Proceedings

Study on Yield Variability in Oil Palm Progenies and Their Genetic Origins †

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Abstract: One of the leading important plantation crops with high revenue returns widely known is *Elaeis guineensis* palm. To-date, yield variability in fresh fruit bunches (YFFB) in Malaysian oil palm plantations is one of the key influences in low palm oil yield. Accordingly, an assessment of *dura*×*pisifera* progenies and their genetic origins on oil palm yield was investigated. Twenty-four derived progenies from 10 genetic sources were adopted as F1 hybrid-single generation and the standard approach for data collection of yield and yield traits was followed for three sequential years. Variance analysis showed genetic differences between the progenies and their origins. Amid the progenies analyzed, 45.83% had YFFB above the trial mean. Progeny HPDP500 had the highest YFFB (191.74 kg/palm/year) and the highest bunch number (YBNO) was recorded in PKDP4474 (20.65 bunches/palm/year), and HPDP500 (20.53 bunches/palm/year). In year-one and year-three, the highest YFFB was reported, while in year-one of data collection, the highest YBNO was recorded. *Dura*-Ulu Remis × Yangambi had the highest YFFB (175.81 kg/palm/year) and Tanzania × Nigeria recorded the highest YBNO (19.06 bunches/palm/year). High heritability and phenotypic coefficient of variation with a moderate genotypic coefficient of variation for all the traits were further revealed. YFFB had a strong positive YBNO relationship (r = 0.676**) and a weak positive average bunch weight correlation (r = 0.378**). For tissue culture and hybridization programs for yield enhancement, progenies and origins with better performance may be used, However, the use of molecular research as a selection criterion seems to be worth further analysis.

Keywords: genetic origins; yield traits; genetic variance; progeny; heritability

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1. Introduction

The Africa oil palm (*Elaeis guineensis* Jacq) is a native of Sierra Leone mostly found along with the coaster areas, which may have extended to other parts of West Africa Nations such as Liberia, Guinea, Guinea Bissau, Ivory Coast, Nigeria, Angola, Tanzania, and Cameroon. However, Ref. [1] reported that the species *guineensis* palm originated from the tropical rainforest in West Africa. Due to modern detections, the epicenter of origin of the palm species *guineensis* Jacq through maximum allelic diversity, is possibly from Nigeria [2]. Oil palm is an extremely gainful source of revenue from tropical areas through exports [3,4]. Per unit area of land, its yield is five times higher than all other oilseed crops [5]. Oil palm is a source of food for an ever-growing population of humans and animals, its products are used as raw materials for industries, biofuel, and above all, it has created countless well-paying jobs for millions of people across the world. In several traditional recipes, one of the compulsory ingredients is locally produced crude palm oil (CPO) [6]. According to Rebena et al. [7] CPO of 80% accounts for approximately 1/3 of the entire edible oil consumption. This is due to it valuable nutritional properties [8].

The use of *dura*×*pisifera* progeny planting materials has led to significant yield improvement in oil palm [9]. However, the continuous variability of fresh fruit bunch (YFFB) yield is highly pronounced in Malaysia oil palm plantations. The YFFB yield in Malaysia for four consecutive years has clearly shown variability in yield as reported by MPOB, [10] and Kushairi et al. [11] as thus: [2015 (18.48 t/ha), 2016 (15.91 t/ha), 2017(19.92 t/ha) and 2018 (17.16 t/ha)]. Africa Countries for example, experience two metric tons (Mt) of palm oil per year, export one Mt/yr and import about eight Mt/yr [12]. Since 1990s, the palm oil sector in Africa has been thriving despite low land output of oil (t oil/ha) and it is presently intensifying [13,14]. However, non-selected and unproductive planting material in the sector has been one of the limiting factors [6,15], inadequate agricultural management practices [16] and yield losses as well as low oil extraction rates (OEC) especially among the small-scale farmers [17].

In Malaysia, oil palm is considered as an important commodity crop with revenue return in 2018, reaching higher than 67.12 billion Ringgit Malaysia and in 2019, a 4.0% visible decline was observed when compared to 67.12 billion Ringgit in 2018 export revenue [18]. A decline in oil yield (OY) palm/ha has been associated with variability in the YFFB yield which has ultimately resulted in serious economic losses in the oil palm industry especially the small-scale farmers. Sarkar et al. [19] reported that higher negative effects on agricultural production than positive impact is due to climate change. Climate change in Malaysia has a significant influence on the variability of oil palm yield, accordingly, the Malaysia oil palm sector sustainability is ultimately affected [19]. A previous investigation carried out by Kushairi et al. [11] reported that the year 2018 was known to be the most challenging period for the oil palm industry in Malaysia with a lower yield of 19.52 t/ha, comprising palm oil prices and exports. The decline in palm oil prices coupled with its weak demand caused a diminish in export earnings in 2018 at 65.12 billion Ringgit Malaysian, compared to 2017 earning of 74.75 billion Ringgit Malaysian [11]. Low oil yield will bring about an economic instability among oil palm growers and the nation at large.

According to Kushairi et al. [11], the year 2018, of 4.1% reduction in the oil palm fresh fruit bunch was noticed when compared to the fresh fruit bunch output of 17.89 tons per hectare in 2017 as against 17.16 tons per hectare in 2018. In different parts of oil palm cultivated country's numerous efforts have been made to identify and to address the causes of low YFFB yield in oil palm plantations, of which palm planting materials are no exception. Thus, this research is intended to assess *dura*×*pisifera* (DP) progenies and their genetic origins on oil palm fresh fruit bunch (YFFB) yield.

Hypothesis of the Study

The hypothesis as follows will be investigated:

H_1. *The performance of the progenies in YFFB yield varies significantly.*
H_0. *There is no significant variation in YFFB yield performance among the progenies.*
H_1. *There is significant variation in Genetic origins' performance for YFFB yield.*
H_0. *There is no significant variation in their performance for YFFB yield.*
H_1. *The genetic variance could influence low YFFB yield in oil palm progenies.*
H_0. *The genetic variance cannot influence low YFFB yield in oil palm progenies.*
H_1. *There is significant variation in yearly performance for YFFB.*
H_0. *There is no significant variation in yearly performance for YFFB.*

2. Materials and Method

A total of 24 D × P progenies (HPDP415, HPDP500, HPDP550, HPDP618, PKDP4118, PKDP4465, PKDP4474, PKDP4482, PKDP4504, PKDP4505, PKDP4529, PKDP4535, PKDP4539, PKDP4540, PKDP4548, PKDP4550, PKDP4570, PKDP4591, PKDP4621, PKDP4648, PKDP4651, PKDP4674, PKDP4679 and PKDP4841 derived from 10 parental origins [(six female *Duras*: Deli-Serdang, Deli-Ulu Remis, Deli-Banting, Deli-Johor Labis, Tanzania, and Angola) and four male *pisiferas*: Yangambi, AVROS, Cameroon and Nigeria)] were planted in 2008 at MPOB Teluk-Intan Research Station, Malaysia at Trial 0.52 at the coordinate of 3° 49′ 3.1100″ N and 101° 3′ 8.9100″ E. These progenies were planted in an Independent completely randomized design (ICRD) in four replications with sixteen palms per family, per replicate and 8.5 m × 8.5 m × 8.5 m planting distance was used. In an eleven years old experimental palms laid-down on a peat-soil, 480 palms were selected from a total palm density of 1930 palms (12.06 hectares) and were monitored for yield and yield components for three consecutive years (2017–2019) initiated by MPOB.

2.1. Data Collection

Three years data recording were done on individually selected progeny palms for the fresh fruit bunch (YFFB), bunch number (YBNO), and average bunch weight (YABW). The data collection of these selected component traits was carried out on a forth-night interval (after every two weeks) or two rounds monthly, following the data standard procedures of Rafii et al. [20,21] and Shabanimofrad et al. [22].

2.2. Statistical Analysis

The calculated mean data by progenies were subjected to version 9.4 of the Statistical Analysis System (SAS) for the analysis of variance employing the general linear model (PROC GLM) due to some missing and uneven distribution of progeny's palms. Descriptive statistics such as mean, coefficient of variation (CV), and standard error (SE) were determined. For mean comparison at a 5% probability level, Duncan's new multiple range tests (DNMRT) were used. SAS (version 9.4) was used for Proc varcomp using restricted maximum likelihood (REML) for variance components estimation and the correlation coefficient was estimated. The genotypic and phenotypic coefficients of variation and heritability were calculated following the procedures and formulae of Burton [23,24], Singh and Chudhary [25], and Johnson et al. [[26].

(a) Heritability estimate (h_B^2):

$$h_B^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

where, h_B^2 = Heritability of broad sense, σ_p^2 = Phenotypic variance, σ_g^2 = Genotypic variance.

Heritability was estimated as categorized by Robinson et al. [27] followed by Johnson et al. [26] as high (>60%), moderate (30–60%), and low (<30%).

(b) Phenotypic coefficients of variation (PCV):

$$PCV = \frac{\sqrt{\sigma_P^2}}{\bar{X}} \times 100$$

where, $\bar{X}$ = Progeny population mean, σ_P^2 = Phenotypic variance.

(c) Genotypic coefficients of variation (GCV):

$$GCV = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

where, σ_g^2 = Genotypic variance, $\bar{X} =$ Progeny population mean.

The genotypic and phenotypic coefficients of variation value estimates were categorized as high (>20%), moderate (10%–20%), and low (0 to 10%) according to Oladosu et al. [28].

3. Results and Discussion

3.1. Experimental Findings on Yield Traits in DP Progenies

Analysis of variance (ANOVA) for yield traits of 24 single crossed *dura* × *pisifera* (DP) progenies presented highly significant differences ($p \leq 0.01$) (Table 1). This result was in agreement with the findings of Arolu et al. [29], they reported in their early studies that the ANOVA of biparental progenies was highly significant for yield and yield traits. This certainly indicated the magnitude of genetic disparity that exists among DP progenies and in terms of selection and breeding programs, they can be exploited for yield improvement. The analysis also showed significant differences ($p \leq 0.01$) among the years for yield traits, inferring inconsistencies in the yield traits performance across the years. However, the interaction between yearly and progeny showed significant differences ($p \leq 0.05$) for YFFB and YBNO, while no significant difference was noticed for YABW. However, due to the homogeneity of the replications, no significant differences were manifested among them.

Table 1. Mean square and estimates of variance components for yield traits among progenies.

Source of Variation	DF	YFFB (kg/palm/year)	YBON (bunch/palm/year)	YABW (kg/palm/year)
Replications (R)	3	318.74 ^{ns}	1,28 ^{ns}	1.06 ^{ns}
Years (Y)	2	1973.68 **	775.92 **	142.38 **
Progenies (G)	23	7102.22 **	88.14 **	23.99 **
Y*G	46	507.90 *	5.23 *	1.57 ^{ns}
Error	186	557.42	3.60	1.23
Variance component				
$\sigma^2{}_g$		645.85 (61.83) $^{+}$	7.60 (65.37)	2.21 (62.60)
$\sigma^2{}_{yg}$		41.43 (3.97)	0.45 (3.87)	0.10 (2.83)
$\sigma^2{}_e$ (ph)		357.22 (34.20)	3.58 (30.76)	1.22 (34.58)
Mean		145.41	15.41	9.34
SE		2.08	2.26	0.12
CV		23.16	27.16	22.50

Note: DF = degree of freedom, YFFB = fresh fruit bunch, YBNO = number of bunches, YABW = average bunch weight, σ_g^2 = genotypic variance, σ_{yg}^2 = year ×genotypic variance, σ_e^2 = error variance, ** = highly significant at $p \leq 0.01$, * = significant $p \leq 0.05$, ns = non-significant $p > 0.05$. The phenotypic variance in percentage are the values in bracket. SE = standard error, CV = coefficient of variation.

Table 1 presents the variance components results obtained in this current study, which showed that superior genetic variability existed among the DP progenies. It was observed that genetic variance (σ_g^2) which varied from 61.83% to 65.37% was found to be higher across the traits analyzed, indicating that variation in DP progeny traits could be attributed to genetic effect which could have influenced the YFFB yield. Whereas, error variance (σ_e^2) was noticed to be low across all the traits, implying that the environmental effect on progeny traits was low.

The mean differences in yearly and DP progenies performance for yield component traits (YFFB, YBNO, and YABW) were presented in Table 2. The best yearly performance for YFFB was observed in year-three and year-one with on significant difference between them and the lowest YFFB was obtained in year-two. Moreover, the lowest YBNO and YABW were noticed in year-two and year-one, respectively. This shows that variability in years' performance could be influenced by differences in climatic factors. The results were in agreement with Oettli et al. [30] findings, they reported that for all regions in Malaysia, a strong variability in annual oil palm yields was observed with noticeable rises and drops at the time of 28 years study period [30]. The dry spell is expected to diminish crude palm oil production, and most cropping schemes are rainfed [31] of which oil palm is no exception.

Table 2. Yearly and progeny means for yield and yield traits of biparental progenies.

YEAR	YFFB (kg/palm/year)	YBON (bunch/palm/year)	YABW (kg/palm/year)
YEAR1 (2017)	153.69a	18.89a	8.00c
YEAR2 (2018)	128.14b	13.35c	9.45b
YEAR3 (2019)	154.40a	14.00b	10.58a
Progeny			
HPDP415	129.55i	11.78ij	11.19ab
HPDP500	191.74a	20.52a	9.48efg
HPDP550	136.35hi	11.73ij	11.47a
HPDP618	142.22fghi	14.50efg	9.62defg
PKDP4118	136.75hi	14.12fhg	9.85def
PKDP4465	138.22hi	15.60ef	9.09fgh
PKDP4474	144.25fghi	20.65a	6.71jk
PKDP4482	89.78k	12.37hij	6.07k
PKDP4504	154.69defgh	15.25ef	9.32fg
PKDP4505	171.80bcd	17.64cd	10.23bcdef
PKDP4529	176.42abc	16.30de	11.03abc
PKDP4535	108.44j	11.84ij	8.62gh
PKDP4539	152.02efgh	17.69cd	8.22hi
PKDP4540	168.31bcde	18.57bc	9.09fgh
PKDP4548	175.01abc	18.28bc	9.63defg
PKDP4550	158.99cdefg	16.41de	9.95cdef
PKDP4570	110.86j	14.09fgh	7.61ij
PKDP4591	180.07ab	16.25de	11.25ab
PKDP4621	94.99jk	10.86j	6.99jk
PKDP4648	141.25ghi	14.58efg	9.72defg
PKDP4651	138.35hi	19.78ab	6.71jk
PKDP4674	158.72cdefg	15.24ef	10.48abcde
PKDP4679	160.48cdef	14.20fg	10.72abcd
PKDP4841	129.91i	12.90ghi	10.09cdef
Mean	145.41	15.41	9.34
SE	2.08	2.26	0.12
CV	23.16	27.16	22.50

Note: PKDP = Porim Kluang. *dura×pisifera,* HPDP = Hulu Paka *dura×pisifera,* YFFB = fresh fruit bunch, YBNO = number of bunches, YABW = average bunch weight, means with the same letters of alphabet within the same column are not significantly different at $p \leq 0.05$ based on Duncan's new multiple range test (DNMRT), SE = standard error, CV = coefficient of variation.

DNMRT revealed variations in the performance of the DP progenies (Table 2). The findings of this study were similar to the result obtained by Arolu et al. [29], they reported that due to differences in progenies, there were sufficient genetic variation for YFFB, YBNO and YABW which gives ample scope for selection. The YFFB yield performance of the progenies ranged from 89.78–191.74 (kg/palm/year) with a trial mean of 145.41 (kg/palm/year) and only 45.83% of the progenies had YFFB yield higher than the trial mean. It was observed that PKDP500 recorded the highest YFFB followed by PKDP4591 and PKDP4482 had the lowest YFFB (Table 2). Similarly, the trial mean for YBNO was 15.41 (bunches/palm/year) and the progenies had a YBNO which varied from 10.86–20.65 (bunches/palm/year) with 45.83% perform better than the trial mean value. It was observed that PKDP4621 recorded the least YBNO, while, PKDP4474 and HPDP500 with no significant differences between them had the highest YBNO followed by PKDP4651. The progenies trial mean for YABW was 9.34 (kg/palm/year) and 58.33% recorded the higher than the trial mean. However, the highest YABW was noticed in HPDP550. DNMRT indicated no significant difference between PKDP4591 and HPDP415 and they recorded the second-highest of YBNO, whereas, the lowest YABW was noticed in PKDP4482. The highest YFFB yield in HPDP500 occurred due to its highest YBNO with a moderate YABW. This result was in agreement with the findings of Myint et al. [32], they reported in their recent research findings that moderate YABW coupled with high YBON resulted in families with highest YFFB yields. In terms of breeding and selection of oil palm, the emphasis has been on YFFB coupled with oil yield [33]. Therefore, as a result, HPDP500 performed the best for YFFB and it could be a good candidate for selection.

The analysed morphological yield traits data showed that YFFB had a moderate positive significant correlation with YBNO (r = 0.67639; *p* = 0.0001) and recorded a weak positive significant relationship with YABW at r = 0.37840; *p* = 0.0001. On the contrary, YBNO exhibited a weak negative significant relationship with YABW at r = −0.34080; *p* = 0.0001. Genotypic and phenotypic levels of dissimilarity could be seen among the natural plant populations in cross-pollinated plants [34] of which oil palm is no exception. For rapid advancement in plant breeding, the basic tools for selection are estimates of heritability, phenotypic, and the genotypic coefficient of variations. A substantial quantity of variation must be seen in the selected component traits to reach ample possibility of reaching the response to selection [32,33,35]. In this study, broad-sense heritability (YFFB 61.83%, YBNO 65.37% and YABW 62.60%) and PCV (YFFB 22.23%, 22.12%, and 20.13%) were found to be high for all traits analyzed, indicating the influence of environmental effect. Whereas, for all the yield traits, GCV was found to be moderate at YFFB 17.48%, YBNO 17.88%, and YABW 15.93%. The PCV was invariably higher than the corresponding GCV on the expression for each trait. Therefore, the hitches of environmental factors that may contribute to low YFFB yield could be considered.

3.2. Parental Origins' Performance in Oil Palm Yield and Yield Traits

The yield trait performance among the genetic origins was presented in Figure 1. The origins' YFFB yield varied from 110.86 to 175.81 (kg/palm/year). Origin Tanzania × AVROS recorded the lowest YFFB yield and the highest YFFB was noticed in origin Deli-Ulu Remis × Yangambi. Similarly, Deli-Banting × AVROS had the least YBNO (11.76 bunches/palm/year) and Tanzania × Nigeria was observed with the highest YBNO at 19.06 bunches/palm/year.

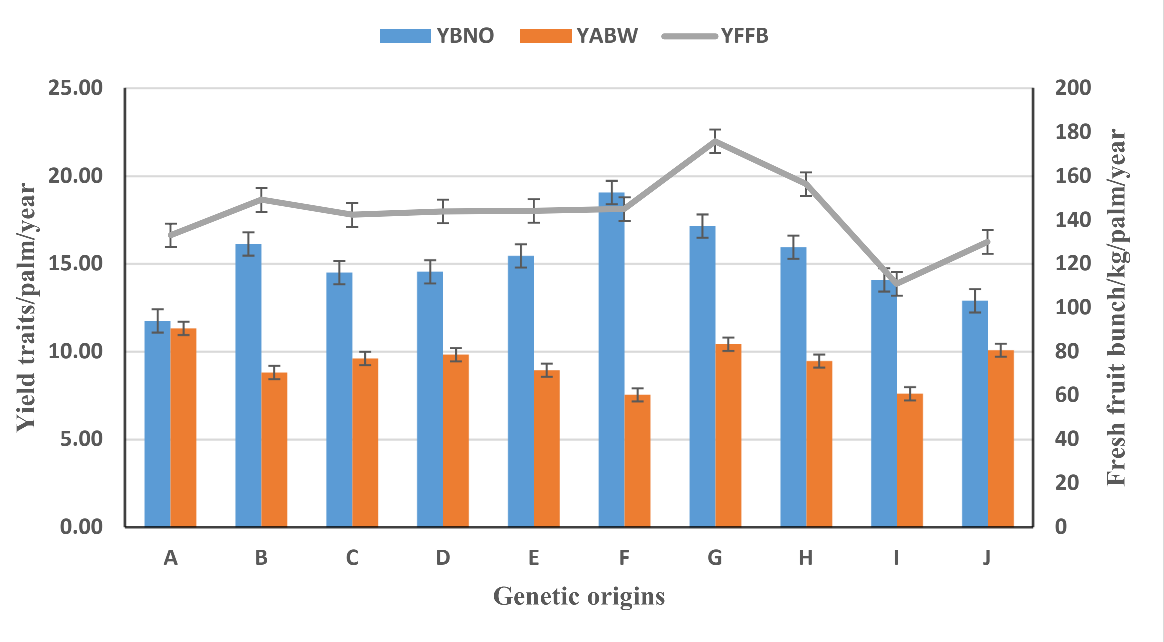

Figure 1. Genetic origins parental performance in yield and yield traits: (**A**) Deli-Banting × AVROS, (**B**) Deli-Ulu Remis × Nigeria, (**C**) Deli-Johor Labis × AVROS, (**D**) Deli Ulu Remis × AVROS, (**E**) Angola × AVROS, (**F**) Tanzania × Nigeria, (**G**) Deli-Ulu Remis × Yangambi, (**H**) Angola × Nigeria, (**I**) Tanzania × AVROS, (**J**) Deli-Serdang × Cameroon.

Also, Tanzania × AVROS had the least YABW at 7.55 (kg/palm/year), whereas, Deli-Banting × AVROS had the maximum YABW (11.33 kg/palm/year). The low performance of Tanzania × AVROS for YFFB was due to its low YABW as a result of its moderate bunch size production. The size of bunches produce determines the YABW, hence due to bigger bunches produced by Deli-Banting × AVROS recorded the highest YABW with the least YBNO produced. The outstanding performance of Deli-Ulu Remis × Yangambi in YFFB yield occurred because of the good combining characteristics of *pisifera* Yangambi. The *pisifera* Yangambi is characterized by high early yields, various growth, thin-shell, ovoid fruit, and thin kernel [36].

4. Conclusions

The fresh fruit bunch yield performance of the 24 DP progenies with a range of 89.78 to 191.74 kg/palm/year was reasonably good. A substantial variation for YFFB was observed among the progenies with progeny HPDP500 as the highest and genetic origins of Deli-Ulu Remis × Yangambi was the most outstanding parent for YFFB. Due to changeability in environmental factors, the annual performance for YFFB was also noticed to have influenced the YFFB yield and year-three recorded the highest YFFB with the least in year-one. Moreover, the YFFB yield was influenced by the genetic effect as a result of the pedigree structure of the progenies used in this study. To further substantiate the YFFB yield, correlation results show a positive significant relationship between YFFB and YBNO, indicating that an increase in YBNO will lead to an increase in YFFB. Heritability and PCV were found to be high in all the traits, while a moderate GCV was noticed in all the traits. However, progeny HPDP500 and origin Deli-Ulu Remis × Yangambi could be exploited for yield improvement in oil palm. High YFFB will bring about an increase in the economy especially for the small-scale farmers. The field quantitative research used in the identification of outstanding progenies and their origins in relation to YFFB demonstrated the potential in investigating and monitoring oil palm yield variability. Oil palm is typically adapted to low rainfall and dry, so palms from these progenies may have the potential to resist heat stress and drought. Also, if joint with molecular research, the knowledge obtained from this study may be more detail in determining the core potential of progenies with maximum genetic variation and minimal accession, accordingly, decreasing the maintenance expenditures of the oil palm sector. We propose future research combines conventional breeding with molecular studies.

Author Contributions: M.R.Y., M.D.A., F.M.I., S.J., and S.S. developed the concept. S.S. carried out the research, M.R.Y., M.D.A., F.M.I., S.J. M.M. and M.M.M. supervised the experiment. S.S., M.J., and O.Y., carried out the calculations and analysis. S.S. draft the manscript. While the proofreading, editing, and finishing were carried out by M.R.Y., M.D.A., F.M.I., S.J., O.Y., and M.J., All authors contributed immensely from planning to the final draft and accepted the published version of the research article.

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