

Microbial Control of Mineral-Bound Carbon

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

Project Goals:

- 1) Assess the magnitude of microbial-driven variation in mineral associated organic matter (MAOM) subsurface decomposition;
- 2) Identify specific community features linked to variation in MAOM decomposition

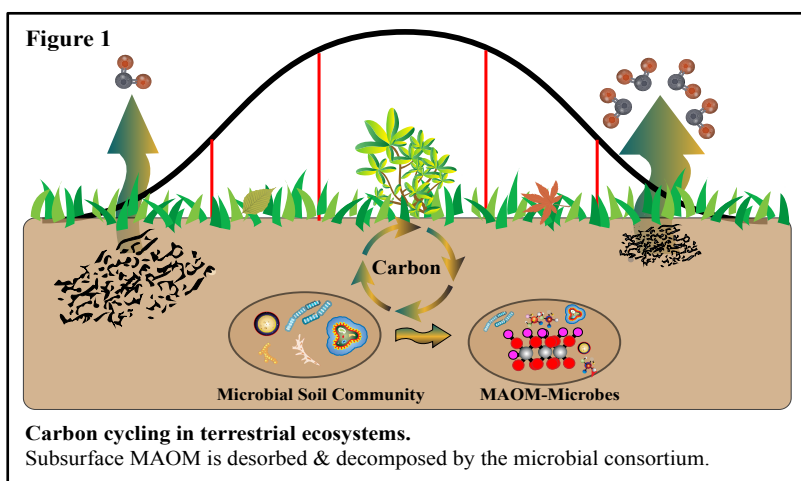
Abstract

The formation of organo-mineral complexes is a key process in long-term stabilization of carbon in soils¹. Because microbes contribute to desorption and transformation of MAOM, microbial community composition is expected to shape MAOM abundance over millennial scales². To inform soil carbon management strategies, the current project examines the range of variation in carbon flow that may occur during MAOM decomposition dependent on community composition. Further, the project aims to identify community features driving this variation, as has been done with surface litter decomposition^{3,4}.

To investigate microbial control of MAOM persistence, we applied a common garden approach by inoculating 103 distinct subsurface soil communities into microcosms. Each microcosm contained a mixture of sterile sand and kaolinite that was pre-loaded with dissolved organic carbon (DOC) obtained from ground Ponderosa pine needles. A total of 206 microcosms were generated and the subsurface soil communities were allowed to desorb and decompose the MAOM, with the loss of MAOM measured as CO₂ efflux. Measurements were taken over a 105-day dark incubation period. ‘High’ and ‘low’ respiration (CO₂) phenotypes were down-selected for community (bacteria and fungi) profiling.

Preliminary results of the ongoing study indicate that microbial-driven variation in desorption and decomposition of (MAOM) is large.

Respiration profiles show greater than 3.5-fold variation across communities, with the cumulative carbon respiration ranging from 0.5 - 1.92% CO₂ (1.2 – 4.2 mg CO₂) over a 105-day incubation. This amounts to between 16.7 and 43.8% of the available mineral bound DOC in the microcosms. Community profiling of the microbial cohorts representing



the ends of this range (the ‘high’ and ‘low’ CO₂ phenotypes) show that some distinctive communities contribute to the observed range of CO₂ efflux. To gain further insight into specific features linked to ‘high’ and ‘low’ respiration, we are applying a machine learning pipeline described previously⁵. Significant features will be used to infer traits that may be driving differences in carbon flow, providing insight into MAOM dynamics.

References

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