

## Microbial response to modified precipitation patterns in tallgrass prairie soil: molecular mechanisms, activity rates and organic matter dynamics

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Goal: Identify microbial physiological responses to modified precipitation in Great Plains prairie soils, and assess the implications for carbon cycling dynamics.

<http://cropandsoil.oregonstate.edu/soils/research/myrold/konza>

A significant amount of carbon (C) is processed and stored in prairie soils: grasslands cover 6.1-7.4% of the earth's land surface and hold 7.3-11.4% of global soil C. Global change models predict that the future precipitation regime across the North American Great Plains will entail less frequent but larger rainfall events. The response of prairie soil microbial C processing and allocation to this scenario of higher hydrologic variability is not known, but will be a key determiner of the future capacity for prairie soil C sequestration. We are approaching this problem by assessing soil microbial function (respiration, C utilization efficiency, extracellular enzyme activity) and molecular indicators of dominant C allocation pathways (soil transcriptome, proteome and metabolome) under ambient and experimentally modified precipitation regimes.

The Rainfall Manipulation Plots (RaMPs) at the Konza Prairie Long-Term Ecological Research (LTER) site in north-eastern Kansas, USA is a replicated field manipulation of the timing and magnitude of natural precipitation that was established in 1998. This experiment does not modify the total amount of growing season rainfall, it imposes extended dry periods and larger, less frequent rainfall events. We collected soil before, during and after rainfall events in both ambient and extended precipitation interval (more "droughty") treatments and measured microbial growth, respiration and potential organic matter degradation responses. Notable results include (1) Equivalent rainfall events caused equivalent microbial respiration responses in ambient and interval manipulation plot soils, but biomass increased after the rainfall in the extended precipitation interval plots only. This implies a greater C use efficiency, or greater potential for belowground C retention, in "droughty" soils. (2) C:N ratio of biomass was increasingly high as soil water content decreased. This implies a physiological and/or population-level shift in the microbiota at low soil water content. (3) Extracellular enzyme activity responses were mixed across the suite of functional groups measured, with one consistent response: cellulose hydrolysis potential was always lower 5 days after rainfall. This implies a decreased dependency on soil organic matter degradation, with a lag period, after rainfall events; perhaps related to plant activity and root exudate deposition belowground.

These results lead to hypotheses regarding microbial physiological adaptation to drought

stress in prairie soils. We are collecting molecular data (454 sequencing and QPCR of bacterial 16S rRNA and fungal ribosomal genes and transcripts, full transcriptomes and proteomes) to test these hypotheses. (H1a) Microbial taxa that respond quickly to increased water availability after drought are more active in soil with an altered precipitation regime history. (H1b) Transcripts and proteins from COGs indicative of growth, not maintenance, will be more abundant after rainfall in the “droughty” plots. (H2a) In soils with low water contents, transcripts and proteins driving trehalose (or other compatible solute) production will be more abundant. (H2b) In soils with low water contents, fungal cells will be more abundant. (H3) Higher root exudate uptake and metabolism 5 days after rainfall events will be evidenced by higher abundance of sugar and amino acid transporters. Directly addressing these mechanistic hypotheses would not be possible without “Omics” approaches.

*This research is sponsored by the DOE-BER, Biological Systems Research on the Role of Microbial Communities in Carbon Cycling Program, under Contract No. DE-SC0004953.*