# The DNA of Cambridge Bay: An analysis of the microbial community within the permafrost layer of Cambridge Bay, Nunavut

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## Introduction

- Permafrost is a permanently frozen layer below the Earth's surface, composed of soil, gravel and sand contained in ice.
- Globally, permafrost environments account for the storage of 1672 petagrams (1672 billion metric tons) of carbon.
- As the permafrost continues to thaw microbial processes will begin to liberate stored carbon as $CO_2$ and $CH_4$.
- Currently, no research has been conducted into the composition of the permafrost microbiome of Cambridge Bay
- An environmental DNA sequencing and bioinformatics approach was taken to describe the microbial community composition in the permafrost of Cambridge Bay and generate a genetic database containing this information
- This data will provide baseline information on microbial community characteristics in these soils that will inform future research evaluating the effects on the microbiome as temperatures continue to rise.

Figure 1. Permafrost core collection near the Canadian High Arctic Research Station in Cambridge Bay.

## Results

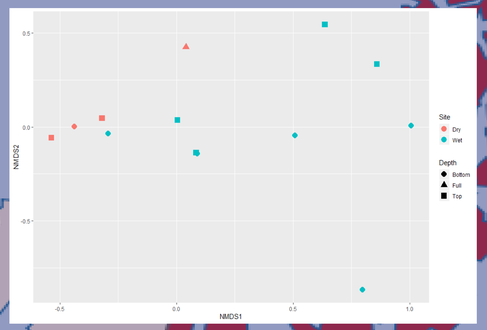


Figure 2. Non-metric multidimensional scaling plot based on Bray-Curtis dissimilarity in community composition between samples at the species level (97% sequence similarity).

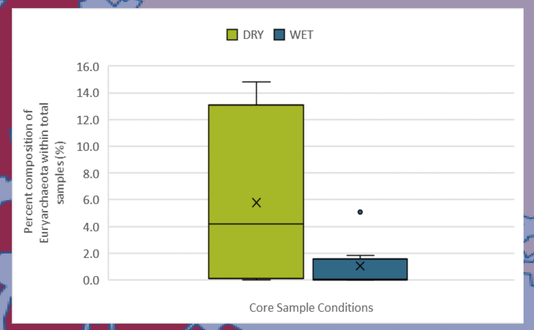


Figure 3. Percentage of Euryarchaeota within total sample composition at wet and dry sites.

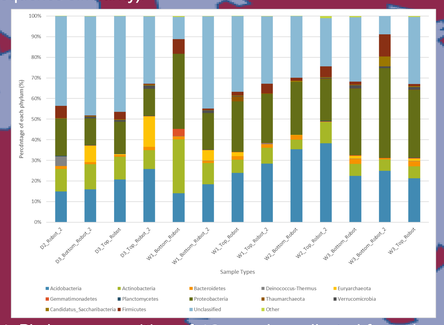


Figure 4. Phylum composition of 13 samples collected from dry and wet sites.

- Figure 2 suggests unique microbial communities within wet and dry sampling sites, indicating that permafrost communities may vary spatially and in response to environmental conditions. The depth of the sample had little impact on the microbes found within the sample.
- There was no significant difference between the wet and dry sites in terms of methanogen (Euryarchaeota) abundance ($t(3)=1.34$, $p>0.05$), despite a wider range in abundance at the dry site shown in Figure 3. This implies that both sites have the potential to be methane sources during periods of thaw if anaerobic conditions arise.
- Figure 4 shows the phylum diversity within the samples. The most prominent phyla were Acidobacteria, Proteobacteria and Actinobacteria. Though these 3 phyla are commonly found in soils, the relative abundance of each may change drastically depending on the environmental conditions that arise post thaw.

## Conclusion

Through this work the microbial community composition in the permafrost of Cambridge Bay was described and a genetic database was created. The methanogenic capabilities of the microbiome were also outlined including a comparison between the wet and dry sites.

This will support future work by providing characteristics of the microbial community within Cambridge Bay, to act as a baseline when evaluating the effects of permafrost thaw on the microbiome as temperatures continue to rise.

## Methods

- Three permafrost cores were collected at two sites from Cambridge Bay, Nunavut; a low-lying coastal site designated "Wet" and a site 200 metres up-slope designated "Dry".
- Cores were processed to remove contaminating non-permafrost material and split into top and bottom sections if the core was >15 cm.
- DNA was extracted from the cores (0.7-0.9 g) using the DNeasy Powersoil kit.
- Two rounds of PCR were used to amplify the 16s rRNA gene and generate libraries for DNA sequencing. Gel electrophoresis was used to confirm the success of PCR steps.
- Template preparation and loading onto an Ion 530 sequencing chip was done with an Ion Chef using an Ion 510 & Ion 520 & Ion 530 Kit-Chef.
- Sequencing was performed on an Ion S5; demultiplexing and read trimming was performed in Torrent Suite 5.10.

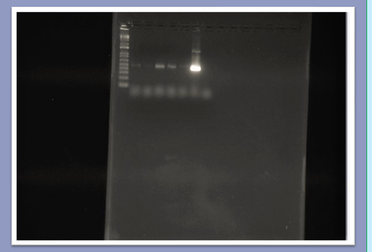

Figure 5. 1.5% agarose gel run at 70V for 30 min to confirm results of second round PCR amplification of 16s rRNA gene amplicons. From left to right: ladder (100 bp), W3_B, D1, D2, D3_T, D3_B, (+), (-)

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