



## **Microbial cells exported from Arctic glaciers: patterns and processes in structuring meltwater assemblages**

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Proglacial streams export large quantities of both supra- and subglacially-derived microbial cells, which have been suggested to play functional and nutritional roles in downstream, estuarine, and coastal habitats. Despite the widespread retreat of northern hemisphere glaciers, very little work has investigated possible environmental controls on the assemblage structure of glacial meltwater streams, and to date no studies have made broad comparisons between different regions of the Arctic. Here, we address two key questions: 1) are glacial meltwater microbial assemblages similar between major Arctic (and sub-Arctic) regions, and 2) can variability within these regions be explained by the physical and chemical characteristics of individual drainage basins?

We compared glacial meltwater assemblages from within six localities (the Greenland Ice Sheet, Disko Island, Iceland, Svalbard, Norway, and Southeast Alaska), differing in lithology, catchment size, and hydrometeorological characteristics, to investigate factors structuring meltwater microbial assemblages. Samples for microbiology and hydrochemistry were taken directly from meltwater streams near the glacier termini. In the laboratory, nucleic acids were extracted from microbiological samples and sequenced for the 16S rRNA gene with Illumina MiSeq. Resulting sequences were quality checked, assigned to OTUs, and analyzed using multivariate methods.

We found all glacial meltwater samples were dominated by Proteobacteria, Bacteroidetes, and Actinobacteria, with Firmicutes and Verrucomicrobia also common in a few localities. Meltwater assemblages prominently clustered geographically, reflecting that regional taxonomic pools and environmental conditions are likely influential in determining assemblage structure. Preliminary analyses further suggest that differences within localities (e.g. Disko Island) may be at least partially explained by individual glacier hydrochemical characteristics (e.g. water chemistry, glacier size, and associated hydrological flowpaths), with greater suspended sediment and dissolved ion concentrations associated with greater proportions of cells originating from the subglacial environment in comparison to supraglacial habitats. The results of our work aid our understanding of how proglacial stream microbial assemblages are structured, and additionally help predict how linkages between glacier microbes and downstream microbial ecosystems may evolve during this current period of climatic warming and increasing glacier melt and recession.