

**GEOBIOLOGY AND SEDIMENTOLOGY OF THE HYPERSALINE GREAT SALT LAKE, NORTHERN UTAH, USA: ANALOGUES FOR ASSESSING WATERY ENVIRONMENTS ON MARS?** Kathleen Nicoll<sup>1</sup> Laura L. Beer<sup>2</sup>, <sup>1</sup>University of Utah, [kathleen.nicoll@gmail.com](mailto:kathleen.nicoll@gmail.com) <sup>2</sup>Colorado School of Mines, [laurabeer@gmail.com](mailto:laurabeer@gmail.com).

**Introduction:** The hypersaline Great Salt Lake (GSL) of northern Utah, USA is a critical regional ecosystem that has not been examined in detail from a geobiological perspective. There are presently only a handful of studies on the biota of this shallow water closed-lake system [1]. Despite interest from industries mining the salt and harvesting the brine shrimp, relatively little is known about the lake's geochemistry, microbial diversity, metabolic activity, and mineralogy, and how these relate together with processes of biosedimentation and fossil preservation.

**Objectives:** We study the composition, architecture, and preservation of modern GSL microbial communities present using genomic (DNA sequencing) and microscopic techniques (SEM, EDAX).

**Initial Results:** Our examination of various sedimentary facies sampled in the modern GSL (figure 1) indicates that microbial communities occur in many of its environments. Microbial communities in the GSL are found in microbial mats, crusts, tufas, oolites, carbonate hardgrounds, stromatolites, open water, and benthos.

Traditional cultivation and isolation approaches on samples from the lake and surrounding features have yielded some Archaea, Bacteria, microalgae and cyanobacteria. Our ongoing phylogenetic studies of microbially-influenced sedimentary structures (MISS, after [2]) including biostromes, microbial mats, as well as benthic and pelagic regions of the lake, are yielding a tremendous amount of information through the application of high-throughput DNA sequencing techniques, including small sub-unit 16S ribosomal RNA (16S ssu rRNA) methods.

**Conclusions and Implications:** Our findings refute the idea that the GSL is "dead" – on the contrary, microbial diversity is a function of the prevailing conditions. Recent work on other microbial mats show that constituent cyanobacteria and other microorganisms secrete extracellular polymeric substances (EPS), which enhance the stability of the sediment [3], and contribute to sedimentation [4]. With this in mind, we endeavour to identify potential biomarkers present in GSL carbonate and siliclastic facies, and to examine their preservation and temporal persistence. Studying the GSL is especially valuable because it is an accessible extreme environment for testing hypotheses regarding biosedimentation, energy pathways, nutrient cycling and eukaryotic evolution on early Earth and Mars.

**References:**

- [1] Eardley, A.J., (1938) *Bulletin of the American Association of Petroleum Geologists*, 22 1305-1411; Carozzi, A.V. (1962) *Journal of Geology*, 70, 246-252. [2] Noffke, N. (2008) *GSA Today*, 18, 4-9. [3] Gerdes, G. et al. (2000) *Sedimentology*, 47, 279-308. [4] Stolz, J.F. (2000) in *Microbial Sediments*. Springer-Verlag 1–8; Dupraz et al. (2008) *Earth Science Reviews* 10.1016/j.earscirev.2008.10.005

**Acknowledgements:** Financial support provided by the University of Utah Creative Research Grant, and the Great Salt Lake Institute.

**Figure 1:** General location of our study area in GSL in Northern Utah. Below, photo of sampled modern microbial mat with MISS (Microbially-influenced sedimentary structures) that is yielding valuable genomic data.

