Bacteriohopanepolyols across environmental gradients in ice-covered lakes of the McMurdo Dry Valleys, Antarctica. E.D. Matys¹, T. Mackey², D.Y. Sumner³, M. Krusor⁴, K. Wall⁵, A. Jungblut⁶, I. Hawes⁷, E. Mueller⁸ and R.E. Summons⁹, ¹Massachusetts Institute of Technology (45 Carleton Street E25-653 Cambridge MA 02139, ematys@mit.edu), ²Massachusetts Institute of Technology (tjmackey@mit.edu), ³University of California Davis (dysumner@ucdavis.edu), ⁴University of California Davis (mldillon@ucdavis.edu), ⁵University of California Davis (kmwall@ucdavis.edu), ⁶Natural History Museum, London (a.jungblut@nhm.ac.uk), ⁷University of Canterbury (ian.hawes@canterbury.ac.nz), ⁸Northeastern University (mueller.el@husky.neu.edu), ⁹Massachusetts Institute of Technology (rsummons@mit.edu)

Abstract: Identifying the diversity, distribution, and functional roles of microorganisms in the environment is essential to understanding ecosystem processes on Earth or elsewhere. Microbial membrane lipids may be used as molecular proxies for identifying microbial communities in contemporary environments [1-3]. Diagnostic compound classes include membrane lipids that are critical to the structural integrity and physiology of cells. Bacteriohopanpolyols (BHPs) are a prime example [4]. In order to apply BHPs and other molecular markers, we must first identify their structural diversity, biological sources, and physiological functions.

The McMurdo Dry Valleys contain numerous icecovered lakes, meltwater ponds, and glaciers with cryoconite holes. They vary in illumination, geochemistry, sedimentation, and microbial community structure. Studies of these extreme environments and the organisms that populate them provide valuable insights into variants of "life as we know it", with implications for the evolution and search for life elsewhere.

The lipid assemblages of these microbial communities have not received extensive study and only recently have they been characterized using genomic approaches [5-8]. Here, we describe the composition of accumulated organic matter in Lakes Vanda, Fryxell, and Joyce, of the McMurdo Dry Valleys. BHPs are of considerable interest due to their recalcitrant hydrocarbon skeleton and potential to serve as biomarkers for particular organisms, metabolisms, or environmental conditions. For example, in our data, the relative abundance of 2-methylhopanoids (2-MeBHP) is unprecedented and may reflect the unusual seasonal light regime of this polar environment [9-11]. Light levels fluctuate seasonally, favoring low-light-tolerant cyanobacteria and possibly specific lipid assemblages.

At 9 m depth in Lake Vanda, benthic microbial mats grow around and under cobbles and boulders and serve as a specific opportunity to test the influence of irradiance on lipid distribution in an otherwise homogenous environment. *In situ* illumination of the mat was modeled to provide an estimate of incident irradiance at any point on the mat surface (37-150 μ mol photons m⁻² s⁻¹; 12). The top layers of the microbial mat were then sampled across the shading gradient from under a rock

overhang to the open water. Surface layers were isolated and extracted for total lipids. Bacteriohopanetetrol (BHT) is a pervasive bacterial membrane lipid and is abundant in all mat surface samples. 2methylbacteriohopanetetrol (2-MeBHT) is also abundant and varies in relation to BHT across the transect. The "2-MeBHT ratio" (2-MeBHT/BHT+2-MeBHT) is highest underneath the boulder at <20% relative irradiance. The 2-MeBHT ratio decreases linearly across the gradient from regions receiving <20% relative irradiance to the open water (100% relative irradiance). This suggests that BHP methylation at the C-2 position may be an adaptation to low irradiance in this polar environment.

By establishing correlations among environmental conditions, microbial community composition, and lipid assemblages in the McMurdo Dry Valleys, our data provide valuable ecological insights as to life in such extreme environments and for the development of biomarkers that allow us to identify similar ecosystems in the Earth's geological record and elsewhere.

References: [1] Wakeham, S.G. and Beier, J.A. (1991) Deep-Sea Research, 38, S943- S968. [2] Brocks, J. J. and Pearson, A. (2005) Reviews in Mineralogy & Geochemistry, 59, 233-258. [3] Castañeda I.S. and Schouten, S. (2011) Quaternary Science Reviews, 30, 2851-2891. [4] Sáenz, J.P. et. al. (2012) PNAS, 109, 14236-14240. [5] Webster-Brown et al. (2015) FEMS Microbiology Ecology, 91, 12. [6] Zhang et al. (2015) Polar Biology, 38, 1097-1110. [7] Jungblut et al. (2016) Applied and Environmental Microbiology, 82, 620-630. [8] Wall et al., in prep. [9] Hawes, I. et. al. (2001) Antarctic Science, 13, 18-27. [10] Hawes, I. and Schwarz, A.M. (2001) Journal of Phycology, 37, 5-15. [11] Hawes, I. et. al. (2013) Biology, Special Issue on Polar Microbiology, 2, 151-176. [12] Mackey (2015) Sand, Mud, and Calcite: Microbial Landscapes on Antarctic Lake Beds (Doctoral dissertation).