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# BROAD SENSE HERITABILITY ESTIMATE OF SOME TRAITS IN CACAO PROGENY TRIAL IN MALAYSIA

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**ABSTRACT** - *The primary goal for most breeding programs in crops is to select genotypes with high yield, resistant to pests and diseases and other desirable agronomic traits while preserving genetic diversity. This paper aimed to estimate component of genetic variation and heritability for specific traits of the cocoa progeny trial in Malaysia. It is very important to understand the inheritance pattern of some traits in generated progenies for breeding strategies especially in the development of superior planting materials. The experiment was laid out in a randomized complete block design of three replications in a progeny trial plot at CRDC Bagan Datuk, Perak. The collected data were subjected to analysis of variance (ANOVA). For this study, the results apply to specific population and environment. This finding would assist cacao breeders to understand the genetics controlling specific traits especially yield and VSD disease tolerance in cacao planting material.*

***Keywords:*** Genotype, genetic variation, heritability, planting material, progeny

## INTRODUCTION

Cacao (*Theobroma cacao* L.), a small understory tree native to the Amazon estuary (Motamayor *et al.*, 2008) is one of the most important perennial crops worldwide. It grows under shade in tropical environments such as Africa, Asia and Latin America regions (Sobowale *et al.*, 2016). The main product of the cacao crop is the seeds called cocoa beans which is used in food and non-food products (Nigam and Singh, 2014).

In producing quality and valuable cocoa beans for the world, breeding study has been playing the important role in cacao crop. The primary breeding objectives for cacao are mostly for yield, resistance to pests and diseases (Lopes *et al.*, 2011) and also bean quality improvements. Usually, plant breeders will always want to combine the useful features of two plants to produce new superior genetic materials. For this study, hand-pollinated seeds received from Papua New Guinea (PNG) and field-planted at Cocoa Research and Development Centre (CRDC) of Bagan Datuk, Perak was used to estimate the heritability of some traits as well as creating new progenies with specific objective such as development of planting materials with high yielding and resistant to VSD disease.

According to Hill (2001), heritability is the proportion of phenotypic variation ($V_P$) in a trait due to variation in genetic values ($V_G$). Phenotypes variation observed between the individuals in a population because of environmental factors and the genes that influence the traits. There is also various interactions between the genes and environmental factors. For the genotype variation of individuals in a population, it occurred at the loci affecting particular traits. The estimation of heritability provides useful genetic information to predict characters transmission from parents to their offspring (Parikh *et al.*, 2016). This would serves as a guide to breeders for the variation observed in particular traits due to genotypic (broad-sense heritability) or additive (narrow-sense heritability) effects (Manga *et al.*, 2018). The selection for the study traits would be easy if heritability of the character is very high.

Through this study, the analysis of genetic control based on hybridization could reveal some information and knowledge on the nature and magnitude of genotypic and phenotypic variability present in the cocoa population. A successful breeding program could be formulated to develop and produce superior planting materials. This paper discusses the overall performance of the progeny trial derived from the bi-parental crosses and to estimate the genetic components and broad-sense heritability in the population. The genetic analysis of the results is to provide and advance knowledge on inheritance pattern of some traits in the generated progenies. The information gained would assist plant breeders for selection of promising genetic materials and further study of the selected traits.

## MATERIALS AND METHODS

### *Plant Material*

Ten progenies (KA2/106 X KEE 42, K 82 X KEE 42, K 82 X KEE 5, KA2/106 X KEE 5, K 82 X KEE 12, KA2/106 X KEE 47, KA2/104 X KEE 12, K 82 X KEE 47, KA2/106 X KEE 23 and KA2/106 X KEE 43) received from PNG was field-planted at Cocoa Research and Development Centre of Bagan Datuk, Perak. The experiment was laid out in three randomized blocks (RCBD) with 64 plants per plot at a planting distance of 3m x 3m triangular under Gliricidia stands as shade trees. Standard cacao culture procedures were used for field maintenance.

### *Phenotypic Assessments and Data Collections*

The tree morphology, pod, bean and yield traits were recorded on a single tree basis. Height of the first jorquette was taken at twenty-two months after field planting. According to Velayutham *et al.* (2013), jorquetting height of cacao tree could affecting the yield. This is because the lengthier jorquette could provide more number of flower cushions leading to higher yield. Girth measurement of the progenies was measured at 30 cm above the ground level in six monthly intervals for four consecutive years. Cacao with good tree girth is expected to produce more number of fan branches which would reflect the trees vigour that favouring higher yield. Both jorquette height and girth measurements were measured by measuring tape and expressed in centimetre.

Pod yield of the individual trees was evaluated bimonthly as one of the main yield components. The data was recorded for nine consecutive years. Dry cocoa beans were prepared according to normal procedure; fermentation of the raw beans for 4-5 days and sun-drying 5-7 days. Pod and bean analysis (PBA) was carried out to determine the bean parameters such as average dried bean weight (ADBW), pod value (PV), bean number per pod (BNP) and other valuable traits according to Haya *et al.* (2007). Pod value is defined as number of pods required to produce one kilogram of dried beans. Estimation of dried bean yield was calculated from PBA results using the formula below:

$$\text{Dried bean yield potential} = \frac{\text{(no. of pod/tree/year) x 1111 trees in a hectare}}{\text{Pod value}}$$

### *Vascular Streak Dieback (VSD) Disease Assessment and Data Collection*

The progenies was evaluated and assessed for vascular streak dieback (VSD) disease to determine their degree of tolerance. The extent of disease symptom severity or damage was quantified following Nuraziawati *et al.*, (2014) by using a disease severity or damage scale which is from 0-6 on progressive damage from chlorosis to defoliation to dieback (Table 1). The scale was used to score the severity of the disease of a plant sub-unit (flush region of seedling or twig or branch of a jorquetted plant).

Table 1. Damage scale of VSD Infection

| **Score** | **Main Symptom** |
|---|---|
| 0 | Apparently uninfected or healthy |
| 1 | Infected leaf, several or most of leaves without symptom |
| 2 | Infected leaf, most or overall showing chlorosis in progress |
| 3 | Most of the infected leaves showing chlorosis and necrosis in progress |
| 4 | Abscise of infected leaves |
| 5 | Abscise of most infected leaves; apparent cessation of first flush growth |
| 6 | Near complete or complete defoliation from abscission of infected leaves; dieback (first flush) in progress as indicated by the drying of twig or stem |

*Chlorosis* : tissue of green leaf change into yellowish due to lack of chlorophyll
*Necrosis* : leaf tissue died indicating scalded or burn mark

The severity score (x) obtained for each evaluated canopy quadrant was then weighted with factor (k) according to the position of the flush; which is based on number of infected quadrant where; 4/4 for all infection quadrant, ¾ for three quadrant, 2/4 for two quadrant and ¼ for one infection quadrant. The disease severity index (DSI) for each tree will be:

$$\text{DSI} = \frac{(x_1k + x_2k + x_3k + x_4k)}{6}$$

The total was divided by number of damage scale classes (6), where $x_1$, $x_2$, $x_3$ and $x_4$ were the value of infection score at each canopy (quadrant). Data collection on VSD disease severity of the trees (DSI) was calculated based on the indexes symptom. The progeny trees were grouped and determined into seven levels of tolerance (Nuraziawati *et al.*, 2014):

0.0 – extremely resistant

0.5 – tolerant

1.0 – less tolerant

1.5 – moderately tolerant

2.0 – less susceptible

2.5 – susceptible

3.0 – extremely susceptible

### *Statistical Analysis*

Data obtained from the assessments were analysed by SAS software package (version 8.2 for windows) to perform analysis of variance (ANOVA). The significance of differences was determined by Tukey’s multiple comparison technique.

### *Estimation of Heritability*

Heritability, the proportion of phenotypic variation is caused mainly by genetic variation among individuals. Heritability and components of genetic variation in this population were estimated for the study traits. The value of heritability always lies between 0 and 1 as a ratio of variance components. The variance components and broad-sense heritability for the progeny population was calculated as follows;

Variance components (from the ANOVA table)

a) Genetic/genotypic variance ($\sigma^2_g$) = (MSG-MSE)/r
b) Error/environmental variance ($\sigma^2_e$) = MSE
c) Phenotype/phenotypic variance ($\sigma^2_p$) = $\sigma^2_g + \sigma^2_e$

Broad-sense heritability was estimated as the ratio of the genetic variance to the phenotypic variance following Manga *et al.*, (2018) as:

$$(H^2) = (\sigma^2_g / \sigma^2_p) = [\sigma^2_g / (\sigma^2_g + \sigma^2_e)]$$

Heritability percentage were categorized as low (0-10%), moderate (20-50%) and high (≥50%) as indicated by Elrod and Stanfield (2002).

## RESULTS AND DISCUSSIONS

The ten progenies differed significantly ($P < 0.05$) from each other for three (jorquette height, yield and VSD disease incidence) out of the four studied traits (Table 2). The mean of the ten progenies for the traits were: jorquette height (114.79 cm), tree girth (26.72 cm), dried bean yield (415.21 kg/ha/yr) and VSD disease incidence (1.25). The coefficients of variation for the four traits ranged between 3.00 (jorquette height) and 17.48 (dried bean yield).

Table 2. Analysis of variance for the study traits

| Source of Variation | DF | Jorquette Height | Tree Girth | Yield | VSD Disease Assessment |
|---|---|---|---|---|---|
| Progeny | 9 | 147.68** | 4.11 | 20227.44* | 0.02* |
| Error | 18 | 11.89 | 2.72 | 5268.85 | 0.01 |
| Mean | | 114.79 | 26.72 | 415.21 | 1.25 |
| CV % | | 3.00 | 6.17 | 17.48 | 5.96 |

The mean performance of the ten progenies for four characters was presented in Table 3. Progeny KA2/104 X KEE 12 gave the highest mean value for jorquette height (124.47 cm) followed by K 82 X KEE 12 (121.15 cm) and KA2/106 X KEE 5 (121.07 cm) meanwhile KA2/106 X KEE 42 gave the lowest value (103.52 cm). The biggest girth measurement (28.18) was recorded by KA2/106 X KEE 5 followed by KA2/106 X KEE 42 (28.07 cm) while the smallest value (24.7 cm) was indicated by KA2/104 X KEE 12.

Progeny of K 82 X KEE 42 gave the highest value for dried bean yield (551.43 kg/ha/yr) followed by KA2/106 X KEE 42 (512.22 kg/ha/yr), KA2/104 X KEE 12 (482.51 kg/ha/yr) and KA2/106 X KEE 5 (460.43 kg/ha/yr). Progeny of KA2/106 X KEE 47 showed the lowest value (294.6 kg/ha/yr) of dried bean yield at the trial plot.

For the disease assessment, progeny of K 82 X KEE 5 recorded the least mean value (1.15) of VSD disease severity index followed by KA2/106 X KEE 43 (1.17), K 82 X KEE 12 and K 82 X KEE 47 (both with 1.19 score index). Lower the DSI is better as it showed less incidence of VSD disease infection. All of the progeny populations were categorized into less tolerant against the disease with the score in the range of 1.0 (less tolerant) to 1.5 (moderately tolerant). From this result, progeny K 82 X KEE 5 represent the most tolerance population against the disease compared to others

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Table 3: Mean performance of ten progenies for four traits

| **Progeny** | **Jorquette height (cm)** | **Tree girth (cm)** | **Yield (kg/ha/yr)** | **VSD disease assessment (DSI)** |
|---|---|---|---|---|
| K 82 X KEE 42 | 107.50cd | 27.46a | 551.43a | 1.29ab |
| KA2/106 X KEE 42 | 103.52d | 28.07a | 512.22ab | 1.23ab |
| KA2/104 X KEE 12 | 124.47a | 24.70a | 482.51abc | 1.34ab |
| KA2/106 X KEE 5 | 121.07a | 28.18a | 460.43abc | 1.26ab |
| K 82 X KEE 5 | 115.57abc | 26.89a | 383.05abc | 1.15b |
| K 82 X KEE 12 | 121.15a | 27.08a | 381.94abc | 1.19ab |
| KA2/106 X KEE 23 | 116.56abc | 25.90a | 380.74abc | 1.33ab |
| KA2/106 X KEE 43 | 108.92cd | 25.24a | 367.14abc | 1.17ab |
| K 82 X KEE 47 | 109.53bcd | 26.23a | 338.04bc | 1.19ab |
| KA2/106 X KEE 47 | 119.62ab | 27.40a | 294.60c | 1.37a |

Means followed by the same letter(s) are not significantly different according to Tukey’s Studentized Range (HSD) Test ($P<0.05$)

From the result obtained (Figure 1), it was revealed that the progeny with the highest jorquette height and biggest girth measurement still producing dried bean yield within the mean value which is considered as high for the trial plot. Meanwhile progeny with the highest VSD disease severity index recorded the least dried bean yield. This indicated that the genotype was more susceptible than others towards the disease.

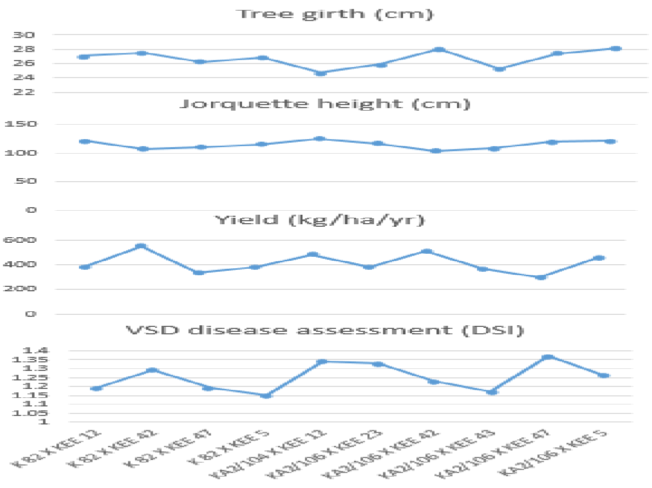

Figure 1: The graph combination of the ten progenies for four study traits

The parents used in this crosses genetic materials has been identified to show promising value for the specific objectives. Regarding the yield observation, clone such as KEE 42 performed good yield compared to others when combine with K 82 and KA2/106. In terms of VSD disease study, clones like KEE 5, KEE 12 and KEE 47 resulted more tolerable genetic materials when combined with K 82 meanwhile KEE 43 when combined with KA2/106.

Table 4 below shows the mean phenotypic and genotypic coefficient of variation and estimation of heritability in the genotypes. The results showed that genotypic coefficient of variation (GCV) lower than phenotypic coefficient of variation (PCV) for all study traits. Broad-sense heritability range of 0.15 – 0.79 was observed. Dried bean yield had the highest value for phenotypic and genotypic coefficient of variation.

Table 4: Mean phenotypic and genotypic coefficient of variances and heritability in the progenies

| **Characters** | **Mean** | **PCV** | **GCV** | **Environmental variance** | **Heritability** |
|---|---|---|---|---|---|
| Jorquette height (cm) | 114.79 | 57.15 | 45.26 | 11.89 | 0.79 |
| Tree girth (cm) | 26.7163 | 3.1824 | 0.4644 | 2.7180 | 0.15 |
| Yield (kg/ha/yr) | 415.2097 | 10255.0446 | 4986.1975 | 5268.8471 | 0.49 |
| VSD disease assessment (DSI) | 1.2525 | 0.0099 | 0.0043 | 0.0056 | 0.44 |

The heritability estimates in the progeny population was high in jorquette height measurement (0.79) compared to other traits which means that the percentage of genetic variation was higher than the environmental factor influence. High broad-sense was indicative of the trait being controlled by genetic factors as opposed to environmental effects. Dried bean yield and VSD disease incidence showed moderate heritability estimate with 0.49 and 0.44 respectively. The girth size of the progeny trees revealed low heritability estimation with only 0.15. This indicated that this trait was highly influenced by the environmental factors such as soil condition, nutrient status and others compared to their genetic factor. The finding from this study showed that high variations in the progenies are mainly due to the genetic factor as well as environmental factors. The result of this trial could be inferred that the diversity exists in the trial plot and can be exploited in cocoa crop improvement research.

## CONCLUSIONS

To conclude, results of the progeny trial showed that genotype effects were significant for dried bean yield, jorquette height and VSD disease assessment except for girth size. This study showed low to high heritability range ($H^2 = 0.15–0.79$). The evaluation of this generated hybrid is a crucial for breeders to understand their genetic potentials in terms of heritability and the collection of the studied agronomic and yield characters. The finding of this study has provided some important information regarding the genetic influence from the parents through the progenies and how much it was accumulated or involved in the progeny trees. Even though the traits expression is controlled by genes, it may partly be influenced by the environment where they were cultivated. This information could assist breeders to select potential and promising genetic materials especially for yield and VSD disease improvement for cacao crop in Malaysia. Result from this trial suggested that progeny of K 82 X KEE 42, KA2/106 X KEE 42, KA2/104 X KEE 12 and KA2/106 X KEE 5 could be selected for acceptable good yield while progeny of K 82 X KEE 5, KA2/106 X KEE 43, K 82 X KEE 12 and K 82 X KEE 47 to be selected in terms of tolerable rate towards VSD disease infection.

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