

## Linking Arctic Lake Sediment Microbial Ecology to Carbon Biogeochemistry

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**Project Goals:** Our objective is to discover how microbial communities mediate the fate of carbon in thawing permafrost landscapes under climate change. We are engaged in a systems approach integrating (a) molecular microbial and viral ecology, (b) molecular organic chemistry and stable and radiocarbon isotopes, and (c) state-of-the-art modeling, along an interconnected chronosequence of permafrost thaw and post-glacial lakes in subarctic Sweden.

**Abstract:** Thawing permafrost peatlands are likely to provide a positive feedback to climate change via methane and carbon dioxide emissions. In particular, Arctic post-glacial lakes in these landscapes have been identified as a significant source of methane to the atmosphere, largely through ebullition (bubbling) of microbially produced methane from the sediments. Lakes and ponds are estimated to contribute approximately two-thirds of total natural methane emissions above 50° N latitude, and post-glacial lakes (formed by glacially carved microtopography) cover more than four times the aerial extent of more intensively-studied thermokarst lakes (*i.e.*, those associated with the physical collapse of Arctic ground as it thaws). Both the production and oxidation of methane are under microbial control in lakes, yet the microbiota of Arctic post-glacial lake sediments have not been examined. Here we combined microbial (metagenomic and amplicon), isotopic, and geochemical characterizations across four sediment cores from two post-glacial lakes to identify key microbes contributing to carbon loss. Aerobic and anaerobic methane oxidation, methylotrophy, and methanogenesis were identified as controls on methane loss and correlated with shifts in sediment carbon geochemistry. Reconstructed population genomes revealed the capacity for carbon transformations differing from previous lineage-specific metabolic predictions, including methylotrophy in Candidate Phylum Aminicenantes and fermentation without the capacity for methanogenesis in the Methanomassiliicoccaceae. Collectively, results support the potential for significant microbial controls on carbon cycling in post-glacial Arctic lakes and reveal unexpected roles for abundant microbial lineages in key carbon transformations.

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