Metagenomics and microbial community profiling across polygon features at the Next Generation Ecosystem Experiment (NGEE)-Arctic Barrow site

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Permafrost soils are one of the world’s largest terrestrial carbon storages. With increasing global temperatures, thawing permafrost is altering Arctic landscapes and becoming a potential source of greenhouse gas (GHG) emissions. As part of the DOE’s NGEE-Arctic project, we focused to resolve the microbial potential and mechanisms leading to GHG emissions at the Barrow Environmental Observatory (BEO). We collected seasonally thawed active layer soil samples along a transect containing high-, flat- and low-centered polygons for three consecutive years. Additionally, five deep cores -up to 3 m- were taken from flat- and low-centered polygons in the same transect. The microbial community compositions along the active layer (horizontal transect) and in the deep cores (vertical transect) were determined by sequencing of 16SrRNA genes and metagenomes. The sequence data was correlated to in-situ GHG flux measurements, geophysical and geochemical soil characteristics. Differences in elevation, polygon futures, soil horizon and moisture content were identified as the main drivers of the microbial community composition differences along the horizontal transect. Especially in flat-centered polygons differences in carbon and nitrogen contents of soil horizons strongly correlated with changes in community composition. Different polygon types shared a large metabolic potential however not all the key metabolic pathways leading to GHG emissions were found across the BEO. For example CH4 production potential was only found in low-centered polygons and extended to permafrost layers. By contrast, CH4 oxidation and CO2 production potential were more prevalent in the high- and flat-centered polygons. Additionally, the metagenome sequence data revealed that capacity for assimilatory nitrate reduction was enriched compared to denitrification and N2O production. The sequencing approach also revealed dramatic shifts in microbial community composition with depth in the deep cores. While active layers were populated with sequences corresponding to Verrucomicrobia (potential methanotrophs) and Acidobacteria, Actinobacteria were more abundant in the mid- and deeper layers. We further investigated permafrost layers have high salt content; since these layers have a potential to contain liquid water and sustain microbial activity below freezing conditions. 16SrRNA gene sequencing revealed anaerobic CH4-producing and -oxidizing Archaea as well as chemolithoautotrophic ammonia-oxidizers within the same permafrost layers, suggesting that nutrients in these layers are tightly regulated and recycled. The long-term goal is to use information gleaned from omics datasets to better inform models that will aid in understanding of the biogeochemical cycles in this complex and fragile ecosystem and how they are perturbed by climate change.