Community Structure of Benthic Microbial Mats, Lake Fryxell, Antarctica. M. Krusor,[1] A. D. Jungblut[2], I. Hawes[3], T. J. Mackey[4], and D. Y. Sumner[1], [1]University of California, Davis, Davis, California; [2]Natural History Museum, London, UK; [3] Waikato University, Tauranga, NZ; [4]Massachussetts Institute of Technology, Cambridge, MA.

Introduction: Microbial communities are often structured by energy sources. On Earth now, light and oxygen from photosynthesis structure most microbial communities [1, 2]. However, the effects of the two are very tightly coupled, and it is not clear how phototrophic microbial mats might be structured in the absence of oxygen or where oxygen is high enough to eliminate anoxia. Understanding these differences can provide insights into how microbial communities might be structured on other worlds, such as on Earth before the Great Oxidation Event and habitable, extraterrestrial planets or satellites.

Background: Lake Fryxell is a physically stable, low-nutrient habitat in the McMurdo Dry Valleys (MDV), Antarctica [3]. The microbial community in the benthic zone of the lake grows in thick, layered mats. When the sun rises above the horizon during the summer months, photosynthetically active radiation (PAR) is available for use by phototrophs [4, 5]. This is the lake's primary energy influx. However, most of the photosynthetic organisms in the microbial mats produce oxygen, influencing the microbial community structure through redox potential. In Lake Fryxell, O_2 concentration and PAR both decline with depth [5].

Methods: In 2012, we collected samples from Lake Fryxell's microbial mats from 9.0, 9.3, and 9.8 m. Temperature, pressure, O_2 concentration, conductivity, PAR, irradiance, O_2 microelectrode profiles, and mat morphology were recorded as well. At 9.0 and 9.3 m depths, PAR was relatively high, and the water was supersaturated with O_2. At 9.8 m depth, PAR was low and lake water was anoxic, but approximately 50 µmol L^{-1} of O_2 was produced by cyanobacteria growing within the microbial mat, creating a mm-thick zone with free O_2 in the mat under anoxic water. Metagenomic sequencing was performed on samples from each depth to assess how variation in community structure correlated with local geochemistry.

Results: Phylogenetic alpha diversity increases with increasing depth into the mat at all lake depths, i.e., with decreasing O_2; and diversity decreases with increasing depth in the lake [Figure 1]. Microbial communities are less diverse and the dominant phototrophs change at lower PAR and O_2 concentrations in deeper water. Further, at 9.8 m, O_2 generated by cyanobacteria creates a habitat for aerobic and microaerophilic heterotrophs under an anoxic water column. Microbial community turnover between mat layers is greater under oxic than anoxic water.

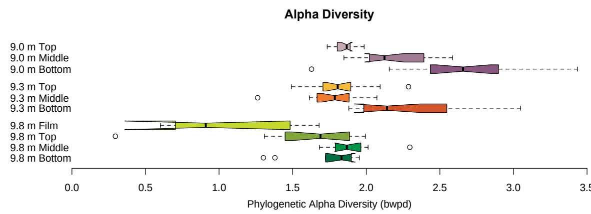

Figure 1. Significant differences in abundance-weighted phylogenetic alpha diversity between samples collected from three lake depths and four microbial mat layers.

Discussion: Mat communities adapt to their environments at numerous levels. Here, metagenomics techniques have revealed that oxygen consumption, generation, and availability appear to drive significant differences in microbial mat community membership and metabolic capacity, coincident with changes in gross mat morphology. Though PAR provides Lake Fryxell's primary source of energy and allows the production of oxygen, oxygen appears to be a major factor determing microbial population distributions across the geochemical gradients in this system.

References: [1] Harris K. J. et al. (2013) *ISMEJ*, 7, 50-60. [2] Jonkers H. M. et al. (2003) *FEMS Microbial Ecol*, *44*, 175-189. [3] Green W. J. and Lyons, W. B. (2008) *Aquat Geochem*, *15*, 321-348. [4] Sumner, D. Y. et al. (2016) *Geology*, *43*, 1-4. [5] Jungblut et al. (2016) *AEM*, *82*, 620-630.