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Phylogenetic study of a basidiomycetous yeast, *Trimorphomyces papilionaceus*, based on the *cob* gene sequence of mitochondria

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The DNA sequence of the *cob*, *ndh3*, *ndh4L*, and 3 tRNA gene regions of of the mitochondrial DNA from a basidiomycetous yeast, *Trimorphomyces papilionaceus*, has been determined. Through the homology comparison of amino acids deduced from *cob* genes, the phylogenetic relationship of *T. papilionaceus* was inferred and compared with previously reported fungi. The ascomycetous yeasts *Saccharomyces cerevisiae* - *Schizosaccharomyces pombe* formed an individual lineage and the basidiomycetous yeast *T. papilionaceus* and the filamentous ascomycetes *Podospora anserina* - *Neurospora crassa* - *Aspergillus nidulans* developed the other separate lineages at a certain point, suggesting that the latter groups once had a common evolutionary stage and then branched at a later stage. The present fungus, *T. papilionaceus*, has yeast and mycelial phases together during the life cycle and might have retained its yeast character all the time throughout its evolution toward the filamentous character.

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Phylogeny of *Phellinus* based on the restriction enzyme analysis of mitochondrial DNA.

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Eleven strains of the genus *Phellinus* were studied to discuss their phylogenetic relationships by utilizing restriction fragment length polymorphisms (RFLPs) of mitochondrial DNAs(mtDNAs). Six of 6 base recognizing restriction enzyme, *Bam*HI, *Bg*III, *Cla*I, *Eco*RI, *Nsi*I, *Pvu*II were used in this study. Restriction profiles of strains for each restriction enzyme were treated as analysis characters to calculate similarity coefficients, which were converted into nucleotide sequence divergence values whose mean values were then arranged in a matrix table. These tables were utilized for phylogenetic analyses using the Neighbor program of the PHYLIP package to construct phylogenetic tree. Two strains of *Phellinus laevigatus* showed high similarity as had been expected. However, one strain of *P. igniarius* and one strain of *P. chrysoloma* showed similarity higher than those between two of *P. igniarius*, or between two of *P. chrysoloma*. The result needed the new analysis different from that of morphologically characterized classification.