

A312 Phylogenetic Classification of *Antrodia* and Related Genera Based on Mitochondrial Small Subunit Ribosomal RNA Gene Analyses

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Antrodia is a genus that causes a brown rot and has been regarded as a polyphyletic group. In this study, whether or not the type of rot is important in taxonomy, intergeneric relationships in polypores and intrageneric relationships in *Antrodia* were examined. Sequences of mitochondrial small subunit ribosomal DNAs were obtained from species of the Polyporaceae and analyzed using PAUP 4.02a. From two phylogenetic trees, four groups were identified: *Antrodia* group, another brown-rot fungi group and two white-rot fungi groups.

Antrodia group included most species of *Antrodia* sequenced in this study, but *A. carbonica* and *A. xantha* formed another small separate cluster which had amyloid skeletal hyphae and trimitic hyphal system. One white-rot fungi group composed of *Antrodiella*, *Diplomitoporus* and *Junghuhnia* was grouped closer to the *Antrodia* group than to the other white-rot fungi group. From this study, the type of rot is recognized as an important character to separate genera. And *A. carbonica* and *A. xantha* need to be grouped into another genus although more evidence is required sometime.

A313 Phylogenetic Study of the Hemiascomycetous Yeasts Based on Chitin Synthase Genes

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Based on conserved amino acid regions for chitin synthases (CHSs) of *Saccharomyces cerevisiae* and *Candida albicans*, two degenerated PCR primers were used to amplify partial genes coding CHSs from seven strains of the hemiascomycetous yeasts. Cloning and sequencing of PCR products showed the existence of fourteen CHSs, which did not involve various introns unlikely with basidiomycetous yeasts. These fragments were identified as members of genes for chitin syntase class I and II by alignment analysis of their deduced amino acid sequences together with the reported CHS genes. Using bootstrap and phylogenetic analysis of the deduced amino acid sequences of class II with those of hemiascomycetous yeasts, the seven strains were divided into three family, Candidaceae, Metschnikowiaceae and Saccharomycetaceae. It agreed well with the previous classification by 18S rDNA sequences. This study showed that CHS fragments could be used as a valuable key for the molecular taxonomic and phylogenetic studies of the hemiascomycetous yeasts.