

Microbial Communities As Carbon Conductors: Elucidating Universal Traits Across Litter Types

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

Project goal:

Determine *common* microbial community traits driving extreme patterns of soil carbon flow across different substrates

Abstract

The LANL Genomic Science SFA aims to inform climate modeling and enable carbon management. The SFA uses genomics approaches to reveal microbial processes affecting biogeochemical cycling (e.g. C and N cycling) in terrestrial ecosystems. This involves discovery of fundamental principles driving the organization and interactions of soil microbes at multiple scales.

We aim to identify microbial traits that consistently predict patterns of carbon flow (soil storage versus mineralization) from decomposition of different litter types. *This research addresses BER grand challenge 2.4, by linking genotype to phenotype in communities that interact to cycle carbon in terrestrial ecosystems.* The proportion of photosynthetically fixed carbon stored in soils over long time periods, and not returned to the atmosphere via respiration, is a significant moderator of atmospheric carbon levels and global climate. The balance between soil carbon storage and mineralization is mediated by micro-organisms that transform plant litter and exudates during decomposition. A relationship between carbon fate in soils and microbial community composition has been regularly postulated and indirectly implied but empirical evidence directly linking the two is lacking. Furthermore, community traits driving major changes in carbon fate are currently unknown. Plant litter quality is a key variable influencing microbial community function. Consequently, comparison of microbial community traits linked to carbon flow from different types of plant litter allows differentiation of universal traits from litter-specific traits. Universal traits are the most useful for carbon flow modelling and management.

We found carbon flux patterns vary substantially when decomposition is undertaken by different naturally occurring microbial communities, irrespective of substrate. To demonstrate this, we placed the same natural communities extracted from soil samples collected from the drylands region of the United States on pine, oak and grass litter in sand microcosms. The microcosms were incubated in homogeneous conditions and cumulative carbon outputs were compared after 45 days. Carbon fate varied widely on all substrates despite consistent conditions within the microcosms. Although grass is generally considered more labile than pine or oak, grass

decomposition produced less CO₂ on average than pine or oak. Dissolved organic carbon outputs were similar among the litter types. Litter type impacted community performance, with the same communities generating different carbon output patterns on the three litters. **Bacteria, not fungi, were the strongest drivers of divergent functional outcomes on pine with both composition and diversity being important.** Comparison of community traits driving carbon fate across the different litter types is ongoing. Elucidating robust traits under controlled conditions is a critical first step toward steering functional variation in naturally chaotic environments.

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