Preliminary evaluation of intra-crosses MPOB-Cameroon and their inter-crosses with MPOB-Zaire breeding population
(*Elaeis guineensis* Jacq.)

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Abstract. Broadening the genetic base of oil palm was as a key action for the improvement of the crop. In this study, fourteen *tenera* progenies from MPOB-CMR x MPOB-CMR and MPOB-CMR x MPOB-ZRE (T x T), crossed according to bi-parental mating design (BIP) were assessed in their fresh fruit bunch (FFB), bunch number (BNO) and average bunch weight (ABWT). The progenies were planted following a randomized complete block design (RCBD) in two replicates. Analysis of variance (ANOVA) revealed that the variability among progenies, for FFB, BNO and ABWT, were highly significant. The contribution of the environmental effects is relatively high for BNO, and this is shown by the low heritability estimated on this character. On the other hand, ABW character showed a high heritability ($h^2_B > 50\%$) at 67.31\%. Progenies deriving from MPOB-CMR x MPOB-ZRE crosses have shown a significantly higher performance compared to those from MPOB-CMR x MPOB-CMR x MPOB-CMR for FFB. Progeny PK1943 (MPOB-CMR x MPOB-ZRE) is the best performer with an average bunch yield of 175.29 kg palm$^{-1}$ yr$^{-1}$.

1. Introduction
Palm oil is the largest produced and traded vegetable oil in the global oils and fats market. The palm oil production contributed about 32% out of 230.08 million tonnes of oils and fats produced globally in 2018. Malaysia as the second largest producer and exporter of palm oil has a huge role to play in fulfilling the increasing global need for vegetable oils and fats. Oil palm (*Elaeis guineensis*), by far is most crucial commodity crop to Malaysia with export revenue from the crop reaching more than RM 67.12 billion in 2018 [1]. In 2019, the Malaysian oil palm industry experienced an enhanced performance as compared to that of in 2018 where significant achievements have been attained in exports, palm oil stocks and prices [2].

The history of the Malaysian oil palm industry can be traced back to the four oil palm seedlings brought from West Africa and planted at the Bogor Botanical Gardens [3]. The *dura* fruit form was planted until a major breakthrough in oil palm breeding, a monogenic inheritance of shell thickness was discovered by Beirnaert and Vanderweylen [4], which had led to further growth of the oil palm industry worldwide. The hybrid between *dura* and *pisifera* palms are known as *tenera*, which have a thinner shell. The switch-over from the thick shell and low oil dura to the thin shell and high oil tenera are more productive as they increase at least 30% of yield [5, 6].

Even though the success in producing improved planting materials was achieved, the genetic base was still considered narrow at that time as the mother palms in seed production was the Deli dura descending from four palms and a limited number of pisifera origins as the pollen source [7]. Noticing
the fact that the genetic base of the current source of mother palms was very narrow, efforts undertaken by the Malaysian Palm Oil Board (MPOB) to broaden the gene pool by collecting *E. guineensis* germplasm materials from its natural habitat in Africa in 1973 and 2010 [8,9]. MPOB-Cameroon (MPOB-CMR) and MPOB-Zaire (MPOB-ZRE) oil palm germplasm had been collected jointly with Unilever in 1984 after the first prospection in Nigeria in 1973 [10]. From evaluation, population from MPOB-CMR showed a high genetic diversity as did those of Nigeria and Sierra Leone [11]. Both MPOB-CMR and MPOB-ZRE were also produced oils with high vitamin E (PS8) [12]. Selected palms from both germplasm populations marked a partial resistance to *Ganoderma* in nursery screening, a serious threat to oil palm industry in Malaysia [13]. While Noh et al. [14] named MPOB-CMR and MPOB-ZRE germplasm collections as possessing more than 20% crude protein in the kernel (PS14). According to Maizura et al. [15], the MPOB-CMR genetic material was listed as MPOB’s oil palm germplasm materials with low lipase traits (PS13).

The on-going breeding programmes, both by MPOB and the industry led to further selection of newer elite *durus* and *pisifera* derived from selected germplasm materials [16]. Therefore, a crossing programme was initiated to assess the potential of *tenera* from *tenera x tenera* crosses, deriving from MPOB-CMR x MPOB-CMR and MPOB-CMR x MPOB-ZRE in term of fresh fruit bunch (FFB), bunch number (BNO) and average bunch weight (ABWT).

### 2. Materials and methods

A total of 14 progenies derived from MPOB-CMR x MPOB-CMR and MPOB-CMR x MPOB-ZRE (T x T) crosses were laid down in a triangular planting system at 9 m apart in Randomized Completely Block Design (RCBD) with 16 palms per plot (progeny) in four replications as presented in Table 1. The fresh fruit bunch (FFB) yield data collection was performed for each individual palm in both replications at interval of three rounds per month. FFB yield would be the sum of bunch weight (BWT) while average bunch weight (ABWT) is the quotient between FFB and bunch number (BNO). BWT and BNO are recorded on individual palm basis at each harvesting round from 36 months after field planting for 4 consecutive years (2003-2009).

#### Table 1. List of progenies and their pedigree

| No. | Progeny | Material | Pedigree |
|-----|---------|----------|----------|
| 1   | PK 1672 |          | 0.218/2108 x 0.219/299 |
| 2   | PK 1677 |          | 0.218/1006 x 0.218/1006 |
| 3   | PK 1683 |          | 0.218/1336 x 0.219/299 |
| 4   | PK 1696 |          | 0.218/2108 x 0.218/1006 |
| 5   | PK 1708 | MPOB-CMR x MPOB-CMR | 0.218/1006 x 0.219/299 |
| 6   | PK 1736 |          | 0.218/1336 x 0.218/1336 |
| 7   | PK 1806 |          | 0.218/135 x 0.219/299 |
| 8   | PK 1894 |          | 0.219/299 x 0.219/299 |
| 9   | PK 1962 |          | 0.218/135 x 0.218/1336 |
| 10  | PK 1918 |          | 0.219/844 x 0.221/739 |
| 11  | PK 1929 |          | 0.218/1006 x 0.221/739 |
| 12  | PK 1932 | MPOB-CMR x MPOB-ZRE | 0.219/271 x 0.221/739 |
| 13  | PK 1943 |          | 0.218/1216 x 0.221/739 |
| 14  | PK 1961 |          | 0.218/1336 x 0.221/739 |
| 15  | PK 2114 | STANDARD CROSS | 0.175/964 x 0.151/2626 |
3. Result and discussion

Analysis of variance (ANOVA) for yield and its components is presented in Table 2. As shown in the table, the replicates (R) item and the interaction between replicate and progeny revealed non-significant difference for FFB, BNO and ABW. The result indicated the consistencies in performance of all the traits studied across the replicates. A highly significant difference (p< 0.01) was observed in progeny for all traits in bunch yield and its components, denoting wide variability observed in the traits studied. In oil palm breeding, having a wide range in yield and its components among the progenies play an important role in selection. The presence of genetic variability will increase the breeding efficiency and lead to better selection gain [17]. This observation follows similar patterns as what has been conducted by Okwuagwu et al. [18] in their bunch yield and its components of dura x tenera oil palm planting materials. Furthermore, a wide variability also has been reported by Marhalil et al. [19] on MPOB-Nigeria dura x AVROS pisifera cross.

The grand mean of fresh fruit bunch (FFB), bunch number (BNO) and average bunch weight (ABWT) were 147.70 kg palm⁻¹ yr⁻¹, 12.71 bunches palm⁻¹ yr⁻¹ and 11.91 kg bunch⁻¹, respectively (Table 3). Further analysis showed that MPOB-CMR x MPOB-ZRE crosses exhibited significantly higher than MPOB-CMR x MPOB-CMR in their FFB and ABWT with 157.24 kg palm⁻¹ yr⁻¹ and 13.35 kg bunch⁻¹, respectively. Among the crosses, PK1943 from MPOB-CMR x MPOB-ZRE scored the highest FFB yield with 175.29 kg palm⁻¹ yr⁻¹, 18% higher than the DxP control. The high FFB yield was supported by a high BNO (14.13 bunches palm⁻¹ yr⁻¹) and moderate ABWT (12.56 kg bunch⁻¹) of the progeny. High FFB yields were also observed in PK1708 (170.40 kg palm⁻¹ yr⁻¹), PK1932 (167.75 kg palm⁻¹ yr⁻¹) and PK1929 (167.05 kg palm⁻¹ yr⁻¹). PK1736 (MPOB-CMR x MPOB-CMR) on the other hand, was found to be the least FFB yield with 90.85 kg palm⁻¹ yr⁻¹, due to its low BNO of 10.47 bunches palm⁻¹ yr⁻¹ and lowest ABWT of only 8.41 kg bunch⁻¹. Duncan New Multiple Range Test (DNMRT) also indicated significant differences between PK1736 and PK1708, PK1929, PK1932, PK1708 and PK1943 for FFB, BNO, and ABW. The result indicated that PK1696 even though with the highest BNO (15.66 bunches palm⁻¹ yr⁻¹), unable to be among the top FFB yielder due to its low ABW (10.36 kg bunch⁻¹). Similarly, PK1961 with a high ABW of 13.69 kg bunch⁻¹, showed below average FFB yield (142.79 kg palm⁻¹ yr⁻¹) due to its low BNO (10.38 bunches palm⁻¹ yr⁻¹). Therefore, it is important to select palms with high BNO and moderate ABW for high FFB yield in selection as suggested by Noh et al. [20].

Variance components and heritability value for the yield and its components were shown at Table 4. The genetic variations (GVC) were 40.08 % (FFB), 19.81% (BNO) and 58.02% (ABWT) to the phenotypic variations (PVC). The high value of GVC to the PVC (> 40%) for both BNO and ABWT obtained, implying high genetic control of these characters. The result was further supported by high heritability value (h²B > 50%) of ABWT (67.31%) and moderate (h²B >30%) for FFB of 33.35%. Meanwhile, broad-sense heritability estimates for BNO was considered as low (h²B <20%) with only 7.85%. The results indicated that ABWT and FFB were more heritable than BNO character. The low heritability value for FFB character was certainly due to the high influence of the environment on that polygenic character. Djonko et al. [21] also observed similar results for having a low heritability for FFB yield in their study of Cameroon-based dura x pisifera oil palm. The low genetic variation and heritability of BNO would limit further breeding and selection for this trait. However, improvement still can be achieved for ABW and FFB since there were sufficient genetic variations.

Table 2. Means squares, variance components and heritability estimates of progenies yield and its component

| Source       | df | FFB   | BNO   | ABWT  |
|--------------|----|-------|-------|-------|
| Replication (R) | 1  | 5319.42 | 0.03  | 51.32 |
| Progeny (P)   | 13 | 8936.91** | 42.88** | 42.81** |
| No | Progeny | Pedigree | Material | FFB (kg palm\(^{-1}\) yr\(^{-1}\)) | BNO (bunches palm\(^{-1}\) yr\(^{-1}\)) | ABWT (kg bunches\(^{-1}\)) |
|----|---------|----------|----------|----------------------------------|---------------------------------|-----------------|
| 1  | PK1672  | 0.218/2108 x 0.219/299 |          | 158.97\(^{ba}\)                  | 14.96\(^{ba}\)                  | 10.96\(^{bc}\)  |
| 2  | PK1677  | 0.218/1006 x 0.218/1006 |          | 122.96\(^{bc}\)                  | 12.39\(^{bc}\)                  | 10.29\(^{bc}\)  |
| 3  | PK1683  | 0.218/1336 x 0.219/299 |          | 158.76\(^{ba}\)                  | 12.53\(^{bac}\)                 | 13.02\(^{ab}\)  |
| 4  | PK1696  | 0.218/2108 x 0.218/1006 |          | 158.58\(^{ba}\)                  | 15.66\(^{a}\)                   | 10.36\(^{bc}\)  |
| 5  | PK1708  | 0.218/1006 x 0.219/299 | MPOB-CMR x MPOB-CMR | 170.40\(^{a}\)                  | 13.69\(^{ab}\)                  | 12.85\(^{ab}\)  |
| 6  | PK1736  | 0.218/1336 x 0.218/1336 |          | 90.85\(^{d}\)                    | 10.47\(^{c}\)                   | 8.41\(^{d}\)    |
| 7  | PK1806  | 0.218/135 x 0.219/299  |          | 129.76\(^{bc}\)                  | 12.09\(^{bc}\)                  | 11.18\(^{bc}\)  |
| 8  | PK1894  | 0.218/299 x 0.219/299  |          | 119.45\(^{bc}\)                  | 12.47\(^{bc}\)                  | 9.56\(^{bc}\)   |
| 9  | PK1902  | 0.218/135 x 0.218/1336 |          | 115.27\(^{bc}\)                  | 12.26\(^{bc}\)                  | 9.66\(^{bc}\)   |
| 10 | PK1918  | 0.219/844 x 0.221/739  |          | 148.50\(^{c}\)                   | 9.75\(^{bc}\)                   | 15.23\(^{b}\)   |
| 11 | PK1929  | 0.218/1006 x 0.221/739 |          | 125.17\(^{c}\)                   | 10.37\(^{c}\)                   | 12.69\(^{ab}\)  |
| 12 | PK1932  | 0.219/271 x 0.221/739  | MPOB-CMR x MPOB-ZRE | 167.05\(^{a}\)                  | 11.91\(^{bc}\)                  | 14.32\(^{a}\)   |
| 13 | PK1943  | 0.218/1216 x 0.221/739 |          | 167.75\(^{a}\)                  | 12.38\(^{bc}\)                  | 13.84\(^{a}\)   |
| 14 | PK1961  | 0.218/1336 x 0.221/739 |          | 175.29\(^{a}\)                  | 14.13\(^{ab}\)                  | 12.56\(^{ab}\)  |
| 15 | PK2114  | 0.175/964 x 0.151/2626 | SC       | 148.50\(^{c}\)                   | 9.75\(^{bc}\)                   | 15.23\(^{b}\)   |
|    | Mean    |          |          | 147.70\(^{ab}\)                  | 12.71\(^{ab}\)                  | 11.91\(^{ab}\)  |

*FFB = fresh fruit bunch; BNO = bunch number; ABWT = average bunch weight; Means with the same small letter(s) in the same column are not significantly different at P < 0.05 with Duncan New Multiple Range Test (DNMRT).

Table 4. Variance components and heritability of yield and its components

| Genetic parameters | FFB    | BNO   | ABWT  |
|--------------------|--------|-------|-------|
| Progeny variance (\(\sigma^2\)) | 355.33 | 0.60  | 2.79  |
| R x P variance (\(\sigma^2_\text{pr}\)) | 365.32 | 2.01  | 0.06  |
| Environmental variance (\(\sigma^2_\text{e}\)) | 1410.20 | 12.59 | 5.44  |
| Phenotypic variance (\(\sigma^2_\text{p}\)) | 2130.85 | 15.19 | 8.29  |
| Genotypic coefficent of variance (GCV %) | 12.76  | 6.08  | 14.03 |
| Phenotypic coefficient of variance (PCV %) | 31.25  | 30.68 | 24.18 |
| GVC/PVC (%) | 40.08  | 19.81 | 58.02 |
| Broad sense heritability (\(h^2_\text{BS}\) %) | 33.35  | 7.85  | 67.35 |

*FFB = fresh fruit bunch; BNO = bunch number; ABWT = average bunch weight; Heritability values are calculated using the formula: Heritability = V\text{Gen}/V\text{P}.
FFB = fresh fruit bunch; BNO = bunch number; ABW = average bunch weight; \( \sigma^2_g \) = genotypic variance; \( \sigma^2_{gr} \) = variance due to genotypes \times replication; \( \sigma^2_p \) = phenotypic variance; \( \sigma^2_e \) = environmental variance; GCV = genotypic coefficient of variation; PCV = phenotypic coefficient of variation; \( h^2_B \) = heritability in broad sense.

4. Conclusion

The analysis of variance (ANOVA) for the bunch yield and its components has revealed that the progeny variability has a high significant effect on the phenotypic expression for fresh fruit bunch (FFB), bunch number (BNO) and average bunch weight (ABWT). Progenies deriving from MPOB-CMR \times MPOB-ZRE crosses have shown a relatively higher performance compared to those from MPOB-CMR \times MPOB-CMR for FFB and ABWT. PK 1943 from MPOB-CMR \times MPOB-ZRE emerged as the best performer in this study with the highest FFB yield of 175.29 kg palm\(^{-1}\) yr\(^{-1}\), supported by a high BNO (14.13 bunches palm\(^{-1}\) yr\(^{-1}\)) and moderate ABWT (12.56 kg bunch\(^{-1}\)). Even though genetic variation and heritability of BNO were low, further breeding and selection still can be achieved for ABW and FFB since there were sufficient genetic variations, contributing of more than 40% to the phenotypic variance and having heritability of more than 20%. Therefore, the male parent of this progeny can be considered for progeny testing with advance dura breeding materials to reduce the dependence of AVROS as the main pollen source in current commercial DxP seed production.

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