


B53E-1934 Fungal and bacterial functional groups explain variance in soil nutrient cycling

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 19:10 - 23:30

 *Poster Hall A-C - South (Exhibition Level, South, MC)*

Abstract

Soil microbes are the driving force behind soil nutrient cycling, yet the role of their composition and function in controlling forest nutrient cycling is poorly understood and rarely used to predict rates of biogeochemical cycling. We aimed to answer: 1) Which microbial traits are the best predictors of soil nitrogen (N) and phosphorus (P) cycling rates in temperate forests? 2) What are the relative contributions of microbial, plant, and abiotic traits in explaining rates of soil N and P cycling? We hypothesized that including fungal and bacterial gene abundances would better predict soil N and P cycling than plant traits and abiotic conditions alone. To test this hypothesis, we designed a field system in New England where variation in microbial community composition was crossed with variation in vegetation composition and soil nutrient content. At 6 sites, we sampled soil along a transect from the forest edge to interior from four stand types: pine, hardwood, hardwood with pine saplings in the understory, and mixed mature pine-hardwood. In each sample, we measured net ammonification, nitrification, and phosphate release rates. We performed high-throughput sequencing of fungal and bacterial rDNA amplicons (16S/ITS), used PICRUSt2 to calculate bacterial gene abundances, and used all published fungal genomes to calculate genus-level gene abundances. Abundances of bacterial and fungal genes coding for decomposition of plant litter were positively correlated with net ammonification (bacterial: $p = 1.6e^{-08}$, $R^2 = 0.27$; fungal: $p = 0.006$, $R^2 = 0.09$) and phosphate release (fungal: $p = 0.002$, $R^2 = 0.23$; bacterial: $p = 0.03$, $R^2 = 0.17$). However, instead of gene abundances, microbial functional guilds were the best predictors of nitrification: N-cycling bacterial abundance positively correlated with nitrification (N cycling: $p = 1e^{-06}$, $R^2 = 0.18$) and ectomycorrhizal abundance was negatively correlated with nitrification ($p = 4e^{-08}$, $R^2 = 0.26$). Using model selection, the best linear models to explain nitrification and phosphate release included microbial, plant, and abiotic traits, and for ammonification

included microbial and abiotic traits. Our results show that multiple microbial traits are important predictors of soil N and P cycling and should be included in future ecosystem-level biogeochemistry models.

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