Something Old, Something New: Systems-Level Insights into Plant-Microbial-Permafrost Carbon Dynamics by Parallel High-Resolution Organic Matter and Microbial Meta-Omics

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Abstract: A fundamental challenge of modern environmental science is to understand how earth systems will respond to climate change. A parallel challenge in biology is to understand how information encoded in organismal genes manifests as biogeochemical processes at ecosystem-to-global scales. These grand challenges intersect in the need to understand the global carbon (C) cycle, which is both mediated by biological processes and a key driver of climate through the greenhouse gases carbon dioxide (CO2) and methane (CH4). A key aspect of these challenges is the C cycle implications of the predicted dramatic shrinkage in northern permafrost in the coming century. Large releases of C from thawing permafrost to the atmosphere are plausible, and a strong potential positive feedback to global warming, but little is known about the controls on such release. What is the interplay of this permafrost "old" C with "new" extant plant-derived C, specifically how do microbial communities interact with these chemical structures in the decomposition/preservation of organic C across a thaw gradient? This proposed work linking microbial dynamics, organic geochemistry and trace gas production will improve models of C cycling in thawing permafrost systems, and clarify the fate of C under future climates.

Recent technical advances at EMSL in high-resolution characterization of organic matter chemistry, and high-throughput proteomic analysis, now permit a uniquely detailed combined approach that will reveal biogeochemical consequences of microbial community dynamics. Complementary microbial metagenome sequencing at the Joint Genome Institute, targeted to increase recovery of current population genomes, will greatly strengthen the population-specific analytical inferences for which microbial groups are actively performing which C transformations. Together, these efforts will improve our understanding of the fate of Arctic and Subarctic C on a changing planet. In this study, we focus on a well-instrumented and highly-studied "model ecosystem" of permafrost thaw and C mobilization, spanning a natural thaw chronosequence. We will characterize in parallel (1) the detailed changes in input C and soil and pore water C chemical structure as it is metabolized and mobilized post-thaw, (2) the microbial community expression that mediates these C transformations and release to the atmosphere and (3) the metagenomes and metatranscriptomes of the peat microbial communities that regulate C flux in permafrost peatlands. This approach will address key outstanding questions about the pathways for C loss under permafrost thaw: how are microbial interactions with plant C and thawing permafrost C determining the loss of these two C pools as C gas emissions? How are microbial community systems interacting with these C substrates to control the ratio of CH4 to CO2 released, a key parameter in simulations of CH4 biogeochemistry used to estimate global emissions? Which are the key microbial lineages performing C transformations in these systems?