

[PS3-D.24]

Evolution of lichens in polar areas

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Distribution of lichens in Antarctic regions was investigated by phenotypic and phylogenetic analysis of lichen samples of the genera *Pseudephebe*, *Umbilicaria*, and *Usnea*. The lichen samples were collected from Leningradskaya and Russkaya Stations, Lindsey Island, Mt. Moses, Maish Nunatak and King George Island. From the phylogenetic tree of *Pseudephebe*, *Umbilicaria* and *Usnea* based on combined sequences of ITS and 28S rDNA, geographical isolation of lichen species in Pacific coast of continental Antarctic was not evident. Instead, samples from long distance were clustered together and contained rDNA sequences of high similarity, implying that lichen species can be easily transferred and widely distributed in Pacific coast of continental Antarctic. Particularly, *Usnea* species with close phylogenetic relationships showed variation in intron possession pattern, implying that introns are easily lost or obtained. However, sequences of introns were generally well conserved in the same phylogenetic lineages. Sharing of same type of introns by lichens from different geographical origin supported the hypothesis of easy geographical distribution of lichen species in Antarctic continent.

Keywords: lichen, evolution, phylogeny