

## **Microbial lineages linked to decomposition outcomes across multiple litter types**

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### **Project goals:**

Determine which bacterial and fungal community members are consistently important to carbon fate in soils during the decomposition of leaf litter. This work was undertaken as part of the LANL Genomic Science SFA, which aims to inform carbon modeling and enable carbon management in terrestrial ecosystems. For more information about the SFA, see here:

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

During plant litter decomposition, a portion of photosynthetically fixed plant carbon is released to the atmosphere, and a portion is retained in soils. An increase in the fraction released as CO<sub>2</sub> may exacerbate global warming, whereas an increase in soil storage may create a carbon sink. A relationship between carbon fate and microbial community composition has been frequently postulated, but disentangling the impacts of community composition from co-varying abiotic factors and litter quality is challenging. Over the last two years, we have presented evidence from experiments with over 800 decomposition microcosms demonstrating that microbial composition can drive substantial differences in carbon flux patterns, at least in the early phase of plant litter decomposition, even when environmental conditions are constant. Using dissolved organic carbon (DOC) abundance as an indicator of carbon flow, we define two contrasting outcomes – high versus low DOC accumulation – and explore the community features linked to each outcome. Here, we identify bacterial and fungal lineages that show consistent links with the two decomposition outcomes among three litter types. Although the litter types generally selected different decomposer communities, numerous bacterial and fungal lineages consistently changed in average relative abundance across all three litters in comparisons of ‘high DOC’ vs ‘low DOC’ communities. This work is a first step towards our goal of identifying universal community features that can influence carbon cycling in disparate environments.

*This work is supported by grants 2015SFAF260 and 2019SFAF255.*