

Understanding the microbial controls on biogeochemical cycles in permafrost ecosystems

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Project Goals: Permafrost soils are one of the world's largest terrestrial carbon stores. The permafrost carbon reservoirs are currently protected from microbial decomposition by frozen conditions. Organic carbon becomes more available for mineralization by microorganisms as permafrost thaws. Microbial metabolism leads to decomposition of soil organic matter, substantially impacting the cycling of nutrients and significantly affecting the arctic landscape. This project use state of the art molecular techniques to resolve complex microbial processes governing the biogeochemical cycles in arctic soils and permafrost to better inform efforts to access uncertainties surrounding ecosystem responses.

Permafrost soils contain a broad diversity of cold-adapted microbes, whose metabolic activity depends on environmental factors such as temperature changes that cause cycles of freezing and thawing in the soil. Permafrost microbial communities are complex, diverse, and active at subzero temperatures. While carbon turnover at depth is proposed to be slower than surface, especially the fate of carbon in deep permafrost, which is currently protected from the warming climate, is uncertain. Permafrost microbiome is a seed bank of mostly novel organisms that have a diverse and broad metabolic potential. In-depth functional characterization of the permafrost microbes is needed to provide a foundation for understanding their responses to thaw. In order to address this gap in our knowledge we performed a pan-Arctic comparative analysis of permafrost metagenomes in which we study biogeography and metabolic functions of permafrost metagenomes assembled genomes (MAGs). This meta-analysis of permafrost MAGs across multiple locations in the Arctic (Alaska, Sweden, Norway, Canada and Russia) quantifies the impact of environmental drivers including but not limited to ice content, topography, continuity, active layer depth, and vegetation on permafrost microbiomes. The microbial communities inhabiting these soils have some common members and metabolic capacity, including the prominence of *Actinobacteria* and dominant functions such as fermentation and stress response. We also observe stark differences in which Eukaryotic and viral populations are represented and in the abundance and biochemistry of methanogens. These results improve our understanding of global variation in permafrost microbiomes. Recognizing geospatial patterns in soil properties and microbiome characteristics across Arctic permafrost landscapes will allow us to better inform on how permafrost microbes can respond to global climate change.

The microbial response to thaw in arctic environments is not uniform and the relationship between permafrost microbiomes and greenhouse gas (GHG) emissions is not well understood. Following

thaw, redistribution of water is a key event that conditions the permafrost for microbial decomposition. While inundation can give rise to low redox conditions and support anaerobic processes, drainage can promote aerobic respiration. Recent metagenomic studies conducted under different thaw scenarios suggest a capacity for utilization of many terminal electron acceptors (TEAs) across intact and thawed permafrost soils. These processes are likely to be active during thaw, although the impact of redox potential and the chemical form of TEAs on GHG emissions after permafrost thaw are not well understood. We initiated batch-scale permafrost incubation experiments dry, natural, and saturated moisture states and under microaerophilic or anaerobic headspaces. Our initial findings following microbial responses to permafrost thaw in short-term (i.e. seasonal) via metagenomics and metatranscriptomics show dominance of fermentation and competition between iron and sulfate reduction processes, highlighting the importance of interactions between iron, sulfur and carbon metabolism. We couple these small-scale manipulation experiments with 1-D controlled thaw and re-freeze soil column experiments. This experimental set-up preserve soil structure during thaw while enabling real time monitoring of GHG fluxes, soil pore water chemistry and microbial communities. After a simulation of thaw and re-freeze event over the whole soil column we analyzed the changes in microbial communities and in soil chemistry via synchrotron fourier transform infrared (sFTIR) spectral imaging at the Berkeley Infrared Structural Biology beamline of the Advanced Light Source (LBNL). Analysis showed that different organic compounds and metabolites were accumulated in post-thaw/refreeze seasonally active top soils (active layer) and permafrost soils. While carbohydrates were enriched in the active layer, permafrost layers showed an accumulation of aliphatic compounds and depletion in carbohydrates.

This project use field observations, laboratory manipulations, and multi-omics approaches to examine how microbial processes, biogeochemical transformations, and hydrology interact during permafrost thaw in different sites in Alaska in order to determine how these factors drive biogeochemical cycles in different arctic soils.

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