Standing at the crossroads: Path analysis highlight potential levers for foresters to preserve fungal taxa richness when changing dominant trees for forest adaptation

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Résumé

Present tree species face near-future risk of living out of their optimal ecologic range because of local consequences of climate change, aggravating forest dieback and impact forest ecosystem services. In order to adapt forests, practices by forest managers are changing and may impact biodiversity, *e.g.* in forest soils hosting complex multi-taxonomic networks. Renewing forest stands with exogenous tree species or varieties is one of the most recommended practices for forest sustainability, hence this study addresses responses of soil fungal communities to tree substitution and the underlying mechanisms behind these changes. Also, this study aims at also documenting the effects of transitioning from coniferous trees to deciduous, as most studies focus on substitution within deciduous or coniferous - that is with general tree traits conservation.
Three substitution treatments were tested over 69 forests stands in Northern France: (1) from mature *Fagus sylvatica L.* towards young *Quercus petraea* Liebl., (2) from mature *Pinus sylvestris* L. to young *Pinus nigra* var. *corsicana* Poir. and (3) from mature *P. sylvestris* to young or *Quercus rubra* L. Organic layer and topsoil were sampled to describe soil fungal community composition by eDNA metabarcoding, and high-throughput sequencing data were taxonomically assigned using the PIPITS bioinformatic pipeline and UNITE reference database. Forest ecological context was further assessed by describing humus forms, phytosociology, stand structure and canopy openness. Fungal and plant community diversities were described with richness and Shannon indices. For a functional approach, dominant tree species identity was translated into a trait value (database TRY) on the plant economic spectrum.

Ascomycota, Basidiomycota and Mortierellomycota richnesses did not correlate significantly with substitution modality, possibly due to variation in stand structure, age or tree diversity. A Structural Equation Model method was used to separate the effect of dominant tree identity, stand age, stand structure and tree diversity on fungal diversity toward four paths: (1) stand vertical structure, (2) understorey microclimate, (3) vegetal diversity, (4) humus form.

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Our results indicate that the main tree species identity and the age affects stand structure variables, altering the understorey microclimate. Age and main tree species identity also had an effect on the humus form affecting understorey plant diversity. Responses of fungal richness varied amongst taxa and between organic layer and topsoil. For instance, in organic layers both Ascomycota and Basidiomycota richnesses increased directly with dominant tree diversity but decreased with second layer tree abundance. In topsoil, Ascomycota richness decreased with dominant tree density and air humidity while Basidiomycota richness directly increased with air humidity, dominant tree diversity and understorey diversity and was modulated by dominant tree identity. Eventually, Mortierellomycota in both layers responded directly to understorey diversity.

In conclusion, change in dominating tree specie and age can impact directly or indirectly the different fungal taxa richness in soil and litter, for instance *via* the alteration of humus layer. However, those effects are not mandatory and forester could leverage it by tree mixing and *ad hoc* management of understorey and stand vertical structure, thus adapting forest stands to global change without losing in fungal richness.

Mots-Clés: Forest adaptation, soil fungal communities, path analysis, soil biodiversity