SUBSURFACE MICROBIAL DIVERSITY AND ECOLOGY OF PLAYA SEDIMENTS AT WHITE SANDS NATIONAL MONUMENT (NEW MEXICO). M. Glamoclija[1], A. Steele[2], M.L. Fogel[3], K. Sirisena[1,2], S. Ramirez[1], I. Widanagamage[1], A. Waldron[1*], M. Zeidan[1*] and S. Potochniak[1*]. [1]Department of Earth and Environmental Sciences, Rutgers University - Newark (m.glamoclija@rutgers.edu), [2]Geophysical Laboratory, Carnegie Institution of Washington, [3]Department of Earth Sciences, University of California at Riverside [1*]Authors are undergraduate students.

Introduction: Sulfates found in Martian sedimentary sequences have been proposed as a part of diagenetic sequences at the Noachian/Hesperian transition, within which fresh water lacustrine environments desiccated and transitioned to more saline environments where sulfates formed [1, 2]. Consequently, playas and lacustrine sequences have been suggested as sites of high astrobiological interest for investigations of biosignatures on Mars [3]. Surface habitats of playas and evaporitic desert environments have been discussed through many publications, and it has been noted that microorganisms living in evaporitic translucent settings will position themselves close to the surface, but not quite exposed to it, to prevent desiccation [4,5,6,7]; in some cases, stratification of organisms within communities has been reported for the first few mm below the surface [8].

Besides the dominant evaporation process, playas are marked by the presence of a shallow groundwater table. The near surface colonization strategy of microbes is an adaptation to explore an extension capillary fringe that will almost reach the surface. In our current work, we focused on the groundwater as the driving force of the subsurface chemistry and potentially distribution of the ecological niches. We drilled about 1 m into the playa sediments to explore this environmental gradient and probe microbial diversity between the surface and 1 m depth down to the groundwater table. We also tested depth profiles of active playa (e.g., Lake Lucero), where we sampled 2 shallow profiles: one in the middle of an area that usually gets flooded and second on the edge of the temporary lake (i.e., the area that dries early in the season). Further, we sampled more stable geologically older and more compact lacustrine sequences along the erosional escarpment too. These older sequences are not as exposed to seasonal playa activity and hence, the moisture content and salinity are more consistent throughout the year.

Here we are combining analyses of mineral assamblages, cation, NH_4 and NO_3 concentrations, $\delta^{15}N$ and organic $\delta^{13}C/^{12}C$ isotopes with 515 Illumina DNA sequencing data.

Results: XRD analysis revealed that samples are mainly composed of gypsum and minor mineral phases as halite and quartz. SEM/EDS (Fig. 1) revealed the presence of amorphous phases: halite, glauberite, magnesium chlorite salt. Diatom frustules were found in more stable, older lithological sequences. Cation analyses showed that general concentrations of Na, Fe, Mg and Sr decreased with depth, consistent with our mineralogical and general lithological observations in which the variety of slat decreases with the depth, however K increased and Ti concentrations were below detection for surface samples and for the deepest sample that directly interacted with groundwater.

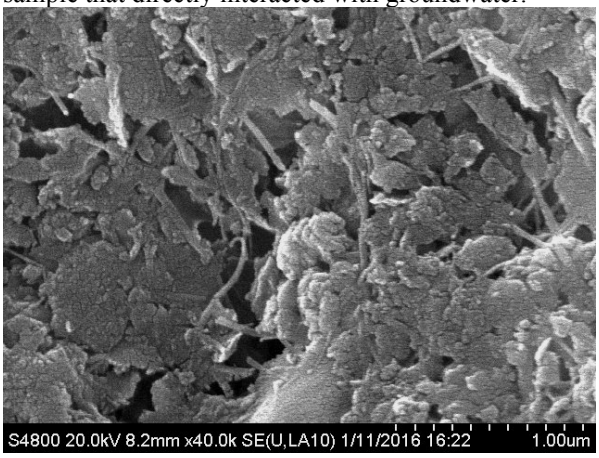

Figure 1. The SEM micrograph of nm in thickness strings found between salt percipitates. These strings/filaments are the sole microbial morphologies observed in the analyzed samples.

The concentrations levels of NH_4 range from 0.93 to 45.6 ppm and in general increase with the depth, while the concentrations for the geologically older strata are more uniform and fall in the range of 1.13 to 1.81 ppm. The NO_3 concentrations fall in the range of 8.73 to 30.43 ppm however the distribution of the NO_3 varies among the sampling sites. The NH_4/NO_3 ratio is the best illustrator for this. The sampling site LL1 that has very shallow groundwater table and has the lowest NH_4/NO_3 ratios associated with the sticky clay horizons. Overall, the concentrations of NO_3 are much higher than these of NH_4 indicating possible presence of oxidizing conditions throughout the depth profile and the contribution from microbial nitrification. The second site LL2 is the driest sampled in the Monument, exhibits an increase in the NH_4/NO_3 ratio with

the depth (0.5 to 4.4 ppm), indicating that few bottom samples may be anoxic. The NH_4/NO_3 ratio is in the range of 0.04 to 0.2 ppm indicating that these samples were predominantly characterized by oxygenated conditions throughout the profile. Similar range is recorded for the geologically older site, which fall in the NH_4/NO_3 range of 0.07 to 0.2 ppm.

Moisture levels in general increased with the depth (from 3 to 53 ppm and at LL1 site getting immersed in the water).

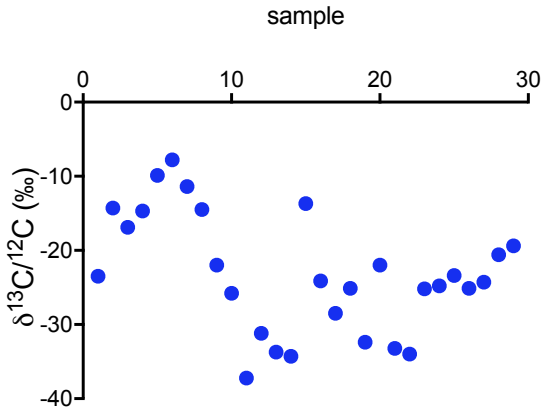

Figure 2. The organic $\delta^{13}C/^{12}C$ isotope data for all of the analyzed samples.

The organic $\delta^{13}C/^{12}C$ values range from -7.8 to -37.2 ‰. The most negative values are indicative (<30 ‰) of methanogens or microbial methane consumption. The $\delta^{13}C/^{12}C$ values that are in range of 25 ‰ are characteristic for microbial organisms.

Based on 515 Illumina DNA sequences, microbial communities in these samples are mainly composed of Eubacteria (around 80%) and in lesser % Archaea. Eukaryotes were detected in only some of the samples and represented with very low diversity of organisms. When using resemblance analysis, S17 Bray Curtis similarity %, all of different depth profiles have very low similarity %, about 10%. It is important to note that the most Bacterial and Archaeal OTUs have been found in surface crusts within a mixture of thenardite, mirabilite and gypsum minerals, groundwater collected from one of the drill holes, and a piezometer from Lake Lucero. These samples have a similar number of OTUs in comparison to groundwater samples collected from a nearby dune field, which has almost twice the number of bacterial OTUs. Groundwater from the playa has more Archaeal OTUs than dune field water, with one of the samples having almost 5x more Archeal OTUs, which varied within the lithological sequences.

Overall, the sequencing data revealed that the microbial taxa (bacteria, archaea, eukaryote) found in the Lake Lucero sediment ecosystem are generally well adapted to the hypersaline, evaporitic conditions. However, it is shown that unique combinations of these hypersaline microbial taxa colonize specialized geochemical microenvironments as they may have diverse genetic potential to survive under various environmental conditions. It is suggested that oxygen content, moisture content, geochemical and mineralogical variations shown across the lithological gradient play crucial roles in defining community ecology. Predicted metabolic diversity and oxygen consumption patterns also support this idea. We acknowledge that 16S and 18S amplicon sequencing approaches may not provide the most accurate results at the genus level, and that metagenomic and metatranscriptomic analyses would be a valuable tool to understand the actual metabolic potential of these organisms.

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