

Influence of Microbial Surface Litter Decomposer Communities on CO₂ Emissions from Natural Soils

Rae DeVan¹, Sanna Sevanto^{2*} (sanna@lanl.gov), Rose Harris², John P. Heneghan², Dea Musa², George Perkins², M. Francesca Cotrufo³, Michaeline B. N. Albright¹ and **John Dunbar**¹

¹Bioscience Division, Los Alamos National Laboratory, Los Alamos, NM

²Earth and Environmental Science Division, Los Alamos National Laboratory, Los Alamos, NM

³Department of Soil and Crop Science, Colorado State University, Fort Collins, CO

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

Project Goals: Test the influence of surface litter decomposer communities that differ in dissolved organic carbon (DOC) production on carbon cycling, balance and emissions in natural soil, and establish predictive links between carbon dioxide emissions, DOC production, and carbon transport to deeper soil layers during surface litter decomposition.

Carbon from terrestrial plant litter decomposition may be incorporated into microbial biomass, respired to the atmosphere as CO₂, or leached into the soil as dissolved organic carbon (DOC). Due to the large amounts of litterfall each year, the fate of this carbon has important implications for global carbon cycling. While most research has focused on climatic and edaphic controls over this carbon, there is strong evidence that microbial community composition can alter C flow during decomposition. The main goals of the LANL Microbial Carbon Cycling SFA are to inform climate modeling and enable carbon management using soil microbial communities. Previous common garden experiments using decomposing litter in microcosms during this project identified soil communities with divergent carbon flows measured as CO₂ and DOC. To understand the effects of microbially driven carbon flow from surface litter decomposition on net ecosystem C flow, we inoculated dual-labeled blue grama plant litter with microbial communities previously identified as either ‘high’ or ‘low’ DOC and incubated the litter on 30 cm, intact soil cores for 8 weeks, with half of the cores containing established blue grama plants. We expected cores inoculated with ‘high’ DOC communities to produce more DOC and less CO₂ compared to cores inoculated with ‘low’ DOC communities.

Our results show that CO₂ flux and DOC concentration peaked in the first 3 weeks of decomposition in all cores, but ‘high’ and ‘low’ DOC microbial communities behaved differently depending on the presence of plants. All cores with live plants produced similar total CO₂, but the ‘low’ DOC cores were more enriched in ¹³CO₂ indicating higher CO₂ release from litter decomposition consistent with expectations. However, in cores without plants, ‘low’ DOC cores produced more total CO₂, but were less enriched than ‘high’ DOC cores. DOC results were similarly flipped depending on the presence of plants. In cores with live plants, opposite to what was expected, inoculation with ‘high’ DOC producing microbial communities resulted in a greater reduction in DOC than inoculation with ‘low’ DOC communities compared to DOC baseline. In cores with no plants, the treatments behaved as expected with the ‘high’ DOC cores

producing more DOC than the 'low' DOC cores compared baseline. In summary, the presence of plants altered the outcome from microbial treatment, and neither set of cores behaved as expected for both carbon flows. 'Low' DOC cores with plants resulted in greater C flow both from CO₂ and DOC compared to 'high' DOC cores, while the opposite trend occurred in cores without plants.

This work was supported by the U.S. Department of Energy Biological System Science Division, through a Science Focus Area Grant (F255SFA2018).