

Influence of fire on native microbial communities in forest soils associated with the fungal pathogen *Armillaria solidipes*

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The virulent root disease pathogen *Armillaria solidipes* causes a white rot of conifers in the western USA, leading to tree mortality and altering forest structure. Few effective methods are available for managing *Armillaria* root disease on the landscape scale. While previous studies have indicated the potential for the soil microbial community, including biological control agents, to influence the disease activity of *A. solidipes*, these communities will likely be impacted by increasingly common wildfires in these forest ecosystems. This research aims to determine the potential influence of varying degrees of wildfire severity on native microbial communities in forest soils associated with *A. solidipes*. In Fall 2022, soil samples were collected from the base of 15 western white pine (*Pinus monticola*) and 15 Douglas-fir (*Pseudotsuga menziesii*) trees in northern Idaho, one year after a wildfire occurred at variable severity across the area. Fungal and bacterial species that potentially act as biological controls for *A. solidipes* were isolated from the soil samples and established in pure culture. Preliminary results from dual culture confrontation tests have identified five fungal species and five bacterial species that are effective at restricting the growth of *A. solidipes* *in vitro*, including multiple *Trichoderma* spp. and *Bacillus* spp. Results from the tagged-amplicon sequencing of the rDNA ITS2 region of fungal DNA and 16S V4-V5 region of bacterial DNA have revealed differences in the richness and alpha diversity of bacterial communities among different levels of fire severity, with unburned soils having higher richness and diversity than burned sites. In contrast, no significant changes in fungal community richness and diversity were observed at 1 year post fire, which suggests either a lack of change following fire or a rapid recovery to pre-fire conditions. However, changes were observed in the relative abundance of some bacterial and fungal families following fire. For example, the bacterial family Enterobacteriaceae, which has previously been associated with *A. solidipes*, was more abundant in soils from less severely burned areas. Additionally, a proliferation of Suillaceae, a family of ectomycorrhizal fungi that can benefit tree health, was found in soils of low-severity burns when compared with both soils from high-severity burns and unburned sites. While further research is required to determine which taxa are important for promoting or suppressing the disease-causing activity of *A. solidipes*, these results suggest the potential for low-severity fires to be part of a management strategy for *Armillaria* root disease. In general, understanding how fire influences the soil microbial communities in areas where *A. solidipes* is prevalent can promote the development of more effective management strategies for *Armillaria* root disease.

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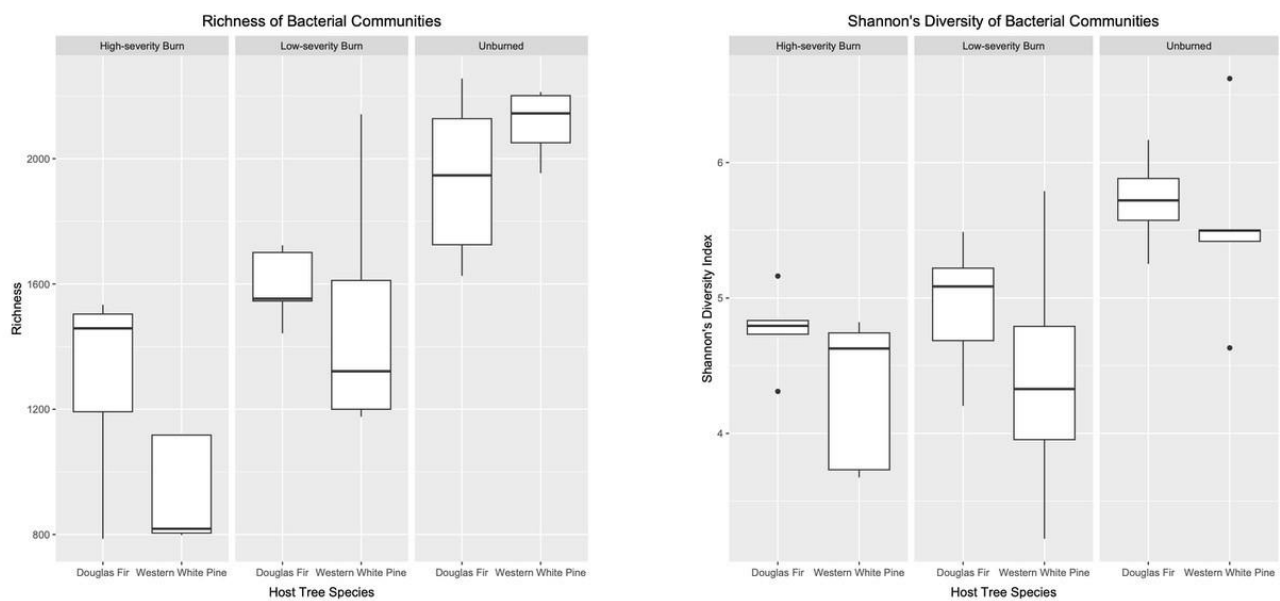


Figure 1: Changes in the richness and alpha diversity, as measured by Shannon's diversity index, of soil bacterial communities with differing levels of fire severity.

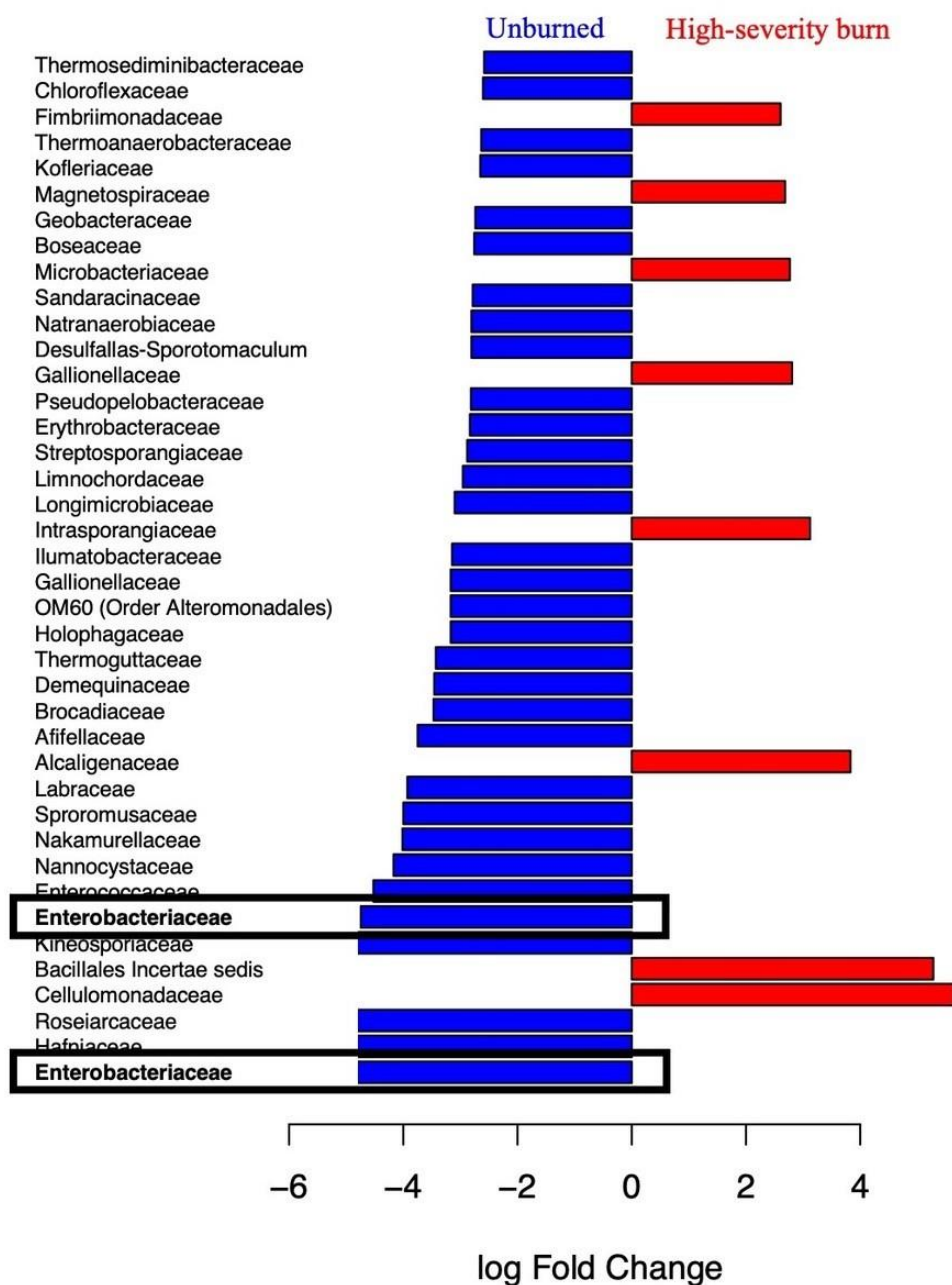


Figure 2: Log-fold change graph indicating bacterial families driving significant differences between soil microbial communities in unburned (blue) and high-severity burn (red) sites. The bacterial family Enterobacteriaceae (bold), which has been previously associated with the microbial community of *Armillaria solidipes*, is more prolific in soil microbial communities of unburned sites.

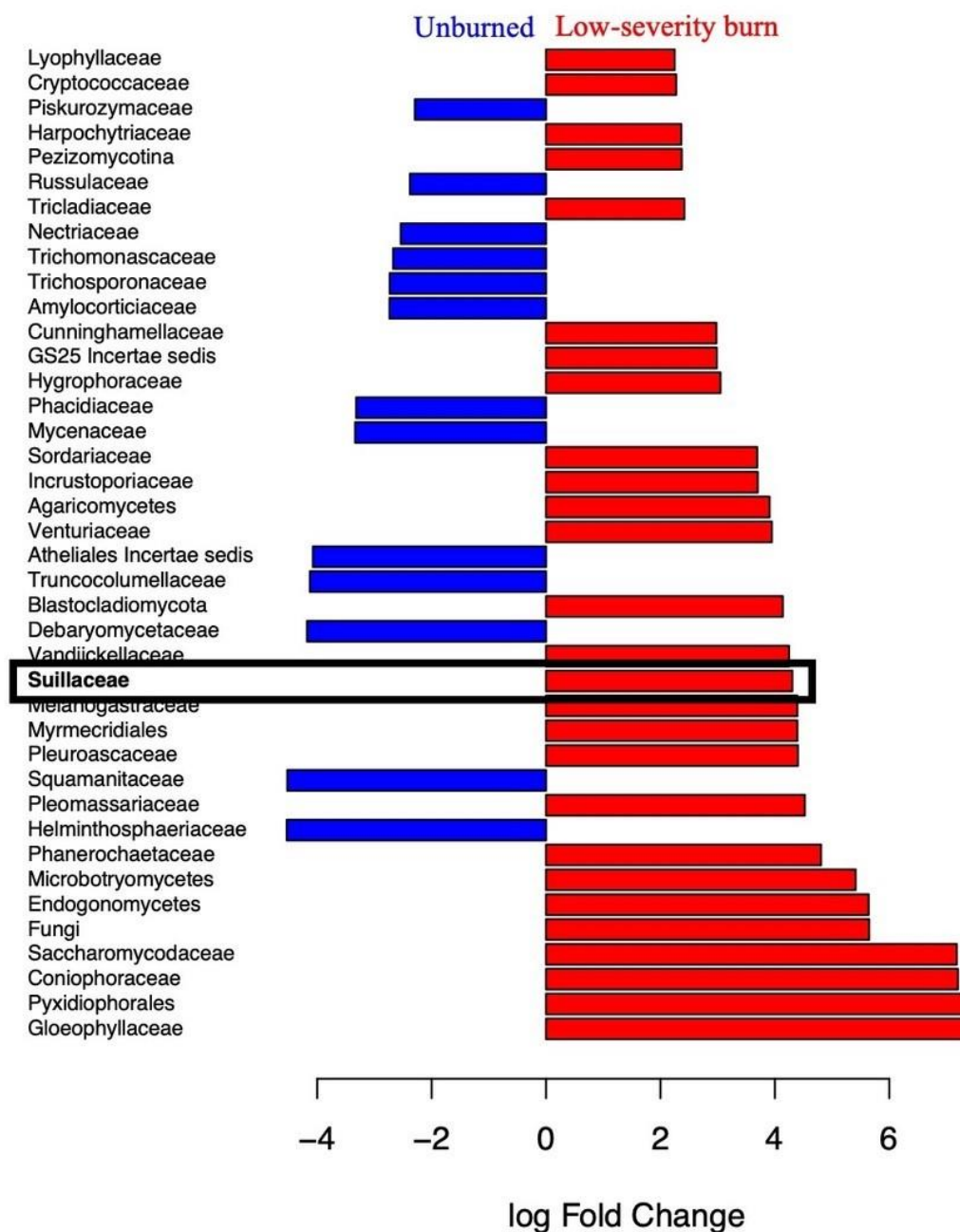


Figure 3: Log-fold change graph indicating fungal families driving significant differences between unburned (blue) and low-severity burn (red) microbial communities. **Suillaceae** (bold), a family of beneficial ectomycorrhizal fungi, is more abundant in soils from low-severity burn sites.

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