Linking microbes to soil metabolism

Kirsten S. Hofmockel[1,2*] (kirsten.hofmockel@pnnl.gov), Racheal Erb[1], Sheryl Bell[1], Adina Howe[1], Will Christer[2], Galya Orr[2]

[1]Environmental Molecular Sciences Laboratory, Pacific Northwest National Laboratory, Richland, WA;[2]Iowa State University, Ames, IA

*kirsten.hofmockel@pnnl.gov

Project Goals: Our project (Microbial drivers of global change at the aggregate scale: linking genomic function to carbon metabolism and warming) works towards a basic understanding of the microbial ecology that regulates cellulose decomposition in grassland soils. We seek to identify the functional traits and community interactions that are responsible for the decomposition of root-derived C and the implications this has for long term soil C storage and release.

Abstract text. Grasslands are a critical yet understudied component of land-atmosphere C exchange. Globally, grasslands represent ca. 30% of global land area and terrestrial net primary productivity (NPP)(Chapin et al. 2002), contain ca. 20% of the world's soil C (Schlesinger 1977, FAOSTAT 2009), and store the majority of their C belowground in root biomass (Neely et al. 2009). Yet, little is known about the microbial pathways regulating cellulose decomposition under field conditions due to the extreme microbial diversity, and the temporal, chemical, and structural complexity of soil ecology. We seek to identify the underlying molecular biology and community ecology that regulates cellulose decomposition in grassland soils.

We examined the microbial interactions and metabolic functions involved in the degradation of cellulose in field experiments, lab incubations, enrichment cultures and modeling experiments. To identify key organisms and enzymes involved in root decomposition, we used fluorescently labeled cellulose nanocrystals (Grate et al) in combination with metatranscriptomics in controlled enrichment experiments. We demonstrate that the community level responses (OD, respiration, 16S amplicons) were not significantly different when soil communities were grown with cellulose or fluorescently labeled cellulose nanocrystals over a 10d incubation, suggesting our experimental platform can be used to track the fate of cellulose through soil decomposer communities. Our results reveal that Proteobacteria, which represent 10% of the native soil community, dominated the community in our cellulose degrading experiments, comprising 32% of the enrichment culture and 80% of the community by day 10. Pseudomonadales were the most abundant, increasing from 2% of the community to greater than 50% during the cellulose enrichment experiment. In contrast Firmicutes comprised 40% of the native soil community, but reduced to 27% by the end of the incubation experiment. Bacillales were the dominant order and decreased from 69% of the community in the soil inoculum down to 20% during the incubation. Based on metatranscriptomic analyses we found that transcripts associated with cellobiosidase (CB; 3.2.1.91) increased in abundance over the experiment, with no significant differences in to

β-1,4-glucosidase (BG; 3.2.1.21) and β-1,4-xylosidase (BX; 3.2.1.37). Organisms assimilating the fluorescently labeled cellulose will be analyzed in conjunction with metatranscriptomic data to understand the basic ecology regulating cellulose decomposition in diverse soil communities. By targeting extracellular enzymes typically measured in biogeochemical field studies and organisms native to the soil community, we aim to link reduced lab studies to field approaches and predictive models.

References

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