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ABSTRACT TITLE: Microbial ecology across polygon features at the NGEE-Arctic Barrow site

ABSTRACT: Arctic soils contain an estimated 12-42% of terrestrial carbon, most of which is sequestered in permafrost. As the permafrost thaws due to global warming, the trapped carbon can potentially be degraded by microbial activity resulting in greenhouse gas (GHG) emissions. On the Alaskan North Slope the collapse and rise of soil due to formation of ice wedges and permafrost thaw create distinct features called polygons. As part of the DOE Next Generation Ecosystem Experiment (NGEE) in the Arctic, we aimed to determine the horizontal and vertical distribution of microbial populations in the polygon features and to determine the potential for GHG emissions due to microbial processes. To determine the horizontal microbial distribution we collected seasonally thawed active layer soil samples along a 500 m transect of polygons (Barrow site 0), including high-centered, transitional and low-centered polygons. In addition, two deep cores (1 m and 3 m depth) were taken from a transitional polygon in the same transect. Prior to sectioning, the cores were CT-scanned to determine the physical heterogeneity throughout the cores. The microbial community compositions along the horizontal transect and in the deep cores were determined by high throughput and deep sequencing of 16S rRNA genes and metagenomes. The sequence data was correlated to GHG flux measurements, geophysical and geochemical soil characteristics. The microbial community composition varied both horizontally and vertically along the polygon transects. Differences in elevation and moisture content were identified as the main drivers of the observed changes. Both the genes for methanogenesis and CH_4-flux measurements were higher in low-centered, wetter polygons compared to high-centered, drier polygons. By contrast, CO_2 production was more prevalent on the ridges of the polygons and in the high-centered polygons. The metagenome sequence data also revealed that the pathway for utilization of nitrate as a nitrogen source was present in the polygon features, but not the complete pathway for denitrification; suggesting that N_2O production capacity was limited. There were also dramatic shifts in community with depth based on profiles obtained from the deep 1m and 3m cores. In the upper layers there were sequences corresponding to Verrucomicrobia (potential methanotrophs) and Acidobacteria. Actinobacteria were more abundant in the mid layers, whereas sequences corresponding to methanogens were abundant in the deeper permafrost layers. To date we have obtained 12 novel isolates from deep layers of the 1 m core, including isolates belonging to fermentative *Clostridia*, *Sporosarcina* spp. and iron reducing *Rhodoferax* spp. as well as several methanogens that grew and produced methane at 2°C. The isolate genomes are currently slated for sequencing at JGI.