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Metagenomic Insights into Microbial Communities and Functions across Arctic Polygonal Grounds

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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. In this project, we applied metagenomics to determine the phylogenetic and functional composition of the soil microbiome from polygonal arctic tundra at the Barrow Environmental Observatory (BEO) in relation to the landscape micro-topography and measured GHG emissions. We collected over 200 active layer and permafrost samples along a transect containing high-, flat- and low-centered polygons for three consecutive years. We found a strong correlation between in-situ GHG fluxes and dominant microbial processes. While polygon type was the primary driver of microbial community composition and distribution of metabolic potential, active layer soil and permafrost microbes shared many metabolic functions that are involved in degradation of complex organic carbon compounds. Yet, not all the key metabolic pathways leading to GHG emissions were found across the BEO. For example CH₄ production and iron reduction processes were constrained to wetter low-centered polygons. By contrast, CH₄ oxidation and CO₂ production potential were more prevalent in the drier high- and flat-centered polygons. CH₄ producing and oxidizing Archaea and chemolithoautotrophic bacteria were detected within the same permafrost layers. We hypothesize that nutrients and available carbon in these layers are tightly regulated and recycled. 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.