Sains Malaysiana 36(2)(2007): 233-242

Stand Structure and the Genetic Diversity of *Koompassia malaccensis* and *Dryobalanops aromatica* in Unlogged and Logged-over Stands

(Struktur Dirian dan Kepelbagaian Genetik *Koompassia Malaccensis* dan *Dryobalanops Aromatica* pada Dirian yang Belum dan yang telah Dibalak)

KIM SU LEE, RATNAM WICKNESWARI & CHEE YEN CHOONG

ABSTRACT

The disturbance level of two nearby logged stands, Compartment 118 and Compartment 69 were studied in Ulu Sedili Forest Reserve, Johor. The mean basal area for trees (trees ≥ 1 cm dbh) in logged stand of Compartment 118 showed 51% reduction in comparison to immediately before logging of the same stand. A similar level of reduction (47%) was observed for mean density of trees in Compartment 118. However, the mean basal area and mean density of tree were higher in 50-year logged Compartment 69 (21% and 122% respectively) compared to Compartment 118 before logging. Concurrently, we examined the effects of logging on genetic diversity of seedling, sapling and mature trees of two important timber species, Koompassia malaccensis and Dryobalanops aromatica using M13 universal primer (multilocus minisatellite DNA) and three other universally-primed primers. Mature trees of K. malaccensis showed 39% reduction in Shannon diversity index (H) in Compartment 69 compared to Compartment 118 before logging detected by M13 universal primer. This may be attributed to the small sample size of the species in Compartment 69. Reduction in H and polymorphic loci (P) for K. malaccensis was higher in seedlings, 5% and 56% respectively in Compartment 69 compared to mature trees (3% and 23% respectively). Contrastingly for seedlings and saplings of D. aromatica, increment in H was higher in Compartment 69 than Compartment 118 immediately after logging, which was 25% and 14% for seedlings while 21% and 14% for saplings, detected by M13 universal primer. The increased genetic diversity detected for this species may be due to its high density in Compartment 118 and Compartment 69. Loss in alleles caused a decline in H of K. malaccensis, especially mature trees in Compartment 69. On the other hand, H of D. aromatica was not affected by loss of alleles.

Keywords: Selective logging; relative disturbance; genetic diversity; Koompassia malaccensis; Dryobalanops aromatica

ABSTRAK

Tahap gangguan ke atas dua dirian pembalakan bersebelahan, Kompartmen 118 dan Kompartmen 69, di dalam Hutan Simpan Ulu Sedili, Johor telah dikaji. Min keluasan basal pokok (pokok ≥ 1 cm dbh) di dirian terbalak Kompartmen 118 menunjukkan penurunan 51% berbanding min keluasan basal pokok sejurus sebelum dibalak di dirian tersebut. Min densiti pokok juga menunjukkan tahap penurunan yang sama (47%) di Kompartmen 118. Namun, min basal pokok dan min densiti pokok adalah lebih tinggi (21% dan 122% masing-masing) di Kompartmen 69 yang dibalak 50 tahun dahulu berbanding Kompartmen 118 sejurus sebelum dibalak. Pada masa yang sama, kami telah mengkaji kesan pembalakan ke atas kepelbagaian genetik anak benih, anak pokok dan pokok matang dua spesies pokok balak yang penting, Koompassia malaccensis dan Dryobalanops aromatica, dengan menggunakan pencetus universal M13 (minisatelit DNA berbilang lokus) dan tiga lagi pencetus universal yang lain. Dalam analisis pencetus universal M13, indeks kepelbagaian Shannon (H) bagi pokok matang K. malaccensis menunjukkan penurunan sebanyak 39% di Kompartmen 69 berbanding Kompartmen 118 sejurus sebelum dibalak. Penurunan ini mungkin disebabkan oleh saiz sampel K. malaccensis yang kecil di Kompartmen 69. Kadar penurunan nilai H dan lokus polimorfik (P) adalah lebih tinggi dalam anak benih (5% dan 56% masing-masing) berbanding pokok matang (3% dan 23% masing-masing) K. malaccensis di Kompartmen 69. Sebaliknya, peningkatan nilai H anak benih dan anak pokok adalah lebih tinggi dalam Kompartmen 69 berbanding Kompartmen 118 sejurus selepas pembalakan bagi pokok balak D. aromatica, iaitu 25% dan 14% bagi anak benih dan 21% dan 14% bagi anak pokok masing-masing untuk Kompartmen 69 dan Kompartmen 118 dirian terbalak. Peningkatan kepelbagian genetik yang dikesan dalam D. aromatica adalah disebabkan oleh kelimpahan pokok balak ini dalam kedua-dua kompartmen tersebut. Kehilangan alel menyebabkan penurunan dalam nilai H pokok K. malaccensis, terutamanya bagi pokok matang dalam Kompartmen 69. Sebaliknya, nilai H bagi pokok D. aromatica tidak dipengaruhi oleh kehilangan alel.

Kata kunci: Pembalakan terpilih; gangguan relatif; kepelbagaian genetik; Koompassia malaccensis; Dryobalanops aromatica

INTRODUCTION

In recent years, the dwindling of forest coverage has received much attention worldwide, especially due to logging. Effects of logging on biodiversity and rainforest ecosystem ranges from alterations of physical structure of the forest to changes in species abundance and composition (Bawa & Seidler 1998; Davies 1998). Though only a small part of trees is harvested, a large portion of the forest may be imparted. Johns (1988) commented about the effects of selective logging caused by skid road construction, log-landing sites and pulling down of neighbouring trees during the extraction of timber trees. The effects can be observed in all forest strata. The immediate consequence of even selective timber extraction is the creation of a new stand structure. Owing to technology limitation, even harvesting of small number of trees may cause loss of forest productivity potential and its genetic diversity.

On the other hand, Cannon et al. (1998) noted that logging removed 62% of dipterocarp basal area. One year after logging, 45% of lowland forest canopy was open (including roads and skid trails) or dominated by low pioneer vegetation, 15% was unaffected and 40% was disturbed in various degrees. In comparison between unlogged and 1-year logged forest, logging reduced both trees density and number of trees species per 0.1 ha plot, for both large and small trees. Removal of trees > 50 cm dbh (diameter at breast height) reduced 43% of small tree species (20 – 30 cm dbh). In an earlier study by Borhan et al. (1987), seedling mortality was found to be 38 – 57% due to mechanized logging. They revealed that destruction of trees < 10 cm dbh was affected by logging practices while crown damage was caused by both logging practices and intensities.

In the *ITTO Year 2000 Objective*, all timber must be harvested from sustainably managed forests by 2000 (ITTO 1992) to ensure continuity of log production and conservation of genetic diversity. Maintenance of genetic resources is an important aspect in sustainable forest management. Genetic diversity is the basis of adaptive flexibility in populations and ultimate evolutionary potential (Ledig 1988; Given 1994; Templeton 1995; Young 1996). Loveless (1992) emphasized the importance of evaluating genetic diversity for developing conservation strategies and effective management guidelines for sustainable forestry. Various studies have been carried out on effects of logging on genetic diversity. Study by Lee et al. (2002b) showed single logging event under Malayan Uniform System did not cause genetic erosion in *Parkia speciosa*. Wickneswari et al. (2000) found the decrease in genetic diversity ranged 5-23% after logging in five tropical tree species which exhibit different life strategies. In addition, *Daemonorops verticillaris* showed slight decrease in alleles (14%) due to damages of individuals. Other studies have reported loss of outcrossing in *Shorea megistophylla* in selectively logged forest (Murawski et al. 1994), and no significant difference in outcrossing rate was detected in *D. aromatica* in primary and secondary forests (Kitamura et al. 1994).

Direct amplified minisatellite DNA (DAMD) is a PCR-based technique. Minisatellite DNA consists of 15-30 bp long sequence motifs repeated in tandem at various loci. The simple repetitive sequences used in DNA fingerprinting are made up of tandemly arranged motifs of only 2 – 10 bp (Epplen 1988; Tautz 1989). Allelic variations are created by the number of core sequence units they contain (Jeffreys et al. 1985). On the other hand, universally-primed PCR (UP-PCR) involves the amplification of genomic DNA with a single universal primer of 8 – 20 nucleotides long (Bulat et al. 1994). DNA hybridization in UP-PCR showed that amplified DNA is primer specific. These universal primers with high specificity are related to nucleotide substitutions in uncoding regions. DAMD has been successfully used in genotyping of *Oryza sativa* (Zhou et al. 1997), wheat (Bebeli et al. 1997) and *Salix* (Chong et al. 1995). Whereas, Lübeck et al. (1999) used UP-PCR to classify *Trichoderma harzianum* into two groups of genotypes and Bulat et al. (1998) studied the genetic relatedness between *Trichoderma* and *Gliocladium* using UP-PCR.

Koompassia malaccensis (Family: Leguminosae), locally known as kempas, is a medium hardwood. This species occurs in peat swamp forest and lowland forest at the elevation of 600 m a.s.l (above sea level). It is found in southern Thailand, Peninsular Malaysia, Borneo, Palawan in Philippines, Sumatra, Riau Archipelago, Banka and Biliton Islands (Appanah & Weinland 1993; Soerianegara & Lemmens et al. 1994). In Peninsular Malaysia, it scatters throughout Kedah, Kelantan, Penang, Perak, Selangor, Negeri Sembilan, Pahang, Malacca and Johor. It is suitable for heavy construction, posts, furniture, floor and railway sleepers.

Dryobalanops aromatica (Family: Dipterocarpaceae), locally known as kapur, is a medium hardwood. It occurs in Sumatra, Riau Archipelago, Borneo and Peninsular Malaysia (Symington 1943). In Peninsular Malaysia, *D. aromatica* is found mainly in two large areas in the east coast, stretching from Pahang-Terengganu border in Baloh Forest Reserve northwards to as far as Sungai Marang in Terengganu, and from north of Sungai Rompin in south Pahang to Panti Forest Reserve in south central Johor (Wyatt-Smith 1963). Besides, it can also be found in Kanching, Rawang, Selangor. *Dryobalanops aromatica* occurs abundantly in the lowlands and hills up to 365 m altitude. It is pollinated by bee viz. *Apis dorsata* and *A. indica* var *cerrana* (Appanah 1981; Ashton 1988). Besides being harvested for its timber for construction uses, it also produces camphor which is used in traditional medication for treating cough, asthma, liver and eye injury.

This study examined the effects of immediate and long term logging on the genetic diversity of *K. malaccensis* and *D. aromatica*. Two forest management units (FMU) located at Ulu Sedili F. R. (Forest Reserve) were chosen for this study. Direct approach was used to study the immediate effect of logging on the genetic diversity of both species in the same compartment before and after logging. An indirect approach was used to study the long-term effect of logging by comparing the genetic diversity

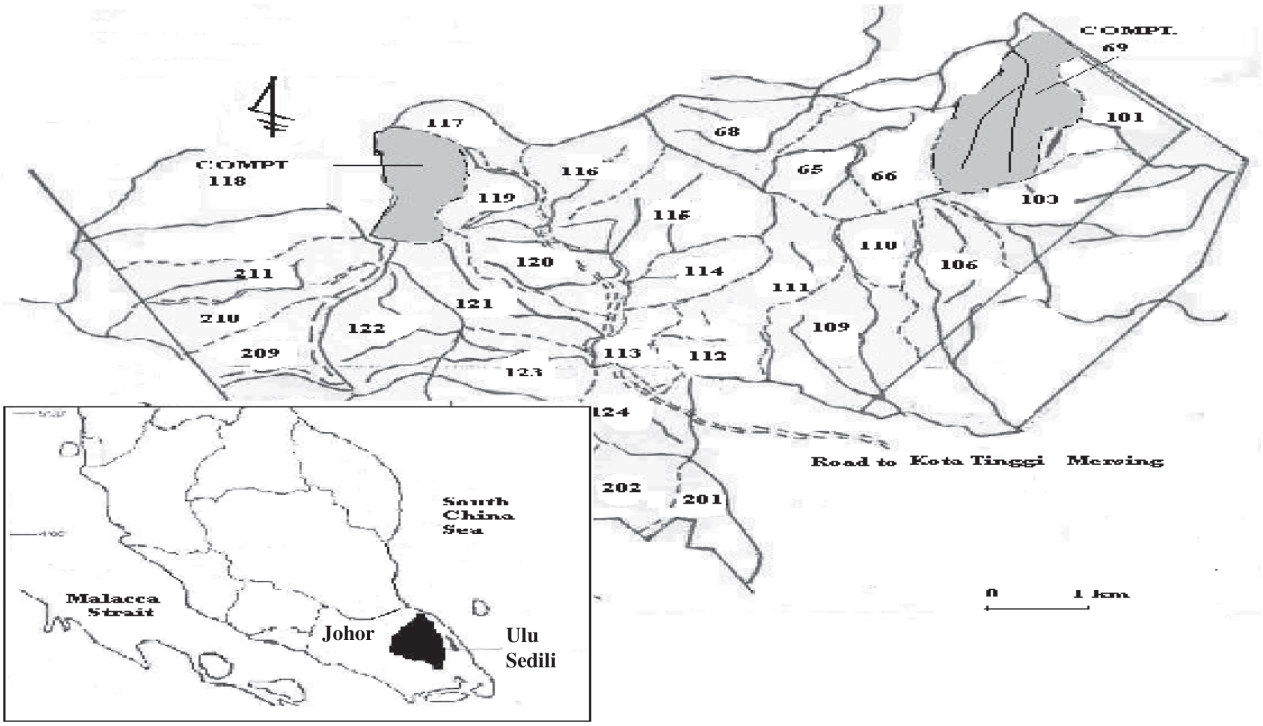

FIGURE 1. Map showing the location of Compartment 118 and Compartment 69 in Ulu Sedili F.R., Johor

in unlogged compartment to that in a nearby logged compartment (logged about 50 years ago). Similar studies have been carried out on *Scaphium macropodum* (Wickneswari et al. 1997a, b; Lee et al. 2002a) and *Parkia speciosa* (Lee et al. 2002b).

MATERIALS AND METHODS

STUDY SITES

Ulu Sedili F. R. is located in Kota Tinggi, Johor, Malaysia (2°10'N latitude, 103°45'E longitude). This forest reserve of 4806 ha has been demarcated as a Genetic Resource Area (GRA) in November 1992 (Lee et al. 2002a). It was divided into 30 compartments which are classified into three different forest management units (FMU): (1) virgin forest, (2) production forest and (3) logged-over forest (Figure 1).

Two compartments in Ulu Sedili F.R. were chosen for this study i.e. Compartment 118 and Compartment 69. Compartment 118 covering 164.3 ha is located at 150 – 800 m a.s.l (above sea level). It was logged in August 2000 under the Selective Management System (SMS). In this system, cutting limit for dipterocarp species is above 50 cm dbh, while for non-dipterocarp species, the cutting limit is not less than 45 cm dbh. In addition, at least 32 trees ha^{-1} for trees with diameter 30 – 45 cm dbh should be retained after logging (Thang 1988). Compartment 69 covering 305.6 ha is located at 50 – 800 m a.s.l. It was logged in 1950's under the Malayan Uniform System (MUS) where the cutting limit for all species is 45 cm dbh (Wyatt-Smith 1963).

ESTIMATION OF RELATIVE DISTURBANCE LEVEL

The pre-harvest inventory on number, species and diameter of all trees > 1 cm dbh were measured from six 20 m × 50 m plots established at different elevations in Compartment 118 in August 1999 and three 20 m × 50 m plots in Compartment 69 in November 1999. Demographic parameters estimated were basal area per unit area (m^2ha^{-1}), number of trees by diamater classes and species richness. The trees were classified into 5 diameter classes, i.e. 5 cm (seedlings and saplings), 5 – 15 cm (poles), 15 – 30 cm (small trees), 30 – 45 cm (medium trees) and > 45 cm (large trees). Post-harvest inventory for Compartment 118 was carried out in March 2001. Due to a landslide in Compartment 118 after logging, demographic data from only three plots could be gathered.

The relative disturbance index (RDI) was estimated using the importance value index (IVI) of the component species and relative importance value index (RIVI) (Curtis & McIntosh 1951; Narayanan & Swarupanandan 1996). The range of the RIVI values calculated for the plots studied were divided into 10 equal classes and assigned an adaptation index (AI) of 1 for the lowest class and 10 for the highest class with increasing order of magnitude. The product of RIVI and the corresponding AI values were summed for each plot to determine the continuum index (CI). The CI values for the study plots were arranged in increasing order of magnitude. An index for the level of disturbance (RDI) was then assigned for each plot based on the relative difference in magnitude of CI. The plot with the lowest CI value was given an index of 1, and the others were determined based on the relative difference in CI.

TABLE 1. Number of samples of *Koompassia malaccensis and Dryobalanops aromatica* collected from Compartment 118 and Compartment 69

Species	Age cohort	Compt. 118		Compt. 69
		Before logging	After logging	
Koompassia malaccensis	Seedling	7	0	4
	Mature	10	0	8
Dryobalanops aromatica	Seedling	41	55	97
	Sapling	43	15	36

DNA EXTRACTION

For each species, 30 – 40 individual trees of each diameter class were sampled (Table 1). Leaf tissues were sampled for seedlings and saplings whereas inner bark tissues were sampled for mature trees. Approximately 4 g leaf or inner bark tissues were used for DNA extraction using modified CTAB method (Doyle & Doyle 1987). Further purification using High Pure PCR Template Preparation Kit (Boehringer Mannheim) was carried out for seedling and saplings of *Dryobalanops aromatica* which contain high secondary metabolite.

DAMD AND UP-PCR ANALYSES

M13 universal primer (Chong et al. 1995) and three single universal primers i.e. UP45, UP3-2 and UP0.3-1 (Bulat et al. 1994) were used for genetic diversity studies. The polymerase chain reaction mixture with a total volume of 25 µl, consisted of 1X PCR buffer (200 mM Tris-HCl pH 8.4, 500 mM KCl), 3 mM Mg^{2+}, 0.2 mM of each dNTP, 10 pmol M13 universal primer, 1 unit *Taq* polymerase and 15 ng of template DNA. PCR amplification using M13 universal primer was carried out in PCR Gene Amp® PCR System 9700 (Perkin Elmer) for one cycle at 94ºC (2 min), 35 cycles at 94ºC (1 min), 45.1ºC (1 min) and 72ºC (2 min), finally one cycle at 72ºC (10 min). For UP-PCR primers, 4 mM Mg^{2+}, 0.6 mM of each dNTP and 2.5 units of *Taq* polymerase were used. Different annealing temperatures were employed: 57.5ºC (UP45), 55.6ºC (UP3-2) and 53.6ºC (UP0.3-1).

PCR products were separated in a 1.5% agarose gel in 1X TBE buffer (1 M Tris-base pH 8.3, 0.9 mM EDTA and 10 mM boric acid,). The electrophoresis was carried out at 85 V for 1 hour. Subsequently, the gel was soaked in 10^{-5} X Gelstar Gelstain® (FMC Corporation) for 1 hour before being visualized under UV light. Polaroid 665 was used for gel documentation.

DATA SCORING AND ANALYSIS

Band size of PCR products (200 bp – 2.070 kbp) was determined by comparing it to 100 bp ladder (GIBCO BRL). Amplified bands were scored as 1 (present) or 0 (absent) regardless of band intensity. Ambiguous or missing data were scored as 9. Each fragment scored was treated as a phenotypic character. Shannon diversity index (*H*) was estimated with the formula: $- \hat{A} p_i \ln p_i$, where p_i is the frequency of phenotype (King & Schaal 1989). Percentage of polymophic loci (P) was also determined.

RESULTS

ESTIMATION OF RELATIVE DISTURBANCE LEVEL

The estimated mean basal area (trees > 1 cm dbh) in Compartment 118 immediate after logging was reduced by 48% (before logging: 33.66 m^2ha^-1; after logging: 17.48 m^2ha^{-1}). 4.55 ha (3%) of the area had been cleared for logging roads, skidding roads and log-landing sites. Therefore, the actual reduction in basal area was 51%. Similarly, mean tree density was reduced by 47%, i.e. from 3507 trees ha^{-1} to 1873 trees ha^{-1}. Figure 2 shows the 50% reduction in basal area for trees ≤ 5 cm dbh and 84% reduction for trees > 45 cm dbh. This was corresponded to reduction in mean tree density of trees ≤ 5 cm dbh of 52%. Trees > 45 cm dbh was reduced by 80% (Fig. 3) due to removal of trees in this class during harvesting. Estimation of relative disturbance index (RDI) showed that basal area (BA) was correlated negatively with RDI (r = - 0.971; p = 0.029) for logged stand (Figure 4). Small CI value indicated the low disturbance level, i.e. for LS-Plot 4, CI = 403.65, RDI = 2.53; CI = 314.36, RDI = 2.00 (LS-Plot 5) and CI = 173.28, RDI = 1.13 (LS-Plot 6) (Table 2). From the demographic data, 89 species (21 dipterocarp; 68 non-dipterocarp) were recorded before logging, but it was reduced to 72 species (19 dipterocarp; 53 non-dipterocarp) after logging.

In comparison to Compartment 118, both the mean basal area and the mean tree density for Compartment 69 were higher, 21% (40.78 m^2ha^{-1}) and 122% (7790 trees ha^{-1}) respectively (Figure 5). In fact, logging had encouraged the regeneration of trees ≤ 5 cm dbh, i.e. 5903 trees ha^{-1} (Figure 6). Contrastingly, 1886 trees ha^{-1} for trees > 45 cm dbh were recorded in Compartment 69. 84 species were recorded in Compartment 69 in which 12 species were dipterocarp.

GENETIC DIVERSITY MEASURES

Long-term effect of logging on K. malaccensis In this study, immediate effect of logging was not determined for *K. malaccensis* due to inaccessibility to three demographic plots caused by landslide. Thus samples from those plots could not be collected. The long-term effect of logging on

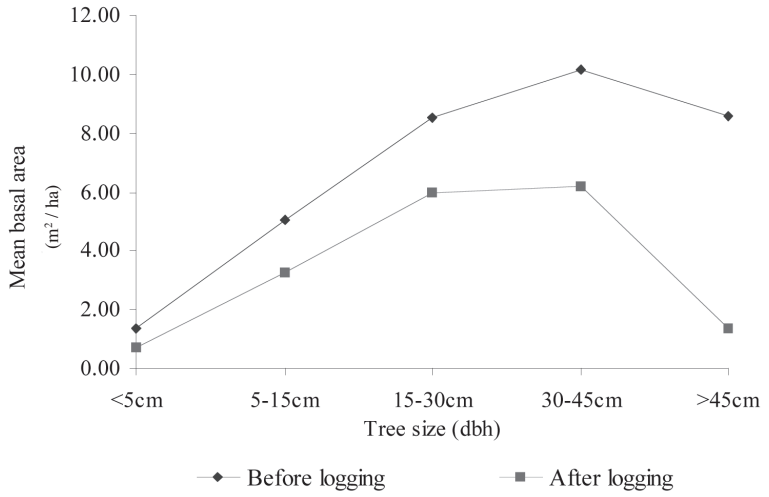

FIGURE 2. Mean tree density (m^2trees ha^{-1}) by diameter classes in Compartment 118 before and after logging

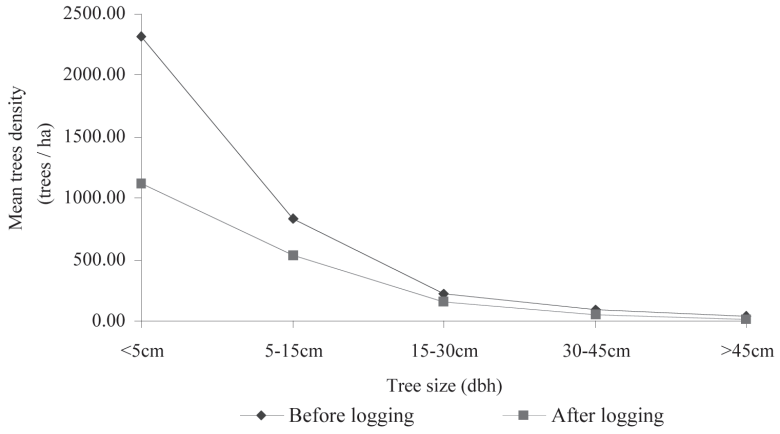

FIGURE 3. Mean tree density (trees ha^{-1}) by diameter classes in Compartment 118 before and after logging

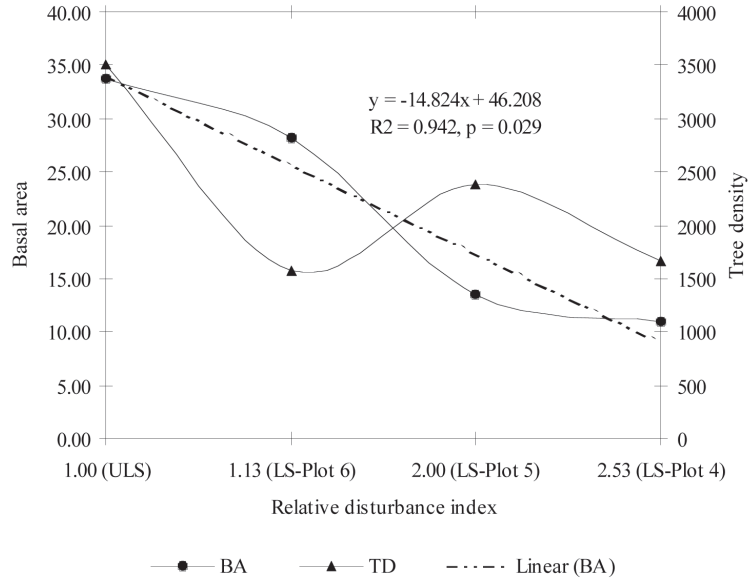

FIGURE 4. Relation between basal area (BA) and tree density (TD) per hectare with increasing relative disturbance index (RDI)

TABLE 2. Relation between basal area (BA) per hectare with increasing relative disturbance index (RDI)

Plot	CI	Difference CI	RDI	[a]% Disturbance	Activities
ULS	154.75	0.15	1.00	0.00	No disturbance.
LS – Plot 6	173.28	0.17	1.13	12.92	Logging under low intensity.
LS – Plot 5	314.36	0.30	2.00	63.55	Logging under low intensity; skidding roads.
LS – Plot 4	403.65	0.38	2.53	65.87	Logging under low intensity; skidding roads; logging roads.
Total	1046.04				

ULS – unlogged stand; LS – logged stand

[a] % disturbance – percentage of disturbance based on basal area (BA)

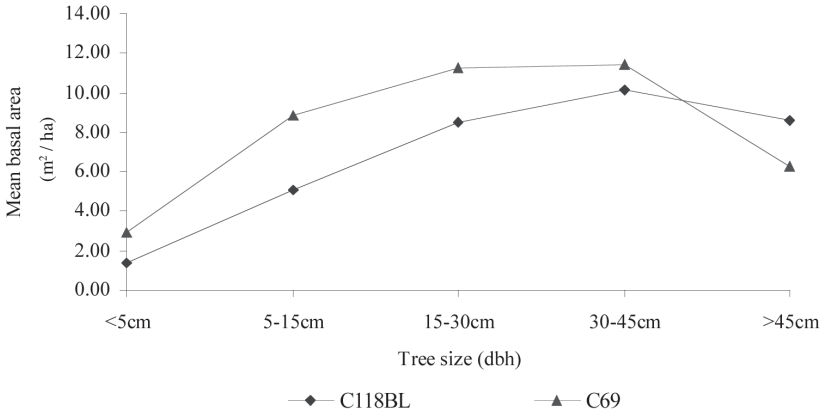

FIGURE 5. Mean basal area (m^2ha^{-1}) by diameter classes in Compartment 69 (C69) compared to Compartment 118 before logging (C118BL)

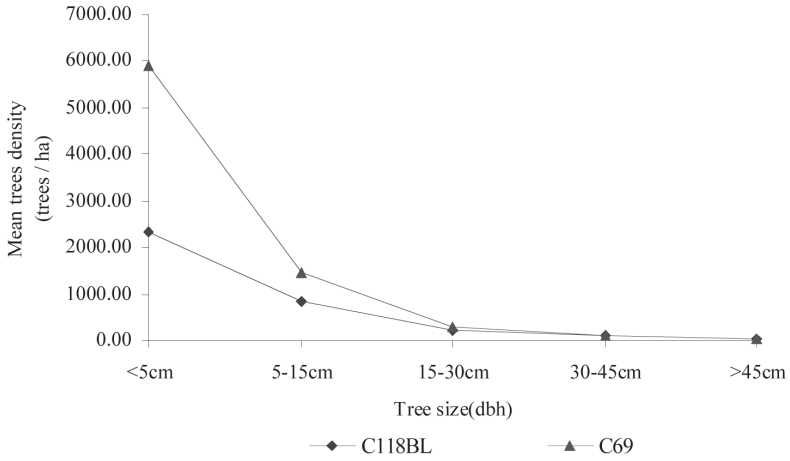

FIGURE 6. Mean tree density (trees ha^{-1}) by diameter classes in Compartment 69 (C69) compared to Compartment 118 before logging (C118BL)

K. malaccensis was observed by allelic loss in seedlings (83%), saplings (65%) and mature trees (50%), which was detected by M13 universal primer. UP-PCR primers viz. UP45, UP3-2 and UP0.3-1 demonstrated allelic loss in saplings (65%), seedlings (56%) and mature trees (18%), corroborating the results generated by M13 universal primer. The primers differed in their capacity to detect polymorphism within different tree diameter classes. The Shannon diversity index for seedlings could not be determined using M13 universal primer since only one sample was amplified for samples collected from Compartment 69. Thus, comparison of changes in this index was impossible. The Shannon diversity index (H) for *K. malaccensis* seedlings in Compartment 69 was lower (H = 0.313) compared to Compartment 118 (H = 0.331) using UP-PCR primers. Mature trees exhibited the lowest H (H = 0.192) (Table 3).

TABLE 3. Mean percentage of polymorphic loci (P) and Shannon diversity index (*H)* per primer for seedlings and mature trees of *K. malaccensis* in Compartment 118 before logging and Compartment 69

Age cohort	Primer	No. of samples analysed		No. of fragments scored	No. of polymorphic loci (P)		Shannon diversity index (*H*)	
		Compt. 118 before logging	Compt. 69		Compt. 118 before logging	Compt. 69	Compt. 118 before logging	Compt. 69
Seedling	M13	-	-	-	-	-	-	-
	UP-PCR	6	3	22	57 (88)	25 (39)	0.331	0.313
Mature	M13	9	7	22	20 (91)	7 (32)	0.317	0.192
	UP-PCR	10	8	25	56 (74)	43 (57)	0.289	0.280

Number in parentheses refer to percentage of polymorphic loci

TABLE 4. Mean percentage of polymorphic loci (P) and Shannon diversity index (*H)* per primer for seedlings and saplings of *D. aromatica* in Compartment 118 and Compartment 69

Age cohort	Primer	No. of samples analysed			No. of fragments scored	No. of polymorphic loci (P)			Shannon diversity index (*H*)		
		Compt. 118		Compt. 69		Compt. 118		Compt. 69	Compt. 118		Compt. 69
		Before logging	After logging			Before logging	After logging		Before logging	After logging	
Seedling	M13	18	30	45	34	15 (44)	25 (74)	20 (59)	0.228	0.259	0.284
	UP-PCR	20	29	43	29	47 (54)	59 (68)	37 (43)	0.218	0.270	0.224
Sapling	M13	27	12	20	29	19 (66)	10 (35)	7 (24)	0.229	0.260	0.276
	UP-PCR	28	11	19	25	62 (82)	28 (37)	18 (24)	0.243	0.256	0.215

Number in parentheses refer to percentage of polymorphic loci

Immediate effect of logging on D. aromatica An increase in number of alleles in seedlings of *D. aromatica* was detected in Compartment 118 immediate after logging (56%). On the contrary, the number of alleles for saplings was reduced by 45%. Table 4 summarizes the Shannon diversity index for seedlings and saplings in Compartment 118 and Compartment 69. Shannon diversity index for seedlings had increased by 14%, from 0.228 before logging to 0.259 after logging (detected by M13 universal primer). Similarly, UP-PCR primers showed increment in *H* for seedlings. Though there was loss of alleles for saplings, an increase in *H* of 14% and 5% respectively was observed using M13 universal primer and UP-PCR primers. Analysis of effect of sample size (N) on genetic diversity parameters showed that increment of allele number and Shannon diversity index for *D. aromatica* seedlings for all primers were not affected by sample size as the sample size before logging (19 – 21 samples) was less than that of after logging (26 – 31 samples). Whereby, allelic loss in saplings was attributed to reduction in sample size (before logging: 25 – 29 samples; after logging: 9 – 12 samples). There were threshold levels in which genetic diversity parameters dropped drastically below certain sample size. These analysis reveal that more than 20 samples were required to estimate change in number of allele while approximately five samples were required to estimate the Shannon diversity index (*H*).

Long-term effect of logging on D. aromatica However, UP-PCR primers detected 20% and 68% lower alleles in seedlings and saplings of *D. aromatica* in the investigation of long-term logging effect. Similarly, M13 universal primer detected 65% lower alleles in saplings but 33% more in seedlings. There were slightly higher in Shannon diversity index for seedlings (25%) and saplings (21%), detected by M13 universal primer in Compartment 69. These results corresponded with UP-PCR primers. The UP-PCR primers detected 3% higher in *H* for seedlings. In contrast, *H* for saplings was lower by 12% (Table 4).

DISCUSSION

ESTIMATION OF RELATIVE DISTURBANCE LEVEL

The reduction of basal area in this study (51%) was lower compared to that reported by Lee et al. (2002a). They noted 57.5% reduction in basal area after logging (trees > 5 cm dbh). Seedlings and mature trees were most affected. 52% of seedlings and 80% of mature trees were damaged after logging in Compartment 118. These results were highly correlated with damage in seedlings and saplings caused by logging practices, i.e. pulling of trees and construction of logging and skidding roads (4.55 ha). 50% and 84% reduction in basal area was observed for seedlings and mature trees respectively in Compartment 118. Lower RDI value (1.13) in LS-Plot 6 compared to LS-Plot 5 (2.00)

and LS-Plot 4 (2.53) also implied that low intensity selective logging caused less damage to forest trees. Guariguata (1998) monitored vegetative and demographic responses to mechanical damages caused by logging on seedlings of *Alseis blackiana* (Rubiaceae), *Protium panamense*, *P. tenuifolium* and *Tetragastris panamensis* (Burseraceae) in lowland forest in central Panama. In these species, percentage mortality after 4 years of logging was significant; bent (21%), snapped (13%) and undamaged controls (6%). Borhan et al. (1987) observed 38 – 57% seedlings mortality when the forest was logged by both tractor and heavy machine. Bertault and Sist (1997) reported that logging affected 40% trees > 10 cm dbh, whilst Wan Razali (1989) and Bertault et al. (1993) suggested that mortality rate would remain high for years before returning to 1 – 2% similar to that in primary forest.

Mean basal area and mean tree density were higher (21% and 122% respectively) in Compartment 69 than that in Compartment 118 before logging. Nicholson (1958) and Wyatt-Smith and Foenander (1962) observed 28 – 45% damages to small and mature trees in lowland forest after 2 years of logging under Malayan Uniform System (MUS). These damages led to creation of space for seedling to regenerate. Seedlings and saplings would use the gap to attain maturity (Whitmore 1983).

EFFECT OF LOGGING ON GENETIC DIVERSITY OF *KOOMPASSIA MALACCENSIS* AND *DRYOBALANOPS AROMATICA*

Logging caused damage to seedlings than mature trees of *K. malaccensis*. Shannon diversity index was lower in seedlings and mature trees (5% and 3% respectively). The lower Shannon diversity index might be attributed to small sample size after logging. Seven (seedlings) and 10 (mature trees) samples were collected in Compartment 118, whilst four and eight samples respectively were collected in Compartment 69. Lee et al. (2002a) showed that logging reduced the population size of *Scaphium macropodum* in a regenerated stand in Pasoh F.R., which had caused significant reduction (32%) in Shannon diversity index. Similarly, low genetic diversity owing to small population was also reported in *Gentiana pneumonanthe* (Raijmann et al. 1994), *Scabiosa columbaria* (Van Treuren et al. 1991), *Eucalyptus albens* (Prober & Brown 1994) and a number of tropical tree species (Wickneswari et al. 1997b).

Reduction in individual number might also reduce outcrossing rate. Murawski et al. (1994) observed increment of 18% in selfing in *Shorea megistophylla* (in Sri Lanka). Leingsiri et al. (1998) also observed reduction of outcrossing in *Pterocarpus macrocarpus* population (in Thailand). Vasek and Harding (1976) and Farris and Mitton (1984) detected decrease in outcrossing in *Clarkia exilis* and *Pinus penderosa* respectively. Besides that, loss in outcrossing can be caused by low gene drifting and low genetic diversity. Destruction of tropical forest by logging might change the competitors among plant species, alteration in pollen and seeds dispersal patterns and contraction in effective population size of plants and animals (Nason et al. 1997).

In contrast, increase of Shannon diversity index was observed immediately and long term after logging for *D. aromatica*. Lim (2002) demonstrated high heterozigosity (H_e = 0.700) and number of alleles (A_a = 5.43) for *D. aromatica* despite loss of polymorphic loci. The high abundance of *D. aromatica* in central Johor (Wyatt-Smith 1963) and pollination by bees may have contributed to its high outcrossing rate (t_m = 0.856) (Kitamura et al. 1994). Konuma et al. (1999) noted that outcrossing rate might not be influenced by tree density if the species has a long-distance pollinator such as *Apis* or *Trigona*. Kitamura et al. (1994) observed outcrossing rate of *D. aromatica* in primary and secondary forests ranged 79 – 86%. Besides, in their study using isozyme analysis, Lee et al. (2001) reported high outcrossing rate in primary forest (t_m = 0.92), followed by logged forest (t_m = 0.77), artificial forest (t_m = 0.66) and plantation forest (t_m = 0.55).

CONCLUSION

Trees ≤ 5 cm dbh suffered most damage caused by tree felling and road construction. On the contrary, canopy opening encouraged regeneration of trees ≤ 5 cm dbh in the long term. Low genetic diversity in seedlings and mature trees of *K. malaccensis* reported in this study is most likely due to the small population size. The high species heterogeneity and abundance of *D. aromatica* in Compartment 118 and Compartment 69 had buffered loss of genetic diversity due to logging.

Determination of trees species density prior to logging can aid in predicting the loss in genetic diversity. Generally, species of high abundance suffer less damage compared to low abundant species. Besides, one of the environmental factors which may be important in determining outcrossing rates is tree density since it infers the genetic diversity. On the other hand, even though current harvesting systems (SMS and MUS) are aimed to minimize damage to the tree species, the cutting limit needs to be modified corresponding to the number of selected individual species. Through the refinement of harvesting guidelines, the genetic diversity of this low abundant species may be retained. Besides, more studies on the low abundant species is important to understand the effect of selective logging on the genetic resources of tropical forests.

ACKNOWLEDGEMENT

We would like to thank the foresters from Operation and Development Unit of Renjer Office, Kota Tinggi, Johor for providing the demographic data for plots in Compartment 118 and Compartment 69, Ulu Sedili F.R. The funding for this study was obtained from the Ministry of Science, Technology and Environment, Malaysia (IRPA Grant 01-02-02-0022).

REFERENCES

Appanah, S. 1981. Pollination in Malaysian primary forests. *Malaysian Forester* 44: 37-42.

Appanah, S. & Weinland, G. 1993. Planting quality timber trees in Peninsular Malaysia - a review. *Malayan Forest Record* No. 38.

Ashton, P.S., Girnish, T.J. & Appanah, S. 1988. Staggered flowering in the Dipterocarpaceae: new insight into floral induction and the evolution of mass fruiting in the aseasonal tropics. *American Naturalist* 132: 44-66.

Bawa, K.S. & Seidler, R. 1998. Natural forest management and conservation of biodiversity in tropical forests. *Conservation Biology* 12: 46-55.

Bebeli, P.J., Zhou, Z., Somers, D.J. & Gustafson, J.P. 1997. PCR primed with minisatellite core sequences yields DNA fingerprinting probes in wheat. *Theoretical and Applied Genetics* 95: 276-283.

Bertault, J-G., Dupuy, B. & Maître, H-F. 1993. Silvicultural research of sustainable management of rainforest. *Proceedings of the Tropical Silviculture Workshop, IUFRO Centennial Conference,* pp. 1-14. Berlin, 1-3 September 1992.

Bertault, J-G. & Sist, P. 1997. An experimental comparison of different harvesting intensities with reduced-impact and conventional logging in East Kalimantan, Indonesia. *Forest Ecology and Management* 94: 209-218.

Borhan, M., Johari, B. & Quah, E.S. 1987. Studies on logging damage due to different methods and intensities of harvesting in a hill dipterocarp forest of Peninsular Malaysia. *Malaysian Forester* 50 (1-2): 135-147.

Bulat, S.A., Lübeck, M., Mironenko, N., Jensen, D.F. & Lübeck, P.S. 1998. UP-PCR analysis and ITS, ribotyping of strains of *Trichoderma* and *Gliocladium*. *Mycology Research* 8: 933-943.

Bulat, S.A., Mironenko, M.V., Lapteva, M.N. & Strelchenko, P.P. 1994. Polymerase chain reaction with universal primers (UP PCR) and its applications to plant genome analysis. In: Conservation of plant gene II: Utilization of ancient and modern DNA. *Missouri Botanical Garden*. Adams, R.P., Miller, J.S., Golenberg, E.M. & Adams, J.E. (Eds.) pp. 113-129.

Cannon, C.H., Peart, D.R. & Leighton, M. 1998. Tree species diversity in commercially logged Bornean rainforest. *Science* 281: 1366-1368.

Chong, D.K.X., Yeh, F.C., Aravanopoulos, F.A. & Zsuffa, L. 1995. DNA fingerprinting willows (*Salix* L.) using polymerase chain reaction with the M13 universal primer. *Scandinavian Journal of Forest Research* 10: 27-31.

Curtis, J.T. & McIntosh, R. 1951. Upland forest communities in the prairie forest border region of Wisconsin. *Ecology* 32: 476-496.

Davies, S.J. 1998. Tropical ecosystem: environmental impacts. In. *Biodiversity Conservation in ASEAN: Emerging Issues & Regional Needs* Ghazally, I. (ed.) England,ASEAN Academic Press Ltd: pp. 14-41.

Doyle, J.J. & Doyle, J.L. 1987. A rapid DNA isolation procedure for small quantities of fresh leaf tissue. *Phytochemical Bulletin* 19: 11-15.

Epplen, J.T. 1988. On simple repeated GATA/GACA sequences in animal genomes: a critical reappraisal. *Journal of Heredity* 79: 409-417.

Farris, M.A. & Mitton, J.B. 1984. Population density, outcrossing rate and heterozygote superiority in Ponderosa pine. *Evolution* 38: 1151-1154.

Given, D.R. 1994. *Principles and practice of plant conservation.* Portland, Oregan: Timber Press.

Guariguata, M.R. 1998. Response of forest tree samplings to experimental mechanical damage in lowland Panama. *Forest Ecology and Management* 102: 103-111.

ITTO. 1992. ITTO guidelines for the sustainable management of natural tropical forest. ITTO Policy Development Series No. 1.

Jeffreys, A.J., Wilson, V. & Thein, S.L. 1985. Hypervariable 'minisatellite' regions in human DNA. *Nature* 314: 67-73.

Johns, A.D. 1988. Effects of 'selective' timber extraction on rain forest structure and composition and some consequences for frugivores and folivores. *Biotropica* 20: 31-37.

King, L.M. & Schaal, B.A. 1989. Ribosomal DNA variation and distribution in *Rudbeckia missouriensis*. *Evolution* 43: 1117-1119.

Kitamura, K., Mohamad Yusof, A.R., Ochiai, O. & Yoshimaru, H. 1994. Estimation of outcrossing rate on *Dryobalanops aromatica* Gaertn. f. in primary and secondary forests in Brunei, Borneo, Southeast Asia. *Plant Species Biology* 9: 37-41.

Konuma, A., Y. Tsumura, C.T. Lee, S.L. Lee & T. Okuda. 1999. Estimation of gene flow in the tropical-rainforest tree *Neobalanocarpus heimii* (Dipterocarpaceae), inferred from paternity analysis. *Molecular Ecology* 9: 1843-1852.

Ledig, F.T. 1988. The conservation of diversity in forest trees. *Bioscience* 38: 471-479.

Lee, C.T., Wickneswari, R., Mahani, M.C. & Zakri, A.H. 2002a. Effects of selective logging on the genetic diversity of *Scaphium macropodum*. *Biological Conservation* 104 (1): 101-118.

Lee, C.T., Wickneswari, R., Mahani, M.C. & Zakri, A.H. 2002b. Maintenance of genetic diversity in *Parkia speciosa* in logged-over forests. *Journal of Tropical Forest Science* 14(2): 163-178.

Lee, S.L. 2001. Mating system parameters of *Dryobalanops aromatica* Gaertn. f. (Dipterocarpaceae) in three different forest types and a seed orchard. *Heredity* 85: 338-345.

Liengsiri, C., Boyle, T.J.B. & Yeh, F.C. 1998. Mating system in *Pterocarpus macrocarpus* Kurz. In Thailand. *Journal of Heredity* 89: 216-221.

Lim, L.S., R. Wickneswari, S.L. Lee & A. Latiff. 2002. Genetic variation of *Dryobalanops aromatica* Gaertn. F. (Dipterocarpaceae) in Peninsular Malaysia using microsatellite DNA markers. *Forest Genetics* 92(2): 127-138.

Loveless, M.D. 1992. Isozyme variation in tropical trees: patterns of genetics organisation. In. *Population genetics of forest trees*, Adam, W.T., Strauss, S.H., Copes, D.L. & Griffin, A.R. (eds.). *Proceedings of the International Symposium on Population Genetics of Forest Trees,* pp. 67-94. Corvalis, Oregan, USA, July 31 – August 2, 1990.

Lübeck, M., Alekhina, I.A., Lübeck, P.S., Jensen, D.F. & Bulat, S.A. 1999. Delineation of *Trichoderma harzianum* into two different genotypic groups by highly robust fingerprinting method, UP-PCR and UP-PCR product cross-hybridization. *Mycology Research* 103(3): 289-298.

Murawski, D.A., Gunatilleke, I.A.U.N. & Bawa, K.S. 1994. The effect of selective logging on inbreeding in *Shorea megistophylla* (Dipterocarpaceae) from Sri Lanka. *Conservation Biology* 8: 997-1002.

Narayanan, I.V. & Swarupanandan, K. 1996. Regeneration dynamics and sylvigenesis in the moist deciduous forests of southwest India. *New Forests* 11: 186-205.

Nason, J.D., Aldrich, R. & Hamrick, J.L. 1997. Dispersal and the dynamics of genetic structure in fragmented tropical tree populations. In. *Tropical Forest Remnants: Ecology, Management, and Conservation of Fragmented Communities,* Laurance, W. F., Bierregaard, R. O., Jr (eds.). pp. 304-320. Chicago, IL: University of Chicago Press.

Nicholson, D.I. 1958. A analysis of logging damage in tropical rainforest, North Borneo. *Malaysian Forester* 21(4): 235-245.

Prober, S.M. & Brown, A.H.D. 1994. Conservation of the grassy white box woodlands: population genetics and fragmentation of *Eucalyptus albens*. *Conservation Biology* 8: 1003-1013.

Raijmann, l.E.L., van Ginkel, W.E., Heckel, D.G. & Menken, S.B.J. 1994. Genetic variation and outcrossing rate in relation to population size. *Gentiana pneumonanthe* L. *Heredity* 8: 1014-1026.

Soerianegara & Lemmens, R.H.M.J. 1994. Timber trees: major commercial timbers. *Plant Resources of South-East Asia* No. 5(1). Bogor, Indonesia.

Symington, C.F. 1943. Foresters' Manual of Dipterocarps. *Malayan Forest Records* No. 16. Malaysia, Universiti Malaya.

Tautz, D. 1989. Hypervariability of simple sequences as a general source for polymorphic DNA markers. *Nucleic Acids Research* 17: 6463-6471.

Templeton, A.R. 1995. Biodiversity at the molecular genetic level: experiences from disparate macroorganisms. In *Biodiversity, Measurement and Estimation*, Hawksworth, D.L. (ed.). pp. 59-64. London: Chapman & Hall.

Thang, H.C. 1988. *Selective Management System: Concept and Practice (Peninsular Malaysia)*. Kuala Lumpur: Forest Department Headquaters.

van Treuren, R., bijlsma, R., van Delden, W. & Ouborg, N.J. 1991. The significance of genetic erosion in the process of extinction. I. Genetic differentiation in *Salvia pretensis* and *Scabiosa columbaria* in relation to population size. *Heredity* 66: 181-189.

Vasek, F.C. & Harding, J. 1976. Outcrossing in natural population. V. analysis of outcrossing, inbreeding and selection in *Clarkia exilis* and *Clarkia temboriensis*. *Evolution* 30: 403-411.

Wan Razali, W. 1989. Summary of growth and yield studies in tropical mixed forests. Proj. Pap. UNDP/RAS/86/049, Forest Research Institute, Malaysia, Kepong, *FRIM Report* No. 49, pp. 17-83.

Whitmore, T.C. 1983. Secondary succession from seed in tropical rain forests. Commonwealth Forestry Bureau, *Forestry Abstracts* 44(12): 767-779.

Wickneswari, R. & Boyle, T.J. 2000. Effects of logging and other forms of harvesting on genetic diversity in humid tropical forests. In *Forest Conservation Genetics: Principles and Practice*, Young, A., Boshier, D., Boyle, T. (eds.). pp. 115-122. Australia: CSIRO Publishing.

Wickneswari, R., Lee, C.T., Norwati, M. & Boyle, T.J.B. 1997a. Effects of logging on the genetic diversity of six tropical rainforest species in a regenerated mixed dipterocarp lowland forest in Peninsular Malaysia. Paper presented at CIFOR Wrap-Up Workshop on Impact of Disturbance, Bangalore, India, August 1997.

Wickneswari, R., Lee, C.T., Norwati, M. & Boyle, T.J.B. 1997b. Immediate effects of logging on genetic diversity of five tropical rainforest species in a ridge forest in Peninsular Malaysia. *CIFOR Wrap-Up Workshop on Impact of Disturbance,* Bangalore, India, August 1997.

Wyatt-Smith, J. 1963. Manual of Malayan Silviculture for Inland Forests. *Malayan Forest Records* 23(1).

Wyatt-Smith, J. & Foenander, E.C. 1962. Damage to the regeneration as the result of logging. *Malaysian Forester* 25(1): 40-44.

Young, A., Boyle, T. & Brown, T. 1996. The population genetic consequences of habitat fragmentation for plants. *TREE* 11: 413-418.

Zhou, Z., Bebeli, P.J. Somers, D.J. & Gustafson, J.P. 1997. Direct amplification of minisatellite-region DNA with VNTR core sequences in genus *Oryza*. *Theoretical and Applied Genetics* 95: 942-949.

School of Environmental and Natural Resource Sciences
Faculty of Science and Technology
Universiti Kebangsaan Malaysia
43600 UKM, Bangi, Selangor D. E.
Malaysia

Received: 18 November 2004
Accepted: 9 February 2007