

## ABSTRACT

### Microbial Diversity during the Polar Night Transition in Lakes of the McMurdo Dry Valleys, Antarctica

T. Vick<sup>1</sup>, L. Amaral-Zettler<sup>2</sup>, J. Priscu<sup>1</sup>

<sup>1</sup>Montana State University, Department of Land Resources and Environmental Sciences, Bozeman, MT, U.S.A.; <sup>2</sup>Joesphine Bay Paul Center/Brown Geological Sciences, Marine Biological Laboratory, Woods Hole, MA, U.S.A.

Microorganisms dominate the water columns of the permanently ice-covered lakes of the McMurdo Dry Valleys (MCM). During the summer, 24-hours of daily sunlight drives primary production by phytoplankton, which provides organic carbon for heterotrophic bacterioplankton. Research on the lakes is typically carried out during the austral spring and summer when logistical support is readily available. During the 2007-2008 International Polar Year, we analyzed genomic DNA samples using massively-parallel 454 tag sequencing to collect the first molecular data to characterize all three domains of life in two permanently ice-covered lakes in the MCM during the transition to the polar night. Duplicate samples were collected from two depths each in Lake Fryxell (FRX) and the West Lobe of Lake Bonney (WLB) once during November (summer) and once during March when almost no sunlight penetrated the water columns of the lakes. Evaluation of taxonomic diversity revealed bacterial communities dominated by members of the Actinobacteria and Bacteroidetes (65% – 75% relative abundance) with Shannon diversity that ranged from 3.07 to 4.03. Diversity was always higher during November relative to March. Members of either the Cryptophytes or Stramenopiles generally dominated the Eukaryal communities, and Eukaryal Shannon diversity (range 1.27 – 2.51) typically increased during March relative to November. The Archaea were dominated by Marine Group I Crenarchaeota, Marine Group II Euryarchaeota, and unknown Archaea. Shannon diversity of the Archaea ranged from 0.46 to 2.38 and was greater during March in FRX and during November in WLB. Seasonal shifts in microbial populations occurred at the OTU level (3% cutoff) in both lakes, indicating that community structures were impacted by the change in solar radiation. Bacterial communities clustered by lake and depth and secondary analysis of clustering via ANOVA showed that a combination of abiotic (photosynthetically active radiation, DOC, conductivity) and biotic (relative abundances of phototrophs and dinoflagellates) were significant in explaining the clustering. Our study is the first to show that community succession is an important aspect of the year-round ecology of the MCM lake ecosystems.