

Poster #9-33**Quantitative, Trait-Based Microbial Ecology to Accurately Model the Impacts of N Deposition on Soil C Cycling in the Anthropocene**Edward Brzostek^{1*}, Ember Morrissey¹, Zachary Freedman¹, Steve Blazewicz², and Peter Weber²¹ West Virginia University, Morgantown, WV;² Lawrence Livermore National Laboratory, Livermore, CAContact: rbrzostek@mail.wvu.edu

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Atmospheric nitrogen (N) deposition resulting from fossil fuel burning in the eastern United States has altered fundamental soil processes, challenging our understanding of whether soils will continue to sequester carbon (C) from the atmosphere and slow environmental change. While evidence shows that N deposition has enhanced C storage in temperate forest soils, it remains unclear whether these effects will persist. Moreover, there is uncertainty as to why some forest soils gain more C in response to N deposition than others. At the heart of this knowledge gap is a failure to link N-induced shifts in microbial biodiversity with their ability to breakdown, assimilate or stabilize soil C. Given that this uncertainty directly impedes the ability of predictive models to project future soil C stocks, there is a critical need to determine how shifts in key microbial traits drive soil C stabilization following N deposition.

Microbial growth, C use, and N use efficiency (the ratio of C or N used to produce microbial biomass vs. the total C or N that a microbes takes up) and turnover (microbial death rate) are keystone microbial traits that control soil processes. Microbes need N as a nutrient to grow, and N deposition could shifts these traits. For example, if high N levels increase C use efficiency and turnover, there will be greater production of dead microbes, which stick to charged soil mineral surfaces and are protected from further microbial attack. To date, there remain limited data on how these traits vary across environmental gradients. Moreover, these N deposition impacts on soil C may likely vary across tree species that differ in the type of symbiotic fungi their roots support: arbuscular mycorrhizal (AM) fungi or ectomycorrhizal (ECM) fungi. AM forests have easier to break down dead plant material, greater bacterial dominance, and more soil N than ECM forests, which could explain why forests differ in soil C responses to elevated N.

The uncertainty highlighted above is mirrored in models used to predict future soil C stocks because they are sensitive to estimates of microbial traits. As measures of microbial traits are sparse, most models assume these traits are the same across environmental gradients, which impedes our ability to predict future soil C stocks. Thus, our objectives are to 1) Quantify variation in taxon-specific and community-level microbial traits across gradients in microbial community composition, mycorrhizal symbioses, and N availability and 2) Integrate this data into a novel predictive framework that enhances our ability to project the regional soil C consequences of historical N deposition in temperate forests.

To meet our objectives, we will link data generated by our novel quantitative stable isotope probing methodology for measuring taxon-specific traits with a state-of-the-art microbial decomposition model. We will measure microbial traits and diversity across three Eastern temperate forest sites of the National Ecological Observatory Network in MA, VA, and TN that span a historical N deposition gradient. At each site, we will use six forest plots dominated by either ECM or AM associated trees thereby leveraging an additional axis of variation in litter quality, soil chemistry, and microbial biodiversity. To isolate N effects, we will incorporate an existing N fertilization experiment in WV. The data we generate will flow into transforming a model that predicts differences between AM and ECM forests in soil C processes.