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Mine runoff continues to provide clues to microbial diversification

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Pink slime at the surface of water trickling through an old mine in California is proving to be a treasure for researchers in their quest to learn more about how bacterial communities exist in nature.

A letter published in today's online edition of *Nature* shows that it is possible to follow what microorganisms are doing in their natural environment by identifying the range of proteins that they produce. The technique, utilized in a microbial community thriving in battery acid-like streams underground at Richmond Mine near Redding, Calif., combines recently developed ways to sequence microbial genes with methods to identify the range of proteins from specific microbial members.

Researchers from Oak Ridge National Laboratory and UC Berkeley discovered that Leptosprillium group II bacteria in these streams are exchanging large blocks of genes. While scientists have seen extensive gene transfer in bacteria, this is the first observation of exchange of huge genomic blocks in a natural microbial community.

"Consequently, this provides important information about the conservation of genetic resources to enable life to survive and thrive," said ORNL's Bob Hettich, a co-author and member of the Chemical Sciences Division. "Ultimately, the basic knowledge gained from this research will lead to a greater understanding of genetic diversity in related organisms and should lead to developments in human health and bioremediation."

The combination of mass spectrometry support from ORNL researchers with extensive reconstruction of genomes from community genomic data at UC Berkeley was key to this work, said Jill Banfield, who led the project. Banfield, a professor in UC Berkeley's Department of Environmental Science, Policy and Management, expects this to have far-reaching implications.

"More important perhaps is the demonstration of our ability to simultaneously identify a large fraction of an organism's proteins and to distinguish them from proteins derived from quite closely related organisms," Banfield said. "This opens the way for detailed studies of how a wide range of microbial communities are structured and how they function."

Hettich agreed that today's powerful molecular tools are playing a vital role in investigating the complexity of how bacterial consortia cooperate and compete in nature. In fact, ORNL mass spectrometry provided the ability to resolve and differentiate peptides that differ by as little as one amino acid.

Nathan VerBerkmoes of the lab's Chemical Sciences Division was instrumental in designing the experiments and acquiring the mass spectrometry data while Manesh Shah of the Biosciences Division provided the bioinformatics horsepower to sort through the massive datasets.

"A key aspect of this paper is the ability to get proteome information on organisms that do not directly have complete genome sequencing information," VerBerkmoes said. "As a result we could study organisms related to those completely sequenced – such as the bacterial clades, or 'cousins,' that are likely to exist in natural environments.

"This also might have implications into helping study human proteomics because not everyone’s individual genome will be sequenced.”

The pink microbial biofilm communities found in the mine runoff provide perfect research subjects because they have fewer organisms than most communities found in nature. The reason, Hettich noted, is that these environmental conditions – a pH of 0.8 -- are too extreme for most organisms to survive. A pH level of 7 is considered neutral and most proteins prefer pH levels between 5 and 7. In addition, the water from the mine often exceeds 120 degrees Fahrenheit. Because of their simpler makeup, the Banfield Laboratory established these communities as a model system in the mid-1990s.

This latest publication builds upon research that was published in May 2005 by Science. In that paper, Banfield, Hettich and colleagues at ORNL describe the bacterial community that thrives in what amounts to sulfuric acid. Their work set the stage for the latest development because it provided the first large-scale proteome dataset for a real-life microbial community with a limited number of members.

Of particular interest to DOE is how this effort relates to its Genomes to Life program, which is focused on identifying and characterizing the molecular machines of life. This study helps extend the initial studies of microbial isolates growth in carefully controlled laboratory settings to more real-world complicated microbial communities.

Source: Oak Ridge National Laboratory

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