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PhD Project Description
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Exploring nitrogen cycling-related traits of boreal forest soil biota using metatranscriptomic markers

In Sweden, managed forests are dominated by secondary forests planted after clear-cutting - the impacts of these practices on belowground carbon and nutrient cycling are of particular importance. On recent clear-cuts, microorganisms may encounter carbon limitation due to the loss of carbon input from roots and litter fall. This could potentially lead to accelerated carbon loss and increased rates of nitrogen mineralization. On the contrary, in the long-term perspective, disruption of ectomycorrhizal symbiosis in clear-cut areas could potentially hinder the turnover of organic stocks, resulting in carbon sequestration and retention of organic nitrogen belowground.

To understand the links between the biological legacies of clear-cutting and nutrient cycling processes, we need information about the response and effect- traits of soil biota. These traits include the decomposition rate of organic matter, nutrient uptake and exchange, and changes in microbial communities. However, such traits are difficult to assess since many soil microorganisms are not easily cultured in the laboratory and current models of links between soil organic matter pools, plant growth, and forestry-related disturbances lack representation of microbial mechanisms. For these models to be relevant for boreal ecosystems, they need to include mechanisms of nitrogen-limitation, which manifests as microbial traits that have downstream consequences for tree growth and belowground carbon storage. Important microbial traits that relate to nitrogen cycling are 1) the capacity to mobilise organic resources (e.g., production of extracellular enzymes); 2) the efficiency by which acquired resources are utilized for biomass growth (i.e., carbon and nitrogen use efficiencies); and 3) the recycling of nutrients during biomass turnover. The relative importance of these adaptations cannot be determined from decomposition experiments, so we propose studying gene expression directly in the field using metatranscriptomics may offer a way forward since transcription of central gene families may correlate with

important microbial traits and help us understand how soil fungi respond to varying levels of nitrogen availability.

To test these ideas, we established a long-term experiment in a low-productive pine forest in northern Sweden that was visited after twelve years, which comprised four levels of harvest intensity: fully clear-cut (0%), 30% or 60% of evenly distributed trees retained, and unlogged (100%) plots. Our focus will be to examine fungal community composition, nutrient stocks, and extracellular protease and chitinase expression by these fungi and the partitioning of resources across treatment groups. Furthermore, we aimed to study the long-term effects on microbial diversity by examining secondary forests planted after clear-cutting (~60 years ago), long continuity forests (only subjected to selective logging), and forests that have never undergone clear-cutting. This comprehensive research will contribute valuable insights into the intricate interplay between forestry practices, microbial communities, and nutrient cycling processes in boreal forests.