Characterization of Icelandic Mars Analog Environment using 16S rRNA Sequencing

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Utilizing Earth analog environments to estimate small-scale spatial and temporal variation in key geochemical signatures and biosignatures will help mission designers ensure future sampling strategies will meet mission science goals. Icelandic lava fields can serve as Mars analog sites due to conditions that include low nutrient availability, temperature extremes, desiccation, and isolation from anthropogenic contamination. We performed the first characterization of soil communities in Fimmvörðuháls. This lava field formed from a basaltic effusive eruption associated with the 2010 Eyjafjallajökull eruption. A triangular grid of sample locations spaced at 1 m, 10 m, 100 m and 1 km intervals was established where the tephra is homogeneous based on visible color, morphology, and grain size. A triplicate sample set at 10 cm spacing was taken at each grid point. High-throughput sequencing of PCR amplicons spanning the V3 and V4 hypervariable regions of 16S rRNA gene was conducted to assess the microbiome taxonomic composition. Sequencing was performed on an Illumina MiSeq using a 500 cycle kit. Sequencing data was analyzed using the QIIME pipeline and R. Based on high-throughput sequencing of 16S rRNA gene amplicons, Proteobacteria and Actinobacteria were the dominant microbial phyla representing over 50% of total sequences in all samples. However, a large number of other phyla (22) were also detected in this ecosystem. Although microbial richness did not vary significantly among samples (Chao1 index; $p>0.05$), the phylogenetic composition (weighted Unifrac metric) of the soil microbiome differed significantly between apparently homogenous sites separated by >1 km ($p<0.05$), suggesting distinct microbial communities despite apparent homogeneity.

References: [1] Amador, E. S. et al. (2015) Planet. Space Sci., 106 1-10. Gentry, D. M. et al. (2017) Astrobio. in press. [2] Klindworth et al. (2013) Nucleic Acids Res, 41(1). [3] Caporaso et al. (2010) Nature Methods, 7(5) 335-336.