The importance of biocrust organics revealed by metabolite sorption studies and in situ imagery

Estelle Couradeau1* (ecouradeau@lbl.gov), Tami L. Swenson1, Benjamin P. Bowen1,2, Vincent Felde3, Joelle Schlapfer1, Daniel Uteau3, Stephen Peth3, Dula Parkinson1, Ferran Garcia-Pichel4 and Trent Northen1,2

1Lawrence Berkeley National Laboratory, Berkeley, CA; 2DOE Joint Genome Institute, Walnut Creek, CA; 3Universität Kassel, Kassel, Germany; 4Arizona State University, Tempe, AZ;

http://www.northenlab.org/research/environmental-exometabolomics/

Project Goals: Understanding the role of microorganisms in soil nutrient cycling and organic matter turnover is a priority of the Department of Energy missions. Within this framework, our project aims at interrogating in situ microbial activity through the combination of pioneering approaches that link microbial community structure to soil organic matter dynamics and physical properties.

Abstract:

Weighing approximately 2400 Gt, soil organic carbon is by far the largest terrestrial pool of organic carbon. Small changes in soil organic matter (SOM) content could have drastic effects on the overall carbon cycle, therefore making SOM stabilization one of the most promising avenues to mitigate greenhouse gas emissions. The soil microbiome is critical in these terrestrial processes including the synthesis, turn-over and eventually the stabilization of SOM. However we still have a limited understanding of how communities encompassing thousands of members process carbon in-situ and how SOM might be stabilized through biological and abiological interactions.

A major challenge moving forward is being able to resolve microbial processes at the relevant spatial and temporal scales to decipher their role in SOM turnover. We use biological soil crust (BSC) as a model system to interrogate the dynamics and interactions of SOM and microbial communities. BSCs are the millimeter size epidermal layer of arid lands, which cover around 20% of Earth’s continental area, a global extension that is predicted to increase due to desertification. BSCs consist of an assemblage of mineral soil particles consolidated into a crust by the addition of exopolymeric substances (EPS), forming the exopolymeric matrix (EPM), which is mainly produced by the filamentous bundle forming cyanobacterium, Microcoleus sp. This cyanobacterium is both the primary producer for, and architect of BSCs, sustaining the development of a diverse microbial community. Despite their ecological importance, little is known about how BSC communities endure long dry periods while remaining viable for rapid resuscitation upon wetting. We hypothesized that biocrusts have the ability to retain nutrients by the EPM and that the bundle-forming is a trait of Microcoleus sp. that serves as an adaptive advantage, slowing the dehydration process and allowing the cyanobacterium to prepare for desiccation.
First, we investigated the ability of biocrust, particularly the EPM, to retain nutrients which would be a critical advantage during limited hydration. A 13C-labeled bacterial lysate metabolite mixture was incubated with non-biologically active (autoclaved) biocrust, the underlying subcrust or EPS extracted from biocrust. Metabolite sorption (retention) was monitored using liquid chromatography/mass spectrometry. Our data demonstrate that both biocrust and its EPS (or more broadly, the EPM) sorbed more metabolites than the subcrust, especially amino acids and organic acids, highlighting the potential role of biocrust in nutrient retention during a wetting event (Swenson et al., 2017).

To glean further insight into how biocrusts function during limited rain events, we used synchrotron based X-ray microtomography to track the water dynamics within an undisturbed BSC core throughout a hydration-dehydration cycle. We resolved the distribution of air, water, soil particles and Microcoleus sp. bundles at the microscale to quantify changes of the pore architecture during wetting and drying. We confirmed that Microcoleus sp. bundles hold water through desiccation, as their volume keeps shrinking even after the soil pore space dried completely.

Altogether, these results suggest that the EPM is crucial for BSC adaptation to pulsatile activity and they retain water longer, allowing more time for the community to prepare for desiccation. Biocrusts may act as a passive filter, capturing a variety of metabolites that could be further used as nutrient source upon the next wetup event. These data also clearly highlight that the use of other in situ techniques might bring complementary information and enhance interpretations of genomics-based microbial community analyses.

References

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