

Dissection of Carbon and Nitrogen Cycling in Post-Fire Soil Environments using a Genome-Informed Experimental Community

Thea Whitman,^{1,*} (twhitman@wisc.edu), Timothy D. Berry,¹ Nayela Zeba,¹ Monica Fischer,² Neem Patel,² Akiko Carver,² Sara Calhoun,³ Andrei Steindorff,³ Matthew Traxler,² Igor Grigoriev,^{2,3} and Thomas D. Bruns²

¹Department of Soil Science, University of Wisconsin-Madison, Madison, WI; ²Department of Plant & Microbial Biology, University of California-Berkeley, Berkeley, CA; and ³US Department of Energy Joint Genome Institute, Lawrence Berkeley National Laboratory, Berkeley, CA, USA

<https://whitmanlab.soils.wisc.edu/research/>

Project Goals: In this work, we aim to dissect the effects of microbes (fungal and bacterial) on carbon (C) and nitrogen (N) dynamics in post-forest fire soils. Our conceptual framework is rooted in systems biology and ecology, while our experimental approach combines genomics, transcriptomics, metabolomics, microbial community profiling, stable isotope techniques, small scale fire systems (pyrocosms), tightly controlled methods for producing labeled pyrolyzed organic matter, and high-throughput monitoring of C mineralization rates. We have three major research objectives: (1) To determine how dominant post-fire soil microbes affect the fate of PyOM; (2) To assess the interaction between N availability and PyOM mineralization by post-fire microbial communities and individual pyrophilous microbes; (3) To define the network of microbial interactions that facilitate PyOM breakdown over time and the key genes involved in this process.

Wildfires are a natural part of many forest ecosystems, with globally important carbon (C) storage and nutrient cycling consequences, and they are increasing in frequency and severity in western North America [1]. Forest fires affect soil C stocks in complex ways. Some C is released into the atmosphere through combustion, while a large percentage of the C is added to the soil in the form of pyrogenic (fire-affected) organic matter (PyOM). Worldwide, it is estimated that 16% of soil organic matter (SOM) is pyrogenic, while in areas with frequent fires, this number may be as high as 80% [2]. Understanding how wildfires affect SOM cycling requires understanding how microbes respond to PyOM and other post-fire soil conditions. However, our understanding of microbial interactions with post-fire soil is in its infancy. Outstanding questions include: Which microbes are capable of degrading PyOM? What are the relevant genes and metabolites associated with this degradation? How does the presence of nutrients such as nitrogen (N) affect post-fire PyOM and SOM degradation? What are the key interactions among post-fire microbes? We have developed resources during our previous DOE grant (DE-SC0016365) that enable us to dissect the post-fire environment. These include: a ¹³C₂ labeling growth chamber, a “charcoalator” for producing PyOM, “pyrocosms” for simulating depth-resolved effects of fire, and a collection of genomic resources including 12 genome-sequenced pyrophilous fungi and more than 80 pyrophilous bacterial isolates. We are now using these in combination with genomics, transcriptomics, metabolomics, and stable isotope techniques to address the following specific objectives: 1) Determine how dominant post-fire soil microbes

affect the fate of PyOM; 2) Assess the interaction between N availability and PyOM mineralization by post-fire microbial communities and individual pyrophilous microbes; 3) Define the network of microbial interactions that facilitate PyOM breakdown over time and the key genes involved.

For Objective 1, we are using cultured isolates, defined post-fire substrates, genomic tools, and mass spectrometry to dissect the metabolic roles of these pyrophilous microbes. This objective ties in directly to Objective 2 (influence of N on PyOM degradation) and Objective 3 (defining the network of microbial interactions), as the realized metabolic activities of the dominant microbes determined in this part of the work will inform our models of these higher order processes. For Objective 2, we are targeting the following questions: (1) How available to microbes are the N-containing compounds that are retained by PyOM and soils during fire? (2) How does the addition of these N compounds affect SOM and PyOM decomposition rates and the microbes responsible for this decomposition? (3) What are the molecular mechanisms by which post-fire increases in mineral N affect PyOM degradation by microbes? We are approaching these questions first by adding N amendments to the series of experiments described in Objective 1 using our collection of isolated fungi and bacteria, and then using natural microbial communities with laboratory incubations. For Objective 3, our goal is to understand the fungal/bacterial interactions that underlie the observed patterns in post-fire nutrient cycling. At the conclusion of this goal, we will have (1) generated a map of interactions between the major fungal/bacterial taxa, (2) categorized the mechanisms underlying these interactions, and (3) leveraged genomics data to identify genes involved in successional transitions. This information will enable us to construct a conceptual model that accounts for the dynamics of this microbial community, and specifically how these interactions influence metabolism and resource utilization in post-fire soils. Together, our findings will be relevant for ecosystem management, post-fire recovery, and fundamental microbial genomics, ecology, and biogeochemistry.

References

1. Westerling, A.L., Hidalgo, H.G., Cayan, D.R., and Swetnam, T.W. 2006. Warming and earlier spring increase western US forest wildfire activity. *Science* 313, 940-943.
2. Lehmann, J., Skjemstad, J., Sohi, S., Carter, J., Barson, M., Falloon, P., Coleman, K., Woodbury, P., and Krull, E. 2008. Australian climate-carbon cycle feedback reduced by soil black carbon. *Nature Geoscience* 1, 832-835.

Funding Statement

This work was funded by the Department of Energy, Systems Biology Enabled Research on the Roles of Microbiomes in Nutrient Cycling Processes program, grant DE-SC0020351 to Thea Whitman, Thomas D. Bruns, Matthew Traxler, and Igor Grigoriev. The work conducted by the U.S. Department of Energy Joint Genome Institute, a DOE Office of Science User Facility, is supported by the Office of Science of the U.S. Department of Energy under Contract No. DE-AC02-05CH11231.