

## GROWTH VARIATION, HERITABILITY AND GENETIC GAIN IN THE FIRST-GENERATION OF *SHOREA LEPROSULA* PROGENY TEST AT KEMASUL FOREST RESERVE, PAHANG, MALAYSIA

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### ABSTRACT

*Shorea leprosula* is a tree species endemic to Southeast Asian rainforest that is highly valued for its timber and resin. Therefore, it has potential to be grown in forest plantations. To achieve this, a tree improvement program was conducted via a progeny trial, consisting of 40 half-sib families planted at Kemasul Forest Reserve (FR), Pahang, Malaysia. The main objectives were to evaluate the growth performances of *S. leprosula* progeny test based on selected growth traits and to estimate the values of heritability and genetic gain. The progeny trial plot was established with 40 half-sib families that originated from 5 populations. The trial plot was laid out in a randomized complete block design (RCBD) with 8 blocks and 4 trees planted per block making the total planted trees amounting to 1280 with a total area of 2.05 hectare. This paper will discuss the variations in the growth performances, heritability ( $h^2$ ) and genetic gain ( $\Delta G$ ) estimated from the following growth traits; diameter at breast height (DBH), total height (HT), clear bole height (CBH), mean crown radius (MCR), crown class, stem form, branch angle, branch size and forking characteristics. Findings showed that the survival rate (47.1%) of *S. leprosula* progeny test in Kemasul FR was relatively low due to an inevitable factor such as disturbance from wild elephant. In addition, the growth variations observed were significantly high ( $p < 0.05$ ) among the important economic traits such as DBH, HT and CBH. Besides, there were high variations observed within the progenies and among the 40 half-sib families. There were five families (F5, F4, F18, F1 and F28) that performed well based on the ordinal ranking. These five families originated from Menyala River FR and Gombak FR. On the other hand, based on the estimation of heritability ( $h^2$ ) and genetic gain ( $\Delta G$ ), the HT trait showed the highest value indicating that this trait could be considered as an important trait in family selection. Furthermore, findings in this study have managed to provide important fundamental knowledge in establishing a seedling seed orchard for *S. leprosula*.

Key words: Breeding strategies, Economic traits, Progenies, Tree selection, Variation

### INTRODUCTION

Forests form a crucial pillar of the Malaysian economy via the timber industry and wood related products. As off 2019, Malaysia's timber and timber-related exports recorded about RM 20.5 billion (approximately USD 4.8 billion) in profit, which was an increase of 0.1 billion from the previous year. Focusing on the price of light red meranti, log price stood firm at MYR 1830/tonne (approximately USD 417), whereas the price for sawn timber increased by 1.1%, MYR 2013/m<sup>3</sup> (approximately USD 459). Inclusively, the market value for timber and wood related products showed an increase in price trend in 2019 (Malaysian Timber Industry Board, 2019).

Current harvesting practices focuses on obtaining timber products from natural forest in a sustainable manner. However, a study conducted by the Forestry Department of Peninsular Malaysia (FDPM) in 1979 demonstrated that there was a need to establish large scale forest plantations to reduce rapid deforestation of natural forests. Establishment of forest plantations to reduce the dependency on the natural forest has long been practiced. For examples, China, India, Japan, Russia, United State, United Kingdom and South Africa already have advanced forest plantations as compared to Malaysia (Abd-Latif et al., 2018).

Realizing the importance of timber and timber-related products, the government of Malaysia has launched the Compensatory Forest Plantation Project (CFPP) in 1982. This is a large scale program, in which a total of 188 000 ha was allocated for the establishment of forest plantations. At the beginning of the project, *Paraserianthes falcata* and *Gmelina arborea* were the main planted species.

However, due to poor growth performance, native species such as *Shorea leprosula*, *Dryobalanops aromatica*, *Hopea odorata*, *Dyera costulata* and *Endospermum malaccense*, and several exotics species such as *Khaya ivorensis*, *Hevea brasiliensis* and *Acacia* hybrid were also introduced (Abd-Latif et al., 2018).

*Shorea leprosula* Miq. or commonly known as “light red meranti” belongs to the Dipterocarpaceae family. This species is indigenous to Peninsular Malaysia, Borneo, Sumatra and Thailand. *S. leprosula* can be found in lowland forests and in hill forests of up to 600 m altitude. It can grow on a wide variety of soil types, such as well-drained soils, clay soils, acidic soils, and periodically flooded alluvium (Chua et al., 2010). The trees can grow up to 60 m in height and 100 cm in diameter at breast height. Its outer bark is greyish brown in colour and shallowly fissured (Ashton, 1982). The trees are harvested from natural forests mainly for its timber and resin (Choo et al., 1983).

Since then, several feasibility studies on the growth performances of *S. leprosula* have been conducted. Among the studies was an establishment of a progeny trial plot. It is a field experiment that allowed for the assessment of genetic variation and the selection of progenies and/or individuals with particular traits that are considered superior. In general, progeny trials are used to compare the performance of specific mother trees or families (Weber & Montes, 2012). The preliminary assessment is crucial to estimate the best family or individuals that can be used as the mother trees for the collection of seeds for plantation purposes. Variations in growth traits are also capable of showing the genetic diversity of the species, which is also important for further selection among the families (Zobel & Talbert, 1984). The main objectives for the establishment of the progeny trial was to assess the growth performances and to estimate the heritability values and genetic gain of the progenies from the selected mother trees.

Heritability is the proportion of phenotypic variance among individuals in a population that is due to heritable genetic effects (Holland et al., 2003). Many studies have shown that growth performances, wood properties and tolerance of plant towards pest and diseases were among the plants’ characteristics that were affected by genetic. Therefore, the estimation of heritability is advantageous in predicting genetic gain. In general, the genetic gain is high when heritability is high (Abengmeneng et al., 2015). Genetic gain is a prediction of a change in the mean value of a trait that occurs with selection within a population. Genetic gain is also a manifestation of genetic improvement (Moose & Mumm, 2008).

Many studies have proved that forest tree breeding can help in increasing the yield from forest plantation production. According to Abd-Latif et al. (2018), trees from the *Shorea* genus, namely *S. leprosula*, *S. roxburghii* and *S. acuminata*, are promising species that should be planted in future plantation programs. Therefore, this study was initiated as an improvement program for *S. leprosula* species via the establishment of a progeny trial plot. The objectives of the study were to evaluate the growth performances among the families, then to assess the estimated broad-sense heritability ( $h^2$ ) and genetic gain ( $\Delta G$ ) based on the phenotypic characteristics; diameter at breast height (DBH), total height (HT), clear bole height (CBH), crown size (CRSZ), crown height (CRHT), stem form (SF), branch angle (BrA), branch size (BrS) and Forking (F). These characteristics were evaluated as the key economic traits, for examples the traits of DBH, HT and CBH are indication of the volume of a timber. Whereas the qualitative phenotypic traits such as SF, BrA, BrS and F indicated the wood quality of the timber.

## MATERIALS AND METHODS

### Preparation of planting materials

Seeds (half-sib) of *Shorea leprosula* were collected from 40 selected mother trees located in five forest reserves in Peninsular Malaysia, which are Forest Reserve (FR) Menyala River, Rengit Hill FR, Bangi FR, Gombak FR and Trantum FR. The five forest reserves were chosen due to the trees being able to produce mature fruits during the collection period.

The 40 selected mother trees (Table 1) were chosen based on the phenotypically superior plus trees characteristics; growth, stem form, wood quality and free from disease and pest infestation. Seeds germination were conducted at FRIM’s nursery. Selection of the seedlings was done at the age of 8 months where the seedlings have reached a height of 45 to 60 cm. The selection was based on uniformity in height and free from disease and pest. The total number of seedlings used in this study were 1280, whereby each half-sib family contained 32 progenies.

### Progeny trial plot establishment

The trial plot was established at Kemasul FR, Pahang, Malaysia which was located at the latitude of 3° 10' N and longitude of 102° 35' E. The total area is 2.05 hectare. In general, the soil series in this area was were Siri Chat and Batu Anam. This study area has a uniform temperature condition, high moisture content, moderate sunlight and free from storm or strong winds. It received north-east monsoon winds between November and March and the south-west monsoon winds from May to September. The study was also replicated at Ulu Sedili FR in Johor but in this paper, only findings from Kemasul FR is discussed.

The trial plot was laid out in Randomized Complete Block Design (RCBD) with eight blocks. Each block consisted of 160 plants, planted in 2 rows with a spacing of 4 m × 4 m. In summary, there were 40 half-sib families in one block, four progenies per half-sib family, making the total planted progenies amounting to 1280.

## Data collection

Growth data were assessed at the age of four years old. Following growth traits were evaluated; diameter at breast height (DBH), total height (HT), clear bole height (CBH), mean crown radius (MCR), crown class, stem form, branch angle, branch size and forking characteristic. For qualitative traits data (crown class, stem form, branch angle, branch size and forking), the progenies were evaluated and graded based on the selection of plus tree grading criteria's (Clark and Wilson, 2005). Each criterion was given a score based on the following index;

(i)	Stem form	1 to 4
(ii)	Forking	1 to 4 (1 = ¼ ; 2 = ½ ; 3 = ¾ ; 4 = top)
(iii)	Branch size	1 to 4 (1 = ½ - ¾ ; 2 = ½ ; 3 = ¼ - ½ ; 4 = ¼ )
(iv)	Branch angle	1 to 4 (1 = 25°; 2 = 45°; 3 = 65°; 4 = 90°)

## Statistical analysis of growth traits

Overall mean for each growth traits were calculated and statistically analyzed by the analysis of variance (ANOVA) to determine the significant differences of means among the families; DBH, HT, CBH, MCR, crown class, stem form, branch angle, branch size and forking using Duncan's multiple range test (DMRT). Data were analyzed using PROC GLM by SAS (SAS Institute Inc. 2014) as per following model:

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

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.

## Analysis of Variances Components, Heritability ( $h^2$ ) and Genetic Gain

Analysis of variances components were analysed using the PROC GLM model by SAS (SAS Institute Inc. 2014), considering that there were missing values of dead trees in the trial plot.

For the families that were reproduced by open pollination technique, the component variances were equal to ¼ from the **additive genetic variance. Phenotypic variances were estimated from the assessment of** family variance, interaction variance between family and block, and variance within plot or location as per following model;

$$\sigma^2_f = \frac{1}{4} \sigma^2_A$$

$$\sigma^2_p = \sigma^2_f + \sigma^2_{fb} + \sigma^2_e$$

where;

- $\sigma^2_f$  = family variance
- $\sigma^2_A$  = additive variance
- $\sigma^2_p$  = phenotypic variance
- $\sigma^2_{fb}$  = interaction variance between family and block
- $\sigma^2_e$  = variance within plot or location

Estimated broad sense heritability ( $h^2$ ) for each growth traits were calculated based on the values of component variances. Interpretation of the component variances was calculated based on the formula by Wright (1976) and Zobel and Talbert (1984). Estimated broad sense heritability ( $h^2$ ) is the ratio of **additive genetic variance to the phenotypic variances** as per the following model;

$$h^2_n = \sigma^2_A / \sigma^2_p = 4 \sigma^2_f / (\sigma^2_f + \sigma^2_{fb} + \sigma^2_e)$$

According to Cotterill and Dean (1990), heritability values for individuals or families can be classified into three categories which are; (i) low when the ( $h^2_n < 0.1$ ), (ii) medium when the  $h^2_n$  (0.1 – 0.3), and (iii) high when the ( $h^2_n > 0.3$ ).

Estimation of genetic gain is calculated based on the following formula (Eldrige et al. 1993; Falconer and Mackay, 1996);

$$G = Sh^2$$

where;

- G = genetic gain
- S = selection differential
- $h^2$  = heritability

Table 1: Details of the 40 selected mother trees of *Shorea leprosula*

No.	Family	Provenance	Latitude and longitude
1	F1	FR Menyala River	02° 48'N 101° 91'E
2	F2	FR Menyala River	02° 48'N 101° 91'E
3	F3	FR Menyala River	02° 48'N 101° 91'E
4	F4	FR Menyala River	02° 48'N 101° 91'E
5	F5	FR Menyala River	02° 48'N 101° 91'E
6	F6	FR Menyala River	02° 48'N 101° 91'E
7	F7	FR Menyala River	02° 48'N 101° 91'E
8	F8	FR Menyala River	02° 48'N 101° 91'E
9	F9	FR Rengit Hill	03° 45'N 102° 19'E
10	F10	FR Rengit Hill	03° 45'N 102° 19'E
11	F11	FR Bangi	02° 55'N 101° 47'E
12	F12	FR Bangi	02° 55'N 101° 47'E
13	F13	FR Bangi	02° 55'N 101° 47'E
14	F14	FR Bangi	02° 55'N 101° 47'E
15	F15	FR Bangi	02° 55'N 101° 47'E
16	F16	FR Bangi	02° 55'N 101° 47'E
17	F17	FR Gombak	03° 17'N 101° 46'E
18	F18	FR Gombak	03° 17'N 101° 46'E
19	F19	FR Gombak	03° 17'N 101° 46'E
20	F20	FR Gombak	03° 17'N 101° 46'E
21	F21	FR Gombak	03° 17'N 101° 46'E
22	F22	FR Gombak	03° 17'N 101° 46'E
23	F23	FR Gombak	03° 17'N 101° 46'E
24	F24	FR Gombak	03° 17'N 101° 46'E
25	F25	FR Gombak	03° 17'N 101° 46'E
26	F26	FR Gombak	03° 17'N 101° 46'E
27	F27	FR Gombak	03° 17'N 101° 46'E
28	F28	FR Gombak	03° 17'N 101° 46'E
29	F29	FR Gombak	03° 17'N 101° 46'E
30	F30	FR Gombak	03° 17'N 101° 46'E
31	F31	FR Gombak	03° 17'N 101° 46'E
32	F32	FR Gombak	03° 17'N 101° 46'E
33	F34	FR Gombak	03° 17'N 101° 46'E
34	F35	FR Gombak	03° 17'N 101° 46'E
35	F36	FR Gombak	03° 17'N 101° 46'E
36	F37	FR Gombak	03° 17'N 101° 46'E
37	F38	FR Menyala River	02° 48'N 101° 91'E
38	F39	FR Trantum	03° 88'N 101° 83'E
39	F45	FR Menyala River	02° 48'N 101° 91'E
40	F47	FR Rengit Hill	03° 45'N 102° 19'E

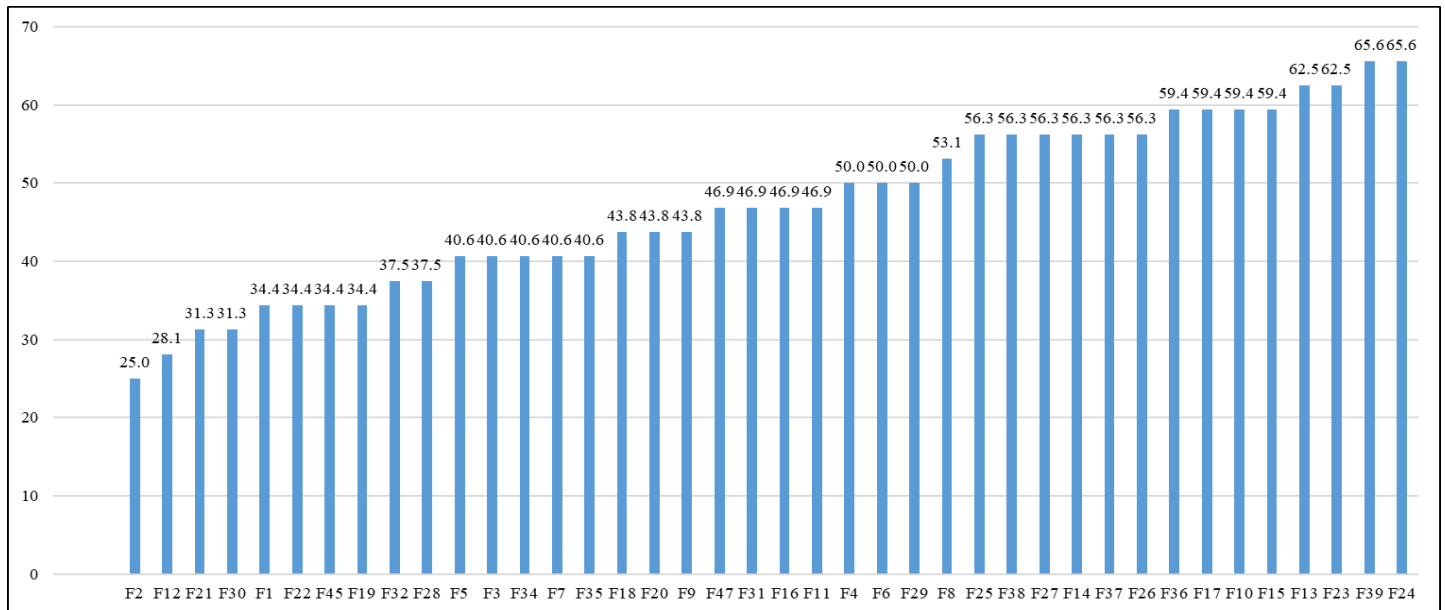
(Note: FR = Forest Reserve)

## RESULTS AND DISCUSSION

### Survival rates

Survival rates of the 40 half-sib families of *S. leprosula* at 4 years old ranged from as low as 25.0% to as high as 65.6% (Figure 1). There were 18 families scored above than 50.0% with F11 and F24 had the highest survival rates of 65.6%. On the other hand, the overall survival percentage of the whole trial plot recorded was 47.1%. This survival percentage indicated that the mortality rates of *S. leprosula* was very high. This could also have meant that *S. leprosula* seedlings were very vulnerable at early age. Most dipterocarp species such as *S. leprosula* need shaded areas at an early age. However, the chosen trial location had moderate sunlight penetration and high moisture content. Furthermore, it has to be noted that the trial plot was located at a natural forest area in which was also the habitat of elephants. Some of the trees were destroyed by the elephants, which was also a main cause of high mortality rates.

Figure 1: Survival rates (%) of the 40 half-sib families of *Shorea leprosula* at 4 years old



### Growth performance

Overall mean of the growth traits (DBH, HT, CBH, crown class, MCR, stem form, branch angle, branch size and forking) from the progeny trial plot of *S. Leprosula* is presented in Table 2. At the age of four years old after planting, mean of DBH and HT recorded was 3.51 cm and 4.41 m, respectively with the estimated increment of 0.60 cm/year and 0.70 m/year, respectively. Results showed there were high coefficient of variation values, indicating there were high variations among the progenies in the half-sib families for the respective traits.

In addition, results showed that the tested progenies in this study have straight stem form in which the mean recorded was in class 4 (recorded value = 3.99). This value indicated that the stem form of overall progenies in the trial plot was slightly crooked but the crookedness is not repetitive and suitable for timber production. Furthermore, branch angle and branch size were in class 3 where the branch angle is in the range of 45° to 65° and branch size is in the range of ¼ to ½ as compared to the main stem diameter. While in term of forking, the mean recorded indicated that the progenies tested were in class 4 whereby there was only one main stem (therefore, there was no forking characteristic recorded).

Study conducted by Naiem et al. on the progeny trial study of *S. leprosula* which had been established at East Kalimantan, Indonesia. From the data, it was observed that the growth performance of the progenies was better at Indonesia. The overall mean of DBH and HT traits recorded were 9.45 cm and 9.1 m, respectively. Among the difference between the two progeny trial plots was the spacing distance, which was 6 × 3m, whereas the spacing distance for this study was 4 × 4m. Their findings indicated that the larger the spacing distance, the better the growth performances of the progenies. In general, both studies showed that there was a highly significant difference in growth variations among the tested half-sib families.

**Table 2: Overall Mean, Standard Deviation (STDEV), Coefficient of variation (CV) and the number of samples (N) for the growth traits of diameter at breast height (DBH), total height (HT), clear bole height (CBH), crown class, mean crown radius (MCR), stem form, branch angle, branch size, forking**

Characteristics	N	Mean $\pm$ STDEV	CV (%)
Diameter at breast height (cm)	603	3.51 $\pm$ 1.65	46.9
Total height (m)	603	4.41 $\pm$ 1.65	37.3
Clear bole height (m)	603	2.16 $\pm$ 0.55	25.6
Crown class	603	2.26 $\pm$ 1.32	58.7
Mean crown radius (m)	603	1.99 $\pm$ 1.06	53.4
Stem form	603	3.99 $\pm$ 1.12	28.0
Branch angle	603	2.64 $\pm$ 0.73	27.7
Branch size	603	2.89 $\pm$ 0.97	33.6
Forking	603	3.96 $\pm$ 0.28	7.1

**Analysis of Variances (ANOVA)**

Analysis of variances (ANOVA) was conducted to determine the variations among the families and how significant are the factors of block, family and the interaction between block and family (block\*family) affecting the growth performances. ANOVA test indicated that there were five growth traits were significant at  $\alpha = 0.05/0.01$ ; DBH, HT, CBH, crown class and branch size on all the sources of variances, block, family and block\*family. While the family factor was shown to have highly significant different on the growth traits of HT, CBH and crown class at  $\alpha = 0.01$  (Table 3). Results indicated that in term of MCR, stem form, branch angle and forking characteristics, the 40 half-sib families perform similarly.

**Table 3. Analysis of variances for diameter at breast height (DBH), Total Height (HT), clear bole height (CBH), crown class, mean crown radius (MCR), stem form, branch angle, branch size and forking**

Source of variance	Df	DBH	HT	CBH	Crown class	MCR	Stem form	Branch angle	Branch size	Forking
Block	7	4.89*	9.58**	0.96**	5.31**	0.84	1.34	0.54	2.04*	0.03
Family	39	3.64*	4.67**	0.49**	2.94**	1.06	1.4	0.51	1.22*	0.04
Block*Family	223	3.17**	2.98**	0.37**	1.79*	1.14	1.4	0.57	1.01	0.06
Error	333	2.2	2.09	0.23	1.45	1.1	1.04	0.5	0.84	0.09
Total	602									

\* Significant difference at 0.05

\*\* Highly significant difference at 0.01

**Analysis of Variance Components**

The analysis of variance components was carried out to estimate the variants for each component; Block ( $\sigma^2_b$ ), Family ( $\sigma^2_f$ ) and the interaction between Block and Family ( $\sigma^2_{bf}$ ), and Error ( $\sigma^2_e$ ) for all the tested growth traits in the study. The variant's value for each component estimated the percentage of contribution of the tested traits, consequently giving a clearer picture on the importance of each component.

The variance components and percentage (%) for total variances of Block, Family and Error for all the growth traits tested in the study were shown in Table 4. For the traits MCR, branch angle and Forking, the values of Block ( $\sigma^2_b$ ) and Family ( $\sigma^2_f$ ) variances were zero (0.00). Forking trait also showed zero (0.00) value for the interaction between Block and Family ( $\sigma^2_{bf}$ ). The zero value (0.00) indicated very low variances from the growth traits.

Family variances ( $\sigma^2_f$ ) for the traits of DBH, HT, CBH, crown class, stem form and branch size recorded were as followed 1.47, 4.38, 3.13, 5.08, 0.82 and 1.06% from the total variances. The variance component values indicated that the traits DBH, HT, CBH, crown class, stem form and branch size contributed to the growth variations among the 40 half-sib families.

**Table 4: Analysis of Variance Components and Percentage (%) for total variances of Block, Family and Error for diameter at breast height (DBH), total height (HT), clear bole height (CBH), crown class, mean crown radius (MCR), stem form, branch angle, branch size and forking**

Component of variances	DBH	HT	CBH	Crown class	MCR	Stem form	Branch angle	Branch size	Forking
Block	0.05	0.13	0.01	0.07	0	0.02	0	0.01	0
	-1.83%	-4.74%	-3.13%	-3.95%	0.00%	-1.64%	0.00%	-1.06%	0.00%
Family	0.04	0.12	0.01	0.09	0	0.01	0	0.01	0
	-1.47%	-4.38%	-3.13%	-5.08%	0.00%	-0.82%	0.00%	-1.06%	0.00%
Block*Family	0.4	0.35	0.06	0.14	0.09	0.18	0.04	0.06	0
	-14.65%	-12.77%	-18.75%	-7.91%	-8.04%	-14.75%	-7.55%	-6.38%	0.00%
Error	2.24	2.14	0.24	1.47	1.03	1.01	0.49	0.86	0.08
	-82.05%	-78.10%	-75.00%	-83.05%	-91.96%	-82.79%	-92.45%	-91.49%	100.00%

Note: Number in the bracket ( ) showed the percentage of contribution (%)

### Ordinal Ranking of the Growth Traits

Based on the ANOVA and analysis of variance components tests, four growth traits (DBH, HT, CBH and crown class) were selected due to a high variations among the families to determine the ordinal ranking of the 40 half-sib families. Results showed that F5, F4, F18, F1 and F28 ranked at the top five (Table 5).

F5 had the best growth performance at DBH, HT and crown class but had slightly lower CBH (ranked 5). In term of survival rate, F5 recorded a survival rate of 40.6% contrary to F24 which has the highest survival rate (65.6%) but has the lowest growth performance (ranked 40). In fact, the top five ranked families based on growth traits, have survival rate lower than 50.0% (34.4 – 50.0%) (Figure 1). Due to the interference of wild animals at this trial plot, the survival rate recorded by each families might be biased. Besides, coefficient of variation (%) recorded by each families on the growth traits tested were slightly higher. This means that there were still high variations of the mean recorded by growth traits.

**Table 5: Ordinal ranking of growth traits showing differences among 40 half-sib families progeny test of *Shorea leprosula* at 4 years after planting in Forest Reserve Kemasul, Pahang, Malaysia**

Family	Provenances	DBH	HT	CBH	Crown class	Mean	Overall Rank
F5	FR Menyala River	1	1	5	1	2	1
F4	FR Menyala River	2	2	2	4	2.5	2
F1	FR Menyala River	3	5	9	6	5.75	4
F25	FR Gombak	4	7	15	7	8.25	6
F18	FR Gombak	5	3	12	2	5.5	3
F13	FR Bangi	6	4	20	3	8.25	7
F23	FR Gombak	7	17	10	17	12.75	12
F28	FR Gombak	8	8	4	9	7.25	5
F36	FR Gombak	9	11	7	14	10.25	9
F21	FR Gombak	10	10	18	11	12.25	10
F32	FR Gombak	11	6	16	5	9.5	8
F17	FR Gombak	12	14	6	18	12.5	11
F38	FR Menyala River	13	16	24	10	15.75	17
F29	FR Gombak	14	20	30	13	19.25	20
F6	FR Menyala River	15	12	19	12	14.5	14
F20	FR Gombak	16	15	13	15	14.75	16
F45	FR Menyala River	17	27	35	26	26.25	26
F3	FR Menyala River	18	13	3	23	14.25	13

F27	FR Gombak	19	18	1	28	16.5	18
F22	FR Gombak	20	9	21	8	14.5	15
F47	FR Rengit Hill	21	21	11	20	18.25	19
F12	FR Bangi	22	23	27	19	22.75	22
F10	FR Rengit Hill	23	22	8	24	19.25	21
F15	FR Bangi	24	25	36	21	26.5	27
F37	FR Gombak	25	30	23	32	27.5	28
F14	FR Bangi	26	29	39	22	29	30
F34	FR Gombak	27	24	26	25	25.5	24
F16	FR Bangi	28	35	37	31	32.75	33
F39	FR Tranum	29	36	32	38	33.75	36
F7	FR Menyala River	30	26	17	29	25.5	25
F11	FR Bangi	31	39	40	34	36	37
F19	FR Gombak	32	28	25	27	28	29
F8	FR Menyala River	33	33	28	33	31.75	32
F26	FR Gombak	34	34	29	37	33.5	35
F30	FR Gombak	35	19	22	16	23	23
F31	FR Gombak	36	32	14	36	29.5	31
F35	FR Gombak	37	38	38	35	37	39
F2	FR Menyala River	38	31	34	30	33.25	34
F9	FR Rengit Hill	39	37	31	39	36.5	38
F24	FR Gombak	40	40	33	40	38.25	40

### Heritability ( $h^2$ ) and Genetic Gain ( $\Delta G$ ) of the growth traits

In general, estimated broad-sense heritability ( $h^2$ ) showed low to medium values for all the genetic traits evaluated which ranged from 0.03 to 0.20 (Table 6) or approximately equal to 3 – 20%. The highest  $h^2$  was observed from the crown class trait (20%) followed by HT (18%) and CBH (13%), whereas the lowest  $h^2$  was observed from the stem form trait (3%). While the traits of MCR, branch angle and Forking recorded a zero value which indicates that the variation within these traits among the 40 half-sib families tested was very low.

Important economic traits such as HT and CBH recorded a medium level of  $h^2$  values. These traits can be key important traits for selection. A study by Naiem et al., (2014) also showed a low to medium values of  $h^2$  recorded for DBH and HT traits. The low values of  $h^2$  might indicate a narrow genetic base of the families. However, the distribution of *S. leprosula* in Malaysia is very wide. According to Lee et al., (2000), the genetic diversity of *S. leprosula* sampled throughout Peninsular Malaysia was considered as high ( $0.369 \pm 0.025$ ).

Overall mean of the four selected growth traits (DBH, HT, CBH and crown class) was used as a baseline to assess the selection differential among the mean of each half-sib families. In this paper, 10 selected half-sib families with the highest mean values for each tested growth trait was calculated for its genetic gain ( $\Delta G$ ) (Table 7). Results showed that the HT trait recorded the highest  $\Delta G$  which was 42% from the F5 family. Findings in this study recorded that there were 22 half-sib families (of 40 half-sib families tested) had mean HT above the overall mean (Supplementary data). Range of the  $\Delta G$  recorded from the 10 selected half-sib families were 6 – 42% for HT, 4 – 13% for DBH, 1 – 6% for CBH and 8 – 16% for crown class. F5 recorded the highest  $\Delta G$  for both DBH and HT traits.

A similar study conducted by Abengmeneng et al., (2015), demonstrated that there was 56% variation in narrow sense heritability in the HT trait of *Ceiba pentandra* at the age of one-year-old. *C. pentandra* is locally known as “kapok” tree, and the species is native to Mexico, South America and West Africa. *C. pentandra* is dominantly harvested for its timber, thus the study was emphasizing on the height trait as the key economic value. On the other hand, the  $\Delta G$  for HT in the study varied from as high as 20.89% above the mean performance, to as low as -29.58% below the mean performance.

Another study on provenance variation of two *Khaya* species, *Khaya anthotheca* and *Khaya ivorensis* indicated that there was no significant variation on the growth performance between the two species at the age of two years old. However, there were significant variations among the progenies tested on both species. Findings in the study recorded the  $h^2$  values of 74% and 51% of the HT trait in *K. anthotheca* and *K. ivorensis* at the age of two years old, respectively. In addition, the  $\Delta G$  in HT recorded on *K. anthotheca* and *K. ivorensis* varied from 0.59% to 26.32%, and 3.2% to 15.56%, respectively. As for the DBH trait, genetic gain



varied from 26.32% above mean performance to as low as -24.76% below the mean performance. The study recommended the progenies that recorded the  $\Delta G$  above the mean performance to be utilised for plantation establishment (Ofori et al. 2007).

**Table 6: Estimated heritability value ( $h^2$ ) for genetic traits**

Genetic traits	Heritability value ( $h^2$ )
Diameter at Breast Height (DBH)	0.06
Total Height (HT)	0.18
Clear Bole Height (CBH)	0.13
Crown class	0.20
Mean crown radius (MCR)	a
Stem form	0.03
Branch angle	a
Branch size	0.04
Forking	a

Note: a showed a negative value for estimated heritability and considered as zero

**Table 7: Selection differential (S) and estimated genetic gain ( $\Delta G$ ) for the traits of diameter at breast height (DBH), total height (HT), clear bole height (CBH) and crown class.**

No.	DBH			HT			CBH			Crown class		
	Family	S	$\Delta G$	Family	S	$\Delta G$	Family	S	$\Delta G$	Family	S	$\Delta G$
1	F5	1.21	0.13	F5	1.81	0.42	F27	0.45	0.06	F24	0.66	0.16
2	F4	0.77	0.08	F4	1.02	0.24	F4	0.34	0.05	F9	0.55	0.13
3	F1	0.67	0.07	F18	0.85	0.2	F3	0.27	0.04	F39	0.52	0.12
4	F25	0.66	0.07	F13	0.71	0.16	F28	0.27	0.04	F26	0.49	0.12
5	F18	0.62	0.07	F1	0.65	0.15	F5	0.21	0.03	F31	0.47	0.11
6	F13	0.57	0.06	F32	0.58	0.13	F17	0.2	0.03	F35	0.44	0.11
7	F23	0.49	0.05	F25	0.55	0.13	F36	0.18	0.02	F11	0.44	0.10
8	F28	0.47	0.05	F28	0.54	0.12	F10	0.11	0.01	F8	0.43	0.10
9	F36	0.46	0.05	F22	0.31	0.07	F1	0.1	0.01	F37	0.43	0.10
10	F21	0.4	0.04	F21	0.28	0.06	F23	0.09	0.01	F16	0.34	0.08

## CONCLUSION

Findings in this study showed that the survival rate of *S. leprosula* progeny test in Kemasul FR, Pahang, Malaysia was relatively low due to the inevitable factor such of wild animals. On the other hand, the growth variations observed were significantly high for important economic traits such as DBH, HT and CBH.

In term of family variations, there were high variations observed within the progenies and among the 40 half-sib families. There were five families (F5, F4, F18, F1 and F28) perform well based on the ordinal ranking. These five families originated from FR Menyala River and FR Gombak. The genetic materials could be further used for future breeding studies and seed sources for conservation and reforestation activities.

Based on the heritability ( $h^2$ ) and genetic gain ( $\Delta G$ ), the HT trait showed the highest value indicating that this trait could be considered as an important trait in family selection. Furthermore, findings in this study have managed to provide important fundamental knowledge to establish a seedling seed orchard for *S. leprosula*.

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## Data archiving statement

All relevant data are within the paper and supplementary material will be uploaded to DRYAD.

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