

## Fungal community shifts in structure and function across a boreal forest fire chronosequence

**Hui Sun<sup>a,b</sup>, Minna Santalahti<sup>a</sup>, Jukka Pumpanen<sup>b</sup>, Kajar Köster<sup>b,c</sup>, Frank Berninger<sup>b</sup>, Tommaso Raffaello<sup>b</sup>, Ari Jumpponen<sup>d</sup>, Fred O. Asiegbu<sup>b</sup>, Jussi Heinonsalo<sup>a</sup>**

<sup>a</sup>Department of Food and Environmental Sciences, University of Helsinki, P.O. Box 56, FI-00014 Helsinki, Finland

<sup>b</sup>Department of Forest Sciences, University of Helsinki, P.O. Box 27, FI-00014 Helsinki, Finland  
<sup>c</sup>Institute of Forestry and Rural Engineering, Estonian University of Life Sciences, Kreutzwaldi 1, Tartu 51014, Estonia

<sup>d</sup>Division of Biology, Kansas State University, 433 Ackert Hall, Manhattan, 66506, USA

Email: [hui.sun@helsinki.fi](mailto:hui.sun@helsinki.fi)

Wildfire is a common natural disturbance in forested ecosystems. It is crucial to understand the responses of soil fungal communities to wildfire as fungi contribute to biogeochemical cycling in soil, by e.g. degrading soil organic matter (SOM) and releasing nutrients from organic sources.

Using high-throughput sequencing of the ribosomal RNA gene markers, coupled with functional gene array, we investigated fungal community structure and its potential function across a boreal forest fire chronosequence (2-152 years post-fire).

Our analyses revealed that boreal forest soil harbored the most diverse fungal community two years after fire and its diversity subsequently decreased with increasing time since fire. Differences in fungal community structure were primarily caused by changes in the abundance of Basidiomycetes and Ascomycetes. Ectomycorrhizal (ECM) fungi contributed to the increase of basidiomycetes over time, with OTUs representing *Cortinarius* and *Piloderma* dominating.

The sites with different post-fire times formed site-specific clusters indicating potential differences in essential biogeochemical processes in soil. The site after fire with highest biological diversity had also the most diverse gene pool. In the mature forest where ECM fungi were the most abundant, the genes involved in the organic matter degradation were as common as in the site where saprotrophic fungi had relatively higher abundance. This supports the hypothesis that ECM fungi could play a role in soil organic matter decomposition and organic N transformations.

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