

Emilia Hannula

(<https://www.nioo.knaw.nl/users/ehannula>)

Supervisor Hans van Veen, NIOO

Fungi are ubiquitous and diverse; the global fungal diversity has been estimated to range upwards from 1.5 million species. At more local scale, fungal diversity is thought to have important consequences for ecosystems. Despite the indications on relationship between fungal diversity and ecosystem function, little is known about this diversity and factors generating and maintaining it. The sheer diversity of life in soil is one of the reasons why soil biodiversity research has lagged behind above-ground studies, especially as majority of the species are not yet been described and can be unculturable. Traditionally, fungi have been divided into discrete ecological guilds, such as leaf litter-decomposers, humus saprobes, white- and brown-rot wood decayers, parasites and mycorrhizal symbionts. However, the actual functionality of individual species, and the synergistic effects among them are often obscure.

Furthermore, even fairly simple systems with defined fungal types, contain fungi with multiple habitats and overlapping functions. However, in more complex systems such as grasslands the functionality of fungal communities is often not known.

Within the EcoFINDERS consortia the fungal diversity is being estimated from five long term observation sites by 454-sequencing technique and this data will be related to other belowground and aboveground parameters. Furthermore, the function of soil fungal communities will be estimated in more detail in one of the sites; a chronosequence of former agricultural lands in different stages of land abandonment located in the Veluwe region in the Netherlands. This will hopefully provide more information about the role of fungi in the establishment of soil microbial communities and their role in the soil functioning. Stable isotope probing approaches will be used to identify soil and plant-associated fungi that respond to ^{13}C and ^{15}N inputs in different soils. The ^{13}C and ^{15}N labeling of intact soil cores collected in summer of 2012 has been performed and soil fungal communities from this experiment will be analysed using PLFA/NLFA-SIP and RNA/DNA-SIP for both community structure and functioning.

Parameters to measure functioning of the fungal communities are being developed and further evaluated with the samples from Veluwe chronosequence. The goal is to develop new and test existing primers to target different fungal functions in order to evaluate the soil fungal communities based on presence and diversity of multiple functional genes. So far, the list of candidate genes include fungal Mn-peroxidases, cellobiohydrolases, laccases, nitrate reductases, glucose oxidases, cellobiosedehydrogenases, oxalate decarboxylase, heme-thiolate peroxidase and 12 different glucosyl hydrolase (GH) families. Fungal cultures have been isolated from the Veluwe soils and all the primers have been tested with DNA from both soil samples and pure cultures. Further analyses will include sequencing analyses of the most suitable candidate genes to compare the functioning of first the Veluwe soils and later possibly also other EcoFINDERS LTOs.