Controllers of Microbial Community Composition in the Ice-Covered Lakes of the McMurdo Dry Valleys, Antarctica. C. L. Grettenberger,¹ K. Wall¹, M. Krusor¹, A. D. Jungblut², I. Hawes³, T Mackey⁴, and D. Y. Sumner¹, ¹Earth and Planetary Sciences, University of California Davis 95616 (clgrett@ucdavis.edu), ²Natural History Museum, London, UK, (a.jungblut@nhm.ac.uk) ³Waikato University, Tauranga, NZ (aquaticresearchsolutions@gmail.com), ⁴Department of Earth, Atmospheric, and Planetary Sciences, Massachusetts Institute of Technology 02139

Introduction: Antarctic lakes serve as habitable oases in the otherwise inhospitable environments of glacier-free valleys. These ice-covered lakes host microbial mats that carpet the shallow depths, commonly with laminated mat and pinnacles that vary in morphology from lake to lake [e.g. 1-4]. Community composition varies between lakes [e.g. 1], between depths within a single lake [e.g. 4], and within the mat structures themselves [e.g. 2]. These community differences may stem from selective filters placed on community composition by local environmental condition such as illumination, nutrient supply, oxidation state, and salinity, which all affect microbial communities. Alternately, geographic barriers may influence community membership by preventing potential members from dispersing to an environment. These mat establishment effects play at least some role because the environment between lakes requires that organisms withstand freeze drying to be transported to any given lake. Thus, the relative roles of colonization and environmental selection in shaping any specific microbial community are not obvious.

Here, we used 16S rRNA gene surveys to examine microbial community composition in Antarctic icecovered lakes at three different scales. Specifically, we addressed 1) within mat 2) within lake and 3) between lake variations. We correlated these differences with geographic and environmental parameters to determine the relative influence of geography and geochemistry on community composition.

Samples and Methods: Lakes Joyce and Vanda microbial mat samples were collected by divers in November 2010 and the samples were sequenced using 505F and 803R primers. We also collected previously published amplicon data from Lake Fryxell. Available geochemical data were also compiled.

Results: We found that while some of the microbial communities representing different morphological components were significantly different, many were not. The variation between communities in different lakes was greater than variations within lakes or within mats. Therefore we suggest that biogeographic factors including limitations on dispersal and establishment control variations in community composition between lakes whereas within lake and within mat geochemical gradients structure communities within the same lake [Fig1]. These patterns of community variation suggest that sampling one "oasis" within an overall inhospitable environment is not likely to capture the diversity of microbial communities that may be present. Even where geochemical conditions might be similar in separate oases, dispersal barriers might lead to divergent community compositions.

References:

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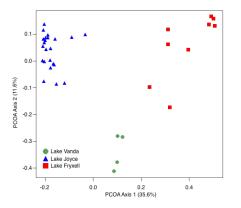


Fig 1. Principal components analysis of microbial communities from lakes Vanda, Joyce, and Fryxell.