

Title: Are the activities of microbial taxa consistent across ecosystems?

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Project Goals: Connecting the composition of microbial communities with biogeochemical process rates has the potential to improve our understanding of, and ability to model, ecosystem function. This project aimed to determine if the growth of prokaryotic taxa is consistent across ecosystems. This work dovetails with our larger goal to characterize *in situ* rates of biogeochemically significant microbial activity at the community scale and for specific taxa. This information will be leveraged to establish whether there is a “phylogenetic imprint” on soil carbon and nitrogen cycling processes that can facilitate better incorporation of microbial data into process-scale modeling efforts.

Soils are a huge reservoir of carbon, yet our ability to predict how this important carbon pool will respond to future climate remains poor. Understanding how soil microbial community composition influences ecosystem biogeochemistry could help resolve this knowledge gap. Our past work demonstrates clear taxonomic patterns in the activity of microorganisms; for instance, some taxonomic groups grow quickly while others grow slowly or not at all. These taxonomic patterns in activity will be most useful for modeling the influence of microbial biodiversity on ecosystem function if they appear consistently across ecosystems. Here we aimed to test the hypothesis that taxonomic identity can explain a significant amount of the variation in prokaryotic growth and carbon assimilation across ecosystems. To this end, we used qSIP with ¹⁸O-water and ¹³C-glucose to measure microbial growth and carbon assimilation in four ecosystems along a climatic gradient in Northern Arizona. These sites consisted of a mixed conifer forest, a ponderosa pine forest, a pinyon-juniper woodland, and a cool desert grassland. While data analysis is still underway, preliminary results suggest an impact of both taxonomic identity and ecosystem type on the activity of microbial populations in soil. This may indicate limited phenotypic plasticity in the activity of microbial populations wherein microorganisms respond to environmental variation but maintain relatively consistent ecological strategies. Characterizing the activity of microbial taxa could result in a paradigm shift wherein microbes are no longer treated as a ‘black box’ in biogeochemical models, leading to dramatic improvements in our ability to understand and predict carbon cycling dynamics in soil.

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