

## Linking Soil Biology and Chemistry Using Knowledge of Exometabolite Substrate Preferences

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<http://www.northenlab.org/research/biological-soil-crusts-biocrusts/>

**Project goals: The Department of Energy has made major investments in soil sequencing efforts that have the potential to revolutionize predictive models of soil nutrient cycling. However, we lack vital data to link sequence data to metabolic transformations in soils. This program aims to help bridge this gap by pioneering new soil metabolomics approaches that link microbial community structure to soil organic matter dynamics.**

The specific connections between soil metabolites and microbial community structure are not well-understood. The dramatic expansion of sequencing data provides a window into microbial community structure and metabolic potential; however, linking these data to exogenous metabolites that microbes process and produce (the exometabolome) remains challenging. Here we explore the ability to use exometabolite profiles of biological soil crust (biocrust) isolates to relate the relative abundance of microbes and metabolites *in situ* (intact biocrusts). Biocrusts are microbial communities that inhabit the surface of soils found in arid regions comprising more than 40% of Earth's terrestrial surface and play a critical role in soil stabilization and nutrient cycling.

Recently we characterized the substrate preferences of seven biocrust bacterial isolates using exometabolomics with the finding that there was very little overlap in metabolite utilization indicating strong niche partitioning (Baran et al, 2015). We next wanted to determine if these metabolite preferences link the relative abundance of these bacteria to soil metabolites in intact biocrusts. To facilitate correlation between soil microbes and metabolites, we focused on the cascade of microbial activity set in motion upon wetting dry soil along a successional gradient. At five timepoints and across four successional stages following wetup, soil water was collected and analyzed by normal-phase liquid chromatography/ mass spectrometry for metabolites and DNA was extracted and sequenced on the HiSeq sequencing platform. Ribosomal protein (L15) was used as a phylogenetic marker.

Biocrust wetting caused a dramatic shift in both microbial community structure and metabolite profiles. Four dominant organisms in the biocrust were close phylotypes of the exometabolite-profiled isolates: a cyanobacterium (*Microcoleus* spp.), two firmicutes (*Anoxybacillus* sp. and *Bacillus* sp.) and an actinobacterium (*Blastococcus* sp.). In general, soil metabolites displayed the expected directionality (positive or negative correlation) with isolate phylotype abundance for 76% of the metabolites examined. Specifically, 78% of the metabolites that were consumed by an isolate were negatively correlated with their phylotypes *in situ* and 73% of released metabolites were

positively correlated. Our results demonstrate the potential of exometabolite profiling in providing a functional link between microbial community structure and chemical composition suggesting that large-scale exometabolite profiling using environmentally relevant metabolites may enhance interpretation of sequence-based microbial community analysis.

## **References**

Baran, R., Brodie, E.L., Mayberry-Lewis, J., Hummel, E., Da Rocha, U.N., Chakraborty, R., Bowen, B.P., Karaoz, U., Cadillo-Quiroz, H., Garscial-Pichel, G. & Northen, T.R. Exometabolite niche partitioning among sympatric soil bacteria. *Nat Commun.*, **6**, 8289 (2015).

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