

**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 in 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.