

Title: Understanding the microbial controls on biogeochemical cycles in permafrost ecosystems

Neslihan Taş^{1*}, Megan Dillon¹, Yaoming Li¹, Craig Ulrich¹, Yuxin Wu¹, Mary-Cathrine Leewis², Mark Waldrop², Susannah Sliebner³, Christopher Chabot⁴, Rachel Mackelprang⁴ and Hoi-Ying Holman¹

¹Lawrence Berkeley National Laboratory, ²The United States Geological Survey, ³GFZ German Research Centre for Geosciences Postdam, ⁴California State University Northridge

Contact: ntas@lbl.gov

Project Lead Principal Investigator (PI): Neslihan Taş

BER Program: Genomic Science

Project: Early Career Research Project

Project Abstract:

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 are one of the world's largest terrestrial carbon storages thus an important focal point for climate change research. With increasing global temperatures, permafrost carbon stores may become available for rapid microbial mineralization and result in increased greenhouse gas (GHG) emissions. Upon permafrost thaw microbial metabolism leads to decomposition of soil organic matter, substantially impacting the cycling of nutrients and significantly affecting the arctic landscape. 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 showed weak correlations to environmental conditions (ice content, topography, continuity, active layer depth, and vegetation) or soil chemistry.

The microbial response to thaw in arctic environments is not uniform and the relationship between permafrost microbiomes and GHG emissions is not well understood. Especially the fate of carbon in deep permafrost, which is currently protected from the warming climate, is uncertain. Following thaw, redistribution of water is a key event that conditions the permafrost for microbial decomposition. We tested the impact of soil moisture availability under microaerophilic and anaerobic conditions via small scale batch experiment. We couple omics (metagenomics and metatranscriptomics) 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). Upon thaw variety of organic compounds and metabolites were accumulated. For example, under saturated high-moisture conditions carbohydrates were depleted and soils accumulated aliphatic compounds. This microbial response was tied to the competition between methanogenesis and iron and/or sulfate reduction processes. 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.