**Molecular phylogeny of Crematogaster subgenus Decacrema ants (Hymenoptera : Formicidae) and the colonization of Macaranga (Euphorbiaceae) trees**

**Abstract**

To elucidate the evolution of one of the most species-rich ant-plant symbiotic systems, the association between Crematogaster (Myrmicinae) and Macaranga (Euphorbiaceae) in South-East Asia, we conducted a phylogenetic analysis of the ant partners. For the phylogenetic analysis partial mitochondrial cytochrome oxidase I and II were sequenced and Maximum Parsimony analysis was performed. The analyzed Crematogaster of the subgenus Decacrema fell into three distinct clades which are also characterized by specific morphological and ecological traits (queen morphology, host-plants, and colony structure). Our results supported the validity of our currently used morphospecies concept for Peninsula Malaysia. However, on a wider geographic range (including North and North-East Borneo) some morphospecies turned out to be species complexes with genetically quite distinct taxa. Our phylogenetic analysis and host association studies do not indicate strict cocladogenesis between the subgenus Decacrema and their Macaranga host-plants because multiple ant taxa occur on quite distinct host-plants belonging to different clades within the genus Macaranga. These results support the view that host-shifting or host-expansion is common in the ants colonizing Macaranga. Additionally, the considerable geographic substructuring found in the phylogenetic trees of the ants suggests that allopatric speciation has also played a role in the diversification and the current distribution of the Decacrema ants. (C) 2003 Elsevier Science (USA). All rights reserved.