

ABSTRACT

The application of biotechnology in forest plantation industry is getting more popular over the last decades and many researches have been conducted to develop marker-assisted selection for tree improvement programme in Malaysia. However, to date, marker assisted selection has not yet widely implemented in Sarawak and conventional breeding would take years to select the best characteristics in trees. Thus, this study was conducted to look into the effectiveness in using Expressed Sequenced Tag derived Simple Sequence Repeats (EST-SSRs) marker to estimate the distribution of genotypes and allele polymorphism of *Acacia mangium* superbulk populations in Sarawak; to determine the relationship or correlation between genetic variation of these populations to environmental and physiological factors and to determine the genetic differentiation of the *Acacia mangium* superbulk populations in comparison with other *Acacia* species. In this study, 93 fresh young leaf samples were collected from three different areas, namely Similajau (Borneo Tree Seeds Seedlings Supply Sdn Bhd. (BTSSSB), Bintulu (DAIKEN) and Kota Samarahan (UNIMAS arboretum) and total genomic DNA of the samples were extracted using modified CTAB method. Thirteen EST-SSR markers were chosen to determine the genetic diversity of *A. mangium* superbulk and fragment analysis was conducted by using ABI PRISM® 3100 Genetic Analyzer and Genemapper™ Version 4.0 software (Applied Biosystems, USA). Statistical analysis performed using PowerMarker software over 13 polymorphic loci revealed that the mean expected heterozygosity or H_e for the three populations was 0.432 and polymorphic information content (PIC) value of 0.398, respectively. Borneo Tree Seeds Seedlings Supply Sdn. Bhd. population showed the highest level of genetic diversity ($N = 40$; $H_e = 0.474$; $PIC = 0.432$) compared to Daiken ($N = 40$; $H_e = 0.458$; $PIC = 0.429$) and UNIMAS Arboretum $N = 13$; $H_e = 0.364$; $PIC = 0.333$). Mean F_{ST}

ranged from 0.411 to 0.533 which indicates that the surplus of homozygotes generally occur within these populations. This might be due to inbreeding factor or partial selfing in *A. mangium* superbulk populations and Mean G_{ST} value of 0.038 further revealed that a low gene differentiation between all populations (at 3.8%), which signifies that these populations are genetically similar to each other. UPGMA dendrogram was also constructed on the *A. mangium* superbulk populations and it revealed that the three populations belong to the same cluster, with BTSSSB and Daiken populations have the highest similarity coefficient (0.890). Future studies should look into the breeding patterns in *Acacia* plus tree populations; the effect of silvicultural regimes in forest plantations to the genetic structure of *Acacia* species; and the effect of interaction between temporal variations in outcrossing rates with temporal and spatial variations in seedling selection towards genetic structure of *Acacia* species.

Keywords: *Acacia mangium* superbulk, EST-SSR, UPGMA, genetic diversity.

**KEPELBAGAIAN GENETIK POKOK *Acacia mangium* TERBAIK (SUPERBULK)
MENGUNAKAN KAEDAH PENANDA JUJUKAN TERUNGKAP TERBITAN
MIKROSATELIT (EST-SSR)**

ABSTRAK

*Penggunaan bioteknologi di dalam industri perladangan hutan menjadi lebih popular pada 10 tahun kebelakangan ini dan banyak penyelidikan telah dijalankan untuk membangunkan kaedah pemilihan pokok menggunakan penanda genetik di Malaysia. Walaubagaimanapun, sehingga kini pemilihan berasaskan penanda genetik belum diamalkan dengan meluas di Sarawak dan pembiakan secara konvensional memerlukan beberapa tahun untuk memilih pokok yang berkarakter baik. Maka, projek ini bertujuan untuk mengkaji keberkesanan penanda jujukan terungkap terbitan mikrosatelit (EST-SSR) bagi menganggarkan taburan genotip dan alel polimorfik pada populasi *Acacia mangium* superbulk di Sarawak; untuk menentukan perhubungan dan korelasi di antara variasi genetik pada populasi *Acacia* tersebut dengan faktor persekitaran dan fisiologi dan menentukan perbezaan genetik populasi *A. mangium* superbulk berbanding spesies pokok *Acacia* yang lain. Dalam kajian ini, 93 daun muda diambil dari tiga kawasan berbeza, iaitu Similajau (Borneo Tree Seeds Seedlings Supply Sdn Bhd atau BTSSSB), Bintulu (DAIKEN) dan Kota Samarahan (Aboretum Unimas) dan jumlah genomik DNA telah diekstrak menggunakan kaedah CTAB yang telah diubahsuai. Tiga belas penanda-penanda EST-SSR ialah dipilih untuk menentukan kepelbagaian genetik *A. mangium* superbulk dan analisis cebisan dijalankan dengan menggunakan ABI PRISM® 3100 Genetic Analyzer and Genemapper™ Version 4.0 perisian (Applied Biosystems, USA). Analisis statistik menggunakan perisian PowerMarker ke atas 13 tempat sebenar polimorf menunjukkan yang purata heterozigot yang dijangka atau H_e untuk tiga populasi ialah 0.432,*

dengan nilai kandungan maklumat polimorfik atau PIC ialah 0.398. Populasi BTSSSB menunjukkan kepelbagaian paras genetic tertinggi ($N = 40$; $H_e = 0.474$; $PIC = 0.432$) berbanding Daiken ($N = 40$; $H_e = 0.458$; $PIC = 0.429$) dan UNIMAS Arboretum $N = 13$; $H_e = 0.364$; $PIC = 0.333$). Nilai min F_{ST} adalah di antara 0.411 dan 0.533 di mana ia menunjukkan lebihan homozigot berlaku dalam populasi ini. Ini mungkin disebabkan oleh pembiakbakaan dalaman atau separa kacukan sendiri di dalam populasi A. mangium superbull dan purata G_{ST} pada 0.038 seterusnya menunjukkan perbezaan gen yang rendah antara semua populasi (pada 3.8%), ini bermakna populasi-populasi ini mengandungi genetik yang sama. Dendogram UPGMA telah yang dibina berdasarkan analisis terhadap persamaan di antara ketiga-tiga populasi A. mangium superbull menunjukkan bahawa ketiga-tiga populasi tersebut terdiri daripada kluster yang sama, di mana populasi BTSSSB dan Daiken mempunyai koefisien keserupaan yang tertinggi iaitu (0.89). Cadangan untuk kajian di masa hadapan adalah untuk mengkaji corak pembiakan pokok yang terbaik untuk *Acacia mangium superbull*; kesan amalan silvikultur di ladang hutan terhadap struktur genetik spesis *Acacia*; dan kesan interaksi di antara variasi waktu untuk kadar kacukan dengan variasi waktu dan ruang di dalam pemilihan anak benih terhadap struktur genetik spesis *Acacia*.

Kata kunci: Acacia mangium superbull, EST-SSR, UPGMA, kepelbagaian genetik