**Poster #1-55**

**Toward the Predictive Understanding of Greenhouse Gas Production in High Latitude Peatlands**

Joel Kostka[1*], Max Kolton[1], Rachel Wilson[2], Malak Tfaily[3], Jeff Chanton[2], William Cooper[2], and Chris Schadt[4]

[1]Georgia Institute of Technology, Atlanta, GA
[2]Florida State University, Tallahassee, FL
[3]Pacific Northwest National Laboratory, Richland, WA
[4]Oak Ridge National Laboratory, Oak Ridge, TN

Contact: joel.kostka@biology.gatech.edu

Arctic and boreal peatlands represent critical regions that cover only 3% of the Earth's land surface but store approximately 1/3 of all soil carbon (C), and currently act as atmospheric C sinks. While future warming and $CO_2$ enrichment should accelerate peat decomposition, uncertainty in the size and reactivity of peat C stocks is cited as a barrier to the reliable predictive modeling of the resilience of belowground C reservoirs to future perturbations and the release of greenhouse gases (GHGs) to the atmosphere. Thus, the goals of this project are to investigate peatland soil organic matter (SOM = peat + dissolved organic matter, DOM) recalcitrance and alternative mechanisms of electron flow as primary controls over belowground C turnover, GHG production ($CO_2$:$CH_4$) ratios, and the response of the microbial C cycle to climatic forcing. The project is being conducted at the Marcell Experimental Forest(MEF), 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, new insights into peatland-specific processes will be incorporated into the land component of the Community Earth System Model to improve climate projections.

We have previously shown (1) that heterotrophic respiration within the peat at SPRUCE is largely driven by DOM and (2) that shallow depths are most susceptible to enhanced warming. Thus any increases in labile organic matter inputs to surface soil, in particular, are likely to result in significant changes to $CO_2$ and $CH_4$ production. Multiple field campaigns were conducted in summer 2017 to capture the whole ecosystem response after 2 years of whole- ecosystem warming (WEW). The DOM metabolome and microbial communities were characterized using advanced analytical chemistry techniques and environmental genomics, respectively. Depth remains the greatest driver of variability across the site, reflecting the trend of increasing humification and parallel microbial community stratification with depth. However, we did find significant correlations between metabolite concentrations and temperature treatment for small sugars, amino acids, and some lipids in surface peat (≤50 cm). In general, small sugars and diacylglycerols increase, while amino acid concentrations decrease with temperature. These results are consistent with increased availability of labile substrates promoting increases in microbial biomass that draw down the pool of available free amino acids in the porewater. Further results suggest that plant stress compounds are increasing, likely in response to warmer temperatures and dryer conditions in the treatment plot which may alter the supply of both C substrates and electron acceptors available for heterotrophic respiration.

Because destructive core sampling is limited within the enclosures, our group is exploring the response of porewater microbial communities to WEW. Surprisingly, microbial diversity in porewater was shown to be equal to or higher in comparison to peat. In response to WEW, preliminary results indicate that microbial diversity declined in porewater and microbial communities show a pronounced shift in composition. In particular, an increase in the relative abundance of methanogens and methanotrophs was observed.