Towards an effective method for microbial cell recovery and genomic analysis from ice cores

Alexander Michaud; Bigelow Laboratory for Ocean Sciences
Pamela Santibanez Avila; Universidad de Magallanes
Dominic Winski; University of Maine
Nathan Chellman; Desert Research Institute
Joe McConnell; Desert Research Institute

Ice cores contain stratigraphic records of microbial cells, buried through thousands of years of snow accumulation and spanning significant climatic periods. It is well established that microorganisms are transported to and preserved within the West Antarctic Ice Sheet. From the total assemblage of microorganisms that land on the ice sheet, we do not know how or if microorganisms survive burial and persist long-term in glacial ice equally. We cannot accurately interpret microbial cell stratigraphic records or utilize these cellular records as proxies until we understand post-depositional processes and the genomic adaptations of microbial cells in glacial ice. Here, we quantify cell concentrations in meltwater from four flow paths of a continuous flow analysis melter system in order to evaluate the efficacy of these flow paths for the successful collection of intact cells archived in ice cores. Using this information, we melted eight sections from the WAIS Divide ice core and quantified the cell concentrations, assayed the viability of the microbial cells, and sorted individual cells for genome sequencing. We will present preliminary data from the flow path cell recovery experiment, and genomic and viability results from the WAIS Divide ice core, with the hope to stimulate further discussion around single cell genomes and how they can be leveraged to complement paleoclimate information from ice cores.