Quantitative stable isotope probing with ^{15}N in soil microbial communities

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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 extend the promising new technique of quantitative stable isotope probing (qSIP) to the study of nitrogen cycling in soil. This work dovetails with our our larger goal to characterize *in situ* rates of biogeochemically significant microbial activity at both 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.

Anthropogenic disruption of the nitrogen (N) cycle is having cascading effects on ecosystems around the global as the cycling of carbon (C) and N are closely linked. In addition to regulating primary production, N availability interacts with other variables to determine rates of soil organic matter decomposition. However, the contributions of microbial taxa to N cycling processes such as immobilization are not well understood. Here we used qSIP with ^{15}N to measure taxon-specific nitrogen uptake by microorganisms in soil. To assess the effects of C availability of N assimilation we considered control and glucose amended soils. Our results indicate that qSIP is sufficiently sensitive to quantitatively differentiate N assimilation among prokaryotic taxa. At the community level, ^{15}N assimilation was enhanced by glucose addition, a pattern mirrored by traditional measurements of nitrogen immobilization. The qSIP analysis revealed strong phylogenetic organization in N assimilation with broad phylogenetic groups exhibiting distinct patters of N uptake. For instance, most phylotypes within Acidobacteria (74%), Actinobacteria (93%), Verrucomicrobia (83%), and Proteobacteria (82%) assimilated more N in the presence of glucose. Conversely all taxa within Firmicutes and Crenarchaeota as well as the majority of Bacteriodetes (84%) had greater N assimilation in the absence of added carbon. These patterns suggest that phylogenetic groups of prokaryotes have distinct and coherent patterns of N uptake that reflect their ecological strategies. The distinct activities of phylogenetic groups provide a basis for understanding how phylogenetic microbial community composition influences N immobilization in soil.

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