Title: Arctic Microbial Permafrost Degradation

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Project Goals:
Permafrost is one of Earth's largest reservoirs of soil organic carbon (SOC). As permafrost thaws, heterotrophic microbial communities degrade the newly-available SOC, often resulting in large and variable fluxes of the greenhouse gases CO_2, CH_4, and possibly N_2O to the atmosphere. Our project will address some questions fundamental to understanding how permafrost thaw affects greenhouse gas emissions. What are the relative contributions of CO_2-consuming vs. net-CO_2-producing processes in thawing permafrost? As SOC degrades, what are the relative production or consumption rates of CO_2, CH_4, and N_2O, which metabolic pathways and microbes drive SOC degradation in thawing permafrost, how are the metabolic pathways affected by SOC composition, and how much of the SOC is degraded? We will address these questions with intact core incubations from Bayelva, Svalbard. This site of continuous permafrost has been warming and thaw depth has increased from ~1 m to ~2 m over the last 20 years.

To determine how permafrost thaw impacts SOC-degrading microbial communities in intact core incubations, we will collect two long cores that go through the current permafrost layer, subsample one of them for DNA and geochemical analyses while in Ny Ålesund, and send the other in coolers to Potsdam, Germany. We will collect nine 2 m cores for transport to Princeton, NJ, where we will monitor pore gas composition and surface fluxes, pore water chemistry and isotopic compositions of dissolved inorganic carbon, dissolved organic carbon, CO_2, CH_4, and N_2O. We will take subsamples for meta-omic analyses at times zero, 1 week after permafrost thaw, after core slumping, and after 12 and 18 months, from four depths in the cores in order to obtain high-resolution molecular information about the microbial functional activities and temporal changes.

Funding from US Department of Energy, Office of Biological and Environmental Research (DE-SC0020369).