MICROBIAL POPULATIONS REFLECT THE GEOCHEMICAL AND PHYSICAL PROPERTIES OF SERPENTINIZATION-HOSTED ECOSYSTEMS. A. H. Howells[1], J. M. Leong[1], T. Ely[1], K. J. Robinson[1], E. L. Shock[1], [1]GEOPIG, Arizona State University-Tempe (alta.howells@asu.edu).

Introduction: As knowledge of the chemical and physical parameters that influence microbial functions increases, the presence and abundance of microbial populations in the environment can potentially inform researchers about active processes. In the subsurface of the Oman Samail Ophiolite, serpentinization, a water-rock reaction, generates reduced, hyperalkaline, H_2-rich fluid. As this fluid comes into contact with the atmosphere, rich in CO_2 and O_2, the resulting disequilibria fuels microbial metabolisms such as hydrogen oxidation, methanogenesis and methane oxidation. These metabolisms are influenced by pH, O_2, H_2 and CH_4 gradients commonly found in Oman systems [1]. By focusing on the distribution and abundance of microbial populations that carry out these metabolisms we can evaluate how interactions of serpentinization-reacted fluids with the atmosphere generates habitability.

Methods: To evaluate how microbial populations reflect the geochemistry of serpentinization-hosted ecosystems, 29 sediment samples were taken from springs in the Oman Samail Ophiolite. These samples came from 4 geographically distinct locations in Oman. Within these locations, samples were taken across pH gradients established by mixing between surrounding surface waters (pH 7-8) and serpentinization-reacted fluids (> pH 11). At 17 of these sites planktonic samples were also taken. The presence and relative abundance of microbial populations were determined by sequencing the 16S rRNA gene. The 16S rRNA gene was amplified and barcoded for sequencing using Illumina MiSeq [2]. OTUs were defined and identified at the genus level using QIIME 2. Geochemical measurements including pH, dissolved methane and hydrogen, major ions, and trace metals were taken and analyzed using methods described in [3].

Results:

Hydrogen Oxidation. The obligate alkaliphilic hydrogen oxidizer, *Hydrogenophaga*, previously isolated from a serpentinization-hosted ecosystem (pH 11.6) in The Cedars, CA [4], is found in all 4 locations. Its preference for H_2-rich, hyperalkaline fluids make it a strong indicator for fresh serpentinzation-reacted fluids. Across the pH gradients this population is most abundant in systems with pH > 11.4.

Methanogenesis. Based on thermodynamic calculations, methanogenesis yields more than an order of magnitude *less* energy per volume of fluid than hydrogen oxidation. Nevertheless, the methanogen *Methanobacterium* is present at >1% relative abundance in 10 of the 29 systems. All of these systems are H_2-rich, ($[H_2]/[CH_4] > 8$). In one system it made up 42% of the community.

Aerobic Methane Oxidation. By comparison with stratified lakes, peatlands, and other ecosystems [5, 6], it may be expected that aerobic methane oxidizers would be most abundant in mixing systems where O_2-rich surface waters meet serpentinization-reacted fluids. In 2 of the 4 locations, the relative abundance of the aerobic methanotroph, *Methylmicrobium*, reached a maximum at ~pH 10. At a third location the maximum was at pH 11.3. Geochemical evidence, including the abundance of Na^+ and Cl^-, indicates that this high pH system has 11-16% influence from surrounding surface water. The fourth location is relatively depleted in methane and no methanotrophs were detected. At this same location, which is also H_2-poor, methanogens comprise <1% of the communities. This speaks to the demand for methane by methane oxidizers and the ability of methanogens to produce it, and raises questions about symbiosis and co-selection. It also suggests a biological contribution to methane measured in serpentinization-hosted ecosystems.

Planktonic Populations. Comparison of planktonic communities with corresponding sediment communities shows enrichments of aerobic methane oxidizers and hydrogen oxidizers in planktonic samples. In contrast, no methanogens were found in any of the planktonic communities. This reflects a demand for O_2 by hydrogen and methane oxidizers, as well as an O_2 intolerance by methanogens.

In summary, hydrogen oxidizers indicate fresh serpentinzation-reacted fluids, methanogens correspond to H_2-rich systems, and methane oxidizers reveal the extent of influence of the atmosphere on serpentinization-reacted fluids. The co-occurrence of methanogens and methane oxidizers indicates a biological origin of methane. Differential distributions of these metabolisms in planktonic versus sediment communities documents the influence of O_2. These results demonstrate the potential use of microbial sequencing data to predict processes occurring in the environment.

References:

[1] Miller H. M. et al. (2016) *Geochim. Cosmochima. Acta., 179*, 217-241. [2] Caporaso J. G. et al. (2012) *ISME J* [3] Shock E. L. et al. (2010) *Geochim. Cosmochim. Acta.,* 74, 4005-4043. [4] Suzuki S. et al. (2013) *Nature Communications.* [5] Bastviken D. et al. (2004), *Global Biogeochem. Cycles, 18*, GB4009. [6] Kip N. et al. (2010) *Nature Geoscience, 3*, 617-621.