

Title: Microbial Community Traits Linked to Carbon Flux Patterns in Soil

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<http://www.lanl.gov/org/padste/adcles/bioscience/bioenergy-biome-sciences/soil-carbon.php>
<http://www.lanl.gov/org/padste/adcles/bioscience/bioenergy-biome-sciences/environmental-microbiology.php>

Project Goals: The LANL Genomic Science SFA is focused on microbial communities in surface soil horizons and their functional processes that influence soil carbon storage and release. The SFA examines soil carbon cycling under conditions of environmental change to understand the metabolic and ecological roles of fungi and bacteria in surface soils in two important temperate biomes – forests and arid grass/shrub lands. In both biomes, fungal and bacterial biomass is concentrated in shallow surface soil strata where C and N cycling are major processes. Advancing fundamental knowledge of soil communities within the context of altered environmental regimes will improve our ability to predict and possibly manage ecosystem contributions to global climate. This involves discovery of fundamental principles at different scales that influence the organization, interactions, and response of soil communities.

For the work presented here, our ongoing aim is to identify microbial community traits linked to different carbon flux patterns. When new organic carbon enters soil ecosystems, a fraction is respired and a fraction is stored for some period of time. The balance between these two general fates determines if soil is a carbon source or sink. Globally, the strongest factors controlling flux patterns are physical-chemical variables (temperature, oxygen, and pH) and biophysical processes (aggregate formation and sorption onto protective mineral surfaces). However, microbial community composition also plays a role.

We found that carbon flux patterns can vary dramatically with subtle changes in the composition of complex microbial communities. To achieve this, we monitored carbon flux patterns from plant-litter-decomposing microbial communities derived from 200 soils from the dry grassland biome of the United States. We exploited the fact that soil microbial communities in a common biome change subtly with spatial distance. Liquid extraction of communities from each sample and transplantation into a common environment (sand microcosms) enabled evaluation of different community configurations without additional confounding factors such as geochemistry and plant cover. We found that communities representing the most divergent carbon cycling outcomes had common traits. This is the first demonstration of specific microbial community traits linked to divergent soil carbon cycling patterns in the same environment.

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