



Untangling the metabolic foodweb in biological soil crust using exometabolomics

Tami Swenson (1), Ulas Karaoz (1), Ana Giraldo Silva (2), Richard Baran (3), Benjamin Bowen (1,4), Ferran Garcia-Pichel (2), Trent Northen (1,4)

(1) Lawrence Berkeley National Lab, Berkeley, CA, USA, (2) School of Life Sciences, Arizona State University, Tempe, AZ, USA, (3) Baran Bioscience, LLC, Berkeley, CA, USA, (4) DOE Joint Genome Institute, Walnut Creek, CA, USA

The connections between soil metabolites and microbial community structure are not well-understood. Here, we focus on a relatively simple, yet critical soil ecosystem, biological soil crusts (biocrusts), which are communities of organisms inhabiting the upper layer of soil in arid environments. Biocrusts persist in a desiccated dormant state for extended periods of time and experience pulsed periods of activity facilitated by infrequent rainfall. *Microcoleus vaginatus*, a non-diazotrophic filamentous cyanobacterium, is the key primary producer in biocrusts in the Colorado Plateau, USA and is an early pioneer in colonizing arid environments. Previously, we observed strong exometabolite niche partitioning among biocrust bacterial isolates enabling construction of a metabolic web model of nutrient exchange between biocrust organisms. We then extended these findings by using our isolate data to link the relative abundance of four dominant bacteria to soil exometabolites in intact biocrust across a simulated wetting event and biocrust developmental stage. Overall, we found that most soil metabolites displayed the expected relationships (positive or negative correlation) with organism abundance.

Our results demonstrate that integrating metabolite profiling, sequencing, and exometabolomics can be used to interpret metagenomes and provides a functional link between biocrust microbial community structure and chemical composition. Current efforts are now focused on continuing exometabolite profiling with additional biocrust isolates (including another primary producer, *M. steenstrupii* and heterotrophs) in order to be able to combine bacteria into functional guilds based on substrate preferences. These data will enable development of increasingly accurate models describing the linkages between biocrust community structure and nutrient cycling.