Microbial Community Composition Controls Carbon Flux Across Litter Types in Short-Term Litter Decomposition

Marie Kroeger[1]* (mkroeger@lanl.gov), Rae Devan[1], Jaron Thompson[2], Renee Johansen[3], La Verne Gallegos[1], Brian Munsky[2], Sanna Sevanto[4], Michaeline B.N. Albright[1], **John Dunbar**[1]

[1]Bioscience Division, Los Alamos National Lab, Los Alamos, New Mexico
[2]Department of Chemical and Biological Engineering, Colorado State University, Fort Collins, CO
[3]Landcare Research, Auckland, New Zealand
[4]Earth and Environmental Science Division, Los Alamos National Lab, Los Alamos, New Mexico

https://www.lanl.gov/science-innovation/science-programs/office-of-science-programs/biological-environmental-research/sfa-microbial-carbon.php

Project Goals

1) Determine the relative importance of substrate (i.e. litter type) and functional state (DOC abundance) to explain the variance in microbial community composition.
2) Determine microbial traits that drive contrasting patterns of carbon flow in short-term litter decomposition among three litter types

Abstract

In terrestrial ecosystems, products of microbially-driven plant litter decomposition are major inputs to the soil organic carbon pool, a key carbon sink. Microbial composition plays an important role in determining the fate of plant litter carbon, which can either be respired as CO_2 or retained in the soil in other forms. However, the microbial community traits that alter carbon flow from litter decomposition are unknown. In this study we sought common microbial traits driving variation in carbon flow from three litter types (pine, oak, and a grass mix) during short-term decomposition in a common garden experiment. We measured carbon flow as carbon dioxide (CO_2) production throughout the 44-day experiment and a final dissolved organic carbon (DOC) measurement. Since we observed a greater than 3-fold microbially-driven DOC range between samples within each litter type and a significant negative correlation between DOC and CO_2 production, we did taxonomic profiling and selected a subset of high and low DOC samples for RNA-Seq analysis to determine differences in functional potential.

Hypotheses: 1) Plant litter type will select for different decomposer communities, but within a litter type, community composition will still vary with DOC abundance (high or low DOC). (2) Some microbial traits driving patterns of carbon flow will be common across the litter types.

Consistent with expectation, litter type explained more of the variance in community composition than DOC (12% and 7% respectively), but DOC constrained by litter type explained the most variance (31%). Bacteria rather than fungi appeared to drive carbon flow. Bacteria represented 82.1% and 82.5% of the differentially expressed microbial genera between low and high DOC, respectively. The limited fungal contribution to differentially expressed genes is consistent with a two-tiered decomposition process: 1) fungi dominate litter deconstruction, releasing DOC and 2) bacteria dominate consumption of DOC. The latter appears to account for

the variation in carbon flow observed in short-term decomposition. Common bacterial metabolic function gene expression signals linked to difference in carbon flow across litter types included biogenesis of cytochromes and selenoproteins, translation, protein secretion, and various carbon metabolism pathways. Observing significant differences at large functional levels that are common across litter types creates testable hypotheses for the mechanisms driving differences in carbon flow. Overall, these findings contribute to the goal of reprogramming carbon flow through microbiome engineering in terrestrial ecosystems to increase soil carbon storage.

*Funding Statement: This work was supported by the U.S. Department of Energy Biological System Science Division, through a Science Focus Area Grant (*2018SFAF255).