Geophysical Research Abstracts Vol. 20, EGU2018-3504, 2018 EGU General Assembly 2018 © Author(s) 2018. CC Attribution 4.0 license.



## Characterizig microbial communities in a rapidly changing, glacially dominated high Arctic watershed

Maria Cavaco (1), Vincent St.Louis (1), Katja Engel (2), Kyra St.Pierre (1), Marek Stibal (3), and Josh D. Neufeld (2)

- (1) Department of Biological Sciences, Faculty of Science, University of Alberta, Edmonton, Canada (cavaco@ualberta.ca),
- (2) Department of Biology, Faculty of Science, University of Waterloo, Waterloo, Canada, (3) Department of Ecology, Faculty of Science, Charles University, Prague, Czechia

Arctic glacial watersheds are being altered by climate change, with current climate models predicting increases in temperature and precipitation in the high Arctic of up to 8.3°C and 40%, respectively, by 2100. These changes will have profound impacts on the Arctic hydrological cycle, including enhanced glacial melt. Current research has identified corresponding changes to the physicochemical parameters of downstream freshwater systems, including changes in fluxes of bioavailable nutrients, pollutants, and turbidity. Alterations to downstream freshwater systems are hypothesized to affect resident aquatic microbial communities, with far reaching and unknown consequences for Arctic biogeochemical cycles and ecosystem services. To address these concerns, we investigated microbial communities and associated physicochemical parameters in the glacially dominated Lake Hazen watershed on Northern Ellesmere Island (81° N; 71° W), used here as a sentinel system for environmental change. We sampled from numerous glacier-fed water bodies over a spring and summer season. Collected water samples were analysed for a suite of physicochemical parameters (e.g., temperature, greenhouse gas content, pH) in parallel with highthroughput 16S rRNA gene data targeting bacteria and archaea. Ordination analysis revealed that samples grouped according to site, with the Lake Hazen microbial community sharing highest overall similarity with major glacialsource rivers. Operational taxonomic units associated with Polaromonas, Rhodoferax, and Flavobacterium genera dominated most waterbodies of this watershed, similar to the findings of other high Arctic freshwater studies. Glacial rivers changed seasonally in response to chemical parameters, such as turbidity and temperature. These data help establish a baseline understanding of the microbial communities from Arctic glacial watersheds so that future research can monitor how the quality of Arctic ecosystems and the services they provide may be changing temporally.