Horizontal And Vertical Profiling Of Microbial Communities Across Landscape Features At NGEE Site, Barrow, AK

Janet K Jansson[1, 2], Neslihan Tas[1], Eoin L. Brodie[1], David E Graham[3], Timothy J Kneafsey[1], Margaret S Torn[1], Yuxin Wu[1], Stan D Wullschleger[3], Susan S. Hubbard[1]

1. LBNL, Berkeley, CA, United States.
2. JGI, Walnut Creek, CA, United States.
3. ORNL, Oak Ridge, TN, United States.

Low- and high-centered polygons in permafrost-dominated ecosystems have distinct geochemical and hydrological characteristics that are expected to alter microbial processes that govern carbon cycle dynamics in Arctic landscapes. Key questions that must be answered if we are to represent these dynamics and their underlying controls into Earth System Models include: 1) Through which pathways is carbon processed in different areas of these polygons? 2) What regulates the release of C as CO2, or methane, and 3) Which microorganisms are responsible? As part of the Next-Generation Ecosystem Experiments (NGEE Arctic) project, we collected samples across a transect of polygon features near Barrow, Alaska. The transect included samples from centers, edges and troughs of high-centered and low-centered polygons, including organic and deeper mineral soil layers. In addition, we took a 1.6 m deep core from our field site and sectioned it vertically to determine the microbial composition at different depths from active layer through upper layers of permafrost. Prior to sectioning, the core was CT-scanned to determine the physical heterogeneity throughout the core. Total DNA was extracted from sub-samples and the microbial community composition in the samples was determined by sequencing of 16S rRNA genes. The resulting microbial profiles were related to corresponding environmental variables. We found that microbial community composition varied according to location across the polygons. Differences in elevation and moisture content were identified as the primary drivers of the observed changes in microbial composition. Methanogenic archaea were more abundant in the centers of low-centered and wetter polygons than high-centered polygons. These data suggest a potential for increased methane production towards the centers of polygons. By contrast, polygon edges had a greater relative abundance of typically aerobic soil microbes that suggests C loss as CO2 would predominate in these environments. A majority of the sequences found could not be reliably classified. Therefore, a current goal is to isolate novel representative organisms from these communities. In addition, we are sequencing the total metagenomic DNA to obtain information about the functional gene composition across the polygon transects. This information will be valuable for prediction of microbial responses to changes in environmental conditions including temperature, moisture, and resource stoichiometry. The long-term goal is to use this information to parameterize or constrain trait-based models of soil biogeochemistry to improve predictions of C flux in thawing permafrost. http://esd.lbl.gov/about/staff/janetjansson/