Linking Microbial Community Structure, Activity and Carbon Cycling in Biological Soil Crust

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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.

Soils play a key role in the global carbon cycle, but the relationships between soil microbial communities and metabolic pathways are poorly understood. Our overall aim is to develop soil metabolomics methods and statistical models to link active microbes to the abundance and turnover of soil metabolites and examine the detailed substrate and product profiles of individual soil bacteria. To achieve these goals, we are using two different soil systems- biological soil crusts (biocrusts) and grassland soils. Biocrusts are communities of organisms inhabiting the upper layer of soil in arid environments. The crust itself is essentially microbial exopolysaccharide linked sand particles and is critical to soil stabilization. Biocrusts persist in a dessicated dormant state for extended periods with rare pulsed activity events following precipitation. *Microcoleus vaginatus*, a non-diazotrophic filamentous cyanobacterium, is the key primary producer in bacterially-dominated biocrusts in the Colorado Plateau and is an early pioneer in colonizing arid environments. Over decades, biocrusts proceed through developmental stages with increasing complexity of constituent microorganisms and macroscopic properties. Since *Microcoleus vaginatus* does not fix nitrogen, metabolic interactions with other biocrust microorganisms in the *Microcoleus vaginatus*-associated 'cyanosphere' presumably play a key role in the cycling of soil organic matter and in determining biocrust community dynamics.

To develop soil metabolomics approaches, a series of extractants (aqueous vs. organic solvents) were compared with soils that were either fumigated with chloroform vapor (to release metabolites from microorganisms) or left unfumigated. Analysis by gas chromatography-mass spectrometry and liquid chromatography-mass spectrometry revealed a breadth of metabolites including sugars, sugar alcohols, amino acids, fatty acids, dicarboxylic acids, sterols, nucleobases and osmolytes. Fumigation prior to extraction had a significant effect on the range and intensity of most metabolites and water was one of the most effective extractants. The inclusion of organic solvent (methanol) facilitated the extraction of fatty acids and sterols.

Exometabolite profiling was used to investigate the utilization of soil metabolites by sympatric bacterial isolates from biocrust (Baran *et al*, 2015). From this we found that *Microcoleus vaginatus* releases a broad range of metabolites. Many of these metabolites were found to be uptaken by heterotrophs but there were surprisingly few metabolites uptaken by all bacteria. This points to competition for a small set of central metabolites and specialization of individual heterotrophs towards a diverse pool of available organic nutrients. We are now

extending these studies to intact soil communities. Specifically, our soil metabolomics methods are being used to analyze the correlations between community structure, activity and soil metabolite dynamics following a laboratory pulsed activity (wetting) event. Biocrusts were wetup with water and metabolites (from porewater) and DNA were extracted at various timepoints up to 49.5 hours post-wetup. Exometabolite analysis revealed a similar breadth of metabolites as soil extracts. In general, many metabolites (*e.g.* amino acids) immediately increased in abundance following wetup and then steadily decreased. However, a few continued to increase over time (*e.g.* xanthine). Interestingly, we have observed xanthine to be released by some *Bacilli sp.* isolated from the biocrust (webofmicrobes.org) and metagenomics and metatranscriptomics show that members of the Paenibacillaceae family increase in abundance in late wetup samples. Previous 16S amplicon data also show a “Firmicutes bloom” following wetup with the new metagenomic data resolving this at genome-level. Ultimately, these approaches will provide an important complement to sequencing efforts linking soil metabolites and soil microbes to enable genomic sciences approaches for understanding and modeling soil carbon cycling.

References

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This work conducted was supported by the Office of Science Early Career Research Program, Office of Biological and Environmental Research, of the U. S. Department of Energy under Contracts No. DE-AC02-05CH11231.