

**DIVERSITY AND METABOLIC POTENTIAL OF MICROBIAL COMMUNITIES IN A CONTINENTAL SERPENTINITE SPRING.** E. R. Dart<sup>1</sup>, P. L. Morrill<sup>2</sup>, and W. J. Brazelton<sup>3</sup>, <sup>1</sup>(University of Utah, Department of Biology, emily.dart@utah.edu), <sup>2</sup>(Memorial University, Department of Earth Sciences, pmorrill@mun.ca), <sup>3</sup>(University of Utah, Department of Biology, william.brazelton@utah.edu).

The geochemical process of serpentinization provides a continuous supply of hydrogen and organic carbon [1]. This may not only create conditions that favor microbial growth but may also meet all of the requirements for a robust and photosynthetically independent biosphere [2]. Additionally, serpentinite systems on Earth may be analogous to systems found on Mars and other planetary bodies [3]. However, serpentinization creates conditions, such as high pH and limited electron acceptors, which may limit microbial growth and diversity [1]. Gaining an understanding of the identity and metabolic potential of microbes that thrive in these environments may provide insight as to whether serpentinization is sufficient to independently support life on this planet and on others.

Some sites of continental serpentinization have springs that feed surface pools. These pools provide easy access to subsurface fluids without the need for invasive sampling techniques such as drilling. However, the identification of microorganisms associated with the subsurface is complicated by two factors, 1) contamination by surface microbes and 2) the presence of microbes that live in the transition zone where hydrogen-rich subsurface fluids meet oxygen-rich surface fluids.

This study focuses on the isolation of subsurface microbes from a continental serpentinite spring in Gros Morne National Park, Newfoundland, Canada. The study was designed to distinguish among potential sources of microorganisms by using a new sampling technique to more effectively isolate subsurface fluids. To capture subsurface fluids, the surface pool was drained, surface fluid input was blocked, and DNA samples were taken from the subsurface source as the pool refilled.

Community dissimilarity comparisons using bacterial and archaeal 16S rRNA gene sequencing indicate that the sampling design led to more direct access to subsurface fluids. These data also show that the bacterial family *Erysipelotrichaceae*, a family previously identified as a likely member of the subsurface community, is significantly enriched in the samples associated with the subsurface (p-value<0.05) [2].

In line with the 16S rRNA data, preliminary analysis of shotgun metagenomic data indicates that metabolic pathways consistent with non-

photosynthetic carbon fixation are present in the samples associated with subsurface fluids while hydrogen oxidation pathways are present in samples associated with surface sources. These results may provide a clearer picture of the diversity and metabolic potential of microbial communities inhabiting subsurface serpentinite environments.

**References:** [1] Schrenk M. O. et al. (2013) *Reviews in Mineralogy & Geochemistry*, 75, 575–606. [2] Brazelton W. J. et al. (2013) *Appl. Environ. Microbiol.*, 79, 3906-3916. [3] Szponar N. et al. (2013) *Icarus*, 224, 286-296.