Next generation sequencing and characterization of biological soil crusts from the western Mojave Desert.

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Introduction:

Biological soil crusts (BSCs) are symbiotic surface soil communities that play pivotal roles in water and nutrient cycling in arid and semi-arid environments [1]. For astrobiology, BSCs serve as potential analogs for life on Mars due to their survivabilities under ultraviolet radiation, low water activities, and wide temperatures ranges. In this presentation, we will describe the characterization of BSCs sampled from the western edge of the Mojave Desert within the Mojave National Preserve in southern California. Our analyses focus on three sites along an elevation transect, where the surface densities along this transect increase with elevation. Herein, we report on the genetic, biochemical, and geochemical analyses of the BSCs, which were conducted as part of a undergraduate training program entitled NASA/CSU Spaceward Bound [2].

Methods:

Samples were collected at three sites along an elevation transect (273 to 685 m over ~ 21.5 km) off of Kelbaker Rd. in the Mojave National Preserve. Surface densities of the BSCs were estimated by pixel analysis of multiple digital images taken at each site. DNA extractions, quantitative PCR, chlorophyll abundances (ethanol extractions & spectral measurements), ATP abundances (benchtop luciferase-based assay), and soil catalase activities (displacement method) were measured within 1-2 days of sample acquisition. Next generation sequencing (454 sequencing, Research and Testing Laboratory LLC) was performed at later dates using the extracted DNA. Geochemical analyses were performed by the Environmental Analytical Lab at Brigham Young University.

Results and Discussion:

The estimated surface densities of the BSCs were 0.89 ± 0.35, 4.4 ± 1.2, and 10 ± 7% coverages at the three sampled sites. Next generation sequencing (NGS) analyses supported the presence of unique bacterial communities at each site, where the most abundant sequences were those from unidentified genera. However, at the phylum level (**Figure 1**), the *Proteobacteria* and *Cyanobacteria* were the most abundant across all sites, where the most represented (and identifiable) cyanobacterial genera were *Microcoleus*, *Phormidium*, *Chroococcidiopsis*, and *Symploca*. Irrespective of surface density, the overall cyanobacterial abundances across the sites were essentially equivalent, which was corroborated by chlorophyll abundance studies. Interestingly, *Nostoc* and *Scytonema* were not detected in our studies. In comparison, the sub-surface communities (below 1 cm) were compositionally unique and lower in overall bacterial abundance (qPCR & NGS). Biochemical analyses showed higher internal ATP concentrations (**Figure 2**) and catalase activities (**Figure 3**) at the higher density sites. Geochemical analyses showed that the soil at the lower elevation site was lower in silt content and higher in heavy metals such as Mo, Co, Ni, and Ti.

Conclusions:

Our preliminary analyses suggest that the BSCs are compositionally unique when compared to those from the eastern sections of the Mojave Desert. Our holistic analyses also suggest that the BSCs along the elevation transect possess differing metabolic activites, and do not necessarily represent differing growth phases of the BSCs. Together with our geochemical results, our studies suggest that the differences in surface densities along the transect are related to the silt and heavy metal (*e.g.*, Mo, Co, Ni, Ti) contents of the corresponding soil. These trends along with more in-depth analyses and the astrobiological significances will be discussed.

Figure 1. Distribution of phyla among the differing sites.

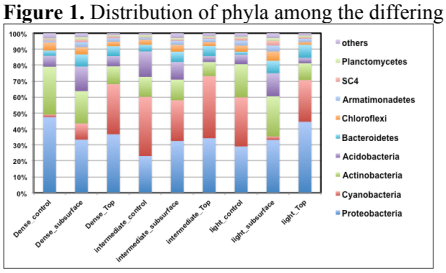


Figure 2. ATP abundances of the BSC and subsurface samples.

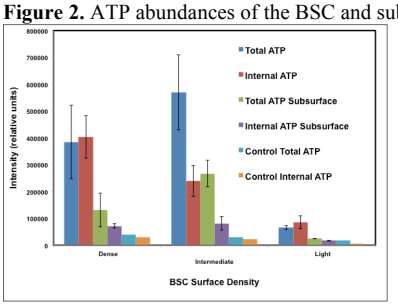
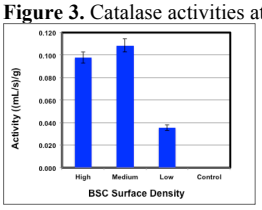


Figure 3. Catalase activities at the differing BSC sites.



References:

[1] Belnap, Lange *Biological Soil Crusts: Structure, Function, and Management*, Springer.
[2] http://www.cpp.edu/~rmogul/spacewardbound.