

Phylogenetic relationship of *Microporus* species in East and Southeast Asia

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Purpose: *Microporus* spp. are widely distributed in temperate East Asia and Paleotropical regions. They play an important role as wood decomposers in the forest ecosystems. However, species recognitions within the genus *Microporus* were inadequate due to their variable morphologies. In this study, phylogenetic relationships of *Microporus* spp. in East Asia (including cool-temperate forests, warm-temperate forests, and subtropical forests) and South East Asia (tropical forests) were investigated to evaluate the species delimitation.

Methods: Deoxyribonucleic acid (DNA) was extracted from the fruiting bodies or mycelia of *Microporus* species. Molecular sequence data from two different regions, namely nuclear ribosomal DNA (nuLSU) and protein-coding genes (RPB2), were generated from the study. Phylogenetic analyses were performed with maximum parsimony and Neighbor-joining method.

Results: The phylogenetic trees based on nuLSU and RPB2 showed that species in *Microporus* consist of a monophyletic group within the family Polyporaceae. A total of 43 collections of *Microporus* from different forest types in Japan and Malaysia were grouped into seven different clades.

Conclusion: This study indicated that the biogeographical distribution range is an important feature for species delimitation of *Microporus* spp. in addition to using the morphological characteristics.