

Cycles of Wetting and Drying Reduce Carbon Efflux and Litter Decomposition in Soil Microcosms

Tayte Campbell^{1*} (tayte.campbell@pnnl.gov), Sophia McKeever¹, John Dunbar², and Vanessa Bailey¹

¹Biological Sciences Division, Pacific Northwest National Laboratory, Richland, WA

²Bioscience (B-11), Los Alamos National Laboratory, Los Alamos, NM

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

Project goals: The aim of this project is to combine metagenomic and metabolomic analyses to understand the microbial influence on carbon cycling in simplified microcosms that mimic soil conditions.

The objective of this research is to understand the different mechanisms through which microbial communities respond to changing moisture levels, and the consequences of these differences to overall soil carbon cycling. Climate change models predict changes in precipitation, with some areas receiving more water inputs and others receiving less. To investigate how moisture variation affects CO₂ efflux and soil carbon stabilization, we used simplified microbial communities in sealed microcosms. Simplified microcosm communities developed from soil inocula allow for the control of environmental factors and provide a tractable level of complexity for mimicking microbial communities in soils.

We collected soils from 95 sites across southwestern grassland and forest soils in the United States and used them to inoculate sand microcosms containing Ponderosa pine needle litter as a carbon source. The soil microcosms were incubated over a three-month period with two treatments: one with constantly wet moisture conditions and one treated with three wetting cycles interspersed with long periods of desiccation. We measured CO₂ efflux throughout the incubation and destructively sampled at the end of the incubation to measure dissolved organic carbon (DOC), pine needle litter decomposition, and to characterize the microbial community using 16S sequencing. From these measurements we aim to use 16S sequencing analyses of the microbial community and chemical analyses on the metabolite profiles to link C fluxes with the microbial communities that drive these processes. We found that soil microbial communities subjected to wetting and drying cycles had 23% less pine needle consumption, 45% less cumulative CO₂ efflux, and 19% less DOC than communities maintained at a constantly wet moisture level. Overall, these findings indicate that wetting events followed by long periods of drought result in lower C degradation, sequestration, and efflux in the soil environment. Further, microcosm samples inoculated from the same soil showed similar intra-treatment trends of C efflux in both treatments, indicating that the microbial community is in fact driving the intra-treatment differences in C cycling.