



Phenotypic Assessment of Oil Palm Diversity through Field-level Screening for Improved Yield Performance on Njala Upland Soil

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

This study was primarily undertaken to assess the fresh fruit bunch (FFB) yield performance among oil palm genotypes on Njala upland soil. To determine the FFB yield, field research was carried out using four oil palm genotypes in an independent complete randomized design in four replications on 160 experimental sample palms. Three years of data were collected on yield and fruit bunch components, and vegetative traits. In the current study, 23 quantitative variables were used to evaluate the performance of four genotypes of oil palm. Through the analysis of variance, the morphological features of the different variants showed a wide range of variation. The traits were found to be influenced by the environment. Genotype Y26666B had the highest FFB yield at 188.31 (kg/palm/year) followed by genotype Y26515A 171.58 (kg/palm/year). It was further examined that FFB yield gap exists among the genotypes and all of them [Y26515A, Y26456A, Y26666B and Y26520C (13.16, 17.86, 11.90 and 17.86 t/genotype/year)], respectively, proved to have high FFB yield gap. This showed that among the elite genotypes (Y26666B and Y26515A), there is a significant opportunity to increase their FFB yield. Correlation (*r*) validated that fruit bunch number had more positive impact on FFB yield than average bunch weight. The findings suggested an alternative method for future studies, hence, genotype Y26666B could be selected as parent for future breeding programs.

Keywords: *Elaeis guineensis*; genotype; phenotypic; trait; variance component; yield gap.

1. INTRODUCTION

The Africa oil palm (*Elaeis guineensis*) is very significant in the South and Central American economies (Meléndez & Ponce, 2016) and as well as in the economy of Africa. In Sierra Leone, its neighboring countries, and the global market for functional foods, oil palm is a rising star. It is possibly the most significant palm species in terms of Agriculture and for more than 7000 years ago, oil palm fruits have been used in primitive societies as a semi wild food basis (Murphy *et al.*, 2021). Almost one third of the vegetable oil produced worldwide comes from the oil palm plant (Tzuan *et al.*, 2022). The highest oil yielder amid oilseed crops worldwide is the species *guineensis*, known as African oil palm which is a native of West and Central Africa (Morley, 2015). Among planted oilseed crops, oil palm is the most oil-yielding per ha, providing a sufficient quantity to fulfil expanding demand (Swaray *et al.*, 2020), accounting for more than 40% of the global edible oil production (Oosterveer, 2015).

Oil palm is well accepted by majority of farmers and its products by consumers in Sierra Leone. Beside from its potential as a foreign exchange earner, oil palm farming allows small-scale farmers to shift from semi-substance to commercial farming. Palm oil is the utmost frequently traded vegetable oil worldwide, and the demand is expected to rise significantly in the future (Vijay *et al.*, 2016). For thousands of years, palm oil has been utilized as food and

medicine. It is an important part of a healthy diet in tropical Africa and Southeast Asia as a natural vegetable oil with an outstanding cooking quality. Medical Doctors and government entities are currently using it to treat particular disorders and enhance nutritional condition. Additionally, it has a higher thermal stability than other vegetable oils and offers superior taste, texture, and quality to dishes and baked goods (Jalloh *et al.*, 2018).

Oil palm planting areas have rapidly expanded and significant levels of oil palm production have been achieved (Kome & Tabi, 2020). From a planted area of 19.04 million ha, palm oil and palm kernel oil production accounted for about 75.17 million tones (one-third) of global total oils and fats output in 2017 (Razmah *et al.*, 2018). According to Barcelos *et al.* (2015), oil palm production could need to reach 240 million tons by 2050.

Oil palm production's main goal is to increase oil-yield and quality, which can be accomplished through genetic improvement of selected traits through breeding programs (Myint *et al.*, 2021). According to Abdullah *et al.* (2011), yield of oil palm is the result of the interrelationship between yield-related features and the final yield. Therefore, to improve oil productivity through breeding, variables that have a significant and direct effect on the oil yield must be evaluated. Palm oil yield is a complicated characteristic that is controlled by either genetic or environmental factors and it could be influenced by several agronomic yield-related

traits, resulting in a low heritability value. The relationship between these qualities is vital for genetic advancement. The correlation results between the attributes should be used as the selection criteria when selecting for high yield. As a result of the complicated relationship between oil yield and yield component features, it's impossible to improve on oil yield without taking into account the traits that contributed to it directly or indirectly (Myint *et al.*, 2021).

Oil palm breeders acknowledge that the present cultivars planted around the world have a narrow genetic base (Arias *et al.*, 2013; Corley & Tinker, 2003). The existing commercial oil palm cultivars narrow genetic base has motivated breeders to place greater emphasis on expanding these genetic resources, as the crop's long-term sustainability yield depends on the use of genetic varieties. Therefore, *Elaeis guineensis* has become an important genetic resource for the development of interspecific hybrids to combat the problem of planting materials in the oil palm industry. Using morpho-agronomic parameters, we examined the phenotypic diversity of four genotypes on Njala upland soil for high yield performance.

2. MATERIALS AND METHODS

Planting Materials: The 17 years old planting material used in this current study is part of the 22 genotypes planted at the back of School of Agriculture and Food Sciences, in 2005 by the Njala University administration, with the aim of making hybridizations among different genotypes to produce quality seedlings for oil palm growers in Sierra Leone as well as West Africa sub-region. Four genotypes (Y26515A, Y26456A, Y26520C and Y26666B) out of the 22 were selected for the purpose of this study.

Experimental Design: The study of yield performance on oil palm genotypes was established in 2021 and ended in 2024. A total land area of 22 ha was planted with 22 genotypes of 3,300 palms. The genotypes were planted in blocks with 10 m × 10 m × 10 m equilateral triangular planting distance between and within plants, and a planting density of 150 palms per genotype per hectare. Six of the genotypes were planted on a homogeneous flat land with the same soil requirement. Therefore, for the purpose of this study, four genotypes were redesigned into four replications using Independent Complete Randomized Design (ICRD), considered as a single palm plot as

described by Swaray *et al.* (2020) and Rafii *et al.* (2001). The four genotypes had 600 palms and 120 palms were considered as border palms. The entire experimental sample palms were 160 and they were selected through systematic random sampling of 10 palms per replication with a total of 40 sample palms per genotype.

Location of Study Area: A field study was conducted in the upland plains behind the School of Agriculture and Food Sciences, Njala University, Njala campus. The said campus is located in the Kori chiefdom, Moyamba District, Southern Sierra Leone, at an elevation of 54 meters (m) above sea level, between latitude 8°06'N and longitude 12°06'W. In general, the area is suitable for oil palm production and expansion due to soil appropriateness and climate. The typical air temperature in the study region (Njala University, Njala-Campus) ranges from 24.4° C to 28.5° C, with an average rainfall of 2500 mm and well-drained clay-loam soil (Johnson *et al.*, 2017).

Procedure and Data Collection: Data were collected on a total of 160 palms, for 36 months and were evaluated for yield components, fruit bunch traits, vegetative characters and yield traits. The data collection lasted for 36 months and on forth night basis following the procedure of Shabanimofrad *et al.* (2013). The yield components which include bunch number (BNO), average bunch weight (ABW) and fresh fruit bunch (FFB) were collected. Data on fruit bunch traits such as fruit bunch length (FBL), fruit bunch circumference (FBC), stock length (STL) and stock circumference (STC) were measured and recorded at every round. The vegetative traits which are considered as one of the vital components in determining yield were measured and it comprised of palm diameter (PD), palm height (HT), frond production (FP), rachis length (RL), petiole length (PL), petiole width (PW), petiole cross section (PCS), leaflet number (LN), number of leaflets per frond (LNF), leaflet width (LW), leaflet length (LL), leaf area (LA) and leaf area index (LAI). To determine single round vegetative measurement on genotypes palms, simplified non-destructive and destructive procedures were used (Breure & Powell 1988; Corley *et al.* 1971).

Estimation of Fresh Fruit Bunch Yield Gap: The FFB yield gap of oil palm genotypes in this study were estimated as the quotient of the actual yield obtained during the study period with respect to potential yield, expressed in percentage using the formula.

Table 1. Estimated mean squares outline for genotypes analysis in this study

S/V	df	MS	MSE
Replications (r)	(r - 1)	MS1	$\sigma^2_e + n'\sigma^2_g + n'g\sigma^2_r$
Genotypes (g)	(g - 1)	MS2	$\sigma^2_e + n'\sigma^2_r + n'r\sigma^2_g$
Error (e)	n - (r + g)	MS3	σ^2_e

Note: degree of freedom = df, source of variation = (s/v), harmonic mean = (n'), genotypes = (g), number of replications = (r), variance = (σ^2), mean squares for source of variation = (MS), expected mean squares = (EMS) based on the sum of squares type three.

$$YG\%/GT = \frac{PY}{AY/GT} \times 100$$

Where:

YG% = FFB yield gap in percentage/genotype,
PY = potential yield of FFB in t ha

AY = actual yield/genotype of FFB in t ha Ruiz et al. (2017) and Feintrenie et al. (2016) potential yields estimates were followed with a range estimate between 12 t ha/year and 25 t ha/year, i.e., FFB <12 t ha/year as low, FFB 12 -25 t ha/year as intermediate and FFB >25 t ha/year as high.

Statistical Analysis: The collected data by individual palms were computed according to their respective genotypes and the means of the data obtained were used for analyses using the Statistical Analysis System (SAS) Version 9.4 (SAS Institute, Cary, NC, USA) application. Due to some missing data, the General Linear Model (PROC GLM) of SAS was used to carried out analyses of variance (ANOVA) among traits of oil palm genotypes. Simple statistics such as Mean, Standard Deviation (SD), Standard Error (SE), Maximum (Max) and Minimum (Min) for Descriptive statistics (DS) were determined for each trait. Also, for genotype means comparison, at 5% level of probability, the Tukey's studentized range (HSD) was used. To determine if oil palm FFB yield was influence by genetic or phenotypic (environment), the variance components were evaluated using Restricted Maximum Likelihood (REML) according to Okwuagwu and Tai (1995). The estimated mean square outline is presented in Table 1.

- a) Genotypic variance estimate (σ^2_g) = (MSG - MSE)/r

where, MSG = mean square of genotype
MSE = mean square of error
r = number of replications.

- b) Error variance estimate (σ^2_e) = MSE
c) Phenotypic variance estimate (σ^2_{ph}) = $\sigma^2_g + \sigma^2_e$

Pearson correlation was followed to determine the significance level at $p \leq 0.05$ and $p \leq 0.01$ among quantitative traits of oil palm genotypes in this study.

3. RESULTS AND DISCUSSION

Analysis of variance (ANOVA) yield component of genotypes on Njala upland soil: The ANOVA for genotypes showed highly significant differences at $P \leq 0.01$, which presented the occurrence of high variability among genotypes in this study. However, replication exhibited non-significant difference in FFB and BNO, but, highly significant difference was observed in ABW (Table 2). This showed that a breeding program could take an advantage of the large amount of genetic variation that exists among the genotypes.

This outcome of this study was consistent with Noh et al 's (2014) findings, who reported the occurrence of significant genotypic variants and inferred that there was sufficient variability in the introgressed oil palm progenies assessed for yield and yield characteristics. Similarly, during the study of the *dura* AVROS $\times$ *pisifera* of MPOB-Nigerian progenies' palms, Marhalil et al. (2013) noticed a highly significant difference ($p \leq 0.01$) of progeny influence on ABW, BNO and FFB, BNO traits.

Performance of Genotypes Yield Component Traits: In Table 3, the performance of the four genotypes of oil palm for FFB, BNO and ABW were presented. The result showed that 50% of the genotypes (Y26666B and Y26515A) performed better than the trial means for FFB, while 25% of the genotypes (Y26666B) for BNO and ABW had higher mean values of 15.63 BNO and 26. 89 ABW than the trial means of BNO and ABW of 11.68 and 18.14, respectively. The highest FFB of 188.31(kg/palm/year), BNO of 15.63 (bunches/palm/year) and ABW of 26.89 (kg/bunch) were observed in genotype Y26666B. The result of this current study indicated that high BNO with moderate ABW resulted in genotype Y26666B yielding the highest FFB

yields. This result agreed with the findings of Myint *et al.* (2019) and Arolu *et al.* (2016) in their yield component results of oil palm genotypes.

However, the FFB results obtained in this study from Y26666B, Y26515A, Y26520C and Y26456A with yield performance of 188.31 (kg/palm/year), 171.58 (kg/palm/year), 129.99 (kg/palm/year) and 129.69 (kg/palm/year), respectively, were higher than the results reported by Myint *et al.* (2019) and Rajanaidu *et al.* (2017). Whereas, the findings of the Senegal germplasm families for FFB yield reported by Myint *et al.* (2019), were comparatively lower than the result reported by Rajanaidu *et al.* (2017), for FFB from Sierra Leone, Guinea, Zaire, Cameroon and Nigeria which exhibited

their corresponding FFB yields of 92.66, 94.03, 102.37, 110.75, kg/palm/year, respectively.

However, the result showed that genotype Y26666B was significantly different from genotypes Y26456A and Y26520C in terms of FFB yield performance, but the result further indicated non-significant difference with genotype Y26515A in terms of FFB yield. High FFB output and oil yields are prioritized during oil palm selection and breeding. This trial was set up primarily to investigate the FFB yield performance among oil palm genotypes. Amiruddin *et al.* (2020) reported that, the analysis of the Tanzanian data showed that the main goal of oil palm breeding efforts is to increase oil yield. Therefore, genotype Y26666B,

Table 2. Analysis of variance and variance component of yield traits of oil palm genotypes

Sources of variation	Df	FFB	BNO	ABW
Replications (r)	3	5022.60 ^{ns}	54.06 ^{ns}	205.10 ^{**}
Genotypes (g)	3	355337.81 ^{**}	319.99 ^{**}	1385.85 ^{**}
Error (e)	153	5257.03	29.10	47.65
Variance components				
σ^2_g		752.13 (12.53)	7.27 (19.99)	33.45 (41.25)
σ^2_e		5252.50 (87.47)	29.10 (80.01)	47.65 (58.75)
σ^2_{ph}		6004.63	36.37	81.10
Mean		154.89	11.68	18.14
SE		6.03	0.47	0.69
SD		76.29	5.92	8.71
Max		478	25	45.2
Min		13	2	6.15

Notes: df = degree of freedom, FFB = fresh fruit bunch (kg/palm/year), BNO = bunch number (bunches/palm/year), ABW = average bunch weight (kg/bunch), σ^2_e = error variance, σ^2_g = genetic variance, σ^2_{ph} = phenotypic variance, SE = Standard Error, SD = standard deviation, ns = non-significant at $p > 0.05$, * = significant at $p \leq 0.05$, ** = $p \leq 0.01$. The phenotypic variance in percentage are the values in bracket.

Table 3. Mean and standard Error ($\pm$) of oil palm genotype yield traits

S/No.	GTP	FFB (kg/palm/year)	BNO (bunches/palm/year)	ABW (kg/bunch)
1	Y26515A	171.58 ^{ab} $\pm$ 13.98	11.60 ^b $\pm$ 0.93	16.02 ^b $\pm$ 1.08
2	Y26456A	129.69 ^b $\pm$ 10.9	10.45 ^b $\pm$ 0.95	14.15 ^b $\pm$ 0.91
3	Y26666B	188.31 ^a $\pm$ 11.15	15.63 ^a $\pm$ 0.85	26.89 ^a $\pm$ 1.5
4	Y26520C	129.99 ^b $\pm$ 9.31	9.05 ^b $\pm$ 0.7	15.50 ^b $\pm$ 0.91
Mean $\pm$		154.89 $\pm$ 6.03	11.68 $\pm$ 0.47	18.14 $\pm$ 0.69
SE				
SD		76.29	5.92	8.71
Max		478	25	45.2
Min		13	2	6.15

Notes: S/No = serial number, FFB = fresh fruit bunch (kg/palm/year), BNO = bunch number (bunches/palm/year), ABW = average bunch weight (kg/bunch), σ^2_e = error variance, SC = standard cross, SE = Standard Error, SD = standard deviation, Max = maximum, Min = minimum, Means with the same letters within the same column are not significantly different at $p \leq 0.05$ based on Tukey's Studentized Ranged (HSD) Test

could be a better candidate for selection and breeding programs based on the FFB result obtained. However, the lowest FFB was recorded by Y26456A (129.69 kg/palm/year). In terms of BNO and ABW, exhibited significant difference at $p \leq 0.05$ based on Tukey's Studentized Ranged (HSD) Test. Genotype Y26666B was significantly different from other genotypes in this study for BNO and ABW (Table 3). This could have led to its high FFB yield. Amiruddin et al. (2015) did analysis on oil palm FFB yield and its component and the result showed that BNO remained more imperative in contributing in the direction of the FFB yield when compared to the oil palm ABW. Whereas the remaining three genotypes showed non-significant variation among them for BNO and ABW. The results further showed that Y26456A recorded the lowest BNO and ABW of values 10.45 (bunches/palm/year) and 14.15 (kg/bunch), respectively. The higher performance of Y26666B genotype could have resulted as a combination of good mother *dura* and father *pisifera* palms. Alwee et al. (2017), reported that the better performance of progenies or genotypes may occur due to the resulting *duras* mated with popular *pisiferas*, which were widely utilized in the creation of commercial oil palm planting materials.

Estimation of Fresh Fruit Bunch Yield Gap of Genotype: The FFB yield gap estimation of genotypes was presented in Fig. 1. The maximum potential FFB yield of 25 t ha/year was used in the determination of each yield gap per genotype. Based on the calculated estimated results (Fig. 1) showed that all the four genotypes in this study indicated that FFB yield gap existed among the genotypes. It was observed that genotypes Y26515A, Y26456A,

Y26666B and Y26520C recorded FFB yield gap of 13.16 t/genotype/year, 17.86 t/genotype/year, 11.90 t/genotype/year and 17.86 t/genotype/year, respectively. In view of soil suitability and climatic factors, the area in which this current experiment was conducted is generally suitable for the cultivation and growth of oil palm.

Nonetheless, the high yield gap of all the genotypes could have occurred as a result of the poor management practices which lag for some years without regular under brushing, pruning, toileting, etc. Fig. 1 showed that genotypes Y26456A and Y26520C recorded the highest yield gap followed by genotype Y26515A. However, genotype Y26666B recorded the least yield gap. All the genotypes used in this field research exhibited high FFB yield gap. Kome and Tabi (2020) in their previous study reported that oil palm of age 9 - 18 years after planting will produce an FFB yield of 11.52 t·ha⁻¹ on average. However, in the absence of lower yield gap progenies or genotypes planting materials for the purpose of selection and breeding for FFB yield improvement, genotype Y26666B could be a better candidate.

Percentage of Palm Types within Genotypes:

Data were also collected on palm types (*dura*, *pisifera* and *tenera*) among the genotype in the study which was presented in Fig. 2. Among the palm types, 6.25% of *dura* palm were observed. Among genotypes, were as the presence of *pisifera* among genotypes was not noticed. However, majority of the palm were proved to *tenera* (93.75%). Therefore, for breeding purposed *dura* mother palm among the genotype could be used as recipient.

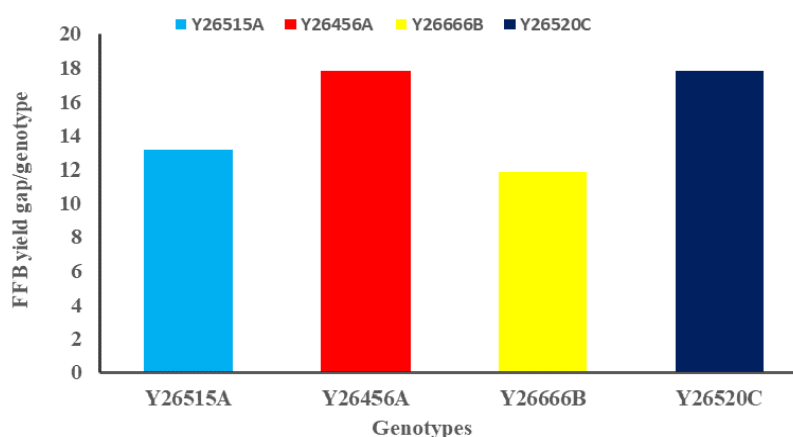


Fig. 1. Yield gap estimation of oil palm genotypes

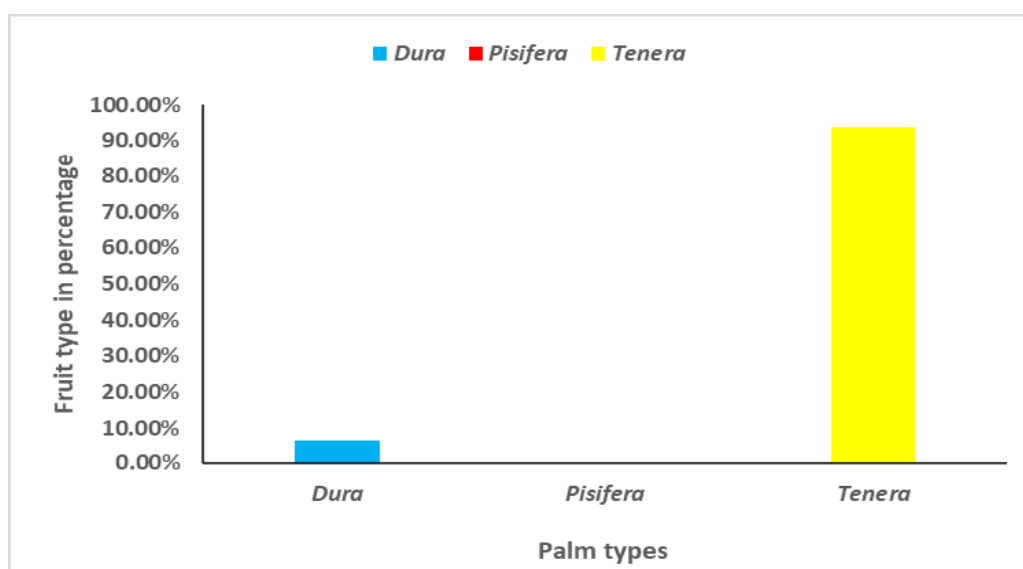


Fig. 2. Palm types among evaluated genotypes

Table 4. Mean squares and estimates for variance components of oil palm genotypes

Sources of variation	df	FBL	FBC	STL	STC
Replications (r)	3	0.27**	4.12*	8.55 ^{ns}	119.83 ^{ns}
Genotypes (g)	3	0.49**	4.07*	129.99**	312.36*
Error (e)	153	0.05	1.61	31.42	107.14
Variance components					
σ^2_g		0.01 (17.37)	0.06 (3.68)	2.48 (7.40)	5.13 (4.57)
σ^2_e		0.05 (82.63)	1.61 (96.32)	30.98 (92.60)	107.14 (95.43)
σ^2_{ph}		0.06	1.67	33.46	112.27
Mean		0.42	0.99	9.58	18.41
SE		0.02	0.1	0.45	0.83
SD		0.25	1.31	5.73	10.55
Max		1.38	11	33	52.67
Min		0.07	0.02	1	3

Notes: df = degree of freedom, FBL = fruit bunch length (m), fruit bunch circumference (m) STL = stock length (cm), STC = stock circumference (cm), σ^2_e = error variance, σ^2_g = genetic variance, σ^2_{ph} = phenotypic variance, SE = Standard Error, SD = standard deviation, Max = maximum, Min = minimum, ns = non-significant at $p > 0.05$, * = significant at $p \leq 0.05$, ** = $p \leq 0.01$. The phenotypic variance in percentage are the values in bracket.

Anova for Fruit Bunch Parameters among Genotypes Trial: The analysis of variance on fruit bunch length (FBL m), fruit bunch circumference (FBC m), stock length (STL cm), stock circumference (STC cm) was presented in Table 4. Based on the analysis carried out in this current investigation, the result revealed highly significant differences at $p < 0.01$ for FBL and STL, whereas significant differences at $p < 0.05$ was observed for traits of FBC and STC. Secondly, the analysis showed that FBL was highly significant among replications and FBC significant, while STL and STC had nonsignificant differences amid the replications.

The variance component of σ^2_e had a range of 82.63 (FBL m) to 96.32 (FBC m), which showed that fruit bunch traits which includes FBL, FBC, STL and STC in this study exhibited the highest σ^2_e . The result in Table 4 presented that the bunch traits were affected by environmental factors, which may have contributed to low size of fruit bunch.

Genotypes Fruit Bunch Parameters: The mean separation analysis using Tukey's Studentized Ranged (HSD) Test at $p \leq 0.05$ showed a significant difference among genotypes for FBL, FBC, STL and STC (Table

5). It was observed that the trial mean for FBL was 0.42 m and it was higher than 50% of the individual genotype mean. Among the genotypes, FBL mean value varied from 0.28 m to 0.54 m and genotype Y26666B recorded the highest followed by genotype Y26520C and Y26515A had the lowest of 0.28 FBL m. The analysis showed that Y26666B was significantly different in their FBL measurement with genotypes Y26515A and Y26456A, but Y26666B was not significantly different with genotype Y26520C. However, Y26520C had a significant variation with Y26515A, but it recorded nonsignificant variation with Y26666B and Y26456A for FBL.

Tukey's Studentized Ranged (HSD) Test showed non-significant differences among the genotypes for FBC. However, the result of FBC highest mean value was recorded by Y26520C of 1.47 m while the minimum mean value was found in Y26515A with 0.91 m and a trial mean of 0.99 m. This may have occurred as a result of their genetic makeup since their parental parents were identical. i.e., most of the derived genotypes may have crossed from the same mother *dura* palms or male *pisifera* palms and therefore, much difference in their FFBC should be detected.

The harvested fruit bunch stock length (STL) was significant among the genotypes with a trial mean value of 9.58 cm. Fifty percent of the genotypes had longer STL than the trial mean and genotype Y26515A recorded the shortest STL (7.17 cm) followed by Y26456A (9.35 cm). The longest STL observed in Y26520C of 11.37 cm followed by Y26666B (10.42 cm). However, HSD analysis showed that Y26520C was not significantly different from Y26666B and Y26456A in STL, but had a significant variation Y26515A. The shorter the stock length, the

larger the oil palm fruit bunch. Therefore, genotype Y26515A could be of better selection for bigger bunch production since it recorded the shortest STL. Even though it had the lowest FFB yield in this study, which could have occurred due to poor management practices such as under brushing, pruning, toileting and other necessary agronomic practices. The existing genotypes were abandoned for some years without any maintenance practices. The stack circumference had a trial mean of 18.41 cm which was also 50% above the genotypes' individual means. The result showed a significant variation among genotypes at $p \leq 0.05$ and Y26666B recorded the largest STC at 20.69 cm and it was significantly different from Y26515A STC of 14.35 cm. Genotype Y26666B had not significant difference with the two remaining genotypes for STC (Table 5). The larger the circumference of the fruit bunch stock, the bigger the bunches and the higher the FFB production among genotypes. This is evidenced that the higher FFB yield production in genotype Y26666B could have occurred due to its larger STC. Therefore, Y26666B could be a better candidate for selection if STC is considered as a trait for FFB yield improvement across genotypes in this field experimental study.

In oil palm breeding, *pisifera* palms displayed strong effects for general combining capacity and homogeneity in their performances after extensive breeding and selection and therefore, the right male parents with better traits for FFB yield improvement must be selected. Oil palm production's main goal is to increase oil yield and quality, which can be accomplished through genetic improvement of selected traits through breeding programs and to improve oil productivity through breeding, variables that have a significant and direct effect on the oil yield must be evaluated (Myint et al., 2021).

Table 5. Fruit bunch variance components mean and standard Error of genotypes

S/No.	GTP	FBL	FBC	STL	STC
1	Y26515A	0.28c $\pm$ 0.03	0.80a $\pm$ 0.16	7.17b $\pm$ 0.9	14.35b $\pm$ 1.22
2	Y26456A	0.40bc $\pm$ 0.03	0.81a $\pm$ 0.07	9.35ab $\pm$ 0.72	19.03ab $\pm$ 1.56
3	Y26666B	0.54a $\pm$ 0.04	0.89a $\pm$ 0.07	10.42ab $\pm$ 0.83	20.69a $\pm$ 1.75
4	Y26520C	0.46ab $\pm$ 0.05	1.47a $\pm$ 0.36	11.37a $\pm$ 1.04	19.56ab $\pm$ 1.94
Mean $\pm$ SE		0.42 $\pm$ 0.02	0.99 $\pm$ 0.1	9.58 $\pm$ 0.45	18.41 $\pm$ 0.83
SD		0.25	1.31	5.73	10.55
Max		1.38	11	33	52.67
Min		0.07	0.02	1	3

Notes: S/No = serial number, GTP = genotype, FBL = fruit bunch length (m), FBC = fruit bunch circumference (m), STL = stock length (cm), STC = stock circumference (cm), SE = Standard Error, SD = standard deviation, Max = maximum, Min = minimum, means with the same letters within the same column are not significantly different at $p \leq 0.05$ based on Tukey's Studentized Ranged (HSD) Test

ANOVA and Variance Component Estimates of Vegetative and Physiological Traits:

Oil palm genotypes grown on Njala upland soil conferred different performance in most of their morphological parameters observed (Table 6). Several vegetative and physiological parameters showed a high significant difference at ($p \leq 0.01$), such as Frond production (FP), Leaf number (LN), Leaf number per frond (LNF), Rachis Length (RAL), Relative leaf area (RLA) and True leaf area (TLA), and Trunk height (TH) exhibited a significant difference at ($p \leq 0.05$). While, Palm diameter (PD), petiole length (PL), Petiole width (PW), Petiole cross-section (PSC), Leaf length (LL), Leaf width (LW), Leaf area (LA) and Leaf area index (LAI) showed non-significant difference at ($p > 0.05$). This result was consistent with that reported by Marhalil *et al.* (2013), in their investigation on the genetic variability of oil palm for yield and vegetative parameters. Similarly, Sunilkumar *et al.* (2015) found a highly significant genetic impact on bunch quality and vegetative components across interspecific oil palm hybrids while evaluating for dwarfness in Indian oil palm genotypes. The highly significant difference among traits indicated that there is a room for selection for future breeding program. This finding demonstrated the considerable genetic diversity that is necessary for the oil palm breeding program to find and utilize the best traits.

Variance components of genetic variance (σ^2_g) values ranged from $<0.01\%$ to 25.64% and σ^2_g recorded the lowest among all the vegetative and physiological traits in this study. Variance components of error variance (σ^2_e) had high values with ranged from 74.36% to 100% for all vegetative and physiological traits analysed, signifying the effect of environment on the said traits of genotypes (Table 6). Precisely, the genotypes were highly affected by the environment with little from genetic effect and this may have influenced the morphological performance of traits of oil palm genotypes for FFB yield.

Performance of Diverse Vegetative and Physiological Traits of oil Palm Genotypes:

The performance of oil palm genotypes for vegetative and physiological traits were presented in Table 7. The palm diameter (PD) is one of the vegetative traits that determines high FFB yield. On the other hand, due to its vigour, a large trunk diameter of a palm tree is not a

characteristic that is preferred for oil palm breeding programs. Smaller trunk diameter is favoured in oil palm breeding programs because it improves nutrient diversion to yield production rather than vegetative growth and maintenance. Though, it might offer a good view for the construction of local bridges. The larger the PD, the better the yield. The PD trial mean value was 0.53 m and had a ranged of 0.51 m to 0.54 with no significant difference amid the genotypes. However, the smallest PD was observed in Y26515A and the largest in Y26666B and Y26520C with the same mean value of 0.54 m.

The production of fronds determines the development of the oil palm inflorescence, which results in the production of the fruit bunch. The potential for a large FFB yield increases with the number of fronds generated by the palm. The trial mean for FP was 28.59 fronds with a range of 25.75 to 31.50 fronds/palm/year. Genotype Y26666B had the highest frond output of 31.50 fronds/palm/year, whilst genotype Y26515A had the lowest frond production at 25.75 fronds/palm/year. The analysis showed that genotypes Y26666B and Y26520C had non-significant difference in FP, but both had a significant variation with genotypes Y26515A and Y26456A. Similarly, Y26515A and Y26456A recorded non-significant difference for FP.

The high FP production in Y26666B led to its high BNO. The high FP production in Y26666B led to its high BNO which resulted in high FFB. The lower production of FP in Y26515A and Y26456A could be the same male palm used in the hybridization for the development of the said genotypes.

The palm leaf number (LN) and = leaf number per frond (LNF) had trial means of 138.84 (no.) and 277.69 (no.), respectively. Genotype Y26666B recorded the highest LN (142.33 no.) and LNF (284.65 no.). Whereas, Y26456A produced the lowest LN (135.95 no.) and LNF (271.90 no.). The more the LN and LNF produced per palm, the better the process of photosynthesis. The genotypes showed non-significant differences for both petiole length (PL) and petiole width (PW) based on Tukey's Studentized Ranged Test at $p \leq 0.05$ (Table 7), with a trial means of 0.77 cm and 0.31 cm, respectively.

Table 6. Genotypes ANOVA and variance component estimate for vegetative and physiological parameters

S/V	DF	PD	TH	FP	LN	LNF	RAL	PL	PW
Replication (r)	3	0.02*	0.47 ^{ns}	54.44*	88.56 ^{ns}	354.23 ^{ns}	0.14 ^{ns}	0.01*	<0.01**
Genotype (G)	3	0.01 ^{ns}	1.98*	261.31**	289.56**	1158.23**	0.69**	<0.01 ^{ns}	<0.01 ^{ns}
Errol (E)	153	0.01	0.63	17.67	69.74	278.97	0.12	<0.01	<0.01
Variance components									
σ^2_g		<0.01 (2.08)	0.03 (5.12)	6.09 (25.64)	5.50 (7.30)	21.98 (7.30)	0.01 (10.80)	<0.01 (<0.01)	<0.01 (2.76)
σ^2_e		0.01 (97.92)	0.63 (94.88)	17.67 (74.36)	69.74 (92.70)	278.97 (92.70)	0.12 (89.20)	<0.01 (100.00)	<0.01 (97.24)
σ^2_{ph}		0.01	0.66	23.76	75.24	300.96	0.13	<0.01	<0.01
Mean		0.53	4.67	28.59	138.84	277.69	4.03	0.77	0.31
SE		0.01	0.06	0.38	0.68	1.36	0.03	<0.01	<0.01
SD		0.08	0.81	4.79	8.62	17.23	0.36	0.05	0.02
Max		0.73	6.78	41	156	312	5.9	0.86	0.35
Min		0.35	2.35	18	113	226	3	0.64	0.2

Notes: S/V = source of variation, DF = Degree of freedom, ns = non-significant ($p > 0.05$), * = significant at ($p \leq 0.05$), ** = highly significant at ($p \leq 0.01$). σ^2_e = error variance, σ^2_g = genetic variance, σ^2_{ph} = phenotypic variance, SE = Standard Error, SD = standard deviation, Max = maximum, Min = minimum. The phenotypic variance in percentage are the values in bracket.

PD = palm diameter (m), TH = trunk height (m), FP = frond production (fronds/palm/year), LN = leaf number (no.), LNF = leaf number per frond (no.), RAL = Rachis Length (m), PL = petiole length, PW = petiole width.

Table 6. Continued

S/V	DF	PCS	LL	LW	LA	RLA	TLA	LAI
Replication (r)	3	<0.01**	138.05 ^{ns}	10.62**	1.60 ^{ns}	31.05 ^{ns}	13.29 ^{ns}	0.78 ^{ns}
Genotype (G)	3	<0.01 ^{ns}	44.19 ^{ns}	0.11 ^{ns}	1.07 ^{ns}	159.14**	32.34**	0.71 ^{ns}
Errol (E)	153	<0.01	115.39	0.99	2.17	15.61	5.49	1.49
Variance components								
σ^2_g		<0.01 (<0.01)	<0.01 (<0.01)	<0.01 (<0.01)	<0.01 (<0.01)	3.59 (18.69)	0.67 (10.89)	<0.01 (<0.01)
σ^2_e		<0.01 (100.00)	114.02 (100.00)	0.97 (100.00)	2.14 (100.00)	15.61 (81.31)	5.49 (89.11)	1.46 (100.00)
σ^2_{ph}		<0.01	114.02	0.97	2.14	19.20	6.16	1.46
Mean		0.24	86.8	4.88	5.75	13.87	7.5	3.91

S/V	DF	PCS	LL	LW	LA	RLA	TLA	LAI
SE		<0.01	0.85	0.08	0.12	0.34	0.2	0.1
SD		0.03	10.7	1.07	1.46	4.31	2.48	1.21
Max		0.29	125	11.32	17.76	31.16	17.14	10.66
Min		0.13	52	3	3.67	4.91	2.7	2.2

Note: S/V = source of variation, DF = Degree of freedom, ns = non-significant ($p > 0.05$), * = significant at ($p \leq 0.05$), ** = highly significant at ($p \leq 0.01$). σ^2_e = error variance, σ^2_g = genetic variance, σ^2_{ph} = phenotypic variance, SE = Standard Error, SD = standard deviation, Max = maximum, Min = minimum. The phenotypic variance in percentage are the values in bracket. PCS = petiole cross-section (m^2), LL = leaf length (cm), LW = leaf width (cm), LA = leaflet area (cm^2), RLA = relative leaf area, TLA = true leaf area, LAI = Leaflet Area Index.

Table 7. Mean and standard error among traits of genotypes

S/No.	GTP	PD	TH	FP	LN	LNF	RAL	PL	PW
1	Y26515A	0.51a ± 0.01	4.86a ± 0.11	27.33b ± 0.33	137.83ab ± 1.26	275.65ab ± 2.52	4.19a ± 0.07	0.76a ± 0.01	0.30a ± 0
2	Y26456A	0.52a ± 0.01	4.80ab ± 0.14	25.75b ± 0.32	135.95b ± 1.51	271.90b ± 3.01	3.96b ± 0.04	0.77a ± 0.01	0.31a ± 0
3	Y26666B	0.54a ± 0.01	4.65ab ± 0.13	31.50a ± 1	142.33a ± 0.92	284.65a ± 1.84	3.89b ± 0.05	0.77a ± 0.01	0.30a ± 0
4	Y26520C	0.54a ± 0.01	4.36b ± 0.12	29.80a ± 0.79	139.28ab ± 1.52	278.55ab ±3.04	4.09ab ± 0.04	0.77a ± 0.01	0.31a ± 0
Mean ± SE		0.53 ± 0.01	4.67 ± 0.06	28.59 ± 0.38	138.84 ± 0.68	277.69 ± 1.36	4.03 ± 0.03	0.77 ± <0.01	0.31 ± <0.01
SD		0.08	0.81	4.79	8.62	17.23	0.36	0.05	0.02
Max		0.73	6.78	41	156	312	5.9	0.86	0.35
Min		0.35	2.35	18	113	226	3	0.64	0.2
S/No.	GTP	PCS	LL	LW	LA	RLA	TLA	LAI	
1	Y26515A	0.23a ± 0.01	86.38a ± 1.65	4.93a ± 0.21	5.90a ± 0.3	15.35a ± 0.61	7.35ab ± 0.36	4.02a ± 0.24	
2	Y26456A	0.24a ± 0	85.52a ± 1.75	4.81a ± 0.2	5.86a ± 0.32	11.49a ± 0.72	6.32b ± 0.4	3.84a ± 0.21	
3	Y26666B	0.24a ± 0.01	87.77a ± 1.73	4.90a ± 0.12	5.68a ± 0.07	15.67a ± 0.53	8.41a ± 0.36	3.76a ± 0.12	
4	Y26520C	0.24a ± 0	87.55a ± 1.68	4.90a ± 0.13	5.55a ± 0.13	12.98a ± 0.65	7.93a ± 0.38	4.03a ± 0.17	
Mean ± SE		0.24 ± <0.01	86.8 ±0.85	4.88 ±0.08	5.75 ±0.12	13.87 ±0.34	7.5 ± 0.2	3.91 ± 0.1	
SD		0.03	10.7	1.07	1.46	4.31	2.48	1.21	
Max		0.29	125	11.32	17.76	31.16	17.14	10.66	
Min		0.13	52	3	3.67	4.91	2.7	2.2	

Note: S/No = serial number, GTP = genotype, PD = palm diameter (m), TH = trunk height (m), FP = frond production (fronds/palm/year), LN = leaf number (no.), LNF = leaf number per frond (no.), PL = petiole length, PW = petiole width, RAL = Rachis Length (m), PCS = petiole cross-section (m^2), LL = leaf length (cm), LW = leaf width (cm), LA = leaflet area (cm^2), LAI = leaflet area index, RLA = relative leaf area, TLA = true leaf area, SE = Standard Error, SD = standard deviation, Max = maximum, Min = minimum, Means with the same letters within the same column are not significantly different at $p \leq 0.05$ based on Tukey's Studentized Ranged (HSD) Test

In the breeding program for oil palms, trunk height (HT), petiole cross-section (PCS) and shorter Rachis Length (RL) are desirable for vegetative traits, in order to develop palms that are compact and can be planted more densely, traits like lower petiole cross-section and shorter rachises are preferred and this could enhance yield per hectare (Myint *et al.*, 2019). For compactness to increase output, for example, Samsul *et al.* (2018) reported that the Malaysian Palm Oil Board (MPOB) had developed the clonal planting material known as CPS2, in which its copied created NGA0.150/2657 (MPOB-Nigeria).

In this current field investigation, TH had a trial mean value of 4.67 m with a range of 4.36 m to 4.86 m. Genotype Y26515A recorded the tallest TH of 4.86 m with non-significant variation with other genotypes, except for genotype Y26520C which recorded the shortest TH at 4.36 m. The RAL ranged from 3.89 m to 4.19 m with a mean value of 4.03 m, while the PCS varied from 0.23 m to 0.24 m² with a trial mean value of 0.24 m². For RAL, significant differences occurred among the genotypes, with the highest from Y26515A which exhibited non-significant with Y26520C, but had a significant difference with Y26456A and Y26666B. The analyses showed non-significant differences among the genotypes for PCS. However, Y26515A recorded the least PCS and the remaining genotypes had the same value (0.24 m).

In addition, the leaf length (LL cm) and leaf width (LW cm) were also recorded and analyzed. The results showed non-significant differences among the oil palm genotypes for these traits. However, a trial mean of 86.8 (LL cm) and 4.88 (LW cm) were obtained and Y26456A recorded the lowest mean (LL 85.52 cm) and (LW 81 cm). The leaflet area (LA cm²) had a trait mean of 5.75 cm² and the mean LA varied from 5.55 cm² to 5.90 cm². Non-significant differences were observed, yet Y26515A showed the maximum LA (5.90 cm²), while genotype Y26520C gave the minimum LA with 5.55 cm².

Also, relative leaf area (RLA), leaflet area index (LAI) and true leaf area (TLA) had trial mean of 13.87, 3.91 and 7.5, respectively. It was observed that non-significant difference occurred amid the genotypes for RLA and LAI (Table 7) among the genotypes. However, statistical significance difference occurred between genotype Y26520C of 7.93 and Y26456A (6.32) for TLA, but genotype Y26520C had non-

significant differences with Y26666B and Y26515A for TLA. Similarly, Y26515A, Y26456A and Y26666B were not significantly different from each other for TLA (Table 7).

The analysed data yielded the following association with reference to yield traits, vegetative and physiological trait components. The 95 percent confidence range of correlation (*r*) used by Koo & Li. (2016) was established to assessed the traits relationships as follows: weak ($r < 0.5$), moderate ($0.5 \leq r \leq 0.75$), good ($0.75 \leq r \leq 0.9$) and perfect ($0.9 < r = 1$) relationships. The quantitative yield traits (BNO and ABW) had a significantly and highly positive relationship with FFB at $r = 0.67^{**}$ and $r = 0.41^{**}$, respectively. This implied that as both BNO and ABW increases, will enhance an increase in FFB yield. This result further validated that oil palm bunch number had more influence on fresh fruit bunch yield than average bunch weight. It could be therefore, determined that improvement in FFB yield, hanged on BNO, which will eventually lead to a surge in oil yield. Therefore, among the yield traits, a substantial presence of genetic relationship exists and thus selection could be done among the genotypes for yield improvement. These yield components normally have an effort in increasing oil yield, which makes them significant for oil palm yield. Findings from de Almeida Rios *et al.* (2018) supported the conclusion made in this study.

4. CONCLUSION

The performance oil palm genotypes on Njala upland soil were evaluated through field research, taking into account 23 traits of oil palm, considering yield and fruit bunch characters as well as vegetative and physiological parameters. Analysis of variance showed that significant variation exists among the genotypes and there was a room for genetic selection. Further analyses were carried out using Restricted Maximum Likelihood estimation for yield and fruit bunch traits including the vegetative and physiological components. The results revealed that all the traits investigated were influenced by the environment with little contribution from genetic variance. Potential yield gap estimation among the genotypes was determined and showed that FFB yield gap existed and it was found to be high in all the genotypes. However, this resulted to high yield gap among the genotypes, based on the poor management practices in the existing oil palm plantation. Furthermore, genotype Y26666B was

identified of having high fresh fruit bunch yielding potential as a result of its high performance in most of the traits examined. Therefore, it could be a hopeful parent for future breeding programs for fresh fruit bunch yield improvement for the achievement higher oil yield. The findings were further validated through correlation coefficient analysis and it was anticipated that there is considerable existence of genetic relationship among the yield traits analysed and hence, selection is possible among the genotypes for yield improvement. Findings reported in this dissertation could have presented more facts in this conventional research if it was done simultaneous with molecular studies.

DATA AVAILABILITY

All data to support the results of this research article is presented within the manuscript.

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DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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