DIFFERENTIAL ABUNDANCE AND EXPRESSION OF ANTARCTIC SOIL MICROBIAL COMMUNITIES: A METATRANSCRIPTOMIC ANALYSIS OF TAXONOMIC AND FUNCTIONAL DIVERSITY. H. N. Buelow[1], A. Kooser[1], D. J. Van Horn[1], and C. D. Takacs-Vesbach[1]. [1]Department of Biology, University of New Mexico, MSC03 2020 Albuquerque, NM 87110, USA

Introduction: The McMurdo Dry Valleys (MDV) are an extreme polar desert region of Antarctica, consisting of exposed soils, relatively free of snow and ice cover. The MDV are thoroughly described as an astrobiological analog, with soils particularly analogous to those of Mars [1], [2]. This unique region is an exclusively microbial ecosystem, lacking higher plant and animal residents. As such, MDV soils are an exceptional study site to describe microbial processes free from many confounding factors common to other terrestrial ecosystems. Microbial life of MDV soils is known to be active during the brief Antarctic summer [3], [4], taking advantage of ephemeral glacial melt water inputs and warmer temperatures. Climate change is increasing warming events in this region, and thus increasing soil moisture and mobilized nutrients in the soils [5]. However, little is known about what functions the resident soil microbes perform, and how these functions change with increasing water and nutrient availability. The experimental research presented here therefore furthers understanding of extreme terrestrial ecosystems, microbial climate change effects, and astrobiology – particularly for Martian soils.

Methods: This project uses a metatranscriptomic approach to investigate summer soil microbial activity in the MDV. Water and organic matter *in situ* treatments were included to increase soil moisture by 10%, providing an experimental basis to consider community responses to environmental pulses relative to unamended controls. The total mRNA transcripts of soil microbial communities were sequenced using Illumina HiSeq and resulting sequences were annotated by MG-RAST, using the GreenGenes and SEED Subsystems databases for taxonomic and functional annotation, respectively. Differential abundance of taxonomy and differential expression of functional reads were analyzed using the phyloseq and DESeq2 packages in R.

Results: Number of reads per sample ranged from 6597242 to 19854970 (9934974 mean), with 42% to 61% of each sample annotated as predicted protein.

Differential abundance. Responses to treatments were variable within individual phyla; some members of a phylum may decrease abundance significantly while other members of the same phylum increase significantly. Key soil bacterial phyla Actinobacteria, Cyanobacteria, and Proteobacteria had the greatest responses to water treatments relative to controls, each with significantly positive and negative abundance changes. For organic matter treatments, members of Firmicutes had the greatest differential abundance increase, consistent with other studies of nutrient additions to these soils [4], [6]. As in water treatments, Actinobacteria and Proteobacteria had some of the strongest abundance responses to organic matter addition relative to controls.

Differential expression. Contrary to the variable responses seen in differential abundance measures, transcript expression tended to show clearer trends at high level functional categories: transcripts within a functional category were either over- or under-expressed relative to controls. Transcripts within 10 Subsystems functional categories were differentially expressed in water addition samples relative to controls. Among these responses, transcripts in categories Motility and Chemotaxis, Carbohydrates, and Phages, Prophages, Transposable Elements, Plasmids were significantly more abundant in water addition samples than controls. For organic matter additions, differential expression occurred across 12 Subsystems functional categories. Increases of transcripts were found in the Amino Acids and Derivatives, Respiration, and Miscellaneous categories. For both water and organic matter additions, transcripts in the Protein Metabolism category were significantly decreased relative to controls, and closer investigation indicates this differential expression largely stems from eukaryotic and archaeal transcripts.

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