Trace elements in ectomycorrhizae determined by neutron activation analysis

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In recent years, interest in the biochemical roles of macrofungi in the environment has increased rapidly. Macrofungi play important roles in biogeochemical cycling of chemical elements in the critical zone and many species are known as effective accumulators of toxic metals.

Ectomycorrhizal fungi live in symbiosis with vascular plants. In this reciprocally profitable relationship, the exchange of nutrients occurs in a mutual organ called ectomycorrhiza (pl. *ectomycorrhizae*). Ectomycorrhizae are formed on fine roots of host plants, distributed throughout the soil profile in both organic and mineral horizons, and are composed of plant biomass and fungal hyphae.

As has been repeatedly demonstrated, metal-adapted mycorrhizal fungi play as an effective biological barrier against metal toxicity in trees. Only few data have been published on concentrations of heavy metals in ectomycorrhizae: a relatively high degree of accumulation of Cd, Cu, Pb and Zn was observed from polluted sites in Norway and Poland.

In this study, we have focused on natural concentrations of trace elements in ectomycorrhizae and fine roots of *Picea abies* from pristine sites above gneissic and granitic bedrocks. Trace elements were analyzed using short-term thermal and long-term epithermal neutron activation analysis. The individual fungal species in analyzed ectomycorrhizal tips were determined by DNA sequencing (rDNA ITS molecular marker, semi-nested PCR).

According to our preliminary results, the most striking accumulation was noted in Cd. Its concentrations, however, varied in a wide range (with the highest content of 50 mg·kg^{-1} dry weight). On the other hand, very low concentrations (mostly below 20 mg·kg^{-1} dry weight) were found for Cu.

Depth-dependent links between surface and subsurface as reflected by microbial community structures in limestone aquifers

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One quarter of the drinking water supply for the world´s population is derived from limestone aquifers, yet they are to date poorly represented in studies focussing on surface-subsurface interactions. Lithoautotrophy might be an important metabolic strategy in these oligotrophic habitats for coupling carbon cycling to the cycling of other elements, e.g. nitrogen, metals or sulphur accumulated from rock weathering. Within the framework of the AquaDiva project we started to explore the influence of surface conditions on the subsurface biosphere. We compared the diversity of microbial communities, some of their key functions, and potential links within food webs in the groundwater of a shallow, suboxic, and a deep, oxygen-rich limestone aquifer located in the Hainich region (Thuringia, Germany) below sites subjected to different land management.

Pyrosequencing of 16S ribosomal RNA revealed a clear separation of the shallow and the deep aquifer based on the structure of the active microbial communities. Results of quantitative PCR targeting *cbbL* and *cbbM* genes encoding RubisCO type I and II suggested that approximately 0.3 to 14 % of the groundwater bacterial population had the genetic potential to fix CO_2 via the Calvin Cycle. Analysis of *cbbM* and *cbbL* transcripts showed that the active CO_2-fixing bacterial communities were dominated by organisms related to *Sulfuricella denitrificans*, *Sideroxydans lithotrophicus*, *Acidithiobacillus sp.*, and *Nitrosomonas ureae* with the latter being more abundant in the deep, oxygen-rich aquifer.

Our data provide strong evidence that chemolitho-autotrophy linked to metabolisms involving sulphur, iron, and nitrogen contributes to the carbon flow in a limestone aquifer. Moreover, analyses of the eukaryotic microbial communities in the groundwater revealed a diverse protist community consisting mainly of bacterial feeders such as ciliates, flagellates and amoeba but also representatives of higher trophic levels such as heliozoa and nematodes, suggesting complex food web interactions. In the light of surface-subsurface interactions, the observed geochemical and microbial patterns point to a depth-dependent impact of surface activities on the aquifer system with the shallow aquifer being more strongly affected by agricultural practices.