Subsurface Biogeochemical Research and Terrestrial Ecosystem Science Joint Meeting April 25-26, 2017
http://doesbr.org/PImeetings/2017/ and http://tes.science.energy.gov/PImeetings/2017/

Poster #55

The response of belowground carbon turnover and heterotrophic microbial communities to warming and elevated CO_2 in peatlands at the ecosystem scale.

Joel E. Kostka[1], Max Kolton[1], Rachel Wilson[2], Jeff P. Chanton[2], William T. Cooper[2], and Chris W. Schadt[3]

[1] Georgia Institute of Technology;
[2] Florida State University;
[3] Oak Ridge National Lab

Contact: Joel Kostka [joel.kostka@biology.gatech.edu]

High latitude peatlands store approximately 1/3 of all soil carbon(C), but wetland-specific processes are underrepresented in global climate models. Using advanced analytical chemistry, ^{14}C and ^{13}C tracing, and next generation gene sequencing, this project quantifies the response of soil organic matter (SOM) storage, reactivity, and decomposition, and the functional diversity of microorganisms to climate change manipulation in peatlands. 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.

Multiple field campaigns were conducted at SPRUCE in summer 2016 to capture the whole ecosystem response after 1 year of whole-ecosystem warming and the immediate biogeochemical response, within days to weeks, after CO_2 enrichment (eCO_2) began. Samples were collected at 1 day, 1 week, 1 month, and 2 months after initiation of eCO_2 treatments and spanning the peak growing season at S1 bog. We determined the concentration and stable isotopic composition of CO_2 and CH_4, and □C ([$\delta^{13}CO_2$+1000]/[$\delta^{13}CH_4$+1000]) values which are an indicator of the CH_4 production pathways. Microbial community composition was characterized using next generation sequencing of SSU rRNA genes. No substantial trends with time or treatment were observed. Our current results indicate that the large store of deep catotelm C remains resistant to anaerobic degradation under conditions that simulate future climatic warming.

Microcosm experiments were conducted with surface peat to examine the response of organic matter decomposition to extreme and prolonged changes in temperature. Microbial community abundance and composition were characterized along with the production of CO_2 and CH_4. Whereas CH_4 production rates exhibited a classic mesophilic response to temperature, CO_2 production showed a large temperature optimum in the psychrophilic range which matched the annual average peat temperature. The relative abundance of methanogenic archaea tracked well with CH_4 production rates, whereas bacterial abundance paralled the CO_2 production rates. Our results indicate that peat microbial communities harbor distinct populations of psychrophilic and mesophilic bacteria. Prolonged exposure to extreme temperature triggered a loss of peat microbial community diversity and a major shift in community composition, with spore-forming members of the *Firmicutes* increasing in relative abundance at high temperatures. Microbial communities crashed at high temperatures similar to those observed, albeit rarely, at MEF.