

Decoding DOM Degradation: How Does Carbon Source and Sunlight Exposure Alter Microbial Metabolism and Expression of Genome-Encoded Metabolic Degradation of Permafrost Organic Matter?

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Abstract: Climate change in the Arctic is progressing rapidly, thawing large areas of permafrost that contain nearly half of the world's soil organic carbon. Conversion of this carbon pool to greenhouse gases has the potential to double the amount of CO₂ in the atmosphere on a timescale similar to human inputs. Once thawed, the fate of this soil C is first to be converted to dissolved organic carbon (DOC), which is then oxidized by microbes and sunlight to CO₂. Recent data show for the first time that newly released DOC from permafrost soils is labile to microbial attack, and that sunlight exposure enhances microbial respiration of this DOC by >40% compared to C held in the dark. The goal of the proposed research is to develop a predictive understanding of how and why photochemical alterations of permafrost DOC lead to increased respiration rates by bacteria. Preliminary analysis of DOC chemical composition before and after light exposure at EMSL demonstrated that sunlight exposure altered a broad range of compounds and functional groups within DOC. We hypothesize that photochemically-altered DOC causes shifts in bacterial species, genomic capabilities, and functional gene expression, all of which contributed to the observed accelerated rate of respiration of permafrost carbon after it's been exposed to sunlight. We propose to use metagenomic and metatranscriptomic sequencing of expressed bacterial genes to identify the genome-encoded, functional metabolic pathways actively used by DOC-degrading bacteria in permafrost soils and to determine how these pathways change when soil DOC is exposed to sunlight in surface waters. We will then compare these results to DOC characterization by low and high-resolution mass spectrometry (Orbitrap and FTICR-MS, respectively) and ¹³C-NMR that show the loss or production of compound classes and functional groups during the experiment. Using the capabilities of JGI and EMSL together, we will determine genes that are differentially expressed and DOC compounds that are differentially modified and respired following light exposure and compared to DOC kept in the dark. We will relate the effects of light exposure on DOC metabolism to the concurrently measured rates of bacterial respiration and production to develop a predictive understanding of the controls on soil C degradation in the Arctic. This proposal combines JGI expertise in metagenomic and metatranscriptomic sequencing and analysis with EMSL instrumentation and expertise for high-resolution chemical analysis of dissolved organic matter. The power of genomics combined with the high-resolution DOC characterization is needed to inform the next generation of models that can better predict the impact of thawing permafrost on global climate change.