Proceedings

2010 한국미생물학회연합 국제학술대회

International Meeting of the Federation of Korean Microbiological Societies

- October 14(Thu)~15(Fri), 2010
- Seoul KyoYuk MunHwa HoeKwan, Seoul, Korea

Organized by

The Federation of Korean Microbiological Societies (FKMS)

Hosted by

The Korean Society for Microbiology and Biotechnology (KMB)
The Korean Society for Microbiology (KSMi)
The Korean Society of Virology (KSV)
The Korean Society of Mycology (KSMy)
The Microbiological Society of Korea (MSK)

Sponsored by

Korean Federation of Science and Technology Societies
Korea National Microorganisms Research Resources Center
Korean Academy of Medical Sciences
National Institute of Health, KCDC
Maeil Dairies Co., Ltd.

한국미생물학회연합
http://www.fkms.kr

Evolution of Antarctic Lichens Revealed by Phylogenetic Analyses

Soon Gyu Hong[1], Chae Haeng Park[1], Ji Hee Kim[1], and Mikhail Andreev[2]

[1]*Division of Polar Life Sciences, Korea Polar Research Institute, KORDI, 7-50 Songdo-dong, Incheon, Korea,*
[2]*Komarov Botanical Institute, Prof. Popov St., 197376, St.-Petersburg, Russia*

The Antarctic is defined geographically as all lands and adjoining ice shelves south of latitude 60°S. Floristically, the Antarctic possesses two vascular plants and diverse bryophytes and lichens. The Antarctic is one of the best places for studying the evolution of lichen-forming fungi because of its geographical locality and diversity of lichens. Lichens are symbiotic organisms of mycobionts (fungi) and photobionts (algae or cyanobacteria). They constitute the main part of Antarctic flora, along with algae and bryophytes. Some lichens are nature's pioneers that are the first to penetrate into the areas emerging from beneath the ice, and have a successful evolutionary strategy to adapt in extreme environmental conditions, and have resulted in diverse, abundant, and important flora in the terrestrial ecosystem of Antarctica. Molecular phylogenetic studies have provided new insights to understanding the evolutionary relationships among phenotiypically recognized species. Recently, collaborative studies among classical taxonomists and molecular phylogeneticists have resulted in a revised classification system of fungi. By extensive molecular phylogenetic studies, many new insights have been found on the matter of polyphyletic taxonomic groups, development of cryptic species, and morphological variation by genetic diversity, geographical distribution, and environmental adaptation. It is now generally accepted that combining morphological and molecular phylogenetic analyses leads to a better understanding of fungal relationships and biodiversity. In this study, results of molecular phylogenetic studies of *Cladonia, Pseudephebe*, *Umbilicaria* and *Usnea* are presented.

The fruticose lichen *Cladonia borealis* grows on soil and humus, sometimes among mosses in light and dry places and is found in polar and subpolar areas. In order to investigate genetic variation and geographical distribution of *C. borealis* from the Antarctic, 50 samples from King George Island (the Antarctic), Punta Arenas (Chile) and Svalbard (Norway) were analyzed. From the multiloci phylogenetic analyses and haplotype network analyses of nuclear ITS and LSU rDNA, mitochondrial small subunit rDNA (mtSSU) and RNA polymerase II (RPB2), it was revealed that *C. borealis* in King George Island is divided into two lineages. *Cladonia borealis* in Svalbard was divided into three lineages including the basal one. From the scenario reconstructed from phylogeny and haplotype network, it is regarded that *C. borealis* has been transferred between Southern and Northern hemisphere at least three times. One of two haplotypes (M1 and M2) of mtSSU was shared among various phylogenetic lineages comprising both of the Antarctic and Arctic lineages, but the second one (M2) was shared only among Svalbard populations. It implies that M2 haplotype is a derived one originated in the Northern hemisphere recently and exchanged among *C. borealis* in Svalbard regardless of phylogenetic lineages.

Distribution of lichens in Antarctic area was investigated by phylogenetic analysis of lichen species of the genera *Pseudephebe*, *Umbilicaria*, and *Usnea*. The lichen species were collected from "Leningradskaya" and "Russkaya" Stations, Lindsey Island, Mt. Moses, Maish Nunatak and King George Islands. From the phylogenetic tree of *Pseudephebe*, *Umbilicaria*, and *Usnea* based on ITS sequences, 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 : lichens, Antarctic, evolution, phylogeny