

Ti: Genetic Diversity Assessment of *Koompassia malaccensis*C. T. Lee^{1,*}, S. L. Lee¹, Q. Z. Faridah², S. S. Siraj²,
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ABSTRACT

A genetic diversity study of *Koompassia malaccensis* based on 19 populations from 18 forest reserves in Peninsular Malaysia is reported. The genetic diversity assessment was based on six polymorphic microsatellites. Overall, all the populations showed high levels of genetic diversity. The allelic richness ranged from 6.0 (Pekan) to 9.3 (Lenggor) whereas the gene diversity ranged from 0.683 (Pekan) to 0.859 (Lenggor). The estimated coefficient of population differentiation (R_{st}) was 0.07, implying that 93% of the genetic diversity was partitioned within populations, with only 7% distributed among populations. From the cluster analysis among the populations, the two peat swamp populations (Pekan and Kuala Langat Selatau) formed a tight cluster even though they are not adjacent to one another. Further analysis including more populations and applying more microsatellites will generate more comprehensive genetic information.

Keywords: Kempas, genetic diversity, population genetics, simple sequence repeats

INTRODUCTION

Koompassia malaccensis Maingay ex Benth. (Leguminosae) is an important tropical timber species distributed in Sumatra, Peninsular Malaysia, Singapore and Borneo (Hou, 2000). It is locally known as kempas and grouped under medium hardwood. It is a very tall tree, easily reaching 55 m in height and has a diameter of 200 cm. It is found in lowland, hill, peat and freshwater swamp forests up to 800 m, but often favouring an altitude not exceeding 150 m. It flowers and fruits regularly and the main flower visitors are bees, *Apis* sp. (Appanah and Weinland, 1993). It produces flowers and fruits all year round with fruits surrounded by a papery wing that spins down. Under the IUCN (1994) version 2.3 criteria, kempas was assigned as lower risk/ conservation dependent (LR/cd) (IUCN, 2006). However, as the demand of its timber is high due to shortage of hardwood, proper conservation measures are crucial to ensure sustainable harvesting.

Knowledge of the distribution of genetic diversity within and among populations of tropical trees is essential in the development of conservation strategies (Hamrick, 1983). Microsatellite markers have been used in population genetic studies for a wide array of timber species (Al-Rabab'ah and Williams, 2002; Novick *et al.*, 2003; Wyman *et al.*, 2003; Lee *et al.*, 2006) due to their ability to detect and describe genetic differences between populations.

This study was carried out using a set of microsatellite loci newly developed for *K. malaccensis* (Lee *et al.*, 2006). The aims were, i) to estimate the genetic diversity levels of *K. malaccensis* in Peninsular Malaysia and, ii) to survey the distribution of genetic diversity within and among populations, and iii) to investigate whether *K. malaccensis* from the peat swamp forests are genetically distinguishable from those of the non peat swamp forests.

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