

NEFOM meeting 22nd to 26th of September 2018 – Oulanka, Finland

Presentation abstracts & Discussion summaries

Climate change effects on fungi

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Earth's climate is changing, and this is already affecting fungi. Fungal fruiting phenology is altering in several important ways in western Europe, although differences vary slightly between countries depending on geography: (1) the autumnal fruiting season for many species has extended considerably, having on average doubled in length in the UK in the last 60 yr; (2) while the majority of saprotrophs now fruit earlier, ectomycorrhizal species tend to fruit later in the yr, though fruiting is curtailed by freezing conditions; (3) in the UK, species ectomycorrhizal with both deciduous trees and conifers tend now to fruit later if associated with the former, but remain unchanged if associated with the latter. This indicates important physiological differences in climate responses between these ecosystems. (4) Many saprotrophic species that used only to fruit in the autumn now also fruit in the spring in the UK, indicating that their mycelia are now active in the winter. (5) The spring fruiting season is also changing. (6) Some species that were fairly specific to the wood, leaf litter or living roots of particular trees species appear to be changing their preferences. With regard to mycelia, elevated temperature and altered water regimes affect fungal growth and rate of wood decomposition directly and indirectly via effects on interacting organisms, including other fungi and grazing soil invertebrates. The latter sometimes moderate climate change effects, in model systems, though responses are complex.

Role of climate in distribution and biogeography of fungi

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Fungi are key players in vital ecosystem services, spanning carbon cycling, decomposition, and varied plant symbioses. However, we have strikingly deficient information on the large-scale distributions of nearly all fungal species, and as a result, we have an incomplete understanding of the evolutionary and environmental factors that shape the patterns of fungal biogeography. This deficiency currently prevents us from anticipating possible shifts in fungi-mediated services in a rapidly changing world. Here, we assemble the largest existing dataset on fungal species distributions by screening >450 sources, and use this dataset to quantify the extent of fungal distributions and their primary drivers. In contrast with previous global and continental studies that indicated strong effects of dispersal and evolutionary history, our analyses identify climate as an important driver of fungal biogeography. Climate not only was the primary constraint on the global distribution of three-quarters of the most common fungi but also shaped fungal communities and their diversity. In contrast to plants and most other taxa, we found limited fungal diversity in the tropics, with fungal richness tending to increase at high latitudes. Climate and its ongoing change may also significantly affect ecosystem functioning because of the narrower climatic tolerances of mycorrhizal than pathogenic fungi.

The DRIVE project: The plant root microbiome diversity and resilience in a changing climate

Unni Vik

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I presented my post-doc project on climate effects on root associated fungi of two plants; the ectomycorrhizal forming plant *Bistorta vivipara* and the arbuscular mycorrhizal forming plant *Potentilla erecta*. The project is situated on the west coast of Norway, where an out-door laboratory for climate effect studies is established. The climate grid of the laboratory covers a gradient ranging 3000 – 750 mm annual precipitation and an mean annual temperature average between 6 and 11 degrees celsius. The project consists of three work packages. In WP1, the fungal communities of the two plants in different climates is investigated by means of high throughout sequencing of the entire root system. In WP2, *B. vivipara* plants, transplanted in the direction of climate change in the Northern hemisphere, is investigated. In 2015 plants were transplanted to warmer, wetter, the combination warmer and wetter as well as internal sites as a control. These will be harvested in 2019 and fungal communities will be sequenced. The third work package is a green house experiment where we will study recruitment of the soil microbiome to the plant roots under different temperatures.

Wood-inhabiting fungal communities across climatic and land-use gradients across Fennoscandia

Jenni Nordén

Norwegian Institute for Nature Research (NINA)

It is critical to understand the environmental drivers of species distributions and population trends for planning efficient conservation, management and restoration actions, and to make realistic projections of future population trends under different management and climate scenarios. Analyses of a set of red-listed and non-red-listed species in Scandinavia showed that the red-listed species had a strong positive response to three spatiotemporal connectivity variables – old-forest connectivity at the scale of 100 km, forest age, volume of deadwood – while the non-red-listed species did not. Large volume of deadwood was only beneficial if the large-scale connectivity was high. In Finland, red-listed species showed to be dependent on connectivity at the local (number of suitable dead trees), landscape (connectivity of old forests at a scale of ca. 5 km) and regional (gradient in the duration of intensive forestry from SW to E Finland) scales. Red-listed species may be dependent on connectivity because of ecological specialisation which creates resources limitation and in turn strengthens dispersal limitation, slow dynamics, rarity, small population sizes, and less light-resistant spores. Based on analyses of 443 species as fruit bodies and 1346 OTUs, temperature and precipitation variables seem to override the effect of connectivity for most, though not all, species at a Scandinavian scale. OTU richness increases to the north, but the fruit body data show the opposite trend. Ongoing work aims to reveal the relative roles of climate, land use, site characteristics, species traits, phylogenetic relatedness and species associations in determining the distribution of individuals species and community composition.

Fungal community shifts along a fire severity gradient in a Boreal forest

Leticia Pérez-Izquierdo

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Boreal forest soils store a major fraction of the global terrestrial carbon. However, fires are pervasive disturbances that may critically trigger the carbon loss from these forest soils and in turn, influence the soil microbial communities with important outcomes over carbon dynamics of northern ecosystems. In this talk, I will present some of the results from my postdoc project in which we have studied the fire impacts on fungal communities, fungal transformations of organic matter and soil nutrients on an ecological gradient in fire severity. The study is part of a larger collaborative venture to investigate ecosystem recovery after the Västmanland fire in 2014, the largest Swedish forest fire in modern times. We sampled plots established in burned (differing in fire severity damage) and un-burned areas. Subplots subjected to logging and non-logging treatments were in turn established in each burned plot. As expected, the fire greatly affected the fungal community, which further consequences on the enzymatic activities related to carbon and nitrogen cycling. Two different fire severity gradients governed these processes: one belowground according to the loss of Carbon and one aboveground according to the death of trees. Among the main fungal responses, we observed a loss of ectomycorrhizal function associated with Manganese peroxidase, phosphatase and chitinase activities after the fire. We did not observed any support for the Gadgil effect in burned areas, probably because of the low quality of carbon, although opportunistic moulds producing cellulose hydrolytic enzymes took over the plots with more remaining carbon. The yeast and *Calyptrozyma* yeast-type living fungi are probably resistant species because they were dominant in the highly burned plots. Gaining knowledge about post-fire ecosystem processes and fungal dynamics will contribute to a better understanding of fire ecology and succession of Boreal forests. Moreover, I will compare briefly these results with those from my PhD where I studied the effect of fire recurrence on fungal communities in fire-prone Mediterranean ecosystems.

Finding meta-transcriptomic markers for carbon use efficiency

Fahri Hasby

Tipping-point in C storage related to mode of mycorrhizal N cycling across the arctic tundra-to-forest transition

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Shrubs and trees are currently increasing in tundra areas across the Arctic, a response linked to recent climate warming. Ecotones between forests, dominated by ectomycorrhizal trees, and heathlands, dominated by ericoid mycorrhizal dwarf shrubs, are naturally found in transitions towards arctic and alpine zones, and may be used as space-for-time substitution to reflect long-term consequences of arctic greening on ecosystem level processes such as nitrogen (N) circulation and carbon (C) sequestration. Here, we present results from a subarctic-to-alpine ecotone from mountain birch forest to heath tundra in northern Sweden. We aimed to test the hypothesis that increasing abundance and activity of ectomycorrhizal fungi with increasing shrubs and trees would lead to faster N cycling through soil pools, and consequently lower C sequestration. We found a strong positive

coupling between tree abundance and ectomycorrhizal fungal growth, both of which were negatively coupled with C sequestration. By DNA-metabarcoding of the fungal communities, we saw that while root-associated ascomycetes were abundant along the entire gradient, there was a sharp dominance shift in the ectomycorrhizal basidiomycete community from species with short-ranged mycelia within the genera *Inocybe* and *Tomentella* in the heath to cord-forming species within *Cortinarius* and *Leccinum* in the forest. Higher C/N-ratios, lower inorganic N levels and lower abundance of functional genes reflecting inorganic N cycling in the forest suggested prevalence of organic N cycling by ectomycorrhizal fungi here. Other studies have suggested that species within *Cortinarius* have retained potential to decompose organic matter by producing Mn-peroxidases likely as a means to access organically bound nutrients, while species within *Inocybe* and *Tomentella* have no such potential. Our results support the idea that the presence and relative decomposition capacity of mycorrhizal fungi rather than different litter input quantities or qualities determine long-term C sink strength across this ecosystem gradient.

Plant-Fungal interactions in alpine ecosystems

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Ectomycorrhizal (ECM) fungi are major players in the establishment of woody perennial plants, but despite their importance, they are largely overlooked in alpine ecosystems. During this NEFOM meeting I presented my PhD project entitled Plant Fungal interaction in alpine ecosystems and highlighted some of the preliminary results. The aims of this project are i) identify the biotic and abiotic factors that influence ECM communities across the European Alps; ii) investigate how ECM communities are shaped in hybrid zones of closely related plant species and iii) generate baseline diversity data for ECM fungi against which to assess the impact of climate change. Mycorrhizal roots were sampled from 47 populations of *Dryas octopetala*, *Bistorta vivipara* and *Salix herbacea* across five countries in the Alps and at a hybrid zone between *Salix purpurea* and *S. helvetica* in a glacier valley in Switzerland. Using community analyses, multivariate statistics, ecological network theory and phylogenetic analyses we will analyse plant-fungal interactions and their drivers of change in these harsh environments. We expect to provide new insights into plant-fungal mutualisms in alpine ecosystems and a better understanding of their resilience to environmental shifts driven by climate change.

The effect of microbial viruses in agroforest ecosystems on three different levels

Veera Brusila

Natural Resource Institute Finland

Microbes are everywhere and are found in every ecosystem on Earth. Hidden and frequently underestimated players in these ecosystems are microbial viruses, which infect

bacteria, archaea, and all the major taxa of fungi. Microbial viruses can have beneficial or harmful impacts on their hosts thus influencing their processes, or they can be cryptic. By altering the host gene expression and behavior, viruses have an influence on every system where their host communities act, consequently on every biological system on Earth. In NEFOM-meeting I introduced my PhD project briefly. My PhD project studies microbial viruses from three different perspectives. The first publication focuses on ability to use mycoviruses, i.e. fungal viruses as biocontrol strategy for economically important tree pathogen. The second publication addresses the question about effect of viruses on mycorrhizas and expands this symbiotic relationship between tree and fungus into three-way interaction. The last publication broadens the picture to ecosystem level: According to a new theory, the soil Microbial Carbon Pump (MCP), atmospheric CO₂ is sequestered into soil in the form of resistant microbial carbon (C). If so, bacterial cell lysis due to virus activity must have an effect on it.

Metatranscriptomics to assess fungal functional ecology in boreal forest

Florian Barbi, Uwe Menzel, Björn Lindahl

Boreal forests represent a large carbon sink, indeed this ecosystem represent 32% of the global carbon store on Earth. Due to the intensive human activity (e.g. forestry, clear-cutting, land use change, fertilization) occurring today in a vast majority of boreal forest, it is essential to advance our understanding of soil processes, to enable informed future policy decisions about forest management and ensure a maintained, and preferably increased, carbon sink. Soil microbial communities play a central role in regulation of soil organic matter dynamics in forest ecosystems and are therefore subject to particular attention. In boreal forest soils, fungi are the main microbial group in term of biomass, and mycorrhizal fungi, living in symbiosis with plant roots, are particularly important in regulating carbon sequestration. New innovative molecular techniques (metatranscriptomics) allow us to open the black box of microbial process in soils, by obtaining massive data of expressed genes from entire microbial communities, and investigate how microorganisms regulate soil organic matter dynamics, directly in the ecosystem. The objective of this study is to develop an approach to highlight fungal functional traits related to soil fungal community ecology. Specifically, to evaluate the mechanisms relative to carbon storage under variation in ecosystem fertility and production. In this purpose, the role of fungal community in carbon transformation, during decomposition and microbial metabolism, is assessing by analyzing expression of genes involved in the production of enzymes implicated in organic matter degradation, stress tolerance and intracellular CO₂ release, at the ecosystem level. The studied site is a native boreal forest presenting a clear split between an N-poor low productive and an N-rich high productive plot. RNAs have been extracted from soil of 16 plots and rRNAs have been removed for a massive Illumina HiSeq sequencing (more than 100 million reads per sample). To decrease the calculation time during bioinformatic analysis and focus on relevant ecological questions, we develop a targeted markers assembly using the HMMER software, based on hidden Markov models. Publically available reference sequence databases (e.g. CAZy or JGI) will be used to guide transcript filtering and identification of expressing organisms. The primary results reveal that fungal traits like decomposition can be describe using a restricted number of functional expressed genes as markers (e.g. cellulases, β -glucosidases, lignin peroxidases). At a larger scale, metatranscriptomic shows that the lignin decomposition process in boreal forest seems drive by both saprotrophs and

mycorrhizal fungi belonging essentially of the *Mycenaceae* and *Cortinariaceae* families. To conclude, the purpose of this pioneer approach is to provide novel insights about the interplay between microbial traits, such as decomposer capacity and metabolic efficiency, and ecosystem level processes, such as carbon sequestration, in order to increase the predictive capacity of ecosystem models.

Effects of long term fertilization on fungal communities in boreal *Pinus sylvestris* forests

Karolina Jörgensen

Factorially untangling saprotrophic, ericoid mycorrhizal and ectomycorrhizal fungal guild effects in the organic horizons

Louis Mielke, Karina Clemmensen, Bjorn Lindahl

I recently began my PhD project at SLU, Uppsala. One experiment I am working on tests the Gadgil Effect and mycorrhizal trait interactions by factorially excluding ericaceous shrubs, mature *Pinus sylvestris* trees and their associated mycorrhizae of a heathland pine forest in central Sweden. This workshop gave motivation to organize preliminary background talk and results while also receiving feedback from other researchers. It helped me put words onto paper and back in a cohesive way.

Fungal interactions have a profound impact on carbon and nitrogen cycling in forest ecosystems because such a large amount of carbon is stored in the soil. Looking at each guild in combination - and isolation - will help us understand the mechanisms involved in decomposition and assimilation of organic matter over a few years. We expect to see ectomycorrhizal fungi hamper decomposition in the litter layer; however, that is not where most of the carbon is stored in the system. The humus layer is a very important component where ericoid mycorrhizal fungi and ectomycorrhizal fungi proliferate. Are their interactions controlling the fate of humus formation in the mor layer? So far we have shown that the treatments work in excluding ectomycorrhizal fungi because respiration rates are much lower in the trenched plots compared to the controls. Next, we will be running enzymatic assays and elemental analyses while also sequencing fungal communities at different depths. This will help us determine the activities and key players of fungi in soil.

Morphological traits predict host-tree specialization in wood-inhabiting fungal communities

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I presented the results of the fifth chapter of my submitted PhD thesis. There we investigated the relationship between dead wood quality (tree species and volume) and fruit body and spore morphology of wood-inhabiting fungal species. We included fungal communities (657 species in total) inhabiting large logs (>15cm in base diameter) of

European aspen, birches, Norway spruce and Scotch pine (total of 192 logs) in 12 semi-natural boreal forests. We found that broadleaved trees had higher species richness than conifer tree species. By using a trait-based hierarchical joint species distribution model, we discovered that species with discomycetoid and pyrenomycetoid (especially on birch) fruit body morphology were specialized on broadleaved dead wood while resupinate and pileate (especially on spruce) species were specialized on coniferous dead wood. Species on broadleaved dead wood had on the average species with larger and more elongated spores, while coniferous logs had species with smaller and more spherical spores. Larger logs had species with larger and more spherical spores than smaller logs. These results may be explained by interactions between the traits as well as between the traits and evolutionary strategies.

Effect of long-term acidification and heavy metal treatment on fungal fruitbody production in subarctic Kevo region

Taina Romppanen

Oulu University, Department of Biology, Finland

I presented my master's thesis. Study site was situated in Kevo subarctic region, where a long-term experimental site was active 1991-2009. Effect of simulated acid rain (pH 3) and heavy metal (CuNi) treatment on fungal fruitbody production, dry weight and species count was studied. Fungal fruitbodies were collected once per year in September for three years (2007-2009). Soil analyses revealed that the nickel and copper concentrations were elevated in the heavy metal treatment plots, and acidification treatment increased the amount of copper in the soil. Data analysis revealed that the effect of soil acidification and heavy metal treatments on observed fungal fruitbody production was low. Some effects were observed in the acidification treatment where it lowered the overall fungal fruitbody production and species count. Especially saprotrophic fungal fruitbody production, dry weight and species count were decreased by acidification treatment. Also combined effect of the treatments was observed on saprotrophic fungal fruitbody dry weight. However, mycorrhizal species, *Cortinarius* species and *Cortinarius armillatus* (coll.) did not seem to react to treatments. Reaction of saprotrophic fungi to acidification treatment was surprising. Contrarily to our expectations before study reaction of mycorrhizal fungi to experimental treatments was not observed. However, our analysis of the selected specific fungal ecological groups and taxons did not explain all variation in the data. Also annual variation of fruitbody production and species count between years was considerable high.

Including fungal community analyses in the Swedish Forest Soil Inventory

Björn Lindahl

A systematic inventory of fungal communities across all forested land in Sweden, based on sequenced ITS markers, reveals clear geographical and ecological patterns in most fungal taxa. Abundances of functional guilds shift from increased abundance of opportunistic moulds and yeasts in the milder climate of the south towards more root-associated ascomycetes (Helotiales, Chaetothyriales and Archaerhizomycetes) at higher latitudes. The inventory also showed that ectomycorrhizal fungi communities are clearly altered by forestry, with species in the genera *Piloderma* and *Tylospora* replacing *Cortinarius* and *Russula* species in more recently disturbed forests. Considering the increasing support for a

pivotal role of *Cortinarius* species in maintaining soil fertility in boreal forests, these patterns call for particular attention. Over-all, it seems urgent that soil fungi are taken into consideration when managing forest ecosystems for sustainability.

Stochastic vs. deterministic processes during AMF community assembly

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A central challenge in ecology is to understand mechanisms determining the assembly of ecological communities. The presence and abundance of species in communities are often explained by the combined effect of dispersal and environmental filtering. Another model, the ecological neutral theory, first described by Hubbell two decades ago, seeks to explain biodiversity patterns by 'neutral' or random processes. In its original version, all trophically similar species in a community are assumed to have the same chance of success, which implies that diversity patterns are shaped by random processes alone. Neutral theory has been used to explain the high plant biodiversity in tropical rainforests, but whether this is reflected in the belowground symbiotic fungal communities is not known. We identified the drivers of community assembly of arbuscular mycorrhizal fungi in the tropical Atlantic forest of Brazil. We found that the extent to which stochastic and deterministic processes affected community assembly depended on the forest type and the spatial scale. In agreement with niche theory, environmental filtering seemed to act at regional scale, while biotic interactions dominated at local scales. This study shows direct evidence that multiple processes are likely operating at the same time and have a great effect in structuring AM fungal communities in rainforests, and that multiple statistical approaches are necessary to reveal the relative importance of biodiversity drivers.

Highlights from the group discussions:

Comments/summaries by participants are grouped under four main themes.

Autecology versus biogeography – how do we meet?

- We discussed how to converge two disjoint current lines of research; 1) one that focus on fewer organisms and on more local (or even lab) scales often with the aim to answer mechanistic questions (how do fungi work) and 2) research with the aim of understanding global biodiversity patterns often without clear connection to fungal driven processes.
- Understanding the role of fungi as part of complex forest systems may not be possible when looking at the role of individual fungal species. Thus, selecting particular functional groups might be a possible solution leading to a better understanding of the ecosystems and the majority of its components by the decision makers and transmitting the message that fungi conservation is needed.

Decomposition & Global Change

- It is a prime priority to understand fungal mediation of responses in decomposition of organic material to global climatic and management changes, as fungi are the main decomposers in Northern ecosystems.
- Identifying genetic markers that reflect functional fungal processes (eg. decomposition, nutrient acquisition) is important.
- Are we using current molecular tools to answer the wrong questions? Using community data provided by HTS techniques has been providing unprecedented resolution assessing microbial community structure and composition. Despite its importance, the use of this source of data on its own should not attempt to answer all types of questions of complex biological systems, but instead, be used in a more integrative and systematic approach.

Conservation biology – do we need to take action?

- Can we manage forests for wood production and at the same time preserve biodiversity?
- One important take home message from this discussion was the importance of the conservation of fungi and their ecological roles does not receive the necessary attention from policy makers (e.g due to the lack of an assigned economic value to the ecosystem service given by fungi).
- Contrasting management practices may be needed to optimize 1) biodiversity, 2) wood production, 3) carbon storage (climate mitigation), and 4) bioenergy production. Thus, all of these services cannot be optimized at the same time in the same stand. This is suggested by trade-offs between forest productivity and soil C storage, which is mediated by fungal community composition.
- FN Agenda 2030: can we optimize biofuel/wood/biodiversity and C stocks at the same time?
- Trees are not completely a renewable energy. There is energy spent on harvesting, handling and for every harvest nutrients are removed from the forest (e.g. base cations). We do not know the long-term consequences of this, as most Northern forests are still only at the end of the first rotation after clear-cut forestry began in the 1950s. In some cases, trees grow less well during second generation.

- There is a need for a systems ecology approach, in which a balance between eg conservational interests and production is found. Both sites will need to compromise – this will be necessary for long-term profitable forestry.
- There is a lack of knowledge about these issues among politicians – should fungal ecologists start lobbying?

NEFOM's future?

- We identified a need to further discuss the role of NEFOM as an integrating community for work around UNITE. Can we as a larger community with many different running projects provide something extra to UNITE? Or is this role (NEFOM started by the group around UNITE) becoming obsolete with larger diversity of bioinformatics tools and databases available? We decided to take up this discussion on the next meeting with a wider representation from all NEFOM groups.
- Should we make a community effort to implement HTS sequence data into UNITE as discussed earlier?
- There was a general agreement that NEFOM should keep a broad fungal ecology focus.
- General agreement on the important role of NEFOM for providing networking opportunities and training (presentations, discussions) particularly for younger scientists.
- The application for extending NEFOM into 2019 is submitted to SNS/EFINORD and the answer will come late November. The main theme we suggested to focus during 2019 is “fungal mediation of C sequestration”.
- From 2020 (application deadline 1st June 2019) NEFOM should find a new coordinator to facilitate varying foci over time!

