Changes in composition and diversity of soil fungal communities along an age gradient of old-growth boreal forests in northwestern Quebec, Canada

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Context

Old-growth forests in eastern Canada are recognized as **unique reservoirs of biodiversity** and **hotspots of fungal diversity**, particularly for **ectomycorrhizal fungi**. Old-growth forests are increasingly recognized as highly heterogeneous and structurally diverse ecosystems, yet little is still known about how **soil fungal communities** vary among different types of old-growth forests.

Objectives

Our objective was to explore how **patterns of composition** and **diversity** in soil fungal communities vary among **old-growth boreal forest type**, and to test the **effect of time since the last fire** (TSF hereafter) on these patterns. The **dating of ancient fires** from 1944 to 1760 years ago found in the **Duparquet Lake Teaching and Research Forest** offers a unique opportunity to evaluate the dynamics of fungal communities in old-growth boreal forests.

Hypothesis

We hypothesized that **(1)** patterns of diversity, community composition, and relative abundances would be taxa- and guild-specific and would not necessarily follow linear trends along successional stages; **(2)** TSF would have significant effects on the diversity and community composition of soil fungal communities, notably through changes in soil physicochemical properties; and **(3)** regardless of successional patterns, the ectomycorrhizal fungi would remain the dominant guild along the post-fire chronosequence.

Material & Methods

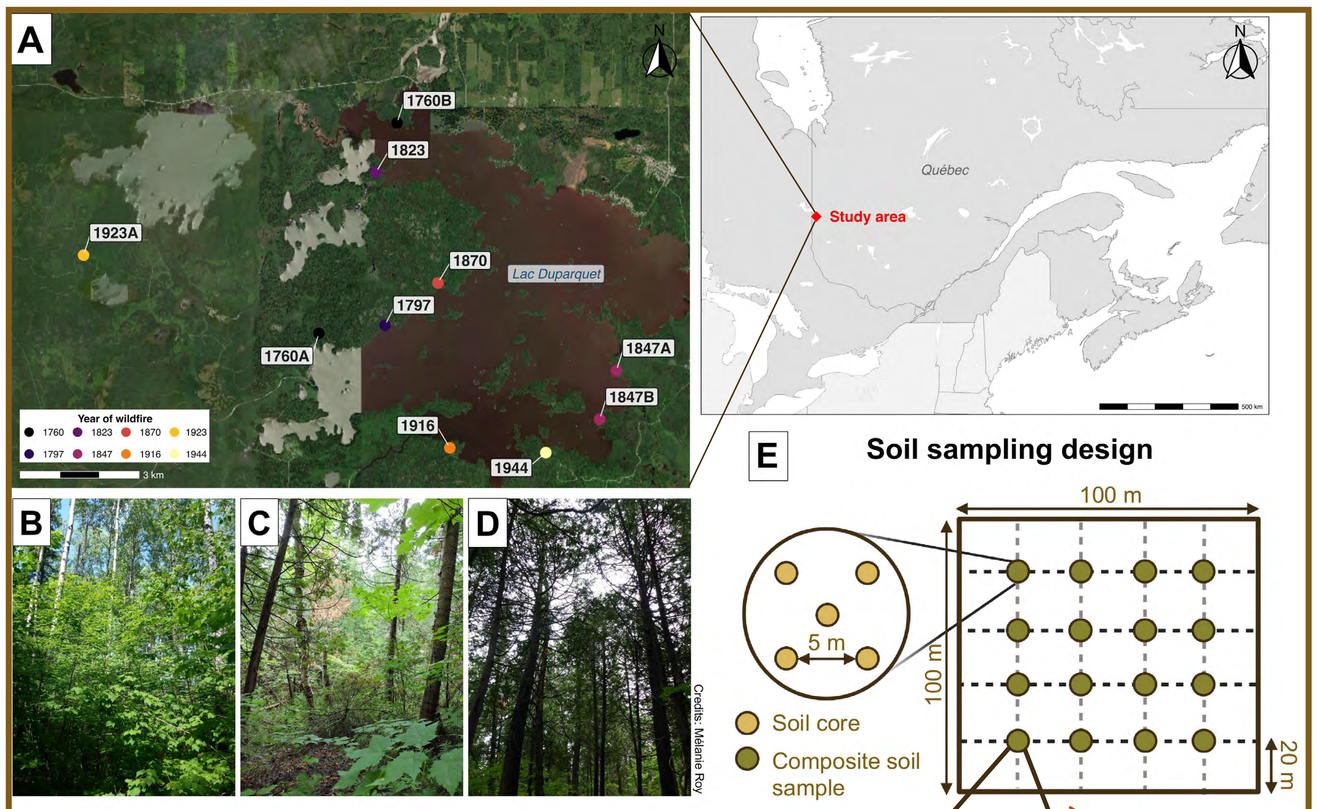

Figure 1. A. Location of the 11 sites (colored points) along the post-fire chronosequence at the Lac Duparquet Teaching and Research Forest (FERLD; 48°30' N, 79°1' W). **B–D.** In situ photographs of deciduous-dominated, mixed, and conifer-dominated stands of the chronosequence, respectively. Photo credit: Mélanie Roy. **E.** Schematic representation of soil sampling design with the 16 composite soil samples collected within each one-hectare plot.

Results

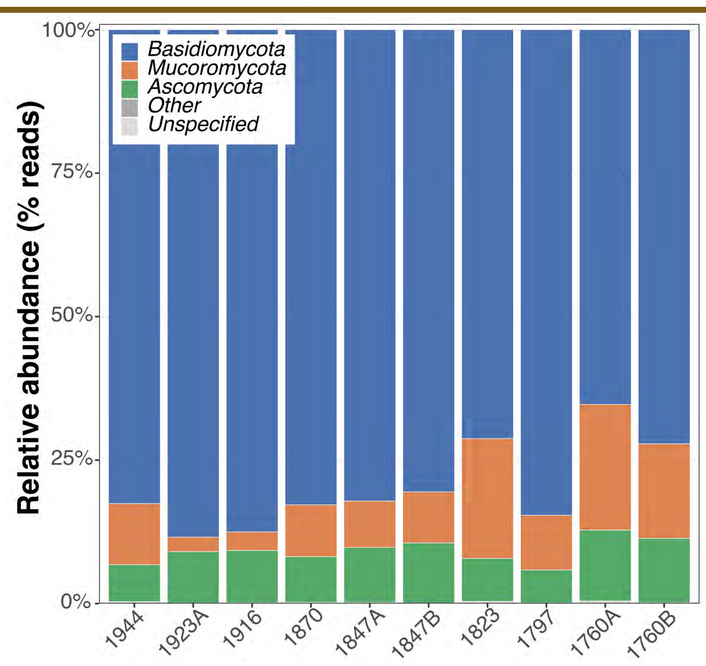

Figure 2. Stacked bar plots of the relative abundance of fungal phyla across the post-fire chronosequence.

- **Basidiomycota**, followed by **Mucoromycota** and **Ascomycota**, were the three most abundant phyla.
- Relative abundance of **Archaeorhizomycetes** significantly increased with TSF, whereas the relative abundance of **ectomycorrhizal fungi** significantly decreased with TSF (DESeq2).
- **Mucoromycota** and **arbuscular mycorrhizal fungi** tended to be more abundant in older old-growth stands.

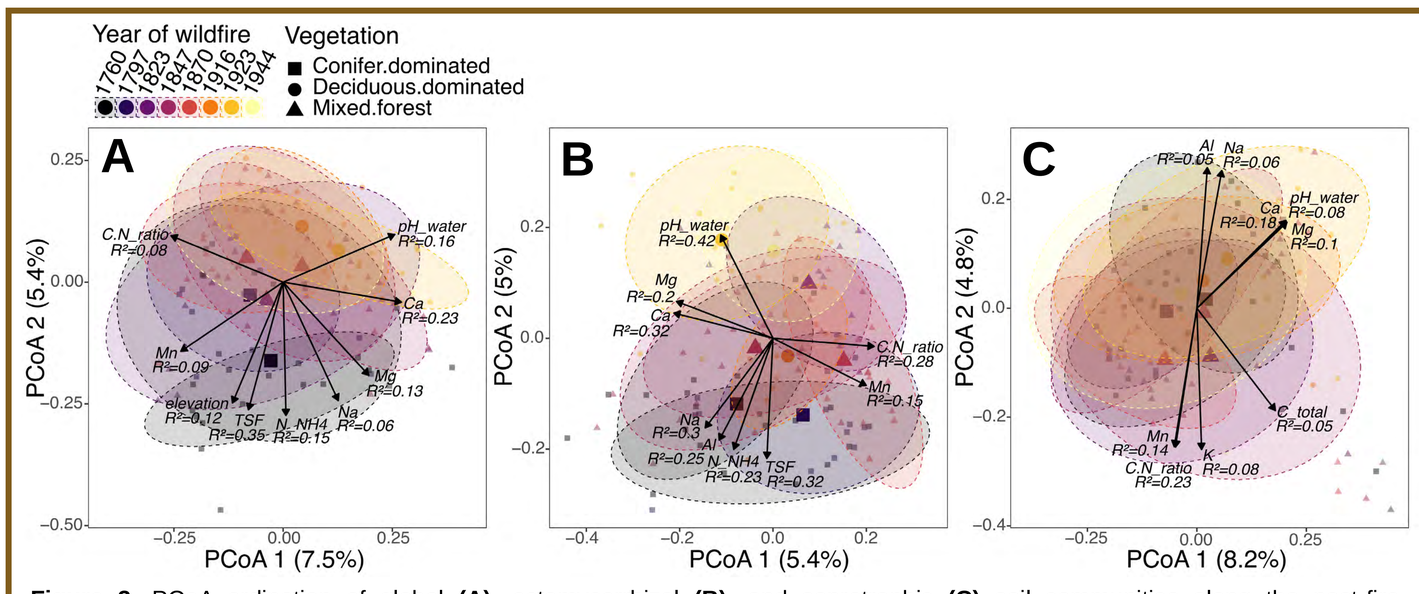

Figure 3. PCoA ordination of global **(A)**, ectomycorrhizal **(B)**, and saprotrophic **(C)** soil communities along the post-fire chronosequence, with physicochemical variables fitted using envfit (only variables with $p < 0.05$ are shown, along with R^2 values).

- Global, ectomycorrhizal, and saprotrophic **community composition differed significantly with TSF** (PERMANOVA test, $p < 0.01$).
- **Beta diversity** (distance to centroid), calculated using betadisper, increased significantly with TSF only for ectomycorrhizal fungi.
- The best-fitting **GAMs** for the global and ectomycorrhizal communities included only TSF as a significant factor influencing the three **Hill numbers (q0, q1, q2)**. For the saprotrophic community, the best-fitting GAMs for the three Hill numbers included as a significant factor only the first principal component (PC1) from a PCA of the **physicochemical variables**.

Conclusion & perspectives

Soil fungal communities are **highly diverse among old-growth forests** and **change across successional stages** alongside the vegetation shifts associated with TSF. However, the relative importance of TSF and soil physicochemical properties in structuring these communities is **taxon-dependent**, raising questions about the **environmental factors driving local-scale heterogeneity** in soil fungal communities within old-growth forests. This type of knowledge will be important for **sustainably integrating funga into forest management** by recognizing the diversity and complexity of soil fungal communities within old-growth forests and ultimately **developing tools to monitor** these overlooked yet essential components of forest biodiversity.

Thanks to our funding partners

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Fonds de recherche Québec
CRSNG NSERC
Ressources naturelles et Forêts Québec
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