## Prokaryotic communities in subglacial outflows in the Alaska Range

Jun Uetake<sup>1</sup>, Tomoaki Morishita<sup>2</sup>, Go Iwahana<sup>3</sup>, Tetsuo Sueyoshi<sup>4</sup>, Keiko Konya<sup>4</sup>

<sup>1</sup> Field Science Center for Northern Hemispherer, Hokkaido University,

<sup>2</sup>Forestry and Forest Products Research Institute

<sup>3</sup>IARC, University of Alaska Fairbanks

<sup>4</sup>Japan Agency for Marine-Earth Science and Technology

It is widely recognized that the cold and oligotrophic supraglacial (glacier surface) area is habitat for microorganisms. However, the microbial communities in subglacial (glacier bottom) area, particularly chemosynthetic autotrophic bacteria capable of synthesizing organic compounds without relying on sunlight, are less understood. In the glaciers in Alaska Range, methane was detected near the glacier terminus, however subglacial microbial communities including methanogenic archaea producing methane, have not been detected yet. Therefore, as part of The Arctic Challenge for Sustainability II (ArCS II) project, we conducted investigations of prokaryotic communities in subglacial meltwater from glaciers in the Alaska Range to show, 1) the difference between subglacial and supraglacial prokaryotic communities, 2) the conditions at the subglacial environment, 3) the possibility of presence of methanogenic archaea.

From June to July 2022, we collected subglacial outflow samples from three glaciers in the Alaska Range (Gulkana Glacier, Canwell Glacier, Castner Glacier) and one near the Chugach Mountains (Matanuska Glacier). Samples were frozen on-site and transported to the laboratory, where those were stored at -60°C until processing. After thawing, approximately 500 mL of each frozen sample was filtered through sterile glass fiber filters, and DNA was extracted using DNA extraction kit. PCR amplification was performed using 16S rRNA gene primers (515F-926R), followed by DNA sequencing. The resulting sequences were grouped into Amplicon Sequence Variants (ASVs) using the R package DADA2, and diversity analysis and visualization were conducted using phyloseq and microViz.

ASVs detected in subglacial outflow and supraglacial samples were mostly specific to their respective environments (Figure 1). However, some ASVs were detected in both environments, indicating the potential flow of microorganisms from the surface to bottom. Bacteria belonging to the *Desulfobulbales* order, which are anaerobic sulfate-reducing bacteria, were more abundant in samples from Castner Glacier, where methane emissions were confirmed. This suggests the presence of anaerobic conditions at the subglacial area and implies the existence of an environment conducive to the proliferation of methanogenic archaea.

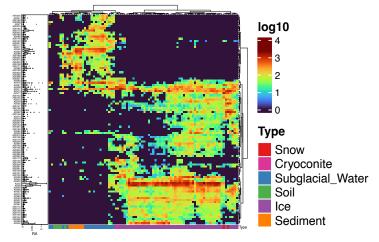


Figure 1. Log transformed abundance of ASVs detected from each environmental type

## References

KONYA, K., IWAHANA, G., SUEYOSHI, T., MORISHITA, T., & ABE, T. Methane flux around the Gulkana Glacier terminus, Alaska summer 2019. *Polar Data Journal*, *6*, 32–42, 2022.