

Phylogenetic Study of the Korean Aphylophorales

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The order Aphylophorales that circumscribed by negative characters such as the absence of gills and the absence of soft, flesh basidiocarps has included many heterogeneous taxa. When the order was proposed, only a few large families were recognized mainly based on hymenophore configuration. Donk [1] put previous taxonomic works together and suggested a completely new classification of the Aphylophorales that comprised 23 modern families instead of 5 groups of the Friesian system. In Donk's system, hymenial configurations were no longer important as familial characters, but microscopic characters such as the mitic system, spore morphology, basidium morphology, and sterile elements like cystidia were emphasized in defining new families. Although Donk's work greatly improved the taxonomy of the Aphylophorales, several families remained artificial and wanted revisions. But recent microscopic studies of basidiocarps and molecular studies of DNAs have shown conventional groupings to be unnatural [2, 3].

Molecular techniques have been applied to mycology and provided a plenty of potential characters for the classification of fungi including Aphylophorales [4, 5]. Molecular techniques are becoming more important and common as means to study taxonomic and phylogenetic relationships among fungi. The ribosomal RNA gene was most commonly used for molecular phylogenetic analyses because it is a very old ancient gene that all organisms have and forms a mosaic pattern of conserved and variable regions, making phylogenetic analyses possible at many taxonomic levels [6]. Other regions used for phylogenetic analyses are nuclear or mitochondrial small subunit rDNAs and large subunit rDNAs, internal transcribed spacers (ITSs), and intergenic spacers (IGS) [7, 8] that can be used for race identification in some fungal species. In addition, protein-coding genes were used for phylogenetic analyses, because of their high contents of functional informations. RNA polymerase II was proved to be valuable for the evolutionary research at the broadest taxonomic level because it is also ubiquitous and contains motifs that have been conserved across the primary kingdoms of life [9].

The Aphylophorales of Korea is still poorly known and only a small part of about 1,200 aphylophoroid fungi has been described. Until recently, the total aphylophoroid species reported in Korea were 411, which belonged to 144 genera and 23 families [10]. Molecular phylogenetic studies were accomplished for Korean aphylophoroid fungi by Kim and Jung [11] and Lee [12], for the Corticiaceae by Lee and Jung [13] and Lim [14], for hymenochaetoid fungi by Jeong [15] and Jeong *et al.* [16], and for Polyporaceae by Hong [17] and Ko [18]. Kim and Jung [11] inferred phylogenetic relationships among 81 aphylophoroid basidiomycetes using the

nuc-SSU region, and 16 clades were discovered and compared to the present families. Lim [14] also utilized the nuc-SSU region for the phylogenetic study of homobasidiomycetes with an emphasis on the taxa of corticioid basidiocarps. Among the recent molecular studies, the most taxonomically inclusive phylogenetic study in Korean Aphyllphorales was achieved by Lee [12]. According to his results, aphyllphoroid fungi formed 13 independent clades which were dispersed in all major clades of Homobasidiomycetes. Those studies provided new informations on phylogenetic relationships between Korean aphyllphoroid fungi and related fungi of homobasidiomycetes and build a phylogenetic scheme and a perspective of Korean aphyllphoroid fungi.

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