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Phylogenetic relationship in *Amanita* species based on ITS1-5.8S rDNA-ITS2 region sequences

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To determine phylogenetic relatedness of the *Amanita* species,common poisonous mushrooms of the Agaricales, internal transcribed spacers (ITSs) and the 5.8S ribosomal RNA gene were amplified by the polymerase chain reaction and then sequenced according to the dideoxy chain termination method . The ITS region provided sufficient variability for phylogenetic analysis within a species. Analysis of the ITS sequence data by distance and parsimony methods revealed a close relationship between *Amaita muscaria and A. tenuifolia* and among *A. aspera, A. citrina, A. rubescens* and *A. pantherina.* Trees generated from the data of the ITS1-5.8S rDNA-ITS2 region by bootstrap analysis
supported all statistically significant branches and provided those relationships.

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Strain LM 182^T, a New Species of the Genus *Catellatospora*

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Soil actinomycete, strain LM 182^T, which was isolated from a gold mine cave in Kongju, was characterized morphologically and chemotaxonomically to study its taxonomic status. This organism formed short chains of nonmotile spores from yellowish vegetative mycelium. The true aerial mycelium was absent. This organism contained *meso*-diaminopimelic and 3-hydroxydiaminopimelic acids, and glycine in the cell wall (wall chemotype II). Arabinose and xylose were present as diagnostic sugars (whole-cell sugar pattern D). Phosphatidylethanolamine was present as a diagnostic polar lipid (Phospholipid type PII), and the major menaquinone was MK-9(H_4). N-glycolyl muramic acid was detected, but mycolic acid was not present. According to its chemotaxonomic and morphological characteristics, this isolate should be placed in the genus *Catellatospora*. However, this organism was different from all previously described species belonging to the genus *Catellatospora* with respect to carbon utilization profiles and cellular fatty acid compositions.