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Bacterial community in sclerotia of *Cenococcum* species and soil in sub-alpine forest, central Japan

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Species of *Cenococcum*, ectomycorrhizal fungi, may be particularly abundant in cold- or nutrient-stressed habitats. The fungus is easily recognized by its jet-black hyphae, and distinct compact masses of fungal mycelium called sclerotia. They are hard, black, comparatively smooth and mostly spherical. Sclerotia are formed in rhizosphere and can provide sufficient inoculums for several years. The purpose of this study is to investigate bacterial community inside sclerotia, with an interest on contribution of sclerotia to microbial diversity in rhizosphere. To investigate bacterial community inside of the fungal sclerotia by 16S rDNA gene clone library, several hundred of sclerotia (ca. 1g) were collected from sub-alpine forest soil in central Japan. Furthermore, three sclerotium grains were applied to investigate internal bacteria community by culture method. The isolated bacterial strains were then proceeded to determine their 16S rDNA partial sequences. The predominant group determined by clone library analysis of 16S ribosomal RNA genes with DNA from the sclerotia was *Acidobacteria* in both sclerotia and soil. Bacterial community of sclerotia showed higher diversity compared to soil. On the contrary, bacterial flora isolated from single sclerotium differed each other. Additionally, the bacterial community was composed by limited species of related genus.