

Erratum to: Comparative chloroplast DNA phylogeography of two tropical pioneer trees, *Macaranga gigantea* and *Macaranga pearsonii* (Euphorbiaceae)

Abstract

Macaranga (Euphorbiaceae) has received much ecological and evolutionary research attention as a genus that includes some of the most conspicuous pioneer trees of Southeast Asian tropical rainforests and because of its manifold associations with ants, including about 30 species that are obligate ant-plants (myrmecophytes). We used sequence data from three chloroplast DNA loci (*ccmp5*, *ccmp6*, *atpB-rbcL*) to assess phylogeographical patterns in species of *Macaranga*, section *Pruinosae*, sampled from various regions of Borneo and the Malay Peninsula. Fortynine chloroplast DNA haplotypes (HT) were identified among 768 specimens from five species, *Macaranga gigantea* (N= 329; 23 HT), *Macaranga pearsonii* (N=347; 21 HT), *Macaranga puberula* (N=24; 4 HT), *Macaranga hosei* (N= 48; 6 HT), and *Macaranga pruinosa* (N=20; 5 HT). Fortyone haplotypes were species-specific, whereas eight haplotypes were shared by two, three, or four species and occupied internal positions in a parsimony network. Population genetic parameters based on haplotype frequencies proved to be in a similar range in the non-myrmecophytic *M. gigantea* and in the ant-associated *M. pearsonii*, which have overlapping distributions in northern and eastern Borneo. A comparison of *GST* and *NST* values revealed a strong phylogeographic structure in both species, whereas colonization pathways suggested by the network topology were different. Both species exhibited similar levels of haplotypic diversity and moderate to high levels of population differentiation. There were no obvious indications for an influence of the symbiotic ant partners on the population structure of their host plants.