Microbial Methane Cycling in Mackenzie Delta Lakes: Comparing Microbial Community Diversity and Activity with Environmental Parameters

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**Background**: Methane, a potent greenhouse gas, is also a substantial source of carbon and energy for ecosystems within Arctic lakes. Complex communities of microbes in the water column and sediment of these lakes play a vital role in the production and consumption of methane, and ultimately influence the net amount of methane that’s released to the atmosphere or cycled through local food webs. Canada’s Western Arctic contains many large and complex lake systems, but research on methane dynamics and microbial communities in the region has been limited. The Mackenzie River Delta floodplain is extremely productive relative to the surrounding tundra landscape, and makes substantial contributions to the global methane budget, especially in the spring when rapid ice break-up causes methane, accumulated under the ice throughout the winter in the Delta’s ~45,000+ lakes, to suddenly escape to the atmosphere (see Figure 1, inset). This project characterizes the structure and activity of methane- and carbon-cycling microbial communities in Mackenzie Delta lakes. This was done by:

1. Analyzing microbial community structure via sequencing of the 16S rRNA gene from lake water DNA samples collected from multiple lakes across the ice cover to ice free season
2. Incubation experiments of lake water with stimulants and inhibitors of methane cycling processes

**Initial results** show that seasonal shifts in lake biogeochemistry – such as dissolved methane and oxygen concentrations, trace metals, temperature, pH, and carbon quality – correspond to shifts in overall microbial community structure (Figure 2); that the main methane- and methyl-cycling microbial groups shift as a function of season, independent of lake origin (Figure 3); that lake waters have microbial communities capable of methane oxidation and production under bulk oxic conditions but are net methanotrophic in the summer (Figure 4); and that the microbial community structure does not change appreciably when exposed to methane-cycling stimulants or inhibitors over a period of 48 hours (Figure 5).

**Study System and Project Design**

![Map of Mackenzie River Delta](Image)

The Mackenzie River Delta in Canada’s Northwest Territories, hereafter referred to as the Delta, is the largest river system in Canada, and the second largest floodplain delta in the circumpolar Arctic region. The Delta floodplain contains over 45,000 lakes, mostly small and shallow, which are incredibly productive compared to the surrounding tundra landscape, and makes substantial contributions to the global methane budget. The Mackenzie River floodplain is extremely productive relative to the surrounding tundra landscape, and makes substantial contributions to the global methane budget, especially in the spring when rapid ice break-up causes methane, accumulated under the ice throughout the winter in the Delta’s ~45,000+ lakes, to suddenly escape to the atmosphere (see Figure 1, inset). This project characterizes the structure and activity of methane- and carbon-cycling microbial communities in Mackenzie Delta lakes. This was done by:

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**Experimental Enrichment of Nutrients and Methanogenesis Inhibition**

Incubation experiments were performed on water from three lakes with differing river-to-lake connection times, biogeochemical properties and carbon quality endpoints. Incubations with various treatments (methanogenesis inhibitor bromo-ethanesulfan (BES), nutrient spike, and combination) were applied to determine methane oxidation (MOX) rates under varying conditions, and Isabel the individual effects of methane oxidation and methanogenesis in the water column.

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