop by the joint JGI/KBase Booth #1311 at the Meeting!

**Microbial Genomics &
Metagenomics (MGM)
Workshop**

September 17-21, 2018

Walnut Creek, Calif.

mgm.jgi.doe.gov

DNA Synthesis Call

White papers due July 31, 2018

<http://bit.ly/JGIsynsciCall>

DNA Synthesis Science proposals are accepted on a continuous basis through JGI's Community Science Program and are reviewed twice a year.

**Look for JGI's presence at
the following conferences:**

Plant Biology 2018

July 14-18, 2018, Montreal, Canada

Stop by the joint JGI/KBase Booth #1200!

**Society for Industrial Microbiol-
ogy and Biotechnology (SIMB)**

August 12-16, 2018, Chicago, IL

Stop by Booth #33 and chat with representatives of the JGI, EMSL, JBEI, the Advanced Biofuels Process Demonstration Unit (ABPDU) and the Agile BioFoundry.

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