

CORRELATING GEOCHEMISTRY AND MICROBIAL COMMUNITY COMPOSITION IN THE DEEP CONTINENTAL BIOSPHERE

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Introduction: If there is or ever was life on an extraterrestrial planetary body, evidence of that life would likely be found below the surface. Some subsurface environments on Earth can be seen as analogs to the subsurface ecosystems on other rocky planets. In Earth's deep subsurface biosphere (DSB), water, organic carbon and chemical energy are often extremely scarce. However, it has been shown that archaea and bacteria are able to persist in the DSB to at least 3.5 km below surface [1]. Understanding how organisms persist, and what markers they may leave behind, is critical in predicting which extraterrestrial bodies may have harbored similar life.

In the current study we investigated sites down to 1.5 km below surface. Our portal to the DSB is a legacy gold mine in Lead, South Dakota—now the Sanford Underground Research Facility (SURF)—hosted within a sulfide-rich, Paleoproterozoic iron-formation [2]. Previous work at SURF used thermodynamic modeling from measured geochemistry to predict energy-yielding metabolic reactions, and showed evidence for chemolithoautotrophic metabolisms [3]. Here, we build upon that work by combining metagenomic sequences with geochemical and 16S rRNA gene sequence data. Correlating these different datasets will give us a better understanding of how life persists in the DSB.

Samples for this study were collected between September, 2013 and March, 2014 from SURF boreholes located between 800-4850 feet below surface. Geochemical data were collected concomitantly with DNA for 16S and metagenomic sequencing.

Results: We found a change in microbial community composition as a function of depth, including a progression from *Proteobacteria*-dominated communities near the surface to *Firmicutes*-dominated communities at depth. The relative abundance of *Archaea* (*Euryarchaeota* and *Thaumarchaeota*) increased with depth. Known metal reducing chemolithoautotrophic organisms were identified in anoxic borehole fluids. A total of 18 phyla belonging to the microbial 'dark matter' [4] were identified. In one location 'candidate phyla' comprised over 20% of the total microbial abundance. Within the metagenomes, thousands of predicted protein-encoding reading frames were identified. Genes involved in

spore formation indicate members of the community are able to go dormant under conditions of extreme energy limitation or environmental perturbation. Evidence for sulfate reducers and methanogens was found both in 16S tag and metagenomic sequences; the abundance of these organisms increased in fluids with relatively high levels of sulfate and methane. Ongoing work includes identification of complete metabolic pathways and correlation of those pathways to phylogenetic markers.

Broader implications: Studying microbial communities in extreme environments on Earth will help us to form testable hypotheses about the existence of communities on extraterrestrial bodies. Combining geochemical metadata with phylogenetic diversity and metagenomic analyses may enable us to predict what metabolic pathways would be likely under extraterrestrial geochemical conditions.

References:

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