

Title: Quantitative, Trait-Based Microbial Ecology to Accurately Model the Impacts of Nitrogen Deposition on Soil Carbon Cycling in the Anthropocene

Edward Brzostek^{1*}, Ember Morrissey¹, Zachary Freedman², Chansotheary Dang¹, Nanette Raczka¹, Juan Piñeiro^{1,4}, Christopher Walter¹, Steve Blazewicz³, and Peter Weber³

¹West Virginia University, Morgantown, WV

²University of Wisconsin, Madison, WI

³Lawrence Livermore National Laboratory, Livermore, CA

⁴University of Cádiz, Cádiz, Spain

Contact: erbrzostek@mail.wvu.edu

Project Lead Principle Investigator: Edward Brzostek

BER Program: ESS

Project: EPSCOR; University Award

Nitrogen (N) deposition has enhanced carbon (C) storage in temperate forest soils. However, it remains unclear whether this soil C will persist as N deposition declines across the region. At the heart of this knowledge gap is the failure to link N-induced shifts in microbial biodiversity with traits that control microbes' 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 N-induced shifts in key microbial traits drive soil C stabilization. To address this uncertainty, our objectives are to: 1) Quantify variations in taxon-specific and community-level microbial traits across gradients in microbial community composition, the distribution of ectomycorrhizal (ECM) and arbuscular mycorrhizal (AM) trees, and N availability and 2) Integrate these data into a novel predictive framework that enhances our ability to project the regional soil C consequences of N deposition in temperate forests. To meet our empirical objectives, we used a suite of quantitative stable isotope probing, metabolomics, and biogeochemical approaches. We continue to build off our findings that decomposition pathways in AM soils have greater flexibility in which microbes are the active decomposers and what they produce than those in ECM soils. To do this, we performed two experiments to examine how N availability and root exudates impact microbial diversity and function. Under elevated N availability, we found evidence for a reduction in functional evenness for both mycorrhizal types with a narrowing of the distribution of active taxa taking up C and N. There was also a negative relationship between respiration and functional diversity suggesting that communities with a higher functional diversity may use resources more efficiently. Under simulated root exudation, we found that microbes in ECM rhizospheres are more efficient at converting exudates into biomass than microbes in AM rhizospheres. We used these results to develop new microbial groups based on substrate preference in our plant-microbial interactions model, FUN-CORPSE. We challenged the model to reproduce results from our laboratory and field experiments and have found that elevated N induces emergent shifts in the dominance of microbes that consume dissolved organic carbon, primary plant material, or microbial necromass. Coupled together, our experimental and model results highlight the importance of integrating state-of-the-art data on microbial traits and function into models to improve predictions of temperate forest responses to global change.