

Microbially-Drive Carbon Flow Persists During Surface Litter Decomposition

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Project Goals: The two main goals of this project were (1) to determine if microbially-driven carbon cycling variation observed in short-term litter decomposition persists over longer timescales and (2) identify the temporal dynamics of microbial traits associated with disparate carbon flow.

Abstract

In terrestrial ecosystems, products of microbially-driven plant litter decomposition are major inputs to the soil organic carbon pool, a key carbon sink. While climate and litter quality impact litter decomposition rates across sites, large intra-site variation in litter mass loss appears to be microbially-driven. During litter decomposition, microorganisms can either mineralize the carbon compounds from plant litter to produce CO₂ through respiration or transform the carbon into other organic molecules. Thus, manipulation of microbial community composition has the potential to alter the ratio of carbon directed toward the atmosphere as CO₂ or funneled to the soil as dissolved organic carbon (DOC), which has the possibility to be stored for longer periods of time. It is clear that microbial composition has a significant effect on litter decomposition; however, it is not understood the underlying mechanisms by which microbial community composition alters carbon cycling at any given point in time, much less over the full cycle of litter decomposition.

To address the gap-in-knowledge we conducted two yearlong experiments, one in the laboratory under controlled environmental conditions and one in the field, where we inoculate non-sterile blue grama plant litter with a 1:40 serial dilution of different soil microbial communities. We measured CO₂ flux and DOC to assess the effect of microbial community composition on carbon flow. We collected blue grama plant litter over the year for microbial community analyses (amplicon, metagenomic, metatranscriptomic sequencing). Overall, we found that microbially-driven DOC variation persists over a year and changing environmental conditions. Furthermore, we observed no significant difference in respiration between low and high DOC microbial communities. This research is still on-going as we wait for microbial sequencing data, DOC characterization data using GC-MS and FTICR-MS, and super resolution FISH microscopy, but we anticipate that the phenotypic differences observed in both laboratory and field conditions will allow us to identify microbial traits driving carbon flow during litter decomposition.

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