



## **Variation of soil arbuscular mycorrhizal fungal communities across land use gradient**

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Arbuscular mycorrhizal (AM) fungi (phylum Glomeromycota) colonize the roots of most terrestrial plants, facilitating mineral nutrient uptake from soil in exchange for plant-assimilated carbon. While investigating functional aspects of plant-AM fungi interactions has been a major focus of research, there is increasing interest in describing and explaining the distribution of AM fungal diversity.

Different management practices has been shown to influence the AM fungal communities while more intense management can bring along the loss of AM fungal diversity. Such a loss may have negative consequences on ecosystem service delivery, primary production and soil sustainability. However, due to cryptic lifestyle of AM fungi, relatively few information is available about variability of diversity and composition of AM fungal communities in the soils from differently managed ecosystems.

To study the variation of soil AM fungal communities in response to the land use intensity, replicated soil samples were collected along land use gradient from intensively managed agricultural fields, organic fields, forest plantations and managed natural forest to primeval forest in Estonia. Soil AM fungal communities were described using molecular tools: DNA extraction, amplicon isolation and 454 large scale parallel pyrosequencing. Glomeromycota sequences were amplified using the SSU rDNA primers NS31 and AML2.

We shall analyse and describe AM fungal community changes along land use intensity gradient and seek finding indicator taxa characteristic to particular land use types. We shall also address changes in the diversity of AM fungal taxa and check whether the decrease of diversity along land use intensity is a ubiquitous phenomenon.