

ABSTRACT

Variations in Bacterial, Archaeal, and Eukaryal Communities during the Polar Night Transition in Lakes of the McMurdo Dry Valleys, Antarctica

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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, providing organic carbon to heterotrophic bacteria and archaea. Changes in microbial activity related to the onset of winter have been previously characterized, showing that heterotrophic bacterioplankton activity slows whereas phytoplankton may encyst or use mixotrophy to survive the polar night. Little is known about taxonomic shifts that might characterize microbial responses to the onset of winter in these lakes. In this study, we used massively-parallel 454 tag sequencing to characterize for the first time all three domains of life in the MCM lakes during the transition from 24-hour sunlight 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 (3% OTU cutoff) 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 (6% OTU cutoff), and Eukaryal Shannon diversity (range 1.27 – 2.51) typically increased during March relative to November. Marine Crenarchaeota and Euryarchaeota (Group I and Group II, respectively) dominated the Archaea (3% OTU cutoff). Shannon diversity ranged from 0.46 to 2.38 and was greater during March in FRX and during November in WLB. To determine whether microbial taxa co-varied over time, we calculated Pearson's correlations between all relative abundance (Bacteria and Archaea) and presence/absence (Eukarya) data across the sample points. Significant correlations (12.4%, $n = 1519896$) are indicative of similar response to seasonal stimuli. Bacteria accounted for 91.1% of significant correlations, while Archaea and Eukarya accounted for 3.1% and 5.8%, respectively. Grazers were some of the most commonly correlated eukaryotic taxa and their correlations with other groups tended to be negative. Network analysis will be used to reveal more specific interactions between members of the domains.