## PROJECT INFORMATION

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| **Project title:** | **Spatiotemporal changes in ectomycorrhizal diversity in European forests** |
| **Project ID:** | **309** |
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## PROJECT DESCRIPTION

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Mineral nutrition is a central to the demography of forest trees (ICP Forests, 2020). In Europe, phosphorus (P) is becoming increasingly limiting for tree growth (Talkner *et al.*, 2015), notably because of an increase of nitrogen (N) availability (Vitousek *et al.*, 2010). Some of the most abundant and widespread European tree species, such as *Quercus robur and Q. petraea*, *Fagus sylvatica*, *Pinus sylvestris* and *Picea abies* rely on ectomycorrhizal (ECM) associations for their N and P supply. Spatial distributions of ECM fungi depend on the presence of their host tree, and are influenced by climate and soil nutrient content but also by atmospheric deposition, notably of N (Cox *et al.*, 2010b; Suz et al. 2014; van der Linde *et al.*, 2018; Lilleskov *et al.*, 2019). Because of the non-linear response of ECM communities to the environment and their complex interactions, small changes in the environmental conditions could drive large shifts in ECM communities, and therefore tree mineral nutrition, pushing forests to a tipping point (Suz *et al.*, 2021). However, recovery of ECM communities following decrease in N pollution is also possible as observed in their fruitbody production (van Strien et al 2018).

In this project, we will investigate spatio-temporal changes in ECM communities along gradients of environmental conditions, particularly climate, soil, and atmospheric deposition. This project is based on a previously published analysis of 137 ECM communities in 137 ICP Forests level II plots, sampled between 2006 and 2015 in 20 countries (van der Linde *et al.*, 2018). We will resample 45 Scots pine and beech sites until summer 2024, to encompass 1) the largest spatial variation in environmental conditions, mostly N deposition, and climate and 2) the largest temporal changes in N deposition and climate since the last sampling.

The sampling and sample processing will follow the same methodology as the first sampling campaign (Cox *et al.*, 2010a; Suz *et al.*, 2014; van der Linde *et al.*, 2018). In each plot, 96 soil cores are collected along 24 transects. In each soil core, three mycorrhizal tips are selected, morphotyped and DNA sequenced for species identification using the ITS region. The change in taxonomic, phylogenetic, and functional diversity will be modelled using a set of Bayesian GLMM with climate, soil and nutrient depositions as explanatory variables (measured in the 5 years before ECM sampling). The asymptotic estimated and effective diversity will be estimated as described in Chao *et al.* (2014). Changes in community composition will be quantified using the same methodological framework as in van der Linde *et al.* (2018). We acknowledge that assessing temporal variation in community composition and diversity can be difficult with two or three time points (Stuble *et al.*, 2021). However, the simultaneous analysis of both “space for time” substitution as well as temporal variation in environmental conditions will allow to ask specific questions, include informative priors and draw robust conclusions (Stuble *et al.*, 2021). Since the first sampling, we expect:

1) Taxonomic, phylogenetic, and functional diversity to be driven by host and environmental characteristics,
2) changes in diversity caused by the changes in environmental conditions (climate, soil, and atmospheric deposition)
3) change in the abundance of nitrophobic species in sites showing changes in N deposition.

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