*Proceedings of the Seventh Round-Table Conference on Dipterocarps*: 10-15

# IMMEDIATE EFFECTS OF LOGGING ON GENETIC DIVERSITY OF *SHOREA CURTISII* (DIPTEROCARPACEAE) REVEALED BY DAMD-PCR MARKERS

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## Abstract

Immediate effects of logging on genetic diversity of *Shorea curtisii* of different age cohorts, i.e. seedlings, saplings and adult trees, were determined using directed amplification of minisatellite-region DNA-PCR (DAMD-PCR) markers. A total of 110 and 85 samples of *S. curtisii* were collected before and immediately after logging in Compartment 118, Ulu Sedili Forest Reserve, Johor, Malaysia. Genetic diversity parameters were estimated based on 33 reproducible fragments/DAMD-PCR loci. Two approaches were used to estimate the genetic diversity parameters, i.e. phenotypic method using Shannon's diversity index (S) and genotypic method with null-allele frequency corrected for deviation from Hardy-Weinberg equilibrium with SSR markers. In general, the reduction of genetic diversity parameters were in the following sequence: saplings < seedlings < adults. There was a significant loss ($p<0.05$) of S, total number of alleles detected and mean expected heterozygosity ($H_e$) in adult trees after a single selective logging event under Selective Management System (SMS). This result is concordant with the results revealed by SSR markers (not reported here) in terms of allelic richness indicating most probably good genome coverage of both markers. The genetic distance matrix generated from SSR data was significantly correlated with DAMD-PCR genotype data ($r = 0.990$, $p<0.05$), indicating a similar genetic structure of *S. curtisii* being depicted by both marker types among the age cohorts tested. Therefore, in general, both DAMD-PCR and SSR markers are sensitive in monitoring genetic diversity changes due to logging and other forms of disturbance.

**Key words:** Selective logging, *Shorea curtisii*, genetic diversity, DAMD-PCR

## Introduction

Maintenance of genetic diversity in forest tree populations that are undergoing population changes, whether natural or human-induced, is seen to be the key to adaptability and continued evolution (Müller-Starck 1985, Namkoong 1991). There is mounting evidence that tree populations which sustain genetic losses are more susceptible to productivity decline and loss of environmental fitness in the event of major environmental changes (Müller-Starck 1985, Bergmann *et al.* 1990, Raddi *et al.* 1994). Loss of genetic diversity immediately after harvesting has been reported in *Pinus strobus* (Buchert *et al.* 1997) and a few other tropical rain forest species (Changtragoon 1997, Wickneswari *et al.* 1999, Lee *et al.* 2002). Inbreeding as a result of logging has been detected in *Shorea megistophylla* (Murawski *et al.* 1994) and *Pterocarpus macrocarpus* (Liengsiri *et al.* 1998) indicating the reduction of mature individuals in the population and limited gene flow.

Sustainable management of natural forests depends on their ability to regenerate after logging. Regeneration determines the genetic diversity in the future forests and their capacity for sustainable production (Veikko & Stahl 2000). Hence assessment of regeneration capacity and genetic diversity would be useful in developing sustainable forest management guidelines and effective conservation strategies. According to Appanah and Mohd Rasol (1990), dipterocarp forests managed under the Selective Management System (SMS) of harvesting practice in Malaysia have the capacity to regenerate after logging. They also reported the fruiting of smaller dipterocarp residuals (> 25 cm dbh) in recently logged forests.