Hydrogenobaculum Population Genomics: Linking Phylogeny, Geochemistry, Genetics, and Ecologic Function.

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Hydrogenobaculum inhabiting the Yellowstone geothermal complex are the focus of a population genomics study. Several pure culture isolates that are phylogenetically 100% identical (full-length 16S rDNA sequence and ITS sequence), but that differ in their ability to grow with H₂ and or H₂S as an energy source are being genome sequenced. This effort is in parallel with a metagenomic study of a mat community in Dragon Spring (our primary study site and a NSF Microbial Observatory) where Hydrogenobaculum is a dominant member (99% of Bacteria PCR clones). Based on extensive chemical analysis of the spring water and ex situ metabolic assays involving mat material, we know that chemolithoautotrophy is a highly relevant metabolism in this spring, which is chemostat-like in nature with respect to temperature, pH, and flux of H₂ and H₂S. Importantly, however, this habitat is also comprised of overlapping temperature and geochemical gradients that provide a continuum of niche opportunities that theoretically could support the maintenance of various genetic alterations that might account for the variation we have observed in ability to utilize H₂ or H₂S. Draft genome coverage of one isolate is being examined for specific functions of interest and metagenome reads are also being studied. Genome sequence revealed novel sequences coding for arsenite oxidases and that have been used for expression and diversity analysis. These and other current developments will be summarized. This work has been supported by the NSF Microbial Observatories and DOE-JGI-Community Sequencing programs, and the NASA-supported Thermal Biology Institute.