

Quantitative, Trait-Based Microbial Ecology to Accurately Model the Impacts of N Deposition on Soil C Cycling in the Anthropocene

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Nitrogen (N) deposition has enhanced 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.

We used quantitative stable isotope probing, metabolomics, and biogeochemical approaches to quantify microbial traits and their impacts on soil C cycling across scales. Under ambient N deposition, we show that soil microbes in AM soils have greater flexibility in their decomposition pathways than those in ECM soils. In AM but not ECM soils, the identity of the soil microbes decomposing litter as well as the resulting metabolites varied as a function of litter quality. Under elevated N, microbial diversity declined for both mycorrhizal types, but there were mycorrhizal-dependent shifts in diversity of taxa using aspartic acid. N fertilization led to diversity declines in AM soil microbes using the C and N from the amino acid. By contrast, ECM soil microbes only showed a decline for N. For both mycorrhizal types, however, our results suggest that there are mycorrhizal-dependent, decomposition pathways that respond differently to elevated N. We used these results to develop new microbial groups that classify microbes based on substrate preference in our plant-microbial interactions model, FUN-CORPSE. When confronted with data from laboratory and field measurements, the refined model was able to capture shifts in decomposition and the mineral stabilization of N. 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.