

## Study of the microbial diversity of a newly discovered East Antarctic freshwater lake, L27C, and of a perennially ice-covered Lake Untersee.

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The microbial communities that reside within freshwater lakes of Schirmacher and Untersee Oases in East Antarctica must cope with extreme conditions that may include cold temperature, annual freeze-thaw cycles, exposure to UV radiation, especially during the austral summer months, low light beneath thick ice-cover, followed by seasonal darkness. The objective of this study was to assess the microbial biodiversity and distribution from samples taken from two freshwater lakes (L27C and Lake Untersee) that were collected during the Tawani 2008 International Antarctic Expedition that conducted research in this region of Antarctica. L27C is a small, previously unreported lake residing 2 km WNW of Maitri Station at Schirmacher Oasis. Biodiversity and distribution of microorganisms within the lake were studied using both culture-independent and culture-dependent methodologies based upon the analysis of eubacterial 16S rRNA gene sequences. Lake Untersee, a perennially ice-covered, ultra-oligotrophic, lake in the Otto-von-Gruber-Gebirge (Gruber Mountains) of central Dronning Maud Land was also sampled and the microbial diversity was analyzed by eubacterial 16S rRNA gene sequences derived from pure cultures. Direct culturing of water samples from each lake on separate R2A growth medium exhibited a variety of microorganisms including: *Janthinobacterium*, *Hymenobacter*, *Sphingomonas*, *Subtercola*, *Deinococcus*, *Arthrobacter*, *Flavobacterium*, *Polaromonas*, *Rhodospirillum rubrum* and *Duganella*. The evaluation of samples from L27C through culture-independent methodology identified a rich microbial diversity consisting of six different phyla of bacteria. The culture-independent analysis also displayed the majority of bacteria (56%) belonged to the Class  $\gamma$ -proteobacteria within the phylum Proteobacteria. Within the Class  $\gamma$ -proteobacteria, *Acinetobacter* dominated (48%) the total microbial load. Overall, L27C exhibited 7 different phyla of bacteria and 20 different genera. Statistical analysis (Shannon-Weaver Diversity Index and Simpson Diversity Index) of the biodiversity of L27C displayed a moderately rich and diverse community. Investigations of the biodiversity and distribution of microorganisms in these lakes will help further our understanding of how the physical environment impact the structure and function within these microbially dominated ecosystems.