

Poster #18

Deep Look into Deep Permafrost: Impact of Warming on Microbial Functions

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BER Program: TES

Project: Ngee Arctic

Project Website: <http://ngee-arctic.ornl.gov/>

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. Especially the fate of carbon in deep permafrost, which is currently protected from the warming climate, is uncertain. In this project, we applied metagenomics and metatranscriptomics to determine the phylogenetic and functional changes in the deep permafrost microbiome from polygonal arctic tundra at the Barrow Environmental Observatory (BEO). We collected permafrost cores ranging from 0.5-3m in depth and analyzed over 200 samples along a transect containing high-, flat- and low-centered polygons in order to determine microbial responses to thaw. BEO permafrost layers were mainly populated with Actinobacteria. Besides depth, pH and changes in the material density were important drivers of microbial community structure. Metagenomes from different permafrost depths also showed elevated potential for CH₄ production in deeper layers while CH₄ production and oxidation potential was detected in near surface permafrost. Moreover deep permafrost layers were also populated by chemolithoautotrophic Alphaproteobacteria. We hypothesize that nutrients and available carbon in these layers are tightly regulated and recycled where permafrost increasingly becomes a CH₄ source with depth. Metagenomics coupled with reconstruction of microbial genomes, detailed measurements of geochemistry and microbial processes aids us in understanding the biogeochemical cycles in Arctic soils and permafrost, and in the future will better inform efforts to resolve uncertainties surrounding ecosystem responses.