Deintensification of land use leads to recovery of soil microbial community composition and function after land use change in Ethiopia

Yoseph Delelegn¹, Witoon Purahong², Ali Nawaz², Hans Sandén¹, Douglas Godbold¹, and Tesfaye Wubet²

¹University of Natural Resources and Life Sciences Vienna ²Helmholtz Centre for Environmental Research UFZ Department of Soil Ecology

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Abstract

Ethiopia has undergone significant land use change during the past centuries, particularly deforestation. These changes have resulted in the loss of topsoil as well as the associated soil ecosystem functions. Grazing exclusion and planting of eucalyptus are measures used to recover degraded lands and reduce deforestation, respectively. Using a gradient of the intensity of land use from natural forest to croplands, we investigated whether these measures also result in restoration of the soil microbial community. We identified the soil bacterial and fungal communities using paired-end amplicon sequencing. A total of 12,765 fungal and 12,325 bacterial OTUs were detected in the five land use types, and only ca. 2% and 17% were shared among the land uses, respectively. Total fungal and bacterial OTU richness was not significantly affected by land use change, but the conversion of forest to cropland resulted in the loss of approximately 40% and 11% of the total native fungal and bacterial OTUs, respectively. Soil pH, C, N, and aggregate stability were key factors corresponding to the overall bacterial and fungal communities that overlapped with the communities. The exclusion of grazing led to an enrichment of soil microbial communities that overlapped with the communities of the natural forest. Our results suggest that remnant native forests act as refugia for microbial communities and that restoration of microbial communities and concomitant recovery of ecosystem function via deintensification of land use is possible. Keywords: ectomycorrhiza, ericoid mycorrhiza, exclosure, microbial diversity, soil enzymes

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