

Microsatellite DNA analysis of two dipterocarp species in a tropical rainforest in Sarawak

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Genetic diversity in natural tree populations has received much attention from foresters, ecologists and geneticists recently. For conservation or restoration of forests, it is important to preserve not only number of individuals, i.e. a quantitative trait, but also high genetic variation, i.e. a qualitative trait, within a plant population. The aims of this study are to elucidate the genetic diversity of dipterocarp tree populations and to discuss how the level of genetic diversity is created and maintained.

The study forest was located in a mixed dipterocarp forest of Lambir Hills National Park (4° 12' N, 114°00' E) in Sarawak, East Malaysia. In the 52 plot established in the forest, all woody plants larger than 1 cm in stem diameter (dbh) at breast height were mapped, and their species and size were recorded (Lee *et al.* 2002). In this study, two dipterocarp emergent tree species, *Dryobalanops aromatica* and *Shorea curtisii*, are selected as focal species. A main pollinator of *D. aromatica* is the giant honey bee (*Apis drosata*), a long-distance pollinator (Sakai *et al.* 2005). On the other hand, *Shorea* species are pollinated by beetles with low mobility (Momose *et al.* 1998).

We picked up fresh leaves from all trees ≥ 30 cm in dbh in the plot (403 trees for *Dryobalanops* and 52 trees for *Shorea*). From the leaves, DNA was extracted by a modified CTAB method (Murry & Thompson 1980). Using microsatellite markers (Ujino *et al.* 1998), genotype of all trees ≥ 30 cm in dbh in the plot (403 trees for *Dryobalanops* and 52 trees for *Shorea*) was discriminated.

Here, we report the genetic variation and genetic structure of the two species in the 52 ha plot.

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