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Evolution and geographical distribution of the lichen genus *Usnea* in Antarctic

Soon Gyu Hong¹, Chae Haeng Park¹, Ji Hee Kim¹, and Mikhail Andreev²

¹Polar BioCenter, Korea Polar Research Institute, KORDI, 7-50 Songdo-dong, Incheon, Korea

²Komarov Botanical Institute, 2, Prof. Popov St., 197376, St.-Petersburg, Russia

Phylogenetic relationships of *Usnea* species collected from different localities in Antarctic, including Leningradskaya, Russkaya, Lindsey Island, Mt. Moses, Maish Nunatak and King Jeorge Island, were reconstructed based on combined sequences of ITS and 28S rDNA. From the tree, geographical isolation of *Usnea* 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 *Usnea* species can be easily transferred and widely distributed in Pacific coast of continental Antarctic. However, *Usnea* species from King Jeorge Island looked isolated from those of continental Antarctic. *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 intron by lichens from different geographical origin supported the hypothesis of easy geographical distribution of lichen species in Antarctic continent.