

Microbial regulation of soil water repellency to control soil degradation

Emily Boak^{1*} (emily_boak@lanl.gov), John Dunbar¹, Marie E. Kroeger¹

¹Bioscience Division, Los Alamos National Lab, Los Alamos, New Mexico

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Project Goals

1. Determine the influence of microbial community composition on the severity and persistence of SWR
2. Identify the metabolites differentially produced from microbial activity in hydrophilic and hydrophobic soils.

Abstract

Soil water repellency (SWR) is a major cause of global soil degradation and a key agricultural concern with an estimated 44 billion dollars lost in the US annually to offset erosion¹⁻². This phenomenon affects soils globally in both natural and cultivated lands³. The effects of climate change will likely exacerbate SWR emphasizing the need to understand the mechanisms driving SWR development and persistence. The importance of the soil microbiome in the development and persistence of SWR has been postulated for decades, but very limited research has been conducted into its role. To address this gap-in-knowledge, we investigated the direct effect of microbial community composition and activity on the development and persistence of SWR in model soils using a “common garden” experiment design. We inoculated microcosms containing model soils (sterile sand, blue grama plant litter, and bentonite clay) with 15 different microbial communities. Respiration was measured throughout the experiment and a soil water drop penetration test was conducted prior to destructive sampling on days 30, 45, and 89. Six microbial communities were found to consistently produce either a hydrophobic (3) or hydrophilic (3) phenotype. We extracted DNA for metagenomics and polar and non-polar metabolites for mass spectrometry.

We found that microbial community composition does affect the development of SWR. Although preliminary, there is some data to support that there is lower microbial diversity in hydrophobic communities, though specific taxa have yet to be identified as involved in SWR development. Preliminary analysis of the metabolomic data shows a significant difference in the functionalities displayed by hydrophilic vs. hydrophobic communities. Somewhat expected, the number of metabolites associated with lipid transport and metabolism is higher in hydrophobic communities, as well as metabolites associated with carbohydrate and coenzyme transport and metabolism. Preliminary data also indicates some differences between time points by community type, with a higher number of metabolites associated with defense mechanisms and signal transduction on day 45 within hydrophobic communities, but not day 89. These initial findings suggest that microbial communities are a key missing factor in this global phenomenon. Further research is necessary to understand the mechanisms driving the development and persistence of SWR *in situ* and under changing environmental conditions and during different stages of colonization. Further research into microbial control of SWR has the

potential to lead to the development of new mitigation strategies of SWR through microbial inoculations in degraded lands.

References:

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