Molecular Analysis of Microbial Communities inhabiting Subglacial Lake Whillans, Antarctica

Amanda Achberger\textsuperscript{1}, Carlo Barbante\textsuperscript{2}, Andrew Mitchell\textsuperscript{3}, Alexander Michaud\textsuperscript{4}, Jill Mikucki\textsuperscript{5}, John Priscu\textsuperscript{4}, Mark Skidmore\textsuperscript{6}, Tristy Vick-Majors\textsuperscript{4}, and Brent Christner\textsuperscript{1}

\textsuperscript{1}Department of Biological Sciences, Louisiana State University, Baton Rouge, LA, 70803
\textsuperscript{2}Department of Environmental Sciences, University of Venice Ca'Foscari, Venice, Italy, 30123
\textsuperscript{3}Institute of Geography and Earth Sciences, Aberystwyth University, Aberystwyth, UK, SY23 3DB
\textsuperscript{4}Department of Land Resources and Environmental Science, Montana State University, Bozeman, Montana, US, 59717
\textsuperscript{5}Department of Microbiology, University of Tennessee, M409 Walters Life Sciences, Knoxville, Tennessee, US, 37996-0845
\textsuperscript{6}Department of Earth Science, Montana State University, Bozeman, Montana, US, 59717

A complex hydrologic system consisting of lakes, streams, and water saturated sediments exists beneath the Antarctic Ice Sheet. Although subglacial aquatic environments are hypothesized to harbor active microbial communities, direct sampling of these potential ecosystems has been lacking. During January 2013, the Whillans Ice Stream Subglacial Access Research Drilling (WISSARD) Project created a ~800 m borehole to access Subglacial Lake Whillans (SLW) and collected water and sediment samples. The biotic and abiotic particulates larger than 10, 3, and 0.2 µm were fractionated and concentrated \textit{in situ} on 142 mm filters using a custom filtration device that was lowered into the lake. In addition, the upper 40 cm of lake sediments were retrieved and sampled at 2 cm intervals. Nucleic acids were extracted from the samples and phylogenetic analysis based on the V4 region of the 16S rRNA gene was used to characterize the prokaryotic microbial community structure in SLW. The significance of the molecular data for deciphering ecosystem processes in SLW are discussed.

This research was supported by the National Science Foundation through grant ANT 0838941 and a Graduate Research Fellowship award to A.A.