

**A303** Phylogenetic classification of *Poria* Based on Gene Sequences of the Mitochondrial Small Subunit Ribosomal DNA

Kim, Seon Young and Jung, Hack Sung  
Department of Microbiology, College of Natural Sciences,  
Seoul National University, Seoul 151-742, Korea

To investigate phylogenetic relationships among strains belong to *Poria* species sensu lato, gene sequences of the small subunit mitochondrial ribosomal RNA were determined for eighteen strains of *Poria* species sensu lato - *Anomoporia bombycina*, *Antrodia malicola*, *Antrodia vaillantii*, *Antrodia xantha*, *Antrodiella americana*, *Antrodiella fissiformis*, *Ceriporia excelsa*, *Ceriporia tarda*, *Ceriporiopsis resinasceus*, *Ceriporiopsis subvermisporea*, *Diplomitoporus* spp., *Donkiporia expansa*, *Junghuhnia separabilima*, *Perenniporia subacida*, *Polyporus palustris* *Poria cocos*, *Poria versipora*, *Wolfiporia extensa*. Phylogenetic analysis was performed with 13 other polypore sequences. The results showed that the genus *Antrodia* was not monophyletic group. The genus *Ceriporia* and *Ceriporiopsis* were also polyphyletic. Other *Poria* strains were scattered among polypores. This results supported previous opinion that the *Poria* are unnatural, polyphyletic group.

**A304** Phylogeny of Phellinus species based on Ribosomal RNA

Wonjin Jeong and Jung, Hack Sung  
Department of Microbiology, College of Natural Sciences  
Seoul National University, Seoul 151-742, Korea

Mitochondrial Small Ribosomal RNA regions was cloned and sequenced in some Phellinus species, including *P. laevigatus*, *P. punctatus*, *P. linteus*. to reveal their taxonomic relationship and the structures of mitochondrial small ribosomal RNA. *P. laevigatus* and *P. punctatus* showed closer relationship with each other than with *P. linteus*. Furthermore, *P. linteus* had a Group I intron.

tRNA-like structures exists in the 3' terminal region of ribosomal RNA coding region. The primary structure showed conserved regions and variable region alternately. The variable region is dissimilar enough to reveal taxonomic structure within species in Phellinus and the conserved region can be used as unique priming site of Phellinus species.