Toward a predictive understanding of the response of belowground microbial carbon turnover to climate change drivers in a boreal peatland.
DE-SC0012088, TES Program; Email address: joel.kostka@biology.gatech.edu

Joel E. Kostka[1], Malak M. Tfaily[2], Xueju Lin[1], Rachel Wilson[3], Jeff P. Chanton[3], William T. Cooper[3], Kaitlin Esson[1], Max Kolton[1], Jack Gilbert[4], Chris W. Schadt[5].
[1]Georgia Institute of Technology; [2]Pacific Northwest National Lab; [3]Florida State University; [4]Argonne National Lab; [5]Oak Ridge National Lab

High latitude peatlands store approximately 1/3 of all soil carbon (C), but wetland-specific processes are generally not included in global climate models. Using advanced analytical chemistry, ^{14}C and ^{13}C tracing, and next generation gene sequencing, this project will quantify the response of soil organic matter (SOM) storage and reactivity, decomposition, and the functional diversity of microorganisms to climate change manipulation in peatlands. The project is being conducted at the Marcell Experimental Forest (MEF), northern Minnesota, where the Oak Ridge National Lab (ORNL) has established an experimental site known as Spruce and Peatland Response Under Climatic and Environmental Change (SPRUCE). In collaboration with SPRUCE investigators at ORNL, new insights will be incorporated into the land component of the Community Earth System Model to improve climate projections.

Prior to completion of the SPRUCE climate enclosures, our objectives were to document trends in the dynamics of organic carbon compounds linked to microbial community composition to elucidate the controls of belowground C turnover and the potential responses to warming. Here we focused on molecular-level characterization of dissolved organic matter (DOM) in pore waters from the S1 bog at the MEF. Ultrahigh-resolution Fourier transform ion cyclotron resonance mass spectrometry (FT ICR MS) and 3-dimensional excitation emission matrix spectroscopy with PARAFAC analysis (EEMS-PARAFAC) revealed that DOM characteristics were most unique in the 50 cm depth zone that was previously identified as the zone where maximum decomposition of soil organic matter is occurring. Nitrogen-and sulfur-bearing compounds were highest at intermediate depth and we have identified for the first time the presence of polycyclic aromatic compounds that contain both nitrogen and sulfur heteroatoms. EEMS-PARAFAC data from S1 bog were combined with data from other bogs and fens around the world in the development of a general peatlands model for DOM fluorescence.

Using next generation sequencing of SSU rRNA genes, metagenomics, and in silico prediction of bacterial functional content, we further showed that the vertical stratification in microbial communities paralleled changes in methane dynamics and organic carbon composition. Multiple lines of evidence consistently point to Type I and Type II methanotrophs, especially Methylomonas and Methylocystis, as the dominant active CH_4-consuming populations in the surface layers of S1 bog. Microbial diversity and members of Alpha/Gammaproteobacteria decreased in relative abundance with depth, while putative anaerobes in the Deltaproteobacteria and Archaea (including methanogens and other functional guilds) increased. To probe the metabolic potential of abundant Archaea, two near-complete archaeal genomes, affiliated with the Thaumarchaeota and Thermoplasmata, were reconstructed from metagenomic data acquired from deep anoxic peat layers. Archaeal genomes revealed the potential to degrade long chain fatty acids (LCFA) via β-oxidation either by syntrophic interaction with methanogens or by coupling oxidation with anaerobic respiration using fumarate or organosulfonates (enriched in humic-like substances) as a terminal electron acceptor (TEA), a result consistent with recent observations of the importance of organic sulfur in organic matter decomposition based on FT-ICR mass spectral characterization.