

Bugs, Big & Small, from Inside & Out, Join Sources of Green Genes to Fill CSP 2010 Pipeline

More than 70 projects were selected for the 2010 Community Sequencing Program (CSP) portfolio. They involve organisms from regions as far north as the Arctic and south to New Zealand. They include proposals to study microbial contaminants in alcohol that could impact biofuel production, microbial communities in the guts of insects from an area geography scholar Jared Diamond once described as "the nearest approach to life on another planet" and a novel bacterial isolate that

could be used to remove heavy metal contaminants from freshwater streams.

"The information we generate from these projects promises to improve the clean, renewable energy pathways being developed now as well as lend researchers more insight into the global carbon cycle, options for bioremediation, and biogeochemical processes," said DOE JGI Director Eddy Rubin. "In translating DNA sequence data into biology, we generate valuable science that improves our understanding of the complex

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processes that support life on the planet, or imperil it."

Following along the lines of previous CSP-approved metagenomic projects involving the

cow, termite and Amazonian stinkbird, Mike Taylor from New Zealand's University of Auckland proposed sequencing microbial communities in side

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Moving Microbial Genomics Forward

BY MASSIE SANTOS BALLON

To get an idea of how many microbes there are on Earth, imagine taking just the smallest type of microbe, the viruses that infect other microbes, and lining them all up in the row. How far do you think that line would reach? From San Francisco to Paris? To the moon? To the sun? The answer: A thousand times the distance across the Milky Way.

Microbes are not only exceedingly numerous, but also extremely diverse, encompassing most of Earth's total biodiversity. This is one reason

why two-thirds of the nearly 5,000 genome projects reported in the Genomes OnLine Database involve microbes. Another factor is the myriad potential applications of microbial research for targeted drug development, bioenergy, bioremediation, agriculture, and other human endeavors. But far more could be done with microbial genomics, according to DOE JGI Genome Biology head Nikos Kyrpides, if researchers would embrace the world of possibilities that extend beyond such human-centric studies.

In an article published in the July issue of the journal *Nature Biotechnology*, Kyrpides reflects on the role of microbial studies in the genomics revolution of the past decade, and considers the factors that have hindered the advancement of the field. Although nearly 1,000 microbial genomes have been sequenced over the past 15 years, he noted that the data obtained has been compromised by the lack of a common language and standardized procedures. Such standards, required for the exchange and integration of

genomic data, still remain to be defined and codified. Due to biases in the selection of genomes for study, vast realms of biodiversity remain unexplored. Data release policies very early on led to what he terms "a violation of a long-standing precept in all scientific fields" when reviewers of submitted publications couldn't access the underlying genomic data.

Kyrpides offers numerous suggestions to meet these and other challenges that face genomics research in the decade ahead. For example,

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Salt Lake's Briny Waters May Harbor Biological Treasures



Photo by Charles Uibel, GreatSaltLakePhotos.com

BY MADOLYN BOWMAN ROGERS

In one of the 2009 Community Sequencing Projects, the DOE JGI are partnering with a consortium of researchers to sequence the genomes of microbial communities in Utah's Great Salt Lake. Researchers believe the lake's harsh environment harbors a wealth of undiscovered biodiversity that may provide new solutions for carbon sequestration and bioremediation, and might even give clues to the nature of life on other planets.

"We believe we're going to find new enzymes and new metabolic routes that have never been seen before," said the project's lead investigator, Bart Weimer, a microbiologist at University of California, Davis. The collaboration also includes researchers at the Utah State University, the U.S. Geological Survey, and the Utah Division of Water Quality.

The Great Salt Lake is the third saltiest body of water on earth, and the saltiest to support life. The salt content varies widely across the lake, but on average the lake is four times saltier than the ocean, and in the North Arm up to 20 times saltier. The lake also contains petroleum seeps,

mercury and other heavy metals, and high volatile sulfur concentrations that give the lake a distinctive rotten-eggs stink. Despite these compounds, the lake supports five million migrating birds each year and is home to brine shrimp and several kinds of algae including diatoms, as well as an untapped diversity of microbial life.

Because the microbes can survive in such an extreme environment, Weimer believes they may contain unique proteins that enable them to chemically fix sulfur and carbon and to detoxify pollutants. Their biochemistry may suggest new methods for sequestering carbon and reducing acid rain, Weimer said, as well as novel pathways for bioremediation of heavy metals, aromatic hydrocarbons, chlorinated compounds and methylmercury (Weimer et al., 2009). Microbial life in the Great Salt Lake might also provide a model for life on planets such as Mars, where sulfate and salt concentrations are also very high.

Since less than one percent of the microbes in the lake can be cultured, most of the microorganisms have never been studied before. The DOE JGI will sequence DNA from four sites in the lake

to provide a baseline picture of microbial diversity. Researchers will combine the DNA data with measurements of microbial metabolites and environmental conditions such as salinity and oxygen to paint a complete picture of the lake's ecology.

"We've done a lot of diversity assessment of the lake in the last two years, and we're not even approaching the limit of microbial diversity," Weimer said. "The services that the DOE JGI will provide are going to eclipse anything that we could do in the next five to ten years."

FOR ADDITIONAL INFORMATION SEE:

Weimer, Bart C., Giovanni Rompato, Jacob Panell, Reed Gann, Balasubramanian Ganesan, Cristian Navas, Martin Gonzalez, Mario Clavel, Steven Albee-Scott. Microbial biodiversity of Great Salt Lake, Utah. 2009. In Saline lakes around the world: unique systems with unique values. pp.15-22. Eds. Oren, A., D. L. Naftz, and W. A. Wurtsbaugh. S. J. and Jessie E. Quinney Natural Resources Research Library, Utah State University Press, Logan. (<http://www.cnr.usu.edu/quinney/itm/publications/nre1>)