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CLASSIFICATION OF NOVEL ACTINOMYCETES FROM GOLD MINE CAVE IN KONGJU, KOREA

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One hundred and eighty-three strains of actinomycetes, which were selectively isolated from a gold mine cave in Kongju using various oligotrophic media, were compared with 262 type strains of 15 genera within the order *Actinomycetales* for 180 unit characters. These strains were clustered by simple matching coefficient (S_{SM}) using UPGMA algorithm. Ninety isolates and 147 type strains of the genus *Streptomyces* were divided to eleven major, 26 minor, and 30 single-member clusters at the 80.5% S_{SM} level. On the other hand, ninety-three non-streptomycete isolates and 15 representative strains of 14 other genera were divided to three major, nine minor, and eighteen single-member clusters at the 80% S_{SM} level. Some of these isolates were further characterized using chemotaxonomic and molecular genetic method. The combination of morphological, chemotaxonomic, and 16S ribosomal RNA gene sequence data indicated that two strains of them belong to two new genera in the order *Actinomycetales*, respectively. Therefore, we propose two new genera for them as follows; *Hongia koreensis* gen. nov. sp. nov. (type strain LM 161) and *Actinospora koreensis* gen. nov. sp. nov. (type strain LM 042).

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TAXONOMIC STUDIES OF ASCOMYCETE FUNGI WITH HAIR ORNAMENTATIONS BASED ON PHYLOGENETIC ANALYSIS

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Chaetomium, a well-known genus of cellulose degrading fungi, includes approximately 300 described species. The genus is cosmopolitan in distribution and occurs on a variety of substrata. Despite its commonness and easily recognized features, the taxonomic status of *Chaetomium* and other related genera is unstable. A major reason for disagreement on the taxonomic position of *Chaetomium* is the uncertainty of the relationships of this genus to other genera or families of pyrenomycetous fungi. The thirty-three taxa were selected for this study based on their taxonomic position or particular morphological characters, which are related with those of *Chaetomium*. Sequences of the 5' end partial 18S subunit ribosomal DNA were analyzed to find the phylogenetic relationships among *Chaetomium* and related genera. The gene phylogeny suggested the inclusion of *Thielavia* within the genus *Chaetomium*, the generic validity of *Achaetomium*, the elevation of *Coniochaeta* to the familial level, and the movement and placement of *Ascotricha* within the Xylariaceae. The analysis helped defining the familial concept of the Microascaceae. The close evolutionary relationship between the Sordariaceae and the Chaetomiaceae was demonstrated.