

COMPARATIVE GENETIC DIVERSITY STUDIES OF *SHOREA CURTISII* (DIPTEROCARPACEAE): AN ASSESSMENT USING SSR AND DAMD MARKERS

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HO, W. S., WICKNESWARI, R., MAHANI, M. C. & SHUKOR, M. N. 2006. **Comparative genetic diversity studies of *Shorea curtisii* (Dipterocarpaceae): an assessment using SSR and DAMD markers.** Genetic diversity of *Shorea curtisii* from different age cohorts, namely, seedlings, saplings and adult trees were determined using six SSR loci and 33 DAMD loci. To quantify genetic diversity in *S. curtisii* we used standard genetic diversity measures for SSR data, and both phenotypic and genotypic methods with null-allele frequency corrected for deviation from Hardy-Weinberg equilibrium (HWE) with SSR markers for DAMD data. Results showed that the genetic diversity measured using DAMD genotypic method was lower than those derived from SSR data based on the same set of samples. This suggests that DAMD allele frequencies corrected from HWE deviation using fixation index derived from SSR data may be underestimated. The genetic distance matrix generated from SSR data was significantly correlated with DAMD 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. The relationship between sample size and genetic diversity measures demonstrated a threshold level, i.e. $n = 20$ and $n = 30$ for seedlings and saplings respectively, and $n = 15$ and $n = 20$ for adult trees revealed by SSR and DAMD markers respectively. Genetic diversity measures dropped drastically below these levels. These results further imply that a highly heterogeneous population was observed in *S. curtisii* from each age cohort. Collectively, both SSR and DAMD markers have good genome coverage in the *S. curtisii* genome.

Keywords: DNA analyses, polymorphisms, genetic distance, tropical timber species, hill dipterocarp forest

HO, W. S., WICKNESWARI, R., MAHANI, M. C. & SHUKOR, M. N. 2006. **Kajian perbandingan kepelbagaian genetik *Shorea curtisii* (Dipterocarpaceae): satu penilaian menggunakan penanda SSR dan DAMD.** Kepelbagaian genetik bagi *Shorea curtisii* daripada kohort umur berbeza, iaitu anak benih, anak pokok dan pokok matang telah ditentukan daripada enam lokus SSR dan 33 lokus DAMD. Bagi menganggar kepelbagaian genetik dalam *S. curtisii* kami menggunakan parameter kepelbagaian genetik piawai untuk data SSR. Bagi data DAMD pula kami menggunakan kedua-dua kaedah fenotip dan genotip dengan frekuensi alel nol dibetulkan penyisihannya daripada keseimbangan Hardy-Weinberg (HWE) dengan penanda SSR. Hasil kajian menunjukkan bahawa anggaran kepelbagaian genetik dengan kaedah genotip DAMD adalah lebih rendah berbanding dengan data SSR menggunakan set sampel yang sama. Ini mencadangkan frekuensi alel nol DAMD yang dibetulkan daripada sisihan HWE menggunakan indeks penetapan daripada data SSR mungkin di bawah jangkaan. Matriks jarak genetik yang dijana daripada data SSR berkorelasi secara signifikan dengan data genotip DAMD ($r = 0.990$, $p < 0.05$). Ini menunjukkan bahawa struktur genetik yang serupa bagi *S. curtisii* telah digambarkan oleh kedua-dua jenis penanda antara kohort umur yang diuji. Hubungan antara saiz sampel dengan kepelbagaian genetik memaparkan satu aras ambang, iaitu $n = 20$ dan $n = 30$ masing-masing bagi anak benih dan anak pokok, serta $n = 15$ dan $n = 20$ bagi pokok matang yang masing-masing dicerap oleh penanda SSR dan DAMD. Nilai kepelbagaian genetik menurun dengan mendadak di bawah nilai ambang. Hasil ini turut menunjukkan bahawa *S. curtisii* daripada setiap kohort umur mempunyai tahap keheterogenan yang tinggi. Secara keseluruhan, kedua-dua penanda SSR dan DAMD meliputi taburan yang luas dalam genom *S. curtisii*.

Introduction

Genetic diversity provides the template for adaptation and evolution of populations and species (Thomas *et al.* 1999). Therefore, preservation and maintenance of genetic diversity of all species are important for both short-term adaptations to environmental change and long-term impact on

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