

## GENETIC PARAMETERS OF *Gmelina arborea* : HEIGHT AND DIAMETER GROWTH

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**LOKMAL, N. 1994. Genetic parameters of *Gmelina arborea* : height and diameter growth.** An open-pollinated progeny trial from 36 plus trees of *Gmelina arborea* was established using randomized complete block design (RCBD). Individual tree height (Ht) and diameter at breast height (DBH) were measured annually. Narrow sense heritability ( $h^2_n$ ), phenotypic ( $\tau_p$ ) and genotypic ( $\tau_g$ ) correlations, and genetic gain ( $\Delta G$ ) were estimated for Ht and DBH from age one to six and age three to six years respectively. Heritability values for Ht ranged from 0.07 to 0.17 while for DBH, it was about 0.12. The values for both traits were very low indicating a very low degree of inheritance.  $\tau_p$  and  $\tau_g$  between Ht and DBH at year one to six were strong ( $> 0.5$ ), indicating that early selection for these traits would be effective. Expected  $\Delta G$  for Ht and DBH were 0.221 m and 0.456 cm respectively. The gains represented an improvement of 4.4% (Ht) and 8.6% (DBH) over the base population. It is suggested that low intensity mass selection followed by high intensity family selection could be carried out to warrant good response in  $\Delta G$ .

Key words: *Gmelina arborea* - progeny trial - open-pollinated - heritability - phenotypic correlation - genetic correlation - mass selection - family selection - selection differential - genetic gain

**LOKMAL, N. 1994. Parameter genetik bagi ciri ketinggian dan diameter bagi *Gmelina arborea*.** Ujian progeni menggunakan biji kacukan terbuka dari 36 pokok terpilih *Gmelina arborea* telah ditubuhkan. Ujian ini menggunakan rekabentuk blok rawak lengkap (RCBD). Ketinggian dan diameter tiap-tiap pokok diukur setiap tahun. Heritabiliti sempit ( $h^2_n$ ), korelasi fenotip ( $\tau_p$ ) dan genotip ( $\tau_g$ ) dan hasil genetik ( $\Delta G$ ) dianggarkan bagi ciri ketinggian (dari umur satu hingga enam tahun) dan bagi ciri diameter (dari umur tiga hingga enam tahun). Nilai heritabiliti bagi ciri ketinggian mempunyai julat dari 0.07 hingga 0.17, manakala bagi diameter pula adalah 0.12. Nilai heritabiliti bagi kedua-dua ciri adalah rendah menggambarkan darjah pewarisan yang rendah. Korelasi fenotip dan genotip bagi ciri ketinggian dan diameter dari umur satu hingga enam tahun adalah tinggi ( $> 0.5$ ), menunjukkan bahawa pemilihan pada peringkat awal bagi kedua-dua ciri-ciri ini akan berkesan. Hasil genetik yang dianggarkan bagi ketinggian dan diameter adalah masing-masing 0.221 m dan 0.456 sm. Hasil genetik ini merupakan peningkatan sebanyak 4.4% (bagi ciri ketinggian) dan 8.6% (bagi ciri diameter) berbanding dengan populasi asal. Pemilihan pukal (mass selection) dengan intensiti rendah diikuti dengan pemilihan famili dengan intensiti tinggi dicadangkan untuk menjamin respon yang baik dalam hasil genetik.

### Introduction

A total area of 300-400 acre were planted with *Gmelina arborea* between the late 1950's and early 1960's at three forest reserves namely Bintang Hijau, Bubu

and Piah, in Kuala Kangsar, Perak, Peninsular Malaysia. Substantial amount of variation was observed in height and diameter at breast height between individuals in these plantations. It is likely that both traits can be improved through proper selection and breeding programs. However, there is little information on heritability ( $h^2$ ) and no quantitative data on the relationship between traits to design multi-trait breeding programs. To the author's knowledge, beside heritability for height and diameter at breast height (Lokmal *et al.* 1990) and heritability for stem straightness, branching habit and healthiness (Lokmal *et al.* 1991), no other report has been published pertaining to this subject on *Gmelina arborea*.

Plus tree selection in breeding programme is solely based on the observed phenotypic value of the trees, and not the genotypic values. It is assumed that favorable phenotypes are the results of an expression of good genotypes. The phenotypic value is made up from genotypic and environmental values or

$$P = G + E$$

where

P is phenotypic value,  
G is genotypic value, and  
E is environmental value.

The environmental value is not known for each individual. However, effect of environmental factors could be estimated by propagating clones or progenies of the families in which the genetic deviations of the members of each family or clone are kept to a minimum. The only way of evaluating the breeding values of the selected individuals is through the test of progenies or clones.

Expressing the genetic control by means of  $h^2$  is the most common method used in forestry and proper interpretation would provide valuable guidelines for the breeding program (Zobel 1961). This information would make the breeding and selection work more reliable and more efficient. Efficiency in  $\Delta G$  through plus tree selection relies on the value of the  $h^2$  of the plus trees. The higher the  $h^2$  value the more efficient would be the genetic gain.

### Materials and methods

In 1981, an open-pollinated progeny trial from 36 plus trees of *Gmelina arborea* selected from Compartments S11 and S13, Bintang Hijau Forest Reserve was established at Field 36, Forest Research Institute of Malaysia (FRIM). A Randomized Complete Block Design (RCBD) was used with each family plot consisting of eight progenies replicated in four blocks. Details of the plot were reported by Lokmal *et al.* (1990). Measurements of height and diameter growth were carried out using clinometer and steel diameter tape respectively. Heritability values for total height and diameter at breast height were estimated from year one to year six and year three to year six respectively.

### Statistical analysis

Analysis using general linear model and variance component was carried out using mixed effect model (SAS 1989) as follows:

$$Y_{ijk} = \mu + b_i + f_j + (bf)_{ij} + \epsilon_{ijk}$$

where

$Y_{ijk}$  : the observation of  $j^{\text{th}}$  family in  $i^{\text{th}}$  block,

$\mu$  : the population mean,

$b_i$  : effect of the  $i^{\text{th}}$  block (fixed),

$f_j$  : effect of the  $j^{\text{th}}$  family (random),

$(bf)_{ij}$  : the effect of interaction between  $i^{\text{th}}$  block with  $j^{\text{th}}$  family (random),

$\epsilon_{ijk}$  : the random error associated with the  $i^{\text{th}}$  block in  $j^{\text{th}}$  family.

Interpretation of variance components was adapted from Zobel and Talbert (1984). Additive variance (breeding values) was estimated as four times of family variance while the phenotypic variance was estimated as a total of family variance, family by blocks and within plots variance (Falconer 1977).

In the formula form, these relations are written as follows:

$$\begin{aligned}\sigma_A^2 &= 4\sigma_f^2 \\ \sigma_p^2 &= \sigma_f^2 + \sigma_{fb}^2 + \sigma_w^2\end{aligned}$$

where

$\sigma_p^2$  : phenotypic variance,

$\sigma_f^2$  : family variance,

$\sigma_{fb}^2$  : family and block interaction variance,

$\sigma_A^2$  : additive variance, and

$\sigma_w^2$  : within plot variance.

Narrow sense heritability was estimated as follows:

$$h_n^2 = \frac{\sigma_A^2}{\sigma_p^2}$$

In addition to the above analysis, analysis of covariance was also carried out using data adjusted for blocks. Phenotypic and genetic correlation coefficients between traits were estimated using the method adapted from Kempthorne (1957) as follows:

## Phenotypic correlation coefficient

$$\tau_p = \frac{\text{Cov}_{xy}}{\sqrt{(\sigma_x^2 \times \sigma_y^2)}}$$

where

$\text{Cov}_{xy}$  : phenotypic covariance between traits x and y,  
 $\sigma_x^2$  : phenotypic variance of trait x, and  
 $\sigma_y^2$  : phenotypic variance of trait y.

## Genetic correlation coefficient

$$\tau_G = \frac{\text{Cov}_{xy}}{\sqrt{(\sigma_x^2 \times \sigma_y^2)}}$$

where

$\text{Cov}_{xy}$  : genotypic covariance between traits x and y,  
 $\sigma_x^2$  : genotypic variance of traits x, and  
 $\sigma_y^2$  : genotypic variance of traits y.

Estimate of genetic gain (G) was done using formula by Falconer (1977), as follows:

$$\Delta G = h_n^2 S$$

where

$\Delta G$  : genetic gain,  
 $h_n^2$  : narrow sense heritability, and  
 $S$  : selection differential.

## Results and discussion

Estimates of variance components for height and diameter at breast height are shown in Tables 1 and 2 respectively.

**Table 1.** Estimated values of all components of variance for height

Component of variance	Age (year)			
	One	Four	Five	Six
Block	0.0045 (1.5)	0.6602 (7.9)	0.8748 (6.3)	1.8833 (10.8)
Family	0.0050 (1.7)	0.1838 (2.2)	0.5828 (4.2)	0.6483 (3.7)
Family × Block	0.0241 (8.1)	3.5185 (41.9)	3.4213 (24.6)	2.6703 (15.3)
Within plots	0.2632 (88.7)	4.0293 (48.0)	9.0438 (64.9)	12.2965 (70.2)

Note : Figures in parentheses are percentages of the respective components of the total variance.

**Table 2.** Estimated values of all components of variance for diameter at breast height

Component of variance	Age (year)			
	Three	Four	Five	Six
Block	0.5846 (5.7)	0.5482 (3.4)	0.4305 (2.0)	0.5468 (1.7)
Family	0.2400 (2.3)	0.6115 (3.8)	0.7321 (3.4)	1.1043 (3.5)
Family × Block	3.2222 (31.4)	4.1769 (25.9)	3.0641 (14.3)	2.4475 (2.8)
Within plots	6.2121 (60.6)	10.7811 (66.9)	17.2246 (80.3)	27.1736 (87.0)

Note : Figures in parentheses are percentages of the respective component of the total variance.

Based on these values, the narrow sense heritability ( $h^2_n$ ) values of both traits are estimated and tabulated in Table 3.

**Table 3.** Estimated  $h^2_n$  values for total height from year one to year six

$h^2_n$	Age (year)		
	One	Five	Six
Height	0.0684	0.1787	0.1660
Diameter	a	0.1205	0.1236

Note : a - unestimatable due to negative estimate of variance family.

Phenotypic and genetic correlations between height and diameter at year one to six are shown in Tables 4 and 5 respectively.

**Table 4.** Phenotypic correlation coefficient  $r_p$  between traits at different ages

Traits	H1	H5	H6	D5	D6
H5	0.63				
H6	0.59	0.95			
D5	0.66	0.92	0.92	0.92	
D6	0.62	0.89	0.91	0.91	0.97

Note: Significant at  $\alpha = 0.05$ .

**Table 5.** Genetic correlation coefficient ( $r_g$ ) between traits at different ages

Traits	H1	H5	H6	D5
H5	0.61			
H6	0.74	0.82		
D5	0.50	0.86	0.96	
D6	0.67	0.78	0.89	0.96

Note: Significant at  $\alpha = 0.05$ .

The estimated values of  $h^2_n$  are very low. Low estimates of  $h^2_n$  for height and diameter, stem form, branching habit and healthiness have been reported by Lokmal *et al.* (1990, 1991). Samuel and Johnstone (1979) in their work on *Picea sitchensis* also found low values of  $h^2_n$  which ranged from 0.14 to 0.27. One of the main reasons was the presence of family and block interaction which reduced the values down to 50%. The interaction term was included in the estimation of phenotypic variance since its value was relatively higher (> 50%) than the family variance component (Tables 1 and 2) as suggested by Shelbourne (1972). The effect of interaction in reducing  $h^2_n$  is well recognized (Shelbourne 1972, Matheson & Raymond 1984, Cotterill 1987, Matheson & Cotterill 1990).

Selection on the basis of early progeny test information is one means of making progress in breeding. The results reported here indicate that early selection with respect to these traits is possible due to strong genetic and phenotypic correlation between traits at age one to six.

In general,  $h^2_n$  values for both traits tended to increase with age. This is a common occurrence in all species (Namkoong & Conkle 1976), since older trees can express their genotype better than the young, and both traits are age-dependent. This was reflected in terms of percentage of family variance components which tended to increase with age (Tables 1 and 2).

Percentage of contribution from components of variance for interaction tended to decrease with age, indicating that the families were more stable as they grew older. The same pattern was reported by Mohn *et al.* (1976), Ying and Morgenstern, (1979), and Nienstaedt and Riemenschneider (1985), in white spruce and Stonecypher *et al.* (1964) in *Pinus taeda*.

Since this experiment was not replicated in other environments, component of family by environment interaction could not be estimated. It is likely that the  $h^2_{\text{f}}$  reported here could be overestimated if applied over a wider range of environments and these figures must be considered as an upper limit. However, unless the family by environment interactions are large, these figures are acceptable.

The estimation of  $h^2_{\text{f}}$  using open-pollinated progenies is based on the assumption of random mating which may not be valid in reality (Squillace 1974). Thus, the deviation from random mating might affect the variability among relatives and this could inflate the estimate of heritability.

It was observed that the within-plot variance component was the largest compared to other variance components for both traits from age one to age six. This finding was in agreement with that observed by Hanover and Barnes (1967) and Samuel and Johnstone (1979). In most cases, the smallest value of variance component was observed either in the component for block or family.

In general, phenotypic correlation coefficients were smaller than their respective genetic correlation coefficient. The same phenomenon was reported by Cotterill and Dean (1992). However, both correlations indicated strong genetic and phenotypic association between traits from age one to six. These results further suggested that early selection, i.e. at the age one year, will deliver about the same amount of  $\Delta G$  as compared to selection at the age of six.

The  $\Delta G$  at the age of six year for height and diameter were 0.221 m and 0.456 cm respectively. On the basis of mean height and diameter of the base population at age six year (5.0 m and 5.3 cm respectively) and mean height and diameter of plus trees at the same age (6.3 m and 9.1 cm respectively with planting density of 1680 trees ha<sup>-1</sup>), these  $\Delta G$  represents an improvement of 4.4% (for height) and 8.6% (for diameter) over the base population. In order to increase  $\Delta G$ , maximizing the selection differential might be rewarding provided genetic diversity of the base population is wide enough to permit it.

## Conclusions

Heritability values estimated for height and diameter at breast height from year one to six were very low. Low intensity of mass selection followed by high intensity of family selection with greater emphasis on good families as well as best individuals of the families should be carried out with respect to these traits. In view of the strong positive phenotypic and genetic correlations between height and diameter at all ages, it was concluded that selection at the early stage is reliable. It is also concluded that selection for one trait will reward  $\Delta G$  in another. This is very important to ensure good response from the selection and hence

high genetic gain. In future, any experiment of this nature should be replicated at least at two different environments so that the genotype by environment interaction could be estimated and hence, accuracy of  $h_n^2$  estimates increased.

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