

Title: Life After Fire: Microbial Community Dynamics Over Time in Fire-Affected Soils

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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.

Abstract text:

Wildfires are a natural aspect of many forest ecosystems that dramatically effects both community composition and nutrient cycling dynamics. Importantly, wildfires are increasing in frequency and severity, and this trend is projected to continue due to climate change. Bacteria and fungi are the first-responders within days-to-weeks after fire. As pioneer species, these organisms are poised to affect the entire trajectory and outcome of post-fire succession and ecosystem recovery. Previous work has demonstrated a clear successional pattern in soil fungal communities that occurs within roughly the first year following fire (1). Furthermore, fungi in the genus *Pyronema* are the first to dramatically dominate the post-fire fungal community, and *Pyronema domesticum* can breakdown the complex aromatic compounds that are characteristic of charcoal and pyrolyzed organic matter (1, 2). We produced a high-resolution dataset describing post-fire succession of both bacteria and fungi at a fine temporal scale following prescribed fires at an experimental pine forest (UC's Blodgett Forest). We collected triplicate soil samples at least once/month for 17 months in four different plots: high-intensity burn, moderate-intensity burn, low-intensity burn, and a no-burn control. In all plots we collected at least one time-point prior to treating the plot with fire. From these soil samples we extracted total DNA, amplified the 16S region of bacteria or the ITS region of fungi, and then sequenced these community amplicons. Here we present our preliminary analysis of this community DNA sequencing data. We show the structure of the microbial communities in each plot, and how these communities change over time in response to fire, soil pH, and seasonal weather patterns. These data provide critical information about the initial stages of post-fire recovery, in particular, the bacterial component of post-fire succession. Additionally, these data point toward key

organisms that warrant further investigation into the specific role they play during post-fire succession.

References/Publications

1. Bruns TD, Chung JA, Carver AA, Glassman SI. A simple pyrococosm for studying soil microbial response to fire reveals a rapid, massive response by *Pyronema* species. *PLoS ONE*. 2020;15: e0222691. doi:10.1371/journal.pone.0222691
2. Fischer MS, Stark FG, Berry T, Zeba N, Whitman T, Traxler MF. Pyrolyzed substrates induce aromatic compound metabolism in the post-fire fungus, *Pyronema domesticum*. *advanced stage of preparation for submission*.

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