Microbial growth and carbon and nutrient use partitioning under peatland warming and elevated CO_2. Jessica Gutknecht, University of Minnesota, Twin Cities

Background: As has been the major thought behind developing the SPRUCE project, the huge carbon store present in peatlands may be threatened by climate change as alterations occur in peatland forest communities, decomposition processes, and other biogeochemical cycles (National Climate Assessment, 2013; Allison and Treseder, 2011). In addition to their role in carbon storage, the organic matrix of peat functions to retain large quantities of minerals such as mercury and sulfur, which are of major concern for pollution in Minnesota and other industrialized areas. Isotopic methods offer a powerful tool for analyzing how microbial communities mediate decomposition or the processing of different elements in any ecosystem. For example, the ^{13}C signature in microbial membrane fatty acids, as well as the quantitative abundance data yielded from those fatty acids, can be used to construct a 'microbial diet' to inform whether fungi and bacteria are using new photosynthate, versus older more recalcitrant carbon sources in general or under elevated CO_2 or climate change scenarios (Herman et al. 2011; Jin and Evans, 2010).

Current plans: With this background and with my newly established GC-Isotope Ratio Mass Spectrometer I am analyzing the ^{13}C signature of lipid profiles from bulk peat in the SPRUCE experiment. To date I have taken samples throughout the peat profile as part of the group peat sampling in all plots from June and September, 2014. Currently we have completed our protocol optimization and are extracting those samples. We plan to have initial data to share by summer 2015. Ultimately, I hope that these data can be combined with other ^{13}C data being collected at the SPRUCE experiment in order to understand how changes in microbial C uptake and carbon use are related to the larger perspective of changing biogeochemistry in peatlands under climate change.

Future plans: My future ideas are in two major directions, and will be the focus of grant writing efforts. First, I plan to continue ^{13}CPLFA analysis together with all group bulk peat sampling efforts as treatments begin. To add to this measurement, I plan to conduct amino sugar analysis (possibly optimizing extraction methods for ^{13}C or ^{15}N analysis). Where the microbial lipid pool is relatively short lived, the amino sugar component of bacterial and fungal cell walls turns over more slowly and represents the microbial contribution to stored organic C. This analysis has been used to demonstrate changes in the microbial contribution to C storage under climate change (Liang and Balser 2012) but has rarely been examined in peatlands.

A second future direction is to expand the work of understanding how changes in the peat matrix alter sulfur cycling, in collaboration with Dr. Brandy Toner, Dr. Ed Nater. Dr. Randy Kolka, and Dr. Steve Sebastyn. Here we would use the principal that as sulfate reduction occurs through microbial sulfate reduction, sulfate becomes enriched in ^{34}S. We will use this information to understand how sulfur cycling and sulfur transformations are changing in peatlands under climate change by comparing isotopic signatures in treated versus untreated plots. Where it would not overlap or would be complementary to other microbial work at SPRUCE, we would also use quantitative PCR methods to quantify the abundance of sulfur reducing bacteria in SPRUCE plots in pore water and bulk peat.

References

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