ASIAN JOURNAL OF AGRICULTURE
Volume 10, Number 1, June 2026
Pages: 17

E-ISSN: 2580-4537
https://doi.org/10.13057/asianjagric/g100173

A comprehensive assessment of phenotypic diversity, multivariate relationships, and trait associations in wild oil palm (*Elaeis guineensis*) collections in Ghana

DICKSON OSEI DARKWAH♥, DANIEL AGYEI-DWARKO, SAMUEL ADU OSEI, BRIGHT FIAWONA, SAMUEL BANAFO, JOHNNY OSSOM SACKITEY, ENOCH SAPEY

Council For Scientific and Industrial Research-Oil Palm Research Institute. P.O. Box 74, Kusi-Kade, Ghana.
Tel: +233-248556687, ♥email: oseidarkwah@yahoo.com

Manuscript received: 21 January 2026. Revision accepted: 9 June 2026.

Abstract. *Darkwah DO, Agyei-Dwarko D, Osei SA, Fiawona B, Banafo S, Sackitey JO, Sapey E. 2026. A comprehensive assessment of phenotypic diversity, multivariate relationships, and trait associations in wild oil palm (*Elaeis guineensis*) collections in Ghana. Asian J Agric 10 (1): g100173. https://doi.org/10.13057/asianjagric/g100173.* The CSIR-Oil Palm Research Institute in Ghana conserves 135 wild oil palm (*Elaeis guineensis*) accessions in its ex-situ gene bank. Due to the narrow genetic base of current Deli dura breeding populations, this study aimed to evaluate the phenotypic diversity and breeding potential of these accessions using multivariate analysis. An augmented experimental design with two replicated Deli dura checks was used to assess 25 agro-morphological traits. Data were analyzed using analysis of variance, cluster analysis, principal component analysis, and Pearson's correlation in R software. Significant variation was observed among accessions for 20 traits. High genotypic coefficient of variation, heritability, and genetic advance as percentage of mean were recorded for fresh fruit bunch yield (25.42%, 90.76%, 49.96%), bunch number (24.32%, 80.18%, 44.92%), and average bunch weight (20.01%, 83.44%, 37.70%). Cluster analysis grouped the accessions into four major clusters independent of geographic origin. Seven principal components with eigenvalues greater than one explained 82.66% of the total phenotypic variation, while both positive and negative trait associations were observed. The findings reveal substantial phenotypic diversity among Ghanaian wild oil palm collections, highlighting their potential for breeding, genetic base broadening, germplasm conservation, and future core collection development, pending validation with molecular markers.

Keywords: Augmented design, evaluation, Ghanaian oil palm germplasm, multivariate analysis, phenotypic diversity

INTRODUCTION

Oil palm (*Elaeis guineensis* Jacq.) is one of the most important oil crops worldwide, with palm oil and palm kernel oil accounting for approximately 40% of global vegetable fat and oil supply due to their exceptionally high yield per unit area (Mardiharini et al. 2021). Palm oil is widely used in food products, cosmetics, pharmaceuticals, and biofuels, making it a versatile and economically significant commodity. The crop plays a crucial role in the livelihoods of millions of smallholder farmers and contributes significantly to the economies of major producing countries, particularly in Southeast Asia and Africa (Faizal and Emdi 2017; FAO 2021; Mardiharini et al. 2021; Supriyanto et al. 2024; Hernawan et al. 2025). Oil palm is native to tropical Africa and a major agricultural commodity in Ghana, where it ranks second only to cocoa in economic importance and supports the livelihoods of over two million peoples (Saleh et al. 2018; GSOPP 2019). The sector contributes substantially to rural employment, income generation, and national food security. Recent government-led initiatives, including the Planting for Export and Rural Development (PERD) program, have further intensified oil palm cultivation by promoting the distribution of improved planting materials to climatically suitable districts.

Globally, oil palm breeding programs are constrained by a narrow genetic base originating from only four palms introduced from Africa to the Bogor Botanical Gardens in Indonesia in 1848, which were subsequently evaluated in experimental plantings in Deli, Sumatra (Corley and Tinker 2016). Repeated cycles of selection within this restricted gene pool have enhanced yield performance, but further reduced genetic diversity, potentially constraining future genetic gains and adaptability, with clear indications of inbreeding depression (Okoye et al. 2018; Mathews et al. 2023). In Ghana, Deli dura palms dominate as female parents in commercial seed production, but their restricted genetic base highlights the need to incorporate diverse germplasm to sustain long-term breeding potential (Darkwah et al. 2020).

Consequently, the evaluation of diverse germplasm, particularly indigenous wild populations, is critical for broadening the genetic base and enhancing selection efficiency in Ghana (Wonkyi-Appiah 2013). Okoye et al. (2018) reported substantial genetic diversity within oil palm populations from Nigerian natural groves and successfully integrated superior accessions into their breeding program. Successful incorporation of exotic and wild germplasm into breeding program has previously resulted in improved traits such as *Fusarium* wilt tolerance, reduced height increment, and favorable plant architecture

(Adon et al. 2021). More recently, Konan et al. (2024) demonstrated significant improvements in oil and bunch yields through the introgression of germplasm of Yocobue origin into second-cycle breeding populations in Côte d'Ivoire. Darkwah et al. (2020) assessed a collection of Ghanaian oil palm accessions using five years of yield records in conjunction with 18 agro-morphological traits without incorporating comprehensive statistical analyses. Notably, a 10-year dataset encompassing vegetative, yield, fruit, and bunch traits is considered sufficient under standard operation of the Oil Palm Research Institute (OPRI), Ghana, to ensure robust assessment of yield performance and architectural stability for selection decisions. Moreover, incorporating additional complementary traits enhances the resolution and reliability of phenotypic diversity.

This extensive multi-trait analysis provides a reliable assessment of phenotypic variability, informing elite parent selection, strategic utilization, and conservation. This study advances previous work by integrating long-term field data and seven additional traits with variance component estimation and multivariate analyses, offering improved resolution of phenotype differentiation and stronger inference on complex trait relationships, which underscores the novelty of this study. Therefore, this study aimed to assess the overall phenotypic diversity within wild oil palm accessions conserved at OPRI, elucidate divergence and similarity among accessions using multivariate analytical approaches, and determine relationships among agro-morphological, yield-related traits and bunch and fruit characters. The study is expected to advance the resolution of phenotypic diversity, enhance selection precision, and identify critical trait combinations associated with yield and adaptability, thereby improving the efficiency of germplasm conservation and utilization strategies.

MATERIALS AND METHODS

Plant samples

Wild oil palm accessions were collected from seven regions of Ghana (Figure 1), i.e., Eastern, Volta, Western, Brong Ahafo, Ashanti, Greater Accra, and Central, during two prospecting exercises conducted in 1996 and 2003. Collection followed the procedures outlined in the IBPGR Oil Palm Descriptor Handbook (IBPGR 1989), targeting open-pollinated palms. During the collection mission, populations (sampling sites) were randomly selected across the natural oil palm belt. At each site, approximately three to ten palms were sampled, and about 100 seeds were collected from each individual palm. Seeds obtained from each palm were maintained separately and designated as individual accessions. A minimum distance of approximately 20 km was maintained between successive sampling sites. Local inhabitants assisted in identifying wild palms and harvesting bunches. The 1996 collection comprised 58 accessions, while 95 accessions were sampled in 2003, totaling 153 accessions, of which phenotypic data were available for 135. Distribution of wild oil palm (*E. guineensis*) accessions used in the study across regions are presented in Table 1. Detailed information on the accessions are given in Table S1. Accessions are discrete germplasm entries maintained in a collection, each representing a genetically distinct or geographically defined sample used for evaluation in diversity and breeding studies. In the present studies, each accession represents one family origin.

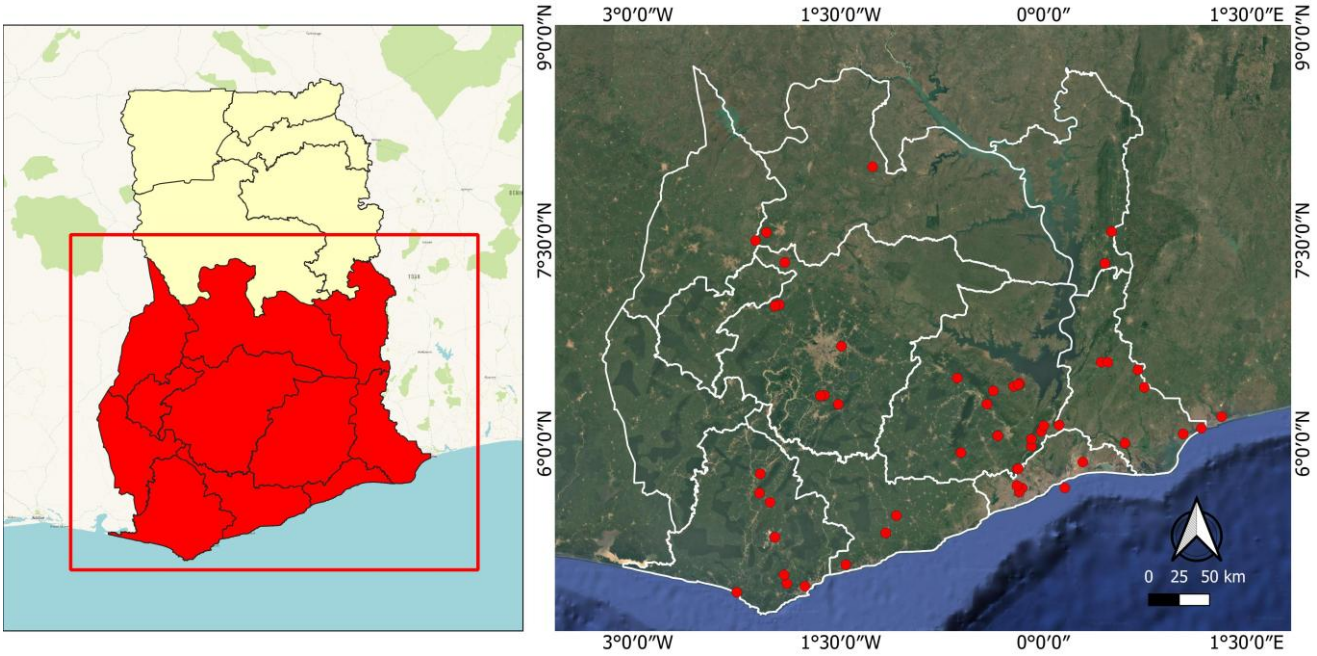

Figure 1. Region and sites of collection of oil palm germplasms

Table 1. Distribution of wild oil palm (*Elaeis guineensis*) accessions across regions

Region	Number of localities	No. of accessions
Volta	12	28
Ashanti	6	20
Brong Ahafo	3	7
Central	3	10
Eastern	16	42
Greater Accra	5	11
Western	9	17
Deli *dura*	-	2
Total	54	137

Procedures

Field experiment

The field trial was conducted at Council for Scientific Industrial Research-Oil Palm Research Institute (CSIR-OPRI) Kusi (0.6° N, 1.45° W), where annual rainfall ranges from 1500 to 2200 mm and temperatures vary between 24 and 34°C. The soils of the experimental site are well-drained and are classified as forest ochrosols under the Ghanaian soil classification system (Owusu-Bennoah et al. 2000), corresponding to Acrisols (Offin series) according to the FAO-UNESCO Revised Legend (FAO/UNESCO 1994). An augmented design was employed, with two Deli dura standard crosses serving as checks. The experiment comprised 15 blocks, each containing nine accessions alongside replicated controls in each block, while the oil palm accessions themselves were not replicated (Darkwah et al. 2020). Data were collected from 10 palms for each accession. The checks were derived from OPRI seed production crosses, including 48D from 851:255D × 851:215D and 621D from the self of 851:215D. Although augmented designs are limited by the lack of replication of test genotypes or accessions, particularly under land-constrained conditions, such as oil palm experiments where palms are established at a 9 × 9 m triangular spacing, they remain highly suitable for evaluating large numbers of accessions. The replication of control genotypes across blocks, enables estimation of experimental variance and minimizes the effects of spatial heterogeneity, thereby improving the reliability of genotype evaluation. The augmented block design was analyzed using a linear model incorporating block effects, replicated checks, and unreplicated test accessions, where replicated controls were used to estimate experimental error and adjust for spatial variation across blocks following procedure described by Ongom et al. (2022) as follows:

Yij=μ+Bi+Cj+Gk+eij

Where, Y_{ij}: Observed value of the j^{th}treatment in the i^{th}block, μ: Overall mean, B_i: Effect of the i^{th}block, C_j: Effect of the replicated check/control genotype, G_k: Effect of the unreplicated test genotype/accession, e_{ij}: Experimental error associated with the observation

Parameters measured

A total of 25 traits were assessed in the study, comprising 16 vegetative traits, 4 yield-related traits, and 5 bunch and fruit character traits. Vegetative traits measured included Leaflet Width (LW), Leaflet Length (LL), Number Of Leaflets (NL), Leaf Area (LA), Total Fronds (TF), Petiole Cross-Section (PCS), Leaf Area Index (LAI), Total Leaf Area (TLA), Leaf Dry Weight (LDW), Average crown Spread (AS), Radius of average spread (Ras), Plant Height (PH), Rachis Length (RL), Height Increment (HI), Frond Dry Weight (FDW), and Frond Index (FI), following standard methods described by Corley (1976) based on 10 years of vegetative data. The measurement methodology and formulas are presented in Table 2. Yield-related parameters such as Fresh Fruit Bunch (FFB) yield was calculated using the formula described by Darkwah et al. (2020) as follows:

$$\mathbf{FFB = NB\ x\ PDH\ x\ ABWT\ x0.001}$$

Where, NB: Number of Bunches, ABWT: Average Bunch Weight (kg), PDH: Planting Density per Hectare, and 0.001: Conversion factor from kg to tons. Bunch Dry Matter (BDM) was estimated following Rajanaidu et al. (2017) as follows:

$$\mathbf{BDM} = \frac{\mathbf{0.53\ x\ FFB\ x\ Planting\ density}}{\mathbf{1000}}$$

Fruit and bunch traits, including single fruit weight, percent mesocarp-to-fruit, percent fruit-to-bunch, percent kernel-to-fruit, and percent shell-to-fruit, were determined using the method of Blaak et al. (1963).

Statistical analysis

Data on vegetative, yield, fruit, and bunch traits were subjected to Analysis of Variance (ANOVA) using the R statistical package (R Core Team 2023). The average values for the 10 palms within each accession were employed for the ANOVA and the estimation of variance components. The error variance was estimated from the replicated check/control treatments and subsequently applied to assess the unreplicated test accessions, with accession means adjusted accordingly for use in all subsequent analyses. Adjusted mean values of phenotypic data collected from oil palm accessions were obtained by conducting augmented analysis of variance using the 'augmentedRCBD' package in R (R Core Team 2023). Block-adjusted means were derived from the checks to correct for spatial heterogeneity before all subsequent analyses, including principal component analysis and cluster analysis. The variance components were used to estimate heritability (h^2), Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), and Genetic Advance (GA) following Estehghari and Farshadfar (2014) with a 10% selection intensity (1.755 from the standard normal distribution table), using the formula as follows:

$$\boldsymbol{h^2 = \frac{\sigma^2 g}{\sigma^2 p}\ x100}$$

$$\mathbf{GCV = \frac{\sqrt{\sigma^2 g}}{X}\ x\ 100}$$

$$\mathbf{PCV = \frac{\sqrt{\sigma^2 p}}{X}\ x\ 100}$$

$$\mathbf{GA = \frac{i\ x\sqrt{\sigma^2 p x\ h^2}}{X}} \times 100$$

Where, $\sigma^2 g$: Genotypic variance, $\sigma^2 p$: Phenotypic variance, i: Selection intensity, and $\bar{X}$: Population mean.

Table 2. Standard procedures for trait measurement and derived trait calculations

Trait	Unit	Measurement methods	Formula
Leaf Area	cm²	Frond number 17 was carefully cut at its base from each palm. The total number of leaflets (n) on both sides of the rachis was recorded. The back region where leaflets narrowed into a V-shape was identified, and 10 upper-rank leaflets were collected from each side just below the V-shape. From these, 6 longest undamaged leaflets were selected and length (L) and mid-width (W) of each measured, with the midpoint determined by folding the leaflet in half.	Leaf Area, (LA) = L∗W∗N∗0.55 Where, L: Leaflet length, W: Leaflet width, and N: Number of leaflets
Total leaf area	m²		Total leaf area $T.\ L.\ A = L.\ A * No.$ of fronds Where, L.A: Leaf Area
Leaf Area Index			Leaf Area Index $\mathrm{LAI} = \frac{T.L.A}{67.57} \times 0.55$ Where, T.L.A: Total Leaf Area, Density is a constant given as 67.57 and 0.55 is a correction factor
Petiole cross-section	cm²	This was assessed by measuring the thickness and width of the petiole using a Venier calliper.	$A = \frac{\pi \times D1 \times D2}{4}$ Where, A: Petiole cross-sectional area (cm²), D_1: Horizontal (major) diameter of petiole (cm), D_2: Vertical (minor) diameter of petiole (cm)
Frond Dry Weight	g		Frond Dry Weight FWD = W ∗ D ∗ 0.1023 ∗ 0.2062 Where, L: Width of the petiole, D: Depth/thickness of the petiole
Total Fronds	Count	All fully developed green fronds were counted, from the central spear leaf down to the lowest unpruned frond on the palm	
Rachis Length	m	Rachis length was measured from the point of insertion of the lower rudimentary leaflets to the tip of the rachis, excluding the terminal leaflets	
Trunk Height	m	Measured from ground level to the exposed base of frond 41 using a measuring tape. Adjacent frond bases were cleared to access the exact attachment point on the trunk	
Spread	m	The canopy spread was measured as the distance from the longest leaf on the North to the longest leaf on the South (NS) and Similarly from the longest leaf on the East to the longest leaf on the West (EW) using a meter rule.	Average Radius $R(as) = \frac{NS+EW}{4}$
Average Spread	m²		Average Spread AS = πr² = R(as)* R(as)*3.14

Multivariate analyses, including Principal Component Analysis (PCA), Wards Hierarchical Cluster Analysis (WHCA), and correlation analysis, were also performed using R software (R Core Team 2023) to examine genetic relationships and trait associations among the accessions. PCA was conducted using prcomp() in the stats package using the correlation matrix, hierarchical clustering was performed with hclust() based on Euclidean distances and Ward's method (ward.D2), and Pearson correlation heatmaps were generated using cor() in stats and visualized with the corrplot package in R. Prior to principal component analysis, variables were standardized to zero mean and a unit variance to eliminate scale effects and ensure equal contribution of all traits, following standard PCA procedures (Jolliffe and Cadima 2016). After standardization, correlation matrix was used since variables were measured in different units to ensure fair contribution in PCA.

RESULTS AND DISCUSSION

Phenotypic variability

This study revealed substantial phenotypic variability among the 135 wild oil palm accessions collected from seven regions of Ghana. ANOVA showed polymorphism in 20 of the 25 morpho-agronomic traits, which contributed to distinguishing the accessions, while traits such as Total

Fronds (TF), Total Leaf Area (TLA), Leaf Area Index (LAI), Frond Dry Weight (FDW), and Frond Index (FI) did not differ significantly (Table 3).

Among the vegetative traits evaluated, leaf area ranged from 2.0 to 7.20 m², with an average of 4.36 m². Rachis length ranged from 1.86 to 6.63 m (mean 3.69 m). Annual height increment in this study ranged from 11.8 to 58.0 cm per year (mean 29.9 cm per year), with maximum values observed in the checks and some accessions reaching 53.46 cm per year (Table 4). For yield traits, accession GHA 8B (accession 90) from Kwaponiase, Eastern region, recorded the highest Fresh Fruit Bunch (FFB) yield of 14.51 tons/ha/yr, driven by high bunch number (13.63) and moderate average bunch weight (7.48 kg) (Table 4). Conversely, GHA 201/02 (accession 2) from Somanya, Eastern region, had the lowest FFB yield (6.18 tons/ha/yr) due to a low bunch number (3.25), despite a moderate bunch weight (7.99 kg).

Significant phenotypic diversity among the germplasm indicates ample scope for selection, reflects the presence of novel alleles that can be conserved for oil palm improvement, and provides opportunities to broaden the genetic base of current breeding populations. The lack of significant variation in TF, TLA, LAI, FDW, and FI suggests relative uniformity of vegetative canopy traits across the evaluated accessions, potentially reflecting strong environmental influence or limited genetic divergence for these parameters.

Vegetative traits are essential for productivity and crop improvement. Soh et al. (2017) noted that key vegetative traits influencing oil palm productivity include plant height, annual height increment, leaf area (or leaf area ratio), and rachis length. Selecting for these traits, together with a high bunch index, can significantly affect yield per palm. Selecting for accessions with sufficient leaf surface area is necessary for effective sunlight capture, supporting photosynthesis and contributing to oil palm growth and yield. Rajanaidu et al. (2017) reported leaf area range of 2.61-7.38 m^2 for MPOB-GHA germplasm, while 4.08-5.17 m^2 for MPOB-CMR accessions (Salim et al. 2023). Murugesan et al. (2020) reported mean rachis lengths of 4.97 m, 6.97 m, and 7.8 m for oil palm germplasm from Guinea Bissau, Tanzania, and Zambia, respectively, which were planted and assessed in India.

Shorter rachis length, smaller petiole cross-section, and lower annual height increment are desirable traits for oil palm breeding programs, as they allow higher-density planting and increase overall productivity (Salim et al. 2023; Norziha et al. 2024). Rajanaidu et al. (2017) reported that the annual height increment of Ghanaian oil palms conserved at MPOB ranged from 6.50 to 58.83 cm per year, with an average of 26.52 cm per year. Tall oil palms typically exhibit high annual height increments of 40-75 cm, as seen in current D × P planting materials (Rajanaidu et al. 2017), with Ghanaian cultivars averaging 50-60 cm per year.

Table 3. Analysis of variance for 25 agro-morphological traits

Traits	Unit	Mean Square		
		Blocks ǂ	Accessions ǂǂ	Residuals ǂǂǂ
Leaf Width (LW)	cm	0.34	0.12 *	0.05
Leaf Length (LL)	cm	82.81	28.02 **	3.92
No. of Leaf (NL)		1429.36	296.55 **	71.46
Leaf Area (LA)	m^2	3.26	0.59 **	0.06
Total Fronds (TF)		24.43	14.54 ^{ns}	20.09
Total Leaf Area (TLA)	m^2	0.04	0.02 ^{ns}	0.01
Leaf Area Index (LAI)		0.05	0.03 ^{ns}	0.19
Petiole Cross section (PCS)	cm^2	34.82	6.25 **	1.70
Leaf Dry weight (LDW)	kg	0.40	0.12 **	0.02
Radius of average spread (Ras)		0.70	0.12 **	0.03
Average Spread (AS)		455.67	62.48 **	9.09
Plant Height (PH)	m	27.31	1.05 **	0.11
Rachis Length (RL)	m	0.94	0.26 **	0.03
Height Increment (HI)	cm/yr	139.78	88.49 **	20.25
Frond Dry Weight (FDW)	kg	257.29	118.14 ^{ns}	76.84
Frond Index (FI)		0.27	0.13 ^{ns}	0.06
Number of Bunches (NB)		11.33	3.88 **	0.95
Average Bunch Weight (ABW)	kg	4.68	2.58 **	0.47
Fresh Fruit Bunch (FFB)	tons/ha/yr	14.06	4.65 **	0.51
Bunch Dry Matter (BDM)	tons/palm/year	0.08	0.03 **	0.005
Single Fruit Weight (SFWT)	g	7.18	2.89 *	1.25
Percent Fruit to Bunch (per FB)		38.13	29.23 **	1.49
Percent mesocarp to fruit (per M)		73.82	51.28 **	1.39
Percent shell to fruit (per S)		62.93	49.18 **	0.92
Percent kernel to fruit (per K)		10.26	13.13 **	1.37

Note: ǂ degrees of freedom for all blocks is equal to 14, ǂǂ degrees of freedom for accessions equal to 136, ǂǂǂ degrees of freedom for residual is equal to 150

Table 4. Phenotypic variability and genetic parameters estimated for 135 accessions

Traits	Min	Max	Mean	Controls mean	CV	PCV (%)	GCV (%)	ECV (%)	HBS	GAM
Leaf Width (LW)	2.68	4.98	3.88	4.10	5.67	8.93	6.85	5.73	58.82	10.84
Leaf Length (LL)	56.20	92.19	72.06	73.90	2.73	8.09	7.61	2.75	88.48	14.78
No. of Leaf (NL)	208.33	328.77	266.21	263.30	3.18	7.38	6.66	3.18	81.49	12.41
Leaf Area (LA)	2.00	7.20	4.36	4.40	5.44	21.05	20.33	5.46	93.26	40.50
Total Fronds (TF)	16.86	35.77	27.59	34.10	15.65	6.05	nc	16.24	nc	nc
Total Leaf Area (TLA)	0.57	1.53	1.11	1.21	8.91	11.21	6.62	9.05	34.83	8.06
Leaf Area Index (LAI)	0.60	1.46	1.00	1.16	42.24	11.15	nc	43.22	nc	nc
Petiole Cross Section (PCS)	4.74	22.94	11.75	13.00	10.88	25.19	22.61	11.11	80.54	41.85
Leaf Dry Weight (LDW)	0.69	3.74	1.44	1.54	9.20	27.48	25.85	9.33	88.48	50.17
Radius of Average Spread (Ras)	2.49	5.01	3.71	3.79	4.34	10.77	9.85	4.36	83.63	18.59
Average Spread (AS)	14.34	79.09	46.17	46.51	6.50	21.55	20.54	6.53	90.82	40.38
Plant Height (PH)	6.74	14.56	10.35	10.49	3.19	17.24	16.94	3.20	96.56	34.35
Rachis Length (Rl)	1.86	6.63	3.69	3.79	4.46	15.06	14.37	4.49	91.11	28.30
Height Increment (HI)	11.8	58.00	29.90	45.36	13.84	23.05	17.45	15.05	57.35	27.27
Frond Dry Weight (FDW)	12.98	82.71	40.29	52.3	20.70	24.32	10.86	21.76	19.96	10.01
Frond Index (FI)	1.69	4.53	3.12	2.91	8.11	11.14	7.74	8.02	48.20	11.08
Number of Bunches (NB)	5.23	14.21	8.05	7.56	12.19	27.15	24.32	12.09	80.18	44.92
Average Bunch Weight (ABW)	5.65	15.12	7.73	8.14	8.83	21.90	20.01	8.91	83.44	37.70
Fresh Fruit Bunch (FFB)	4.10	14.51	8.84	9.08	8.06	26.68	25.42	8.11	90.76	49.96
Bunch Dry Matter (BDM)	0.17	1.27	0.69	0.71	7.54	26.63	25.52	7.60	91.85	50.45
Single Fruit Weight (SFWT)	1.50	12.70	5.71	7.80	18.43	22.39	10.92	19.55	23.79	10.99
Percent Fruit to Bunch (per FB)	42.88	71.24	56.78	50.87	2.19	8.67	8.40	2.15	93.85	16.79
Percent mesocarp to fruit (per M)	23.67	74.02	43.82	42.80	2.70	17.02	16.81	2.69	97.51	34.24
Percent shell to fruit (per S)	16.10	56.20	41.33	40.35	2.34	17.64	17.48	2.33	98.26	35.75
Percent kernel to fruit (per K)	6.90	49.85	14.85	16.85	7.72	23.95	22.61	7.89	89.14	44.04

Note: nc: Not computed

Palms with shorter annual height increments are valuable for breeding slow-growing, compact varieties. Selecting short-statured palms with high yields increases the likelihood of developing progenies that combine superior productivity with reduced height growth. For example, Nigerian Population 12 (dura) exhibits high FFB (200 kg/p/yr) and an annual height increment of 15-19 cm per year; crossing it with pisifera increased FFB by 16.7% and reduced height by 22% compared to controls (Arolu et al. 2016). Slow-growing oil palms prolong economic lifespan, simplify harvesting, and reduce labour costs (Barcelos et al. 2015; Azni et al. 2017). Accessions exhibiting high yield performance and other desirable traits are presented in Table 5.

The findings in terms of yield indicate that high FFB can result from a combination of high bunch number and moderate bunch weight, supporting previous studies (Arolu et al. 2016; Myint et al. 2019; Salim et al. 2023), but contrasting with Kushairi et al. (2003), who suggested that FFB is driven by heavier bunch weight and fewer bunches. In comparison with other germplasm studies, the MPOB-GHA germplasm showed less variation (9.29-15.25 t/ha/yr) (Rajanaidu et al. 2017), the mean yield for Zambian and Tanzanian germplasm planted in India (15.47 t/ha/yr and 12.36 t/ha/yr, respectively (Murugesan et al. 2020), and for MPOB-CMR accessions (11.18-18.65 t/ha/yr) (Salim et al. 2023) was higher than the mean in this study (8.84 t/ha/yr). Importantly, 51% of the accessions exceeded the control's mean FFB yield (9.08 t/ha/yr), demonstrating the high yield potential and adaptive value of Ghanaian wild germplasm as a genetic resource for breeding. High-yielding, genetically diverse oil palm accessions can be introgressed into elite breeding populations to enhance productivity or selected as parental material for targeted breeding programs. The observed differences among vegetative, yield, fruit, and bunch characters across the various studies are likely attributable to genotype × environment interactions, variations in crop management practices, and inconsistencies in data collection methodologies.

Genetic parameters

Evaluating genetic variability is essential in oil palm breeding, as it indicates the potential for selecting and improving key traits. In this study, the Genotypic Coefficient of Variation (GCV) ranged from 6.62% (TLA) to 25.85% (LDW), while the phenotypic coefficient of variation (PCV) ranged from 6.05% (TF) to 27.48% (LDW) (Table 4). According to the classification by Khan et al. (2022), traits with GCV less than 10% are considered low, 10-20% moderate, and greater than 20% high. About 65% of the traits exhibited moderate to high GCV, with nine traits, Leaf Area (LA), Petiole Cross-Section (PCS), Leaf Dry Weight (LDW), Average Spread (AS), Number of Bunches (NB), Average Bunch Weight (ABWT), Fresh Fruit Bunch Yield (FFB), Bunch Dry Matter (BDM), and kernel-to-fruit ratio (per K), showing high GCV. The observed phenotypic variability suggests the presence of substantial diversity among the accessions and indicates potential for broadening the genetic base and providing ample scope for selection and improvement in Ghanaian oil palm breeding programs. However, these inferences are derived solely from phenotypic evaluations using

augmented design, which may be influenced by environmental effects and genotype × environment interactions, potentially inflating estimates of variability. Therefore, integration of molecular marker analyses would further strengthen the resolution and validation of the diversity patterns observed in this study. Traits such as TF and LAI had GCV and h^2 as not computed (nc) i.e zero and might be attributed to no detectable genetic variation among the evaluated accessions as revealed in the ANOVA table for those traits.

For all traits, PCV exceeded GCV, highlighting environmental influence on trait expression, however, narrow differences between PCV and GCV for traits, such as LW, LL, NL, LA, PCS, LDW, Ras, A/S, PH, RL, NB, ABWT, FFB, BDM, per M, per FB, per K, and per S, suggest strong genetic control, making them reliable targets for selection. Broad-sense Heritability (HB) ranged from 19.96% (FDW) to 98.26% (per SF). A recent classification for heritability thresholds in plant breeding categorizes heritability as low (<30%), moderate (30-60%), and high (>60%) (Kumar et al. 2024b). In this study, most traits showed high heritability, indicating that the observed variation is largely genetic and may result in a better response to selection. Traits with lower heritability, such as TF, FDW, and LAI, were largely monomorphic and influenced by environmental or non-additive genetic factors (Khan et al. 2022). High heritability estimates were observed for Bunch Number (BN), Average Bunch Weight (ABWT), and Fresh Fruit Bunch (FFB), consistent with the findings of Sapey et al. (2015) and Darkwah et al. (2020). However, these results contrast with Corley and Tinker (2016), Bakar et al. (2022), and Norziha et al. (2024), who reported lower heritability for the same traits. Variations in heritability across studies may reflect differences in the genetic composition of the genotypes, environmental influences, genotype × environment interactions, and the specific conditions under which the evaluations were conducted.

Genetic Advance (GA) quantifies the expected improvement in a trait resulting from a specific selection intensity. It also indicates the potential for a selected population to exceed the performance of the original population. When expressed as a percentage of the mean, GA provides a meaningful measure of selection response, particularly when interpreted alongside heritability and the genetic coefficient of variation. Genetic advance as a percentage of the mean (GAM) ranged from 8.06% (TLA) to 50.45% (BDM). Genetic advance as a percentage of the mean was categorized as low (<10%), moderate (10-20%), and high (>20%) (Kumar et al. 2024a). In the present study, most traits showed moderate to high genetic advance (GAM), consistent with the results reported by Constantin et al. (2017).

Traits with high heritability and high genetic advance indicate potential breeding value, suggesting that selection is likely to be effective in early breeding generations (Jafar et al. 2023; Kumar et al. 2024b). Conversely, traits with high heritability, but low genetic advance generally reflect lower breeding value and may indicate dominance or epistasis, which restrict the potential for genetic improvement through simple selection (Kumar et al. 2024b). Accordingly, traits such as Leaf Area (LA), Rachis Length (RL), Height Increment (HI), Petiole Cross-Section (PCS), Number Of Bunches (NB), Average Bunch Weight (ABWT), Fresh Fruit Bunch Yield (FFB), and mesocarp fraction (per M) showed both high heritability and high genetic advance, suggesting these traits have comparative breeding value. Our results demonstrate strong potential for effective selection, with a high likelihood of achieving substantial genetic improvement in subsequent breeding generations.

Principal components analysis

Principal Component Analysis (PCA) was conducted to evaluate the contribution of individual traits to overall variation among 135 oil palm accessions. Following standard criteria described by Ekezie (2013), seven principal components with eigenvalues ≥1 were retained, collectively explaining 82.66% of the total variation in 25 agro-morphological traits (Table 6). PC1 accounted for the largest proportion of variation (34.41%) and was dominated by vegetative traits, while PC2 (14.03%) primarily represented yield-related traits, including ABWT, BDM, FFB, and NB. The subsequent components (PC3-PC7) contributed progressively smaller proportions of variation, ranging from 10.41% to 4.05%, and reflected traits such as leaf morphology, frond characteristics, and fruit composition. Similar patterns have been observed in other crops, where seven principal components captured 87–89% of total variation, highlighting the effectiveness of PCA in differentiating oil palm accessions and providing a basis for targeted selection in breeding programs (Vasić et al. 2008; Li et al. 2015).

Table 5. Selected accessions with superior yield and desirable phenotypic traits

Accessions	Height increment per year	Bunch number	Av. Bunch weight	Fresh fruit bunch	% Mesocarp to Fruit
GHA 211/01	28.88	9.32	10.20	13.79	62.65
GHA 212/03	31.39	8.63	10.72	13.27	46.53
GHA 218/01	31.92	11.78	7.42	13.03	49.13
GHA 227/01	23.47	11.55	8.09	13.46	54.10
GHA 5	36.75	10.03	9.31	13.66	44.53
CONTROL	45.36	7.56	8.14	9.08	42.80

PC1 and PC2 were plotted to examine relationships among the 135 accessions (Figure 2). The score plot revealed both phenotypically distinct accessions at the edges, such as 25, 34, 47, 62, 68, 82, 86, 90, 97, 104, 106, 121, 124, and 135, and closely positioned or overlapping accessions, including 120 and 89, 102 and 71, 58 and 59, and 38 and 35, indicating similarity. Divergent accessions with superior agronomic traits are ideal candidates for crossing to exploit heterosis and mitigate inbreeding depression, which can substantially reduce oil palm yield under continuous selfing (Bakoumé et al. 2015). Maintaining only a subset of similar accessions, confirmed via molecular markers, can facilitate the creation of a core collection, typically 5-20% of the total germplasm, reducing maintenance costs while maximizing efficient land use (van Hintum et al. 2000).

Table 6. Latent vector scores of principal component analysis

Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7
ABWT	-0.34	0.37	-0.05	-0.50	0.40	-0.30	-0.21
AS	-0.88	0.25	0.02	0.10	0.18	0.01	0.05
BDM	-0.16	0.88	-0.14	-0.11	-0.33	0.08	-0.12
FDW	-0.88	-0.21	0.25	0.08	-0.08	0.16	-0.11
FFB	-0.14	0.89	-0.15	-0.15	-0.31	0.09	-0.11
FI	-0.32	-0.16	-0.80	-0.20	-0.16	-0.20	-0.03
HI	-0.38	0.23	0.25	-0.04	0.45	0.40	-0.12
LA	-0.91	-0.08	-0.32	-0.05	-0.05	-0.12	-0.01
LAI	-0.68	-0.31	0.25	-0.21	-0.29	0.14	-0.24
LDW	-0.70	0.10	0.39	0.00	0.08	0.02	0.03
LL	-0.77	0.09	-0.24	0.12	0.06	-0.14	0.23
LW	-0.71	-0.05	-0.35	0.03	-0.06	-0.30	-0.14
NB	0.12	0.64	-0.15	0.23	-0.57	0.33	0.11
NL	-0.70	-0.13	-0.22	-0.27	-0.14	0.13	-0.12
PCS	-0.87	0.05	0.34	0.13	0.09	0.00	0.02
perFB	0.16	0.23	0.28	0.29	-0.21	-0.61	-0.19
perK	0.01	0.10	-0.62	-0.17	0.29	0.13	0.48
perM	-0.18	-0.07	0.57	-0.66	-0.31	-0.15	0.17
perS	0.19	0.02	-0.29	0.79	0.18	0.08	-0.44
PH	-0.39	0.61	0.19	0.06	0.28	0.00	0.13
Ras	-0.82	0.27	0.10	0.25	0.16	0.01	0.14
RL	-0.58	0.18	0.24	0.45	-0.07	-0.22	0.21
SFWT	0.28	0.43	-0.09	-0.46	0.34	0.02	-0.39
TF	-0.64	-0.52	-0.03	-0.04	-0.16	0.29	-0.18
TLA	-0.88	-0.24	-0.35	0.02	-0.07	-0.01	-0.05
Eigen value	8.6	3.51	2.6	2.19	1.61	1.14	1.01
Variance (%)	34.41	14.03	10.41	8.75	6.43	4.58	4.05
Cum. variance (%)	34.41	48.44	58.85	67.6	74.03	78.61	82.66

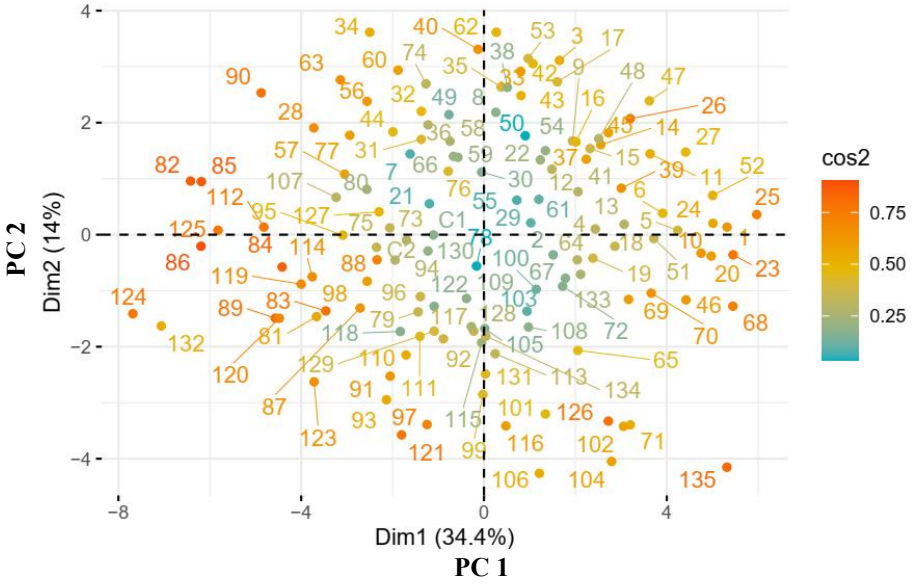

Figure 2. Principal Component score plot (PC1 1 vs. PC2) of Ghanaian oil palm germplasm derived from 25 standardized agro-morphological traits

A PCA biplot was used to examine the relationships between accessions and traits and to identify the most influential variables (Figure 3). Traits such as SFWT, %K, NB, and %FB correlated positively with PC1, whereas BDM, PH, ABWT, and HI were negatively associated. For PC2, BDM, FFB, PH, ABWT, AS, and HI contributed positively, while FDW, LAI, TF, and TLA contributed negatively. In PCA biplot interpretation, the angle between trait vectors reflects the strength and direction of the relationship: acute angles (< 90°) indicate positive correlations, right angles (~90°) indicate negligible correlation, and obtuse angles (>90°) indicate negative correlations (Kavian et al. 2023). For example, NB and SFWT were positively correlated on PC1, and BDM and FFB on PC2. Accessions 47 and 34, located in separate quadrants, exhibited superior NB and ABWT, respectively.

Clustering pattern assessment

Cluster analysis comprises a set of multivariate techniques designed to group individuals or objects into relatively homogeneous clusters based on shared characteristics while maximizing differences among groups (Backhaus et al. 2023). In this study, the similarity and divergence among the 135 oil palm accessions were assessed using Ward's hierarchical clustering method across 25 agro-morphological traits. Ward's method was selected for its proven efficiency and widespread use in hierarchical clustering analyses (Mikrou and Sapidis 2025). The analysis grouped the accessions into four major clusters, indicating substantial variation among the traits evaluated (Figure 4). These results align with previous studies by Taeprayoon et al. (2015) and Teh et al. (2017), who also identified four clusters when characterizing oil palm germplasm. The first cluster comprised 32 accessions (23%) and included three subclusters, characterized by relatively lower annual height increment, higher Bunch Dry Matter (BDM), increased fruit-to-bunch (per FB) and mesocarp-to-fruit (M/F) ratios, and reduced shell-to-fruit (S/F) and kernel-to-fruit (K/F) proportions. Both Deli dura controls were included in this cluster. The second cluster contained 18 accessions (13%) with two subclusters, distinguished by larger leaf width and length, greater leaf area, higher number of leaflets, and taller plant stature. The third cluster consisted of 41 accessions (30%) organized into two subclusters, with palm code 50 identified as an outlier. This group was characterized by a higher per S, elevated per FB, lower per K, and moderate to high bunch yield, representing yield-related traits that make these accessions promising candidates for inclusion in hybridization and selection programs. The fourth and largest cluster, comprising 46 accessions, was characterized by moderate bunch yield alongside elevated Petiole Cross-Section (PCS) and Leaf Dry Weight (LDW), reflecting a combination of structural and productivity traits.

Cluster analysis enables the assessment of genetic diversity, identification of superior accessions, and selection of genetically distant parents for hybridization, thereby maximizing heterosis, improving yield, oil content, and stress tolerance, and mitigating inbreeding depression by highlighting diverse populations for crossing. Additionally, clustering supports efficient germplasm management, reduces redundancy, and aids in predicting breeding outcomes, making it an indispensable strategy for enhancing the effectiveness and precision of oil palm improvement programs. In the present study, the two Deli dura materials used as checks were grouped within the same cluster and were connected by the shortest node length, indicating a high degree of similarity between them. This observation confirms the narrow genetic variability and limited allelic diversity of Deli dura materials, despite their extensive use as maternal parents in commercial seed production (Corley and Tinker 2016). Therefore, the results underscore the need for introgression with genetically diverse germplasm to broaden the genetic base and enhance the long-term effectiveness of oil palm breeding programs. Furthermore, accessions linked by very short internode distances, such as pairs 33 and 35, 83 and 87, 110 and 111, and 121 and 131, exhibited a high degree of genetic similarity, suggesting possible redundancy within the collection. Upon validation using molecular marker analyses, one accession from each closely related pair could be eliminated to minimize duplication and promote more efficient conservation and management of the germplasm.

Inbreeding depression has been identified as a significant factor reducing oil palm performance, particularly because oil palm is an obligate outcrossing species. Successive rounds of inbreeding increase homozygosity, exposing deleterious recessive alleles that negatively affect fitness, resulting in poorer growth, reduced reproductive success, and lower yield components. In self or closely related parental lines, inbreeding depression has been associated with substantial declines in fruit bunch production of up to 40–60% compared with outcrossed material, primarily due to reductions in both bunch number and bunch weight (Corley and Tinker 2016; Ooi et al. 2023). To mitigate inbreeding depression, accessions with superior agro-morphological performance can be selected from distinct clusters and intercrossed to exploit heterosis and enhance progeny vigour and yield potential. Observations on heterosis and inbreeding reduction are predictive and indicate potential breeding benefits; however, their validation requires empirical testing through controlled crosses. These results provide hypotheses for hybrid vigour and inbreeding management, rather than confirmed outcomes. Accessions from different regional collections are often clustered together, indicating no clear association between genetic diversity and region of collection. This pattern suggests that geographic origin did not significantly influence the genetic structure of the collection. The lack of association between clustering patterns and geographic origin may be attributed to gene flow, extensive movement of oil palm planting materials across regions due to its diverse utility and economic importance and shared breeding history, which reduces geographic differentiation among accessions. Similar observations have been reported in previous oil palm germplasm studies conducted by Li-Hammeda et al. (2016), Sapey et al. (2017), Saleh et al. (2018), Darkwah et al. (2020) and Zolkafli et al. (2025). Recent analyses using

SSR markers further confirm this pattern, attributing it to historical gene flow, shared ancestry, and germplasm exchange (Zhou et al. 2015; Masanja et al. 2025). The distribution of accessions from the seven regions across the four clusters is shown in Table 7.

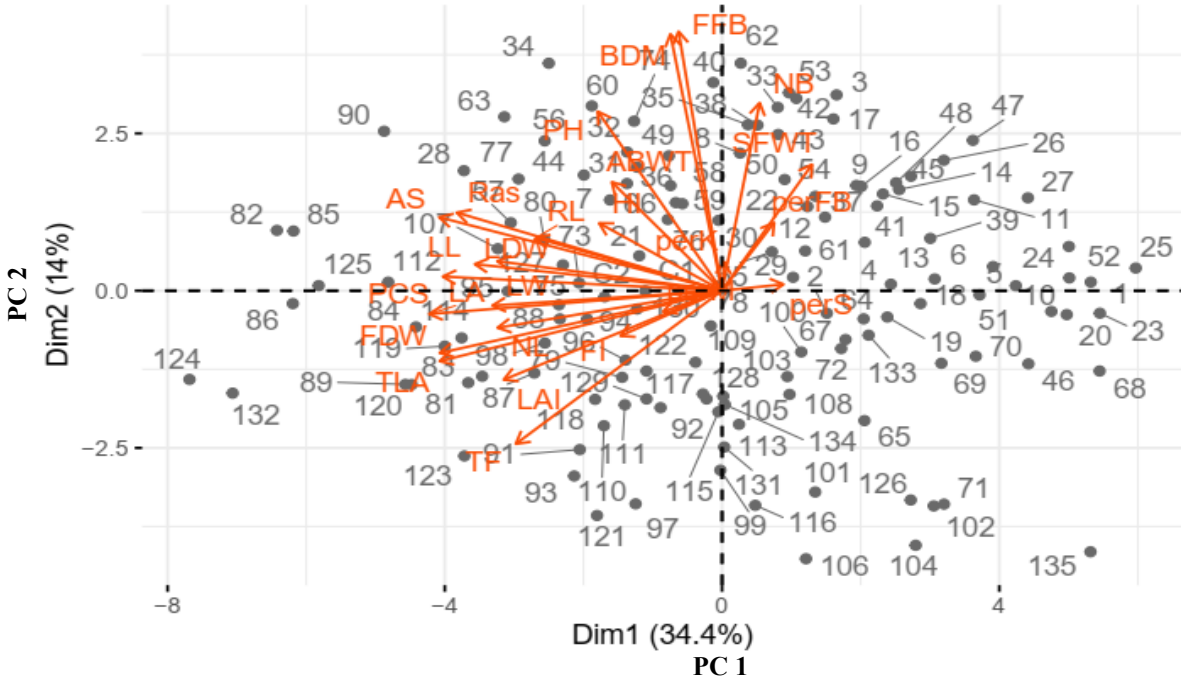

Figure 3. PCA biplot of 135 Ghanaian oil palm accessions and 25 standardized agro-morphological traits, integrating trait and accession relationships

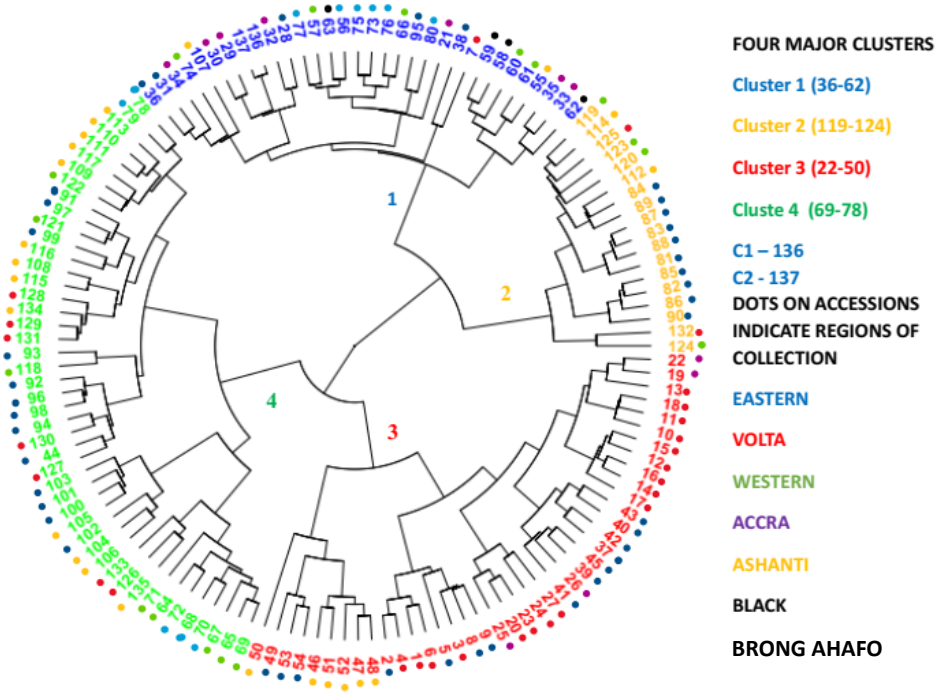

Figure 4. Dendrogram of 135 Ghana oil palm accessions based on 25 agro-morphological traits using Ward's hierarchical clustering distance metric

Correlation among agro-morphological traits

Pearson's correlation analysis was used to quantify associations among the 25 agro-morphological traits evaluated across the 135 Ghanaian oil palm accessions (Figure 5). The strength of Pearson's correlation coefficient is commonly interpreted by its absolute value: values ≥ ±0.90 indicate very strong relationships, ±0.70 to ±0.90 strong associations, ±0.50 to ±0.70 moderate relationships, ±0.30 to ±0.50 low associations, and values below ±0.30 weak correlation (Mukaka 2012). Strong positive significant correlations were observed, with the highest between FFB and BDM (r = 0.99), while weak associations were detected between NL and % M/F, as well as NL and HI (r = 0.17). Fresh fruit bunch yield showed significant positive correlations with both bunch number (r = 0.71, p ≤ 0.001) and average bunch weight (r = 0.39, p ≤ 0.001). In contrast, bunch number and average bunch weight were negatively correlated (r = −0.31, p ≤ 0.001), reflecting their antagonistic relationship. This pattern is consistent with previous reports in oil palm germplasm studies (Darkwah et al. 2020; Suzana et al. 2020; Salim et al. 2023). Overall, the results indicate that higher FFB yield can be achieved through an optimal balance between bunch number and bunch weight, where a high bunch number combined with moderate bunch weight maximizes productivity.

Table 7. Regional distribution of accessions across the four clusters

Region	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Ashanti	1	2	4	13
Brong Ahafo	5		2	
Central	5			5
Eastern	5	10	14	13
Greater Accra	6		5	
Volta	3	4	16	7
Western	5	2		8
Control	2			
Total	32	18	41	46

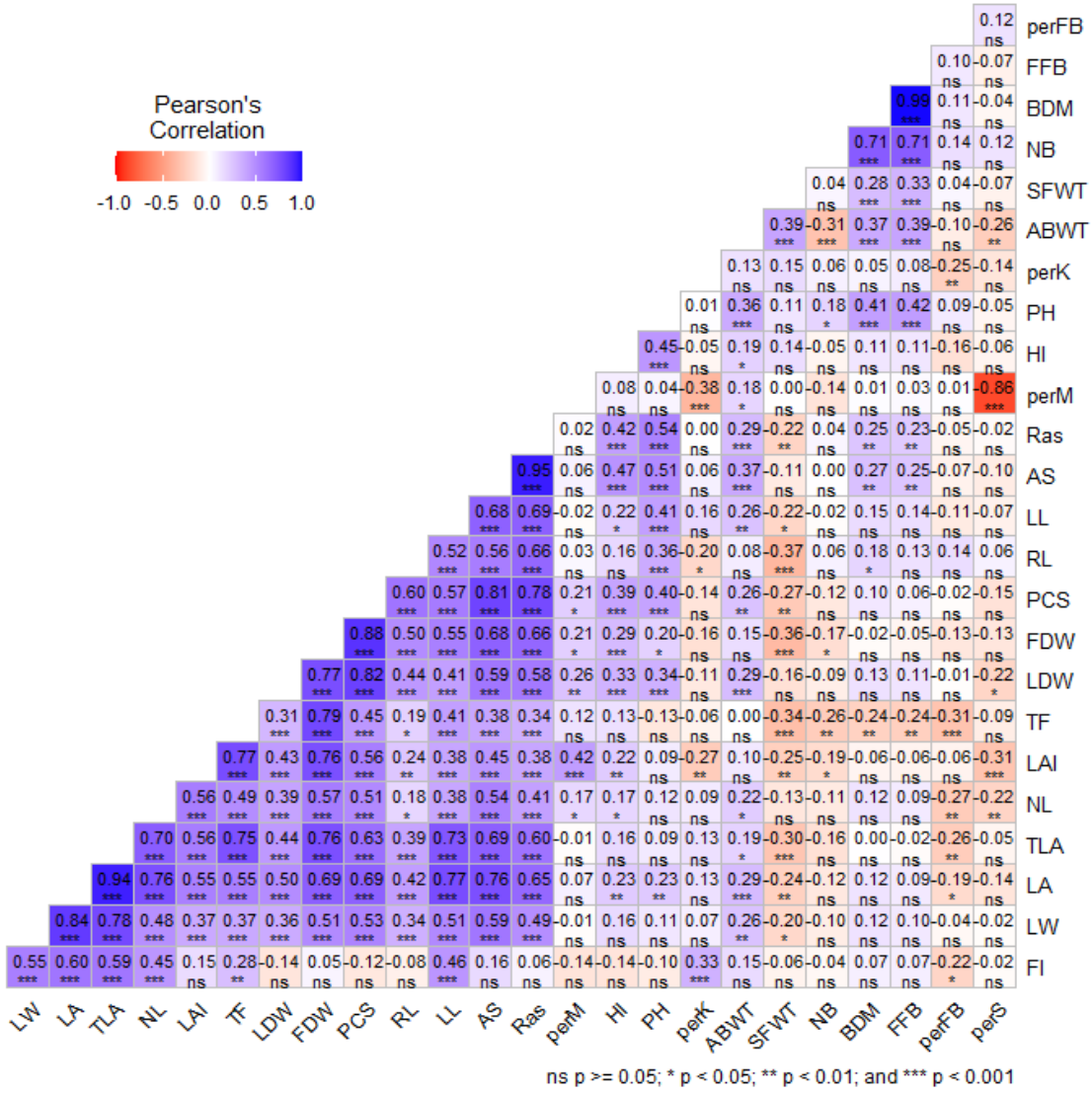

Figure 5. Heat map showing Pearson's correlation coefficients matrix for 25 agro-morphological traits in 135 Ghanaian oil palm accessions. ns: Not significant (p ≥ 0.05), *: Significant at p < 0.05, **: Highly significant at p < 0.01, ***: Very highly significant at p < 0.001

Among vegetative traits, LA showed a significant positive correlation with RL ($r = 0.42$, $p \leq 0.001$) and PCS ($r = 0.69$, $p \leq 0.001$), while PCS and RL also exhibited a moderate positive correlation ($r = 0.60$, $p \leq 0.001$). Plant height (PH) showed a significant positive correlation with height increment (HI; $r = 0.45$, $p \leq 0.001$), consistent with Balakrishna et al. (2018), who reported $r = 0.97$ for Indian oil palm genotypes. HI also correlated positively with RL ($r = 0.16$) and PCS ($r = 0.39$, $p \leq 0.001$). Traits defining compact palms, slow height increment, short rachis, and thin petiole are interrelated (Pangaribuan et al. 2019; Salim et al. 2023), suggesting that indirect selection for one trait could effectively improve the others.

Bunch and fruit traits were predominantly negatively correlated. Percent fruit-to-bunch (per FB) showed negative associations with percent shell (per S; $r = -0.25$, $p \leq 0.001$) and percent kernel ($r = -0.14$), while percent mesocarp (per M) was strongly inversely correlated with shell thickness (per S; $r = -0.86$, $p \leq 0.001$), corroborating the findings of Shi et al. (2019) and Salim et al. (2023). These results indicate that selecting for high mesocarp content to maximize oil yield will inherently reduce shell thickness, whereas breeding for thicker shells, which are useful for industrial applications, will reduce the mesocarp proportion.

In conclusion, substantial phenotypic variation was observed among the 135 oil palm accessions from seven Ghanaian regions, with 20 of the 25 agro-morphological traits showing polymorphism. High genotypic coefficient of variation, heritability, and genetic advance for key yield- and architecture-related traits (including LA, PCS, LDW, NB, ABW, FFB, and BDM) indicate strong potential for effective selection and strategic use of elite accessions in future breeding. Principal component analysis highlighted the key traits driving phenotypic variation and enabled efficient identification of diverse, high-value accessions for targeted selection in oil palm breeding. Cluster analysis demonstrated broad phenotypic diversity among the accessions and identified both divergent and redundant groups. The distinct clustering also supports the selection of genetically distant parents to reduce inbreeding depression and enhance heterosis in breeding programs. This provides a sound basis for developing a compact core collection that maximizes diversity while improving conservation efficiency. This study was based on phenotypic data collected using an augmented design, with limited replication and environmental control, which may not fully capture genetic variation among accessions. Therefore, molecular characterization is required to confirm genetic redundancy and inform core collection and breeding decisions. Trait association analysis identified key correlations that can be exploited for indirect selection, enabling more efficient improvement of yield and related traits. These relationships support faster genetic gain and informed selection in oil palm breeding programs. Given the extensive phenotypic variation observed within the collections, Genome-Wide Association Studies (GWAS) could be used to validate the phenotypic clusters identified in this study.

ACKNOWLDEGEMENTS

The authors gratefully acknowledge the CSIR-Oil Palm Research Institute (CSIR-OPRI), Ghana, for providing financial support for the collection, conservation, and evaluation of the oil palm germplasm used in this study. Special appreciation is extended to Mr. Daniel Agyei-Dwarko for his invaluable contributions to the prospection, collection, and conservation of the wild oil palm accessions. The authors also thank the staff of the Crop Improvement Division, CSIR-OPRI, for their dedicated assistance in data collection and field evaluations. Their technical support and cooperation were instrumental to the successful completion of this research.

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Table S1. Source of the accessions used in the study

Accession	Latitude	Longitude	Location	Region
GHA 201/01	6°05.39N	0°01.021 W	SOMANYA-SRA	Eastern
GHA 201/02	6°05.39N	0°01.021 W	SOMANYA-SRA	Eastern
GHA 201/05	6°07.983N	0°00.136 E	ODUMASE-KROBO	Eastern
GHA 201/04	6°07.983N	0°00.136 E	ODUMASE-KROBO	Eastern
GHA 202/02	6°36.081N	0°25.530 E	HO E.P HEAD Q.	Volta
GHA 202/01	6°36.099N	0°28.522 E	HO E.P HEAD Q.	Volta
GHA 203/ 01	6°32.714N	0°41.873 E	AGORTIME KPETOE	Volta
GHA 203/02	6°32.713N	0°41.873 E	AGORTIME KPETOE	Volta
GHA 203/03	6°32.713N	0°41.873 E	AGORTIME KPETOE	Volta
GHA 205 /05	6°06.852N	01°10.035 E	AFLAO-AVAKORME	Volta
GHA 205 /04	6°06.852N	01°10.035 E	AFLAO-AVAKORME	Volta
GHA 205 /01	6°08.210N	0°06.911 E	DENU-KOPEHIA	Volta
GHA 205 /02	6°08.210N	0°06.911 E	DENU-KOPEHIA	Volta
GHA 205 /06	6°11.982N	01°19.012 E	AFLAO-AVAKORFE	Volta
GHA 205 /03	6°08.210N	0°06.911 E	DENU-KOPEHIA	Volta
GHA 204/ 01	6°24.968N	0°44.676 E	ZIOFE	Volta
GHA 204/02	6°24.968N	0°44.676 E	ZIOFE	Volta
GHA 206/01	6°04.317N	01°01.901 E	KLIKOR AFUTA (AGBOZUME)	Volta
GHA 206/02	6°04.326N	01°01.979 E	KLIKOR AFUTA (AGBOZUME)	Volta
GHA 207/ 01	6°00.173N	0°36.143 E	SOGAKORFE NEW TOWN	Volta
GHA 207/ 02	6°00.158N	0°36.140E	SOGAKORFE NEW TOWN	Volta
GHA 207/03	6°00.234N	0°36.117 E	SOGAKORFE GLOVER KOFE	Volta
GHA 208/01	5°51.920N	0°17.392 E	DAWA	Greater
GHA 209/01	5°40.421N	0°09.412 E	MADINA SOCIAL WELFARE	Greater
GHA 209/ 02	5°40.325N	0°09.477W	MADINA SOCIAL WELFARE	Greater
GHA 209/ 03	5°40.325N	0°09.477W	MADINA SOCIAL WELFARE	Greater
GHA 209/04	5°38.695N	0°10.708W	EAST LEGON OKPONGLO	Greater
GHA 209/05	5°38.605N	0°10.708W	EAST LEGON OKPONGLO	Greater
GHA 209/06	5°38.605N	0°10.708W	EAST LEGON OKPONGLO	Greater
GHA 209/07	5°41.436N	0°11.795W	NORTH LEGON AGBOGBA	Greater
GHA 209/08	5°41.436N	0°11.795W	NORTH LEGON AGBOGBA	Greater
GHA 210/02	5°41.434N	0°11.795W	DODOWA MANYA	Greater
GHA 210/03	5°48.916N	0°11.795W	DODOWA MANYA	Greater
GHA 211/01	5°48.916N	0°11.263W	GYANKAMA-BAHAI	Eastern
GHA 211/02	5°48.924N	0°11.235W	GYANKAMA-BAHAI	Eastern
GHA 211/03	5°48.922N	0°11.236W	GYANKAMA-BAHAI	Eastern
GHA 211/04	5°48.922N	0°11.236W	GYANKAMA-BAHAI	Eastern
GHA 212/01	5°58.868N	0°05.342W	ABIRIW-PC	Eastern
GHA 212/02	6°02.025N	0°05.388W	BEPOASE- ADUKROM	Eastern
GHA 212/03	6°02.025N	0°05.388W	BEPOASE- ADUKROM	Eastern
GHA 213/01	6°17.511N	0°25.049W	BOSOSO	Eastern
GHA 213/02	6°17.511N	0°25.049W	BOSOSO	Eastern
GHA 214/01	6°23.392N	0°22.300W	BEGORO-DANSO	Eastern
GHA 214/03	6°23.392N	0°22.300W	BEGORO-DANSO	Eastern
GHA 214/02	6°23.392N	0°22.300W	BEGORO-DANSO	Eastern
GHA 215/01	6°29.109N	0°38.275W	NEW JEJETI	Eastern
GHA 215/ 02	6°29.109N	0°38.275W	NEW JEJETI	Eastern
GHA 215/03	6°29.109N	0°38.275W	NEW JEJETI	Eastern
GHA 217/01	6°21.463N	01°37.203W	DENYAME-KUMASI	ASHANTI
GHA 217/02	6°21.463N	01°37.203W	DENYAME-KUMASI	ASHANTI
GHA 217/03	6°21.463N	01°37.203W	DENYAME-KUMASI	ASHANTI
GHA 217/07	6°21.463N	01°37.203W	DENYAME-KUMASI	ASHANTI
GHA 218/01	07°01.588N	01°57.216W	KUNTUNSO	BRONG AHAFO
GHA 218/02	07°01.588N	01°57.216W	KUNTUNSO	BRONG AHAFO
GHA 218/03	07°62.735N	01°15.862W	KUNTUNSO	BRONG AHAFO
GHA 219/01	07°33.644N	02°02.892W	MAAMPEHIA TECHIMAN	BRONG AHAFO
GHA 219/02	07°33.644N	02°02.892W	MAAMPEHIA TECHIMAN	BRONG AHAFO
GHA 220/01	07°30.019N	02°07.759W	KWADWO NSOWAAKROM WENCHI	BRONG AHAFO
GHA 220/02	07°30.019N	02°07.759W	KWADWO NSOWAAKROM WENCHI	BRONG AHAFO
GHA 221/01	5°46.665N	2°05.630W	WASA-AKROPONG LOWCOST	Western
GHA 221/03	5°38.104N	2°05.951W	BAWDIE-ACHIASE	Western
GHA 221/02	5°46.665N	2°05.630W	WASA-AKROPONG LOWCOST	Western
GHA 221/04	5°34.026N	2°01.271W	BOGOSO-PRESBY LAND	Western
GHA 222/03	5°18.551N	1°59.219W	TARKWA-CYANIDE	Western

GHA 222/02	5°18.529N	1°59.208W	TARKWA-CYANIDE	Western
GHA 222/01	5°18.538N	1°59.134W	TARKWA-CYANIDE	Western
GHA 223/01	4°54.173N	2°16.091W	ANKOBRA- RIVER BANKS	Western
GHA 223/03	4°54.173N	2°16.091W	ANKOBRA- RIVER BANKS	Western
GHA 224/03	4°56.815N	1°45.868W	NTANKORFUL CEMETERY	Western
GHA 225/02	5°06.422N	1°27.701W	AYENSUDO	Central
GHA 225/03	5°06.422N	1°27.701W	AYENSUDO	Central
GHA 226/01	5°20.448N	1°09.998W	ABURA DUNKWA NEW	Central
GHA 226/03	5°20.448N	1°09.998W	ABURA DUNKWA NEW	Central
GHA 227/01	5°28.122N	1°05.224W	ASSIN OCHISO-AWOYO NO.2	Central
GHA 227/02	5°28.122N	1°05.284W	ASSIN OCHISO-AWOYO NO.2	Central
GHA 227/03	5°28.122N	1°05.284W	ASSIN OCHISO-AWOYO NO.2	Central
GHA 227/04	5°28.122N	1°05.284W	ASSIN OCHISO-AWOYO NO.2	Central
GHA 227/ 05	5°28.122N	1°05.284W	ASSIN OCHISO-AWOYO NO.2	Central
GHA 233/02	5°28.122N	1°05.224W	ASSIN OCHISO-AWOYO NO.2	Central
GHA 301/02	6°08 482N	0°00.587	AGOMENYA	Volta
GHA 1	6°25.44 N	0°13.25W	Abesre	Eastern
GHA 2	6°25.44 N	0°13.25W	Abesre	Eastern
GHA 3	6°25.44 N	0°13.25W	Abesre	Eastern
GHA 4	6°25.44 N	0°13.25W	Abesre	Eastern
GHA 5	6°26.68 N	0°10.60W	Kwaopeniase	Eastern
GHA 6	6°26.68 N	0°10.60W	Kwaopeniase Yokwenya	Eastern
GHA 7	6°26.68 N	0°10.60W	"	Eastern
GHA 8A	6°26.68 N	0°10.60W	"	Eastern
GHA 8	6°26.68 N	0°10.60W	"	Eastern
GHA 8B	6°26.68 N	0°10.60W	"	Eastern
GHA 9	6°26.26 N	0°11.22W	"	Eastern
GHA 10	6°26.26 N	0°11.22W	"	Eastern
GHA 11	6°03.48 N	0°20.28W	Adidi /Nankese	Eastern
GHA 12	6°03.48 N	0°20.28W	Adidi	Eastern
GHA 13	6°03.48 N	0°20.28W	"	Eastern
GHA 14	6°03.48 N	0°20.28W	"	Eastern
GHA 15	6°03.48 N	0°20.28W	"	Eastern
GHA 18	5°56.03 N	0°36.65W	Sekyi Nkwanta (Oworam)	Eastern
GHA 19	5°56.03 N	0°36.65W	Sekyi Nkwanta (Oworam)	Eastern
GHA 20	5°56.03 N	0°36.65W	Sekyi Nkwanta (Oworam)	Eastern
GHA 21	5°56.03 N	0°36.65W	Sekyi Nkwanta (Oworam)	Eastern
GHA 22	5°56.03 N	0°36.65W	Sekyi Nkwanta (Oworam)	Eastern
GHA 23	5°56.03 N	0°36.65W	Sekyi Nkwanta (Oworam)	Eastern
GHA 24	6°43.19 N	1°29.66W	Kwamo	Ashanti
GHA 25	6°43.19 N	1°29.66W	Kwamo	Ashanti
GHA 26	6°43.19 N	1°29.66W	Kwamo	Ashanti
GHA 27	7°01.07 N	1°59.14W	Bonakrom	Ashanti
GHA 28	7°01.07 N	1°59.14W	Bonakrom	Ashanti
GHA 29	7°01.07 N	1°59.14W	Bonakrom	Ashanti
GHA 30	6°21.24 N	1°38.96W	Akasamu /Jawbu	Ashanti
GHA 31	6°21.24 N	1°38.96W	Akasamu /Jawbu	Ashanti
GHA 32	6°21.24 N	1°38.96W	Akasamu Jawbu	Ashanti
GHA 33	6°21.24 N	1°38.96W	Akasamu Jawbu	Ashanti
GHA 35	6°17.47 N	1°31.06W	Fomena	Ashanti
GHA 36	6°17.47 N	1°31.06W	Fomena	Ashanti
GHA 37	6°17.47 N	1°31.06W	Fomena	Ashanti
GHA 38	6°17.47 N	1°31.06W	Fomena	Ashanti
GHA 39	4°58.05 N	1°53.85W	Mpohor/ Ayiem	Western
GHA 40	4°58.05 N	1°53.85W	"	Western
GHA 41	5°01.86 N	1°55.07W	Adum Dominase	Western
GHA 42	5°01.86 N	1°55.07W	"	Western
GHA 43	5°01.86 N	1°55.07W	"	Western
GHA 44	5°01.86 N	1°55.07W	"	Western
GHA 45	5°01.86 N	1°55.07W	Adum Dominase (Ampeasem)	Western
GHA 46	7°34.00 N	0°30.20E	Menuso Agbokordzi/Kadjebi	Volta
GHA 47	7°34.00 N	0°30.20E	"	Volta
GHA 48	7°34.00 N	0°30.20E	"	Volta
GHA 50	7°34.00 N	0°30.20E	"	Volta
GHA 51	7°34.00 N	0°30.20E	"	Volta
GHA 52	7°19.86 N	0°27.22E	Bowiri Kyirahi/Jasikan	Volta
GHA 53	7°19.86 N	0°27.22E	"	Volta

GHA 54	7°19.86 N	0°27.22E	"	Volta
GHA 55	7°19.86 N	0°27.22E	Bowiri Kyirahi	Volta
GHA 56	7°20.34 N	1°54.79W	Dumkofo/Nkekasu A/R	Ashanti
GHA 57	7°20.34 N	1°54.79W	"	Ashanti