

**GEOCHEMICAL INFLUENCES ON SEDIMENT BACTERIAL COMMUNITIES IN A SERPENTINIZATION-HOSTED ECOSYSTEM.** A. Howells<sup>1</sup>, A. T. Poret-Peterson<sup>2</sup>, A. Cox<sup>2</sup>, P. Canovas<sup>2</sup>, and E. L. Shock<sup>2,3</sup>, <sup>1</sup>School of Life Sciences, <sup>2</sup>School of Earth & Space Exploration, <sup>3</sup>Department of Chemistry and Biochemistry, Arizona State University, Tempe, AZ.

**Introduction:** Serpentinization is widespread across the solar system. On Earth, serpentinization generates habitats where various microbial metabolisms can be fueled by the products of water-rock reactions (e.g., methane, hydrogen, organic compounds) [1]. We have sampled a number of hyperalkaline springs (pH>10) in the Samail Ophiolite in northern Oman, and find that the fluids are enriched in methane, hydrogen, calcium, dissolved organic carbon, ammonium, and sulfide, and severely depleted in magnesium, dissolved inorganic carbon, nitrate, and sulfate relative to neighboring surface waters.

The enrichment or depletion of particular carbon and energy sources and other geochemical constituents in hyperalkaline springs and surface waters provides an opportunity to study how geochemistry potentially structures microbial communities in these springs. Furthermore, in Oman, hyperalkaline seeps have pH values as high as 11.8, which exceed the known upper pH limit for microbial growth in chemostats (pH 11.4), but at considerably lower salinities suggesting the presence of novel alkaline-tolerant microbial populations [2]. In this study we compared sediment microbial community composition and diversity among Oman hyperalkaline springs, surface waters (~pH 8), and fluids resulting from mixtures of surface waters and hyperalkaline springs (~pH 9-10) as functions of geochemical composition.

**Methods:** Spring water geochemical measurements and sediment community composition analysis were conducted at 4 surface water locations, 3 mixing fluids, and 7 hyperalkaline springs. Geochemical parameters included pH, dissolved methane and hydrogen, major ions, metals, and other parameters described in [3]. Microbial community composition was characterized by sequencing the V4-V5 region of the bacterial 16S rRNA gene amplified from sediment DNA extractions. OTUs were identified using UPARSE [4] and classified via RDP Classifier [5]. Canonical correspondence analysis (CCA) was used to relate geochemical parameters to bacterial community composition followed by permutations to test for significance of correlations [6].

**Results:** Preliminary CCA revealed that bacterial community composition is significantly correlated ( $P < 0.05$ ) with pH, dissolved inorganic carbon, sulfate, and magnesium. Community composition is also marginally correlated with calcium and phosphorus ( $P = 0.07$ ). The relative abundance of OTUs showed that the sedi-

ment communities of the hyperalkaline springs are mostly dominated by Firmicutes and Proteobacteria. Among the Proteobacteria, the most abundant OTU was classified as *Hydrogenophaga*, suggesting that hydrogen oxidation may be an important energy source in these springs, although these organisms are metabolically flexible. Representatives of Firmicutes are known to perform fermentation and may potentially use dissolved organic carbon in these springs. Moreover, these organisms are known to produce hydrogen, also a product of serpentinization, which is elevated in these springs. In two hyperalkaline springs, OTUs affiliated with Cyanobacteria/Chloroplast were the most abundant, despite the potential limitation of dissolved inorganic carbon in these springs. OTUs classified as Bacteroidetes were more abundant in some of the surface waters. The alpha diversity of the hyperalkaline spring sediments is overall much lower than in the surface waters and mixing fluids. Sediments of the mixing fluids tend to be the most diverse.

This preliminary work reveals that the difference in geochemical composition of the hyperalkaline spring and surface waters are drivers in shaping sediment bacterial community composition and diversity in these systems. Furthermore, these hyperalkaline springs provide an abundance of energy sources for organisms such as *Hydrogenophaga*. And while geochemistry is playing a distinct role in shaping community composition and diversity, we can quantify how the organisms in these environments contribute to the observed geochemical composition.

#### References

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