



Fungal community in sclerotia of Japanese Beech forest soils in north eastern Japan

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Sclerotia are resting structures of ectomycorrhizal fungi and appear as a response to unfavorable environmental conditions such as desiccation. They are hard, black, comparatively smooth and mostly spherical. Sclerotia are formed in rhizosphere and the ^{14}C ages of sclerotia from A horizons of volcanic ash soils may range from modern until ca. 100~1,200 yr B.P. Most sclerotia-forming fungal species are known to be host-specific plant pathogens and therefore their abundance may indicate the presence of their host plants. The purpose of this study was to investigate fungal communities in sclerotia with an interest in describing the existing or may have previously existed host plant community. To investigate fungal community inside of sclerotia by 16S rDNA gene clone library, several hundred of sclerotia (ca. 1g) were collected from *Fagus crenata* forest soil in north eastern Japan. The rDNA ITS regions were then amplified by the PCR using primer pair ITS-1F/ITS-4. Aliquots of the amplified DNA were digested with restriction endonucleases AluI, Hae III, and HhaI to obtain ITS-RFLPs. To obtain the fungal community profiles a quenching fluorescence primer was used for real-time quantitative PCR (qPCR) assay to monitor the PCR amplification and then used for T-RFLP. The predominant group determined by clone library analysis from the sclerotia was Ascomycota: *Arthrinium arundinis*, which has been reported to be one of the soil fungal species responsible for bamboo degradation and a pathogen for many species belonging to Poaceae family.