

## Organism interactions and substrate range are the primary mechanisms linked to divergent carbon flow during litter decomposition

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### Project Goals

- 1) Generate hypotheses regarding mechanisms behind microbially driven differences in carbon flow from complex microbiome data
- 2) Use machine learning approaches to identify key microbial taxa linked to differences in carbon flow

### Abstract

The LANL Microbial Carbon Cycling 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. Toward this end, we screened 206 soil communities decomposing plant litter in a common garden microcosm environment and examined features linked to divergent patterns of carbon flow. Carbon flow was measured as carbon dioxide (CO<sub>2</sub>) and dissolved organic carbon (DOC) from 44-days of litter decomposition. Two large groups of microbial communities representing “high” and “low” DOC phenotypes from original soil and 44-day microcosm samples were down-selected for fungal and bacterial profiling. Metatranscriptomes were also sequenced from a smaller subset of communities in each group. Our results suggest that the high and low DOC phenotypes are a manifestation of both ontogenic effects (time dependent differences), and innate functional differences in the microbial communities. A later stage of successional development could yield low DOC, and thereby reflect an ontogenic effect. However, the difference in average respiration rate between the high and low DOC groups clearly indicates innate differences in physiology. To gain further insight, using machine learning approaches, we identified *features*—traits at the organism, pathway, or gene level—linked to the high and low DOC phenotypes. The features pointed to several potential mechanisms driving differences in carbon flow including organism interactions, substrate range and substrate affinity. Further confirmation and elucidation of innate functional constraints can inform strategies for soil carbon management.

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