

Microbial Ecology of Hypersaline Paleolake Sediments Along a Geological Transect in the Great Salt Lake Desert, Utah: A Habitability Model for Early Mars. K. L. Lynch¹, J. Munakata Marr¹, B. H. Horgan², J. Hanley³, K. A. Rey⁴, R. J. Schneider¹, W. A. Jackson⁵, S. M. Ritter⁴, and J. R. Spear¹. ¹Colorado School of Mines, 1500 Illinois Street, Golden, CO 80305 (kllynch@mines.edu), ²Purdue University, West Lafayette, IN. ³Southwest Research Institute, Boulder, CO, ⁴Brigham Young University, Provo, UT, ⁵Texas Tech University, Lubbock Texas

Introduction: Martian paleolake basins are prime habitability targets for the Mars 2020 mission [1, 2]. While it is unclear whether or not Mars ever hosted a large ocean [3], martian paleolakes are excellent proxies for a Hadean-like origin-of-life environment [4,5]. The majority of terrestrial paleolakes transitioned to modern day evaporite basins with clay, sulfate and chloride compositions similar to the aqueous minerals identified across the martian surface, are known to harbor a diverse array of microbial life, and enhance the preservation of organic matter & fossils. As such, these terrestrial systems are considered excellent analogs for habitability studies that will be useful for identifying and exploring paleolake systems on Mars [6].

In this study we investigate the microbial ecology, along mineralogical and geochemical gradients, of a terrestrial paleolake basin in an effort to: 1) Characterize the biological diversity within an understudied environment 2) Assess the correlation, if any, between the microbial diversity and the mineralogical and geochemical variation present in the basin. 3) Assess the influence of this relationship on biomarker preservation as a model for paleolake systems on the red planet.

Field Site: The Great Salt Lake Desert (GSLD) is one of two remnants, the other being the Great Salt Lake, of the ancient Lake Bonneville, the largest of several North American paleolakes from the Pleistocene Epoch (~32,000 to 16,200 B.P.). Of the three main sub-basins of the GSLD, only the isolated Pilot Valley has remained relatively untouched, and thus is the focus of this investigation.

Pilot Valley is a closed basin system with a subsurface hydrology comprised of three distinct aquifers: an alluvial fan aquifer, a deep basin-fill aquifer at a depth of ~30 meters, and a shallow brine aquifer that encompasses the upper ~6 meters of the basin sediment fill. The shallow-brine aquifer is maintained by ground water flow from mountain front recharge of the alluvial aquifer flanking the Silver Island Range [7]. The only loss mechanism from the Pilot Valley basin is capillary wicking and evaporation from the playa surface [8].

Methods: Sediment core samples down to depths of 2 meters were taken from a defined horizontal transect lying along geochemical and mineralogical gradients in the Pilot Valley basin. Mineralogy of the sediments was determined by X-Ray Diffraction (XRD), automated scanning electron microscopy

(QEMSCAN), and visible-near-infrared spectroscopy (VNIR). DNA was extracted from each sample and subjected to 454 pyrosequencing of the 16S rRNA gene. The resulting data was processed using the Qiime workflow software and analyzed using ecological statistic packages in Qiime, PAST and R.



Figure 1. Satellite Image of the Great Salt Lake Desert & key Sub-basins: Bonneville Salt Flats & Pilot Valley. Image courtesy of Google Earth.

Summary: Results show an expected dominance of the archaeon *Halobacteria* across the study transect. However, the diversity within the bacterial domain is markedly different from other hypersaline systems and most notable is the high abundance of *Gemmatimonadetes*. Preliminary alpha and beta diversity analyses of the data set suggest that shifts in the microbial community are driven by vertical variations in the mineralogy, thus likely affecting which microbial species and subsequent biomarkers will get preserved within the sedimentary layers of the basin.

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