53. 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: Develop a new omics-driven technical approach that couples multiple- element stable isotope probing with nanoscale secondary ion mass spectrometry (NanoSIMS) and phylogenetic microarrays to investigate the functional processes of the microbial community involved in soil carbon cycling. This technique 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 "phylogenetic 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.

For the past several decades, connecting biogeochemistry and microbial genomics has been a high priority in microbial ecology. Yet, techniques that actually link element flow and genomic information are scarce. In this project, we are using the Chip-SIP method to measure isotopic composition of major elements (C, N, H, and O) of nucleic acid sequences representing individual microbial taxa. RNA is extracted from an environmental sample after exposure to isotopically labeled substrates. The nucleic acids from the entire microbial community are then exposed to a microarray containing small probes that target the 16S rRNA genes of a large variety of microorganisms so that nucleic acids extracted from the environmental sample bind to matching probes. Then, the entire microarray is placed under a nanoscale secondary ion mass spectrometer, which sequentially analyzes the RNA bound to each probe for isotopic composition. In this way, element flow in the natural environment into individual microbial taxa can be determined.

Our work relates to key unknowns about soil carbon cycling and stability. The methods we are developing will allow us to examine relationships between soil microbial diversity and the processing of soil C. We hypothesize that there is a phylogenetic signal in the microbial biogeochemistry of the soil C cycle, explaining the variation in the degradation of soil organic matter in response to external forcing. The information generated will help to better understand the functional significance of the identity of microorganisms in complex, natural communities.

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