56. Microbial Community and Functional Responses to Rainfall Manipulations in a Prairie Soil

Ari Jumpponen[1*] (ari@ksu.edu), Lydia H. Zeglin[2], Peter J. Bottomley[2], Charles W. Rice[1], Maude M. David[3], Emmanuel Prestat[1,3], Janet K. Jansson[3], Susannah G. Tringe[5], Nathan C. VerBerkmoes[4], Robert L. Hettich[4] and **David D. Myrold[2]**

[1]Kansas State University, Manhattan, KS; [2]Oregon State University, Corvallis, OR; [3]Lawrence Berkeley National Laboratory, Berkeley, CA; [4]Oak Ridge National Laboratory, Oak Ridge, TN; [5]Joint Genome Institute, Walnut Creek, CA

http://cropandsoil.oregonstate.edu/content/meta-omics-analysis-microbia-carbon-cycling-responses-altered-rainfall-inputs-native-prairie-soils

Project Goals: Prairie soils are important stocks of sequestered carbon. However, responses in soil carbon processing to predicted environmental change are still unknown. This project aims to determine soil microbial community and functional responses to ambient and altered precipitation schemes with a specific emphasis on microbial processes that are fundamental to soil carbon dynamics. To do this, the project combines an array of omics tools ranging from targeted locus sequencing to soil transcriptomics and proteomics.

Large pools of carbon (C) are processed and stored in prairie soils: grasslands cover 6.1-7.4% of the earth's land area and store 7.3-11.4% of global soil C. Current global change predictions suggest that precipitation may change little in annual volume, but more in frequency, resulting in more variable regimes across the North American Great Plains with less frequent but larger rainfall events. Between these large pulse events, soil systems will experience extended and often extreme droughts. Despite the importance of prairie soils and therein-residing microbial communities for C sequestration, our understanding of microbial community and functional responses or the resultant C processing to the variability in soil hydrology is cursory at the best. Our current program has assessed soil microbial communities (PLFA- and qPCR-inferred biomass, bacterial 16S RNA and DNA; fungal 28S RNA and DNA), microbial function (respiration, C utilization efficiency, extracellular enzyme activity (EEA)) and microbial gene expression (soil transcriptomic and proteomic analysis, focused on components of C processing pathways) under ambient and altered precipitation schemes. We have taken advantage of the Rainfall Manipulation Plot (RaMP) infrastructure at the Konza Prairie Long-Term Ecological Research site in the Flint Hills region in NE Kansas. The RaMPs provide a long-term replicated (n=6 per treatment) field experiment that aims to mimic predicted shifts in precipitation intervals, while keeping the total precipitation volumes unchanged. In the course of our current program, we sampled soils before, during, and after rainfall events from experimental units that represent ambient rainfall (Ambient) as well as experimental units that experienced a 50% increase in the dry intervals between precipitation events and fewer but larger rainfall resulting in same precipitation volume over the growing season, simulating "droughty" conditions (Altered).

Results to date indicate that rainfall events caused rapid and similar microbial respiration responses in Ambient and Altered treatments. Further, microbial biomass increased rapidly after the rainfall, more so in the Altered plots. These results suggest that increasing precipitation intervals may increase microbial C use efficiency and lead to greater potential for C sequestration belowground. Concurrent with these responses, biomass C:N ratio and fungal:bacterial ratio increased as soil water content decreased; however, our next-generation sequence data suggested only minor community responses. These results suggest that

(i) coarse changes in relative abundance of microbial domains (bacteria vs. fungi) dominate within-domain taxonomic responses, and/or (ii) physiological shifts within the communities are more prevalent than community turnover as a result of altered precipitation frequency and soil water contents.

Both QPCR and gene expression data suggest bacterial sensitivity to rainfall manipulation, in that bacterial 16S rRNA gene abundance was lowest in the driest soils, and relative abundance of mRNAs for oxidative phosphorylation was highest immediately after rainfall (like microbial respiration). Our results also highlight microbial EEA responses. Rainfall induced bulk soil cellulolytic activity and expression of bacterial cellobiose transport genes in moist soils, but not in dry soils. This result suggests rapid processing of available organic matter once soil water contents increase, and that a threshold of microbial respiration and/or labile C availability must be exceeded to induce SOM decomposition.

Beyond identifying microbial mechanisms that contribute to enhanced soil C storage potential in drier soils, the gene expression data also suggest shifts in stress-related and C-processing metabolic pathways. Corresponding proteomes for each soil transcriptome are complete, and are being aligned to better understand microbial function at the protein level in field samples. Also, our efforts to improve resolution and annotation of Omic data likely provide further insight into soil microbial functional responses. Extended dry conditions caused the most notable shifts in both microbial structure and function, highlighting the importance of extreme events and preceding conditions in understanding soil microbial C cycling dynamics. The combination of multi-Omic and activity-level data acquisition confirmed that dynamic soil water content affects microbial C cycling processes at both the cellular and ecosystem levels. In all, our results suggest that, while sensitive to rainfall events and seasonal drying, microbial communities and activities are resilient over multi-annual time scales to shifts in precipitation frequency and express a variety of physiological strategies to cope with drought stress in prairie soils.