Multiple-Element Isotope Probes, NanoSIMS, and the Functional Genomics of Microbial Carbon Cycling in Soils in Response to Chronic Climatic Change

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Project Goals: The goal of this project is to develop new omics-driven technical approaches that couple multiple-element stable isotope probing with phylogenetic analysis to investigate microbial community functional processes involved in soil carbon cycling. These techniques will be used to identify soil bacteria and fungi involved in organic carbon degradation, examine the impacts of shifting environmental variables on their functional processes, and determine if there is a "phylogentic imprint" on the soil carbon cycle. The capability to quantify *in situ* microbial growth rates both at the community scale and for specific taxa will be the primary advantage of this new methodology. The project will leverage several long-term field research sites (ponderosa pine and mixed conifer forests) that have been subject to experimental climate change manipulation. The information generated in this work will help to establish whether phylogenetically specific imprints are observed on soil carbon cycling processes and facilitate better incorporation of omics-derived data into process-scale modeling efforts.

Soils are a huge reservoir of carbon, exceeding phytomass and atmospheric carbon combined. Anthropogenic increases in CO_2 are expected to augment primary productivity and thus enhance carbon transfer from the atmosphere to the soil potentially increasing soil carbon storage. However, the consequences of enhanced primary production on soil carbon storage remain unclear as microbial decomposition activities respond dynamically to fresh carbon substrates. Specifically, the decomposition of native soil organic C can be reduced or enhanced in response to fresh carbon inputs, a phenomenon known as the "priming effect". We used quantitative stable isotope probing with ^{13}C-labeled glucose and ^{18}O-labled water to measure individual and community level activity in order to understand how microbial activity mediates priming in soil. Initially labile carbon addition decreased soil carbon mineralization (negative priming) but over time repeated additions increased the mineralization of soil carbon (positive priming). This shift in activity was associated with an increased relative abundance of Proteobacteria and TM7 and a decrease in the proportion of Acidobacteria and Actinobacteria. By comparing changes in ^{18}O assimilation (growth) due to labile C addition with the amount of ^{13}C assimilation from the added substrate, we assessed the changes in soil carbon utilization

induced by fresh carbon inputs. Initially labile carbon was being consumed in lieu of soil organic matter, a phenomena often called preferential substrate utilization, causing the negative priming. After repeated carbon additions, labile carbon increased the growth of most prokaryotic taxa. This additional growth was achieved using a mixture of the added carbon and the soil organic matter resulting in enhanced native carbon mineralization explaining the positive priming. To understand how responses to labile carbon addition were distributed across bacterial taxa we categorized changes in activity and tested for phylogenetic clustering. Most bacterial taxa were involved in priming, and these organisms were not phylogenetically clustered. This suggests that increased growth and soil carbon utilization in response to fresh carbon inputs is routine among bacteria and does not require specialized physiological or ecological attributes. Consequently, priming may not be strongly constrained by bacterial biodiversity in soil.

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