# Recovery of Soil Fungal Community: Monoculture Plantation versus Natural Regeneration

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The recovery of ecosystem functioning to the natural forests is one of the main challenges of forest restoration worldwide these days. While monoculture plantations have been the most common practice of forest restoration, a number of studies have demonstrated that these forests have lower levels of biodiversity and ecosystem functioning, especially in terms of carbon storage, than natural forests. Forests in the northern area identified as a critical carbon sink, monoculture plantations have been expanding rapidly on the deforested land but there is a growing interest in natural regeneration (also as known as passive forest restoration). Some studies have compared vegetation recovery with and without human intervention. However, little is known about the succession of soil fungi during forest development even though they play a vital role in regulating multiple ecosystem functions such as nutrient cycles, plant growth and carbon budget. Here we aimed to compare the successional development and the recovery of soil fungal communities among different forest types.

The study sites were the Teshio experimental forest of Hokkaido University located in the northern part of Hokkaido, Japan (Fig. 1). We established 33 study sites in three forest types: natural forest, *Picea-glehnii* plantation and secondary forest. To assess the fungal succession trajectory in each forest restoration type, these sites were designed to have different stages of forest development (chronosequence approach from 0 to 50 years). Soil samples were collected in three replicates at each plot and sequenced using DNA metabarcoding. The procedures used for bioinformatics analyses followed those described by Matsuoka et al., 2019. The Jaccard dissimilarity index between all samples was calculated and visualized using principal coordinate analysis (PcoA). We showed the change in OTU richness and the dissimilarity index along the forest age, and then fitted a linear model on the soil fungal community data.

The Ascomycota was the most abundant bacterial phylum, followed by the Basidiomycota, Mucoromycota, Chytridiomycota, Zoopagomycota, Cryptomycot and Blastocladiomycota, as well as 5% of the OTUs could not be identified to phylum. OTU richness significantly decreased with time in plantations but not significantly in natural regeneration forests (Fig. 2). In the plantation, there was no relationship between the Jaccard dissimilarity index with natural forest and forest age while the index significantly decreased in the regeneration forest (Fig. 3). In addition, the fungal communities of the secondary forest became similar to those in the natural forest as the stage developed (Fig. 4).

We found that there were different successional patterns of fungal communities across the forest restoration types. Previous studies confirmed that the plant community plays an important role in the soil microbial community structure via litter chemical properties and root exudation. Differences in tree species composition could have affected the soil fungal community structure. Moreover, our findings imply that natural regeneration could be a successful approach for restoring fungal communities.

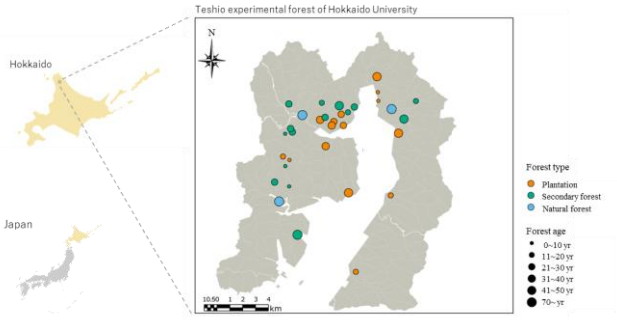


Fig. 1: The study site of the Teshio experimental forest of Hokkaido University. Different colors of points refer to three different forest types. Orange, plantation; Green, secondary forest; Blue, natural forest.

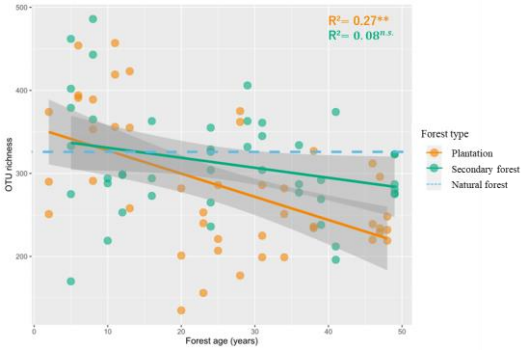


Fig. 2: Operational taxonomic unit (OTU) richness of fungi during forest succession. Different colors of points refer to three different forest types. A dotted line indicates the average number of OTUs in all plots of natural forest.
** $P < 0.01$.
n.s. $P > 0.05$.

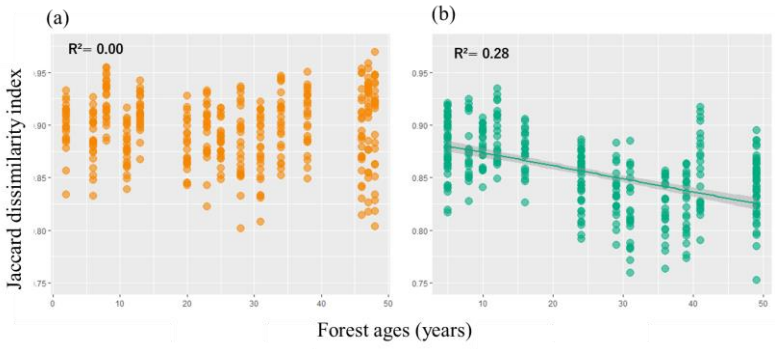


Fig. 3: Relationships between forest age and similarity of fungal communities. Jaccard similarity coefficient with natural forest calculated (0: similar, 1: dissimilar) for all plots of plantation (a) and secondary forest (b). If linear regression with forest age appears significant for $p < 0.05$, the trend line and 95% credible intervals are given.

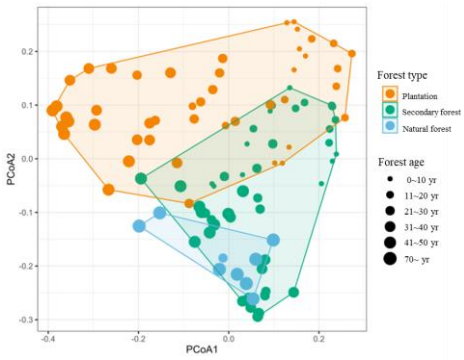


Fig. 4: Principal coordinate analysis on the Jaccard similarity index matrix of all plots highlighting the three different forest-type.

## References

Matsuoka, S., Sugiyama, Y., Sato, H., Katano, I., Harada, K., and Doi, H, Spatial structure of fungal DNA assemblages revealed with eDNA metabarcoding in a forest river network in western Japan, Metabarcoding and Metagenomics, 3, 37–47, 2019.