

## **Systems Biology Reveals Diversity in Key Environmental Cleanup Microbe**

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Georgia Tech assistant professor Kostas Konstantinidis displays Shewanella microbes that have the ability to "inhale" certain metals and compounds and convert them to an altered state, which is typically much less toxic. Credit: Georgia Tech Photo: Gary Meek

(PhysOrg.com) -- Researchers have completed the first thorough, systemlevel assessment of the diversity of an environmentally important genus of microbes known as Shewanella. Microbes belonging to that genus frequently participate in bioremediation by confining and cleaning up contaminated areas in the environment.

The team of researchers from the Georgia Institute of Technology, Michigan State University and the Pacific Northwest National Laboratory analyzed the gene sequences, proteins expressed and physiology of 10 <u>strains</u> of Shewanella. They believe the study results



will help researchers choose the best Shewanella strain for bioremediation projects based on each site's environmental conditions and contaminants.

The findings, which further advance the understanding of the enormous microbial biodiversity that exists on the planet, appear in the early online issue of the journal <u>Proceedings of the National Academy of Sciences</u>. This research was supported by the U.S. Department of Energy through the Shewanella Federation consortium and the Proteomics Application project.

Similar to a human breathing in oxygen and exhaling carbon dioxide, many Shewanella microbes have the ability to "inhale" certain metals and compounds and convert them to an altered state, which is typically much less toxic. This ability makes Shewanella very important for the environment and bioremediation, but selecting the best strain for a particular project has been a challenge.

"If you look at different strains of Shewanella under a microscope or you look at their ribosomal genes, which are routinely used to identify newly isolated strains of bacteria, they look identical. Thus, traditional microbiological approaches would suggest that the physiology and phenotype of these Shewanella bacteria are very similar, if not identical, but that is not true," explained Kostas Konstantinidis, an assistant professor in the Georgia Tech School of Civil and Environmental Engineering. Konstantinidis, who also holds a joint appointment in the School of Biology, led the research team in analyzing the data.

Using the traditional method for determining interrelatedness between microbial strains -- sequencing of the 16S ribosomal gene -- the researchers determined that the 10 strains belonged to the same genus. However, the technique was unable to distinguish between most of the strains or define general properties that would allow the researchers to



differentiate one strain from another. To do that, they turned to genomic and whole-cell proteomic data.

By comparing the 10 Shewanella genomes, which were sequenced at the Department of Energy's Joint Genome Institute, the research team found that while some of the strains shared 98 percent of the same genes, other strains only shared 70 percent. Out of the almost 10,000 protein-coding genes in the 10 strains, nearly half -- 48 percent -- of the genes were strain-specific, and the differences in expressed proteins were consistently larger than their differences at the gene content level.



A team of researchers, including Georgia Tech's Kostas Konstantinidis, analyzed the gene sequences of 10 Shewanella strains and found that nearly half of the almost 10,000 protein-coding genes were strain-specific. Credit: Georgia Tech Photo: Gary Meek

"These findings suggest that similarity in gene regulation and expression constitutes an important factor for determining phenotypic similarity or



dissimilarity among the very closely related Shewanella genomes," noted Konstantinidis. "They also indicate that it might be time to start replacing the traditional microbiology approaches for identifying and classifying new species with genomics- or proteomics-based methods."

Upon further analysis, the researchers found that the genetic differences between strains frequently reflected environmental or ecological adaptation and specialization, which had also substantially altered the global metabolic and regulatory networks in some of the strains. The Shewanella organisms in the study appeared to gain most of their new functions by acquiring groups of genes as mobile genetic islands, selecting islands carrying ecologically important genes and losing ecologically unimportant genes.

The most rapidly changing individual functions in the Shewanellae were related to "breathing" metals and sensing mechanisms, which represent the first line of adaptive response to different environmental conditions. Shewanella bacteria live in environments that range from deep subsurface sandstone to marine sediment and from freshwater to saltwater. All but one of the strains was able to reduce several metals and metalloids. That one exception had undertaken a unique evolution resulting in an inability to exploit strictly anaerobic habitats.

"Let's say you have a strain of Shewanella that is unable to convert uranium dissolved in contaminated groundwater to a form incapable of dissolving in water," explained Konstantinidis. "If you put that strain in an environment that contains high concentrations of uranium, that microbe is likely to acquire the genes that accept uranium from a nearby strain, in turn preventing uranium from spreading as the groundwater flows."

This adaptability of bacteria is remarkable, but requires further study in the <u>bioremediation</u> arena, since it frequently underlies the emergence of



new bacterial strains. Konstantinidis' team at Georgia Tech is currently investigating communities of these Shewanella strains in their natural environments to advance understanding of the influence of the environment on the evolution of the bacterial genome and identify the key genes in the genome that respond to specific environmental stimuli or conditions, such as the presence of heavy metals.

Ongoing studies should broaden the researchers' understanding of the relationship between genotype, phenotype, environment and evolution, he said.

Source: Georgia Institute of Technology

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