Abstracts

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MICROBIAL COMMUNITY IN ANTARCTIC LICHENS

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Lichens are symbiotic association of fungal (mycobiont) and photosynthetic algal or cyanobacterial (photobiont) partners. Contribution of the two major partners has been well known, but composition and role of other components of lichen ecosystems has not been evaluated carefully. Recently, microbial community in the lichen thalli has been revealed by cultivation of microorganisms, FISH imaging, and sequence analyses. It was also suggested that bacteria, archaea and microfungi associated with lichens (microbiont) have important roles in lichen ecosystem by biodiversity and meta-proteome analyses. In the current study, microbial community composition in *Cladonia, Umbilicaria, Usnea*, and 3 crustose lichens from King George Island, Antarctica was analyzed by pyrosequencing of bacterial 16S rDNA, eukaryotic LSU rDNA, and algal ITS region of nuc rDNA. Proteobacteria, Acidobacteria, Actinobacteria, and Bacteroidetes in bacterial community and Dothideomycetes, Eurotiomycetes and Lecanoromycetes in lichen-associated fungal community were the major phyla in the Antactic lichen ecosystems. Microbial phylotype composition from the same or related lichen species were more closely related than those of different lichen species. Sequencing results of LSU and ITS regions of nuclear rDNA and plastid 16S rDNA of algal species indicated that each lichen thalli contain diverse photobionts. In most cases a major photobiont constituted higher than 97% of total photobiont community, but in some cases, the second major photobiont comprised upto 20% of total photobiont community. These results imply that lichen thalli is a complex ecosystem composed of lichenized fungi, diverse photobionts and microbionts such as bacteria and microfungi. It also suggests that studies for all partners of lichens are required to understand ecology and physiology of lichens.

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