

## **Microbial controls on biogeochemical cycles in permafrost ecosystems**

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**Project Goals: The permafrost carbon reservoirs are currently protected from microbial decomposition by frozen conditions. Upon permafrost thaw 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 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 pan-Arctic analysis of permafrost MAGs across multiple locations (Alaska, Sweden, Norway, Canada and Russia) showed stark differences in microbial populations and metabolic functions that are not strong driven by environmental conditions (ice content, topography, continuity, active layer depth, and vegetation) or soil chemistry. 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. We initiated batch-scale permafrost incubation experiments dry, natural, and saturated moisture states and under microaerophilic or anaerobic headspaces. Via metagenomics and metatranscriptomics we dissect the microbial response leading to fermentation and competition between methanogenesis and iron and/or sulfate reduction processes, highlighting the importance of interactions between iron, sulfur and carbon metabolism. We couple omics methods

with analysis of 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 variety of organic compounds and metabolites were accumulated in thawed permafrost soils. Especially under saturated conditions while carbohydrates were depleted, soils accumulated aliphatic compounds.

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.

*This research is supported by DOE Early Career Program by the Office of Biological and Environmental Research in the DOE Office of Science.*