

Phylogenetic position of *Trimorphomyces papilionaceus* based on 5S rRNA sequence

Yong Her, Young-Won Kang, Hack Sung Jung* and Yong-Ha Park¹

Department of Microbiology, College of Natural Sciences and Research Center for Molecular Microbiology, Seoul National University, Seoul 151-742 and ¹Korean Collection for Type Cultures, Genetic Engineering Center, Korea Institute of Science and Technology, Daejeon 305-606, Korea

Submitted September 2, 1992

EMBL accession no. X67494

The sequence of the cytoplasmic 5S rRNA from *Trimorphomyces papilionaceus* (UBC 75-7237-d), a basidiomycetous yeast of the Tremellaceae, was determined by the direct chemical method for sequencing RNA (1) and compared to the known 5S rRNA sequences of 19 basidiomycetous fungi. The 5S rRNA of *T.papilionaceus* consists of 118 bases whose sequence fits the secondary model of the 5S rRNA of basidiomycetes proposed by Huysmans *et al.* (2) and belongs to the type B (3). Based on Knuc values, the closest fungus to *T.papilionaceus* was *Tilletiaria anomala*, another basidiomycetous yeast of the Sporobolomycetaceae, showing 25 nucleotide differences of 0.128 1/2Knuc value.

According to the dendrogram (Figure 1) based on Knuc values of 5S rRNAs of 20 basidiomycetous fungi, right after the separation of type A and B 5S rRNA groups, *T.papilionaceus* has separated from the type B group in the first place, meaning that this species is the oldest one among the type B fungi. And the sequence of *T.papilionaceus* does not fit any of the five sequence clusters proposed by Walker and Doolittle (4). For the present, the 5S rRNA of *T.papilionaceus* represents a cluster of

its own, suggesting a possibility that this species diverged at a fairly early stage during the evolution and has developed a separate phylogenetic branch within basidiomycetous fungi.

ACKNOWLEDGEMENTS

We thank Dr. Bandoni, University of British Columbia, for providing the *T.papilionaceus* strain. The present research was supported by the KOSEF research grant for SRC (Research Center for Molecular Microbiology, Seoul National University).

REFERENCES

1. Peattie, D.A. (1979) *Proc. Natl. Acad. Sci. USA* **76**, 1760–1764.
2. Huysmans, E., Dams, E., Vandenberghe, A. and de Wachter, R. (1983) *Nucleic Acids Res.* **11**, 2871–2880.
3. Blanz, P.A. and Unsel, M. (1987) In de Hoog, G.S., Smith, M.Th. and Weijman, A.C.M. (eds.) *The expanding realm of yeast-like fungi — Ribosomal RNA as a taxonomic tool in mycology*. Elsevier Science Publishers, Amsterdam, pp. 247–258.
4. Walker, W.F. and Doolittle, W.F. (1983) *Nucleic Acids Res.* **11**, 7625–7630.

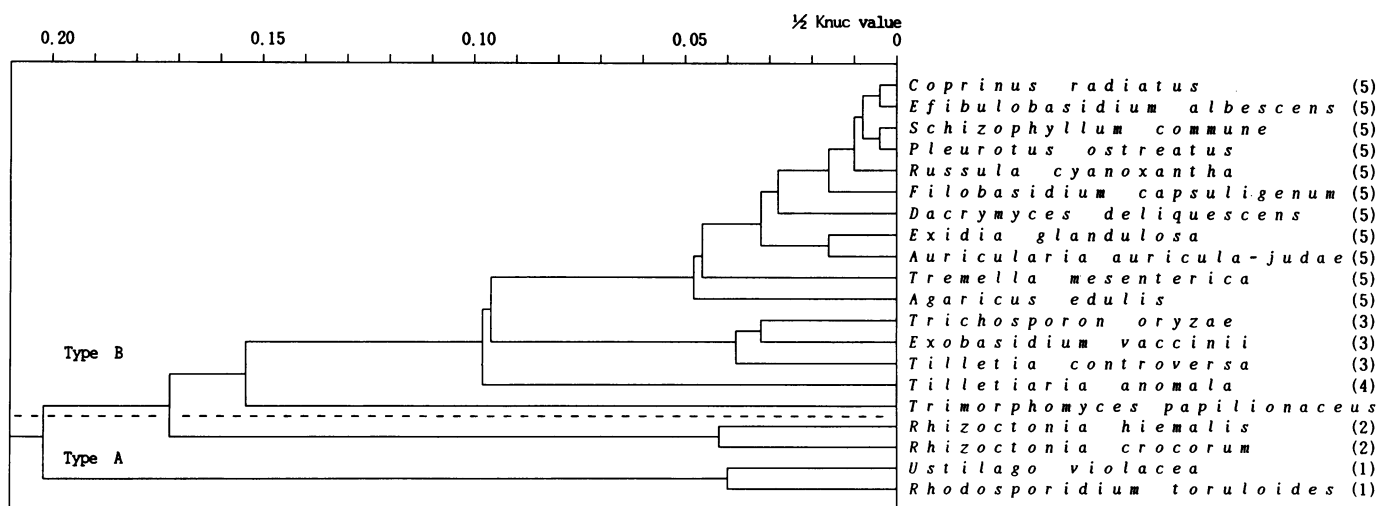


Figure 1. Relationships between basidiomycetous fungi based on their 5S rRNA nucleotide sequences. The dashed line separates type A and B organisms and the numbers on the right side correspond to the clusters proposed by Walker and Doolittle (4).

* To whom correspondence should be addressed