

Functional genomics of pyrophilous fungi – determining the fate of pyrolyzed carbon in post-fire soils

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https://genome.jgi.doe.gov/Pyrophilous_Fungi

Project Goals: Our overall goal is to understand how the post-fire fungal community affects the fates of pyrolyzed carbon and soil carbon in early post-fire soil environments. We will address this overall goal in the context of the following objectives: 1) Develop improved genomic and other -omic resources for the dominant fungi in this system. 2) Determine the temporal response of soil microbes to fire and to pyrolyzed organic matter additions under controlled conditions. 3) Characterize the extractable fractions of pyrolyzed organic matter, their temporal patterns of degradation, their effects on soil organic carbon mineralization, and the soil microbes driving these processes.

Forest fires are a necessary disturbance in forest ecosystems and historically occur at regular intervals. Although forest fires are a natural occurrence, severe forest fires affect larger areas of land than is expected for their fire regimes, causing damage to wildlife and human communities. Forest fire recovery depends on the ecological succession of soil microbial organisms as well as flora and fauna, but little is known at the microbial level. What is known is that forest soil changes greatly after fire, with an enrichment of dead biomass and partially pyrolyzed or “charred” carbon compounds. Soil chemistry also changes, with melted waxes, lipids and cutins creating hydrophobic conditions that can lead to erosion and landslides. In the direct aftermath of forest fires, post fire soils are dominated by pyrophilous fungi, or filamentous fungi that are known to fruit exclusively on burned soil. As the earliest soil fungal colonizers, pyrophilous fungi may have an important role in post fire soil recovery and may help determine the fate of post fire soil carbon, but little is known about the organisms or their adaptation to their environment. Here, we have sequenced, annotated, and compared the genomes of 10 pyrophilous fungi (7 Ascomycetes and 4 Basidiomycetes) to 24 of their non-pyrophilous relatives and found expansions in gene families related to substrate metabolism, stress response capabilities, and secondary metabolites. Amongst pyrophilous ascomycetes species, we found expansions in many substrate utilization genes including CAZymes such as curdlanases (GH132), cutinases (CE5), carbohydrate binding modules (CBM 50), chitin binding modules (CBM 14), and phospholipases. Expanded protease families include serine aminopeptidases, metalloproteases, Caspases (C14B), and ubiquitin-specific proteases. On the basidiomycetes pyrophilous species, we found several rapidly expanded families such as xylanases (GH10), xylan esterases or cutinases (CE5), multicopper-oxidase (AA1), metalloproteases, p450, ABC/MFS transporters,

and DNA repair gene XPG1. *Coprinellus angulatus* genome showed the highest rate of expansions compared with genomes of other *Coprinellus* species, totaling 61 families (22 containing signal peptide) and 584 genes including heat-shock protein hsp70, chitin synthase III and signaling proteins G-alpha/Pkinase. This study will help us increase our knowledge of adaptive advantages that have evolved in pyrophilous fungi and the role of these organisms in post fire succession.

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