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Original Research Article

Genetic Diversity Analysis of Cocoa (*Theobroma cacao* L.) Clones for Breeding and Selection in Nigeria

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Abstract: Cocoa productivity is constrained by several challenges, including aging cocoa trees, limited availability of improved planting materials, pest and disease infestations, and the effects of climate change. The genetic diversity present among cocoa clones is therefore essential for developing superior hybrid cultivars that can address these issues and contribute to sustainable production. This study assessed the genetic diversity of forty cocoa clones established in an existing germplasm plot at the Cocoa Research Institute of Nigeria (CRIN), Ibadan, using a randomized complete block design with six replications. Seven quantitative pod traits were evaluated and analyzed statistically. Significant differences ($P < 0.001$) were observed among the forty clones for all traits measured. The clones exhibited wide variation in pod weight (203.33–837.67 g), number of beans per pod (33.67–56.67), bean weight per pod (52.50–174.00 g), pod length (12.17–27.70 cm), pod width (6.07–9.00 cm), pod thickness (0.5–1.87 cm), and hundred dry bean weight (58.00–154.00 g). Yield-related traits showed strong positive correlations with one another ($P < 0.001$). The first three principal component axes accounted for 76.2% of the total variation, and cluster analysis grouped the clones into five distinct categories. High phenotypic and genotypic coefficients of variation, along with high heritability and genetic advance, were recorded for pod weight, bean weight per pod, and hundred dry bean weight, while number of beans per pod and pod length exhibited high heritability with moderate genetic advance. These traits can therefore serve as key selection criteria in cocoa breeding programs.

Keywords: Heritability, Cocoa Clones, Genetic Diversity, Germplasm, Eigenvector, Clustering, Genetic Advance.

INTRODUCTION

Cocoa (*Theobroma cacao* L.) is a valuable tropical crop in the *Malvaceae* family. As the main ingredient in chocolate, beverages, and other products, cocoa plays a significant role in the global economy. Millions of people worldwide consume these products (Kongor and Dimas, 2023) generating substantial revenue for governments in producing countries. In fact, cocoa is a major foreign exchange earner, contributing significantly to the GDP of these nations (Kehinde, 2022; Oyekale 2022). The crop thrives in tropical and subtropical regions, with West Africa dominating global production (Kongor *et al.*, 2024). Nigeria is a major cocoa exporter, ranking sixth globally, with production rising from 280,000 metric tonnes in 2022 to 340,000 metric tonnes in early 2024. Despite this increase, the country still lags behind the top three cocoa producers (Sunpress, 2025). Nigerian cocoa production faces significant challenges, including aging trees, pests and diseases, climate change, insecurity, and limited access to improved planting materials. However, breeders can tap into the genetic diversity of cocoa to address these issues and boost productivity. The genetic diversity of cocoa (*Theobroma cacao* L.) is a critical factor in the sustainability and productivity of cocoa production worldwide, particularly in Nigeria, which is one of the largest cocoa producers in Africa. Cocoa is not only a significant agricultural commodity but also a vital source of income for millions of farmers and contributes significantly to the country's economy (FAO, 2020). Nigeria's cocoa genetic resources are rich and varied, comprising numerous local and introduced varieties. Understanding and preserving the genetic diversity of cocoa clones is essential for developing high-yielding, disease-resistant, and climate-resilient varieties that can withstand the challenges posed by pests, diseases, and

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changing environmental conditions (Adebayo *et al*., 2020; Asare *et al*., 2019).

Cocoa conservation is unique due to its recalcitrant seeds, which can't withstand drying or long-term storage. Instead, clonal germplasm is preserved through vegetative propagation methods like grafting, budding, and rooted cuttings. These collections provide breeders with valuable parental material, preserving rare alleles for important traits (Lavoie *et al*., 2022). Cocoa clonal germplasm collections in field genebanks and research centers are a vital source of genetic variation for breeding programs. These collections preserve essential genetic diversity, enabling the development of cocoa varieties with improved traits such as disease resistance, higher yields, better quality and environmental adaptability. This genetic foundation is crucial for sustainable cocoa improvement. Genetic diversity within plant genetic resources provide breeders with opportunities to develop new cultivars with desirable traits, such as high yield, large seed size, pest and disease resistance, drought tolerance, and photosensitivity (Govindaraj, *et al*., 2014).

Genetic diversity is crucial for cocoa's long-term breeding and production success, enabling improvements in yield, resilience, adaptability, and quality. Preserving and utilizing this diversity is essential for maintaining stable cocoa farming systems, ensuring global chocolate industry growth, Protecting against genetic erosion and reducing production risks. A good knowledge of the extent of genetic variability of key morpho-agronomic traits of cocoa clones is imperative for genetic conservation and utilization of the crop in breeding programs targeted at improving the high beans quality, yield and related traits required by the global, regional and local demands for cocoa beans. The detection of significant variations in associated traits serves as a premise for selection and improvement of cocoa genotypes. Agro-morphological characterization is the first step in the assessment of genetic variability and identification of desirable traits of interest (Lahai *et al*., 2025). This study aims to explore the genetic diversity of cocoa clones in Nigeria, assessing the implications for breeding and conservation efforts. By employing conventional breeding methods, this research seeks to provide insights into the genetic variability present within Nigerian cocoa populations and to identify superior clones that can contribute to sustainable cocoa production in the face of ongoing agricultural challenges.

MATERIALS AND METHODS

The experiment was conducted in the existing germplasm plots of the Cocoa Research Institute of Nigeria (CRIN), Ibadan. The plots are located at 07.02°N latitude and 03.09°E longitude, at an elevation of 122 meters above sea level. A randomized complete block design (RCBD) was adopted, consisting of six replications with ten trees per block for each clone, planted at a spacing of 3 m × 3 m. The study involved forty cocoa clones fifteen from local germplasm plots and twenty-five from international germplasm plots. Data were collected from fifteen uniformly matured and ripe pods per clone, following the procedure described by Adewale *et al*., (2013). The parameters recorded included pod weight (g), number of beans per pod, weight of beans per pod (g), pod length (cm), pod width (cm), pod thickness (cm), and hundred dried beans weight (g).

All collected data were analyzed using the Statistical Analysis Software (SAS) version 9.2. Analysis of variance (ANOVA) was performed using the PROC GLM procedure, and significant differences among treatment means were determined using Duncan's Multiple Range Test (DMRT). Trait correlations were assessed using the Analyst option in SAS, while Principal Component and Cluster Analyses were conducted with PROC PRINCOMP and PROC CLUSTER, respectively. The variance components were used to compute the genotypic and phenotypic coefficients of variability, heritability (in the broad-sense) and genetic advance, according to the methods of Burton (1952), Johnson *et al.* (1955) and Kumar *et al*., (1985).

Genotypic coefficient of variation = $\left(\sqrt{\sigma g} \middle/ \bar{x}\right) X100$ …….(1)

Phenotypic coefficient of variation = $\left(\sqrt{\sigma ph} \middle/ \bar{x}\right) X100$…...(2)

where: σ_g and σ_{ph} are the genotypic and phenotypic standard deviations, respectively and $\bar{x}$ is the grand mean for the character under consideration.

The PCV and GCV value were ranked as described by Siva-Subramanian and Menon (1973)

0 to 10% - Low

10 to 20% - Moderate

> 20% - High

Broad sense heritability was estimated as the ratio of the genetic variance to the phenotypic variance and expressed in percentage following Toker (2004) as Broad Sense Heritability

$(H) = \sigma^2 g/\sigma^2 p \times 100$ ……………………… (3)

$\sigma^2 p = \sigma^2 g + \sigma^2 e$ …………………………… (4)

Where

$\sigma^2 g$ = genotypic variance

$\sigma^2 p$ = phenotypic variance

$\sigma^2 e$ = environmental variance

The values of heritability percent was classified as per Johnson *et al*., (1955)

0 to 30 percent = Low

31 to 60 percent = Moderate

Above 60 percent = High

Genetic advance (GA) was computed according to the formula by Johnson *et al.*, (1955).

$$GA = \frac{\sigma^2 g \times K}{\sqrt{\sigma^2 p}} \quad \ldots\ldots\ldots\ldots\ldots\ldots (5)$$

Where k = 2.06 (selection differential at 10%)

$\sigma^2 g$ = genotypic variance
$\sigma^2 p$ = phenotypic variance

The values of Genetic advance are classified as per the method of Johnson *et al.*, (1955).
Less than 10 percent = Low
10 – 20 percent = Moderate
More than 20 percent = High

RESULTS AND DISCUSSION

The mean performance of the evaluated cocoa clones for seven (7) yield traits is presented in Table 1. There was a highly significant ($P \leq 0.001$) difference among the forty clones for all the traits evaluated. Clone MAN15-2 exhibited the highest mean values for the number of beans per pod (56.57), weight of beans per pod (174.00 g), and pod length (27.70 cm). In contrast, PA120 recorded the lowest mean values for pod weight (203.33 g), number of beans per pod (33.67), and pod length (12.17 cm). Similarly, EET59 showed superior performance in pod width (9.90 cm) and hundred dried bean weight (154.00 g), while N38 and GF24 had the lowest values for pod width (6.07 cm) and hundred dried bean weight (58.00 g), respectively. Clone T22/28 recorded the lowest mean value for weight of beans per pod (52.50 g), whereas T86/2 had the smallest pod thickness (0.50 cm). The success of breeding programs depends on genetic variation. This study found significant genetic diversity, breeding potential and selection opportunities. This finding is consistent with the report of Deepa *et al.*, (2019), who also observed significant differences among cocoa clones for the studied traits. The Cocoa clones showed notable differences in yield traits, this diversity offers opportunities for future breeding and improvement and greater genetic variability increases chances of achieving desirable outcomes.

The eigenvalues, variance proportions of the four principal component (PC) axes, and the eigenvectors of seven morphological traits are presented in Table 2. The first principal component (PC1) accounted for 51.0% of the total variation, while the first three components together explained 76.2% of the total variability. The remaining three components contributed 13.4%, 11.9%, and 8.8% for PC2, PC3, and PC4, respectively. Morphological traits with character loadings of 0.2 or higher were considered significant contributors to each principal component axis. Seven yield traits pod weight, number of beans per pod, weight of beans per pod, pod length, pod width, pod thickness, and hundred dried bean weight loaded heavily on PC1. Four traits number of beans per pod, weight of beans per pod, pod thickness, and hundred dried bean weight were most influential for PC2. Three traits number of beans per pod, pod thickness, and hundred dried bean weight loaded strongly on PC3, while PC4 was predominantly defined by five traits: number of beans per pod, weight of beans per pod, pod length, pod width, and pod thickness. Principal component analysis (PCA) identified patterns of trait co-variation among cocoa clones, revealing differential trait contributions, significant trait influences and Trait importance. Each trait contributed uniquely to total variation, all assessed traits impacted variation among cocoa clones and collective trait contributions enabled effective classification of cocoa clones. The PCA results aligned with previous research (Adewale *et al.*, 2013), highlighting the value of phenotypic traits in describing and differentiating cocoa genotypes. The analysis showed that individual traits varied in their influence on total variability.

Table 1: Mean performance of forty cocoa clones evaluated for seven yield traits

Clones	PdWT	NoBP	WtBP	PdLT	PdWidth	PdThick	DW100B
PA120	203.33g	33.67d	56.33h	12.17l	6.73g-i	0.83b-e	78.00g-k
MAN15-2	738.17a-c	56.67a	174.00a	27.70a	9.07a-f	1.47ab	126.33a-c
PA150	370.17e-g	47.67a-d	66.33gh	19.87b-h	7.23c-i	1.13b-e	84.00f-k
PLAYAALTA	378.50e-g	48.33a-d	107.83b-h	21.33b-f	7.63a-i	1.17b-d	110.00b-g
SPEC 54	609.33a-f	46.67a-d	112.10a-h	24.00a-d	8.63a-h	1.20b-d	92.67d-j
C77	541.67a-f	53.33ab	123.83a-g	20.83b-f	8.50a-h	1.23a-d	116.07b-f
POUND7	530.33a-f	49.00a-d	140.67a-f	17.07f-l	8.23a-i	1.33a-d	125.23a-d
LCTEET46	385.50d-g	46.67a-d	62.83gh	13.23i-l	6.53hi	1.87a	75.33jk
EET59	758.50ab	44.33a-d	145.17a-e	21.53a-f	9.90a	1.37a-d	154.00a
IFCS	466.00b-g	45.00a-d	123.00a-g	17.93d-l	6.73g-i	0.83b-e	93.00d-j
VENC4	558.33a-f	50.00a-c	102.00c-h	19.50c-i	9.40a-d	0.90b-e	90.00f-k
MXC67	692.00a-d	49.00a-d	166.83ab	20.87b-f	9.30a-e	1.33a-d	92.33d-j
MOCOROGO	614.50a-f	50.00a-c	121.17a-g	18.30d-l	9.53a-c	0.93b-e	90.00f-k
ICS1	606.17a-f	48.33a-d	100.17c-h	23.37a-e	8.93a-g	0.97b-e	124.33a-e
IMC47	559.83a-f	51.67ab	85.83d-h	18.20d-l	8.07a-i	1.37a-d	83.33f-k
UF676	433.33c-g	46.67a-d	80.50f-h	25.50a-c	9.50a-c	1.00b-e	93.00d-j

Clones	PdWT	NoBP	WtBP	PdLT	PdWidth	PdThick	DW100B
PA107	441.83c-g	45.00a-d	95.00d-h	19.03d-i	8.00a-i	1.37a-d	77.67g-k
APA4	662.50a-e	40.67b-d	163.17a-c	21.33b-f	8.90a-g	1.27a-d	141.00ab
CATIE1000	542.67a-f	49.33a-d	123.17a-g	19.67b-h	8.80a-h	1.03b-e	93.00d-j
BE10	606.17a-f	53.33ab	123.33a-g	19.93b-h	9.57ab	1.47ab	94.67c-j
SCA6	437.53c-g	50.00a-c	110.33a-h	17.30e-l	7.63a-i	0.97b-e	75.67i-k
T85/799	435.00c-g	52.67ab	148.70a-d	20.10b-h	7.97a-i	1.10b-e	98.00c-j
GF24	570.33a-f	47.67a-d	87.10d-h	20.37b-g	8.87a-g	1.37a-d	58.00k
AMAZ15-15	432.33c-g	40.33b-d	83.83e-h	17.63e-l	7.03e-j	1.43a-c	84.67f-k
AMAZ15-2	837.67a	51.67ab	92.67d-h	25.90ab	9.83a	1.33a-d	94.67c-j
T12/11	375.50e-g	40.33b-d	104.43b-h	16.43f-l	7.67a-i	1.07b-e	108.40b-i
T9/15	413.17d-g	43.33a-d	88.33d-h	18.53d-k	7.13d-i	1.20b-d	101.83c-j
T53/5	435.17c-g	44.33a-d	98.67d-h	18.63d-j	7.73a-i	0.97b-e	93.33c-j
T65/7	461.83b-g	47.33a-d	96.63d-h	12.67cj-l	6.70g-i	0.73de	105.00c-j
T53/8	472.83b-g	48.67a-d	102.50c-h	20.40b-g	8.27a-i	1.10b-e	111.13b-f
T82/27	574.33a-f	42.67a-d	102.67c-h	17.20e-l	7.27b-i	1.00b-e	108.87b-h
T57/22	466.83b-g	40.33b-d	81.53e-h	16.53f-l	7.10d-i	1.37a-d	107.07c-j
T30/13	415.33d-g	39.33b-d	76.17gh	15.43f-l	6.87f-i	1.07b-e	90.33f-k
T65/35	316.00fg	38.33b-d	70.00gh	13.23i-l	7.87a-i	0.97b-e	74.67jk
T86/2	313.50fg	43.00a-d	95.83d-h	14.20g-l	7.30b-i	0.50e	89.33f-k
T12/5	370.00e-g	35.00cd	100.00c-h	20.47b-g	7.13d-i	1.00b-e	100.00c-j
T22/28	382.17d-g	34.67cd	52.50h	17.50e-l	7.60a-i	1.23a-d	103.03c-j
T16/17	450.83b-g	42.00a-d	88.33d-h	13.85h-l	7.43b-i	0.80c-d	91.33e-j
T101/15	532.83a-f	43.00a-d	102.53c-h	12.67j-l	7.17d-i	0.73de	101.00c-j
N38	329.33fg	35.67cd	55.67h	12.30kl	6.07i	0.83b-e	76.00h-k
Fsign	***	***	***	***	***	***	***

Means followed by the same letter(s) are not significantly different according to DMRT (P<0.05)

NB: PdWT-Pod weight, NoBP- Number of beans per pod, WtBP- Weight of bean per pod, PdLT-Pod length, PdWidth-Pod width, PdThick-Pod thickness, and DW100B- Hundred dried bean weight

Table 2: Eigen values and factor scores of characters associated with the first four principal component axes in cocoa clones

Characters	PCA1	PCA2	PCA3	PCA4
PdWT	0.452	0.008	-0.016	-0.003
NoBP	0.353	-0.202	-0.563	-0.453
WtBP	0.419	0.297	-0.126	-0.362
PdLT	0.403	-0.136	0.049	0.590
PdWidth	0.435	-0.162	-0.119	0.420
PdThick	0.252	-0.546	0.699	-0.370
DW100B	0.284	0.727	0.403	-0.052
Eigenvalue	3.567	2.939	1.830	0.616
Variance (%)	51.0	13.4	11.9	8.8
Cumulative (%)	51.0	64.4	76.2	85.0

Eigenvectors ≥0.2 are in bold

NB: PdWT-Pod weight, NoBP- Number of beans per pod, WtBP- Weight of bean per pod, PdLT-Pod length, PdWidth-Pod width, PdThick-Pod thickness, and DW100B- Hundred dried bean weight

The phenotypic correlation coefficients among the seven evaluated traits of the cocoa clones are presented in Table 3. A positive and highly significant (P<0.001) correlation was observed between the number of beans per pod and pod weight (r = 0.495). The weight of beans per pod showed a highly significant (P<0.001) and positive association with both pod weight and number of beans per pod (r = 0.626 and 0.513, respectively). Similarly, pod length exhibited highly significant (P<0.001) and positive correlations with pod weight, number of beans per pod, and weight of beans per pod (r = 0.535, 0.423, and 0.442). Pod width was highly significant (P<0.001) and positively correlated with pod weight, number of beans per pod, weight of beans per pod, and pod length (r = 0.693, 0.467, 0.536, and 0.639). In addition, pod thickness showed significant (P≤0.05) and positive correlations with pod weight, number of beans per pod, weight of beans per pod, pod length, and pod width (r = 0.361, 0.208, 0.236, 0.335, and 0.315). The hundred dry bean weight also had highly significant (P<0.001) and positive associations with pod weight, weight of beans per pod, pod length, and pod width (r = 0.407, 0.491, 0.337, and 0.273). Understanding correlations between traits is crucial for designing effective breeding programs. In this study, the yield traits showed positive correlations, indicating that selecting for one trait can simultaneously impact others. This association can be expressed through observable relationships between traits, genetic relationships between traits, and environmental influences on trait relationships. These correlations inform breeding decisions and can enhance the efficiency of selection and improvement programs.

The UPGMA analysis grouped the cocoa clones into five major clusters at a dissimilarity coefficient of 100 (Figure 1), indicating a high degree of genetic diversity among the clones. The ability of UPGMA to distinctly separate the clones into clear groups confirms the reliability of morphological and quantitative traits for classifying cocoa clones. At the similarity level of 100, five distinct clusters were identified. Group I contained one clone, Group II comprised four clones, Group III had one clone, and Group IV also included four clones, while Group V consisted of twenty-two clones (Figure 1). Clones in Cluster V exhibited the highest mean values for all the evaluated traits (Table 4).

The phenotypic and genotypic coefficients of variation (PCV and GCV), broad-sense heritability, and genetic advance (as a percentage of the mean) for the traits evaluated in the cocoa clones are presented in Table 5. The results revealed that the GCV values were slightly lower than the corresponding PCV values, this indicates that environmental effects had minimal influence on the observed variability, implying that the differences were primarily attributed to the genetic makeup of the genotypes. Both PCV and GCV showed relatively high values across all the traits studied, and heritability estimates exceeding 50% were recorded for every character.

Relatively high genetic advance values were recorded for pod weight (439.94%), weight of beans per pod (99.33%), and hundred dry bean weight (64.17%). The traits pod weight, weight of beans per pod, and hundred dry bean weight exhibited high heritability along with high genetic advance, suggesting that they are controlled by additive gene action. This implies that selection based on these traits would be effective and beneficial for breeding programs. Comparable findings were also reported by Deepa *et al*., (2019) and Lahai *et al*., (2025).

Table 3: Phenotypic correlation coefficient among seven quantitative characters of cocoa clones

Characters	**PdWT**	**NoBP**	**WtBP**	**PdLT**	**PdWidth**	**PdThick**	**DW100B**
PdWT							
NoBP	0.495***						
WtBP	0.626***	0.513***					
PdLT	0.535***	0.423***	0.442***				
PdWidth	0.693***	0.467***	0.536***	0.639***			
PdThick	0.361***	0.208*	0.236**	0.335***	0.315***		
DW100B	0.407***	0.142ns	0.491***	0.337***	0.273***	0.137ns	

NB: PdWT-Pod weight, NoBP- Number of beans per pod, WtBP- Weight of bean per pod, PdLT-Pod length, PdWidth-Pod width, PdThick-Pod thickness, and DW100B- Hundred dried bean weight

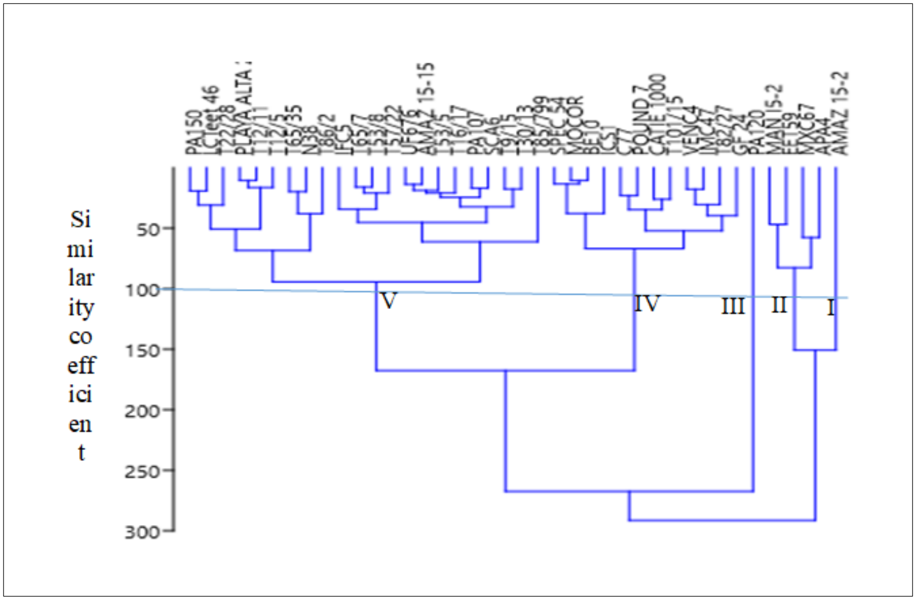

Figure 1: Dendrogram showing grouping similarities among forty cocoa clones for yield traits across the germplasm

Table 4: Cluster means showing intra-cluster variability of the seven traits

Cluster groups					
Characters	**I**	**II**	**III**	**IV**	**V**
Pod weight (g)	837.67	2851.17	203.33	6846.49	8982.68
Number of beans per pod	51.67	190.17	33.67	585	954.66
Weight of beans per pod(g)	92.67	649.17	56.33	1324.57	1988.94
Pod length (cm)	25.90	91.43	12.17	231.11	382.09
Pod width (cm)	9.83	37.17	6.73	102.97	163.12
Pod thickness (cm)	1.33	5.44	0.83	13.53	23.71
Hundred dried bean weight (g)	94.67	513.66	78	1177.17	2042.79
Cluster Population	1	10	9	1	4

Table 5: Estimates of genetic parameters of traits of cocoa clones

Traits	Mean	PCV	GCV	Heritability (%)	Genetic Advance (%)
Pod weight (g)	493.04	50.60	46.81	85.61	439.94
Number of beans per pod	45.40	23.64	21.19	80.36	17.80
Weight of beans per pod(g)	102.79	53.56	50.13	87.58	99.33
Pod length (cm)	18.57	36.97	35.53	92.34	13.06
Pod width (cm)	8.00	23.91	22.26	86.61	3.41
Pod thickness (cm)	1.12	44.64	40.92	84.00	0.87
Hundred dried bean weight (g)	97.66	34.90	33.36	91.40	64.17

CONCLUSION

The findings of this study revealed that the forty cocoa clones showed considerable variation across the seven traits assessed. The potential for genetic improvement and the development of high-yielding cocoa varieties largely rely on the magnitude and nature of genetic variability present in the germplasm. Cluster analysis using UPGMA grouped the cocoa genotypes into five distinct clusters. Traits exhibiting high heritability along with high genetic advance are reliable indicators for selection, as they are less affected by environmental factors. Additionally, correlation analysis showed interrelationships among traits, highlighting key component traits that can be targeted for effective yield improvement through selection. Several cocoa clones with outstanding quality traits were identified in this study. Using these superior clones as parents for future hybridization could yield progenies with enhanced heterotic performance. The inclusion of these promising clones in future breeding programmes is anticipated to enhance cocoa productivity in Nigeria.

REFERENCES

- Adebayo, A. H., Ojo, M. O., Olorunfemi, A. M. (2020). Assessing the genetic diversity of cocoa (Theobroma cacao L.) using molecular markers in Nigeria. *Journal of Agricultural Science and Technology*, 22(4), 234-245.
- Adewale D. B., Adeigbe O.O., Adenuga O.O., Adepoju A.F., Muyiwa A.A., Aikpokpodion P.O. (2013). Descriptive and discriminatory significance of pod phenotypic traits for diversity analysis of cocoa genotypes *esci journals j. plant breed. genet.* 01 (03) 131-137
- Asare R., Sarpong D. B., Owusu-Ansah E. The role of genetic diversity in the improvement of Theobroma cacao: Implications for breeding programs. *African Journal of Biotechnology*, 2019. 18(5), 234-244.
- Burton, G. W. Quantitative inheritance in grasses, *Proceedings of the Sixth International Grassland Congress*, 1952 Pennsylvania State College, USA, 17, 23 August 1952, pp. 277-283.
- Deepa, R., Balakrishnan, S., Jegadeeswari, V., Thiribhuvanamala, G., Kumaravadivel., N. (2019). Study of variability, heritability and genetic advance for yield attributing characters in cocoa clones. *The Pharma Innovation Journal* 2019. 8(5): 466-469
- FAO. (2020). Cocoa market review. Food and Agriculture Organization of the United Nations. Retrieved from FAO website
- Govindaraj, M. Vetriventhan, M. Srinivasan (2014). Importance of Genetic Diversity Assessment in Crop Plants and Its Recent Advances: An Overview of Its Analytical Perspectives. *Hindawi Publishing Corporation Genetics Research International* Volume 2015, Article ID 431487, 14 pages http://dx.doi.org/10.1155/2015/431487
- Johnson, H. W., Robinson, H. F., (1955). Comstock, R. E. Estimate of genetic and environmental variability in soybean. *Agronomy Journal*. 47: 314-318
- Kehinde, A.D. (2022). Access to trade credit and its impact on the use of European Union (EU) approved pesticides among smallholder cocoa farmers in Ondo State, Nigeria. *Heliyon.* 8(12):12409.
- Kongor, J.E., Owusu, M., Oduro-Yeboah C. (2024). Cocoa production in the 2020s: challenges and solutions. CABI Agriculture and Bioscience https://doi.org/10.1186/s43170-024-00310-6
- Kongor, J.E., Rahadian, Aji M.D. (2023). Processing of cocoa and development of choco late beverage. Natural products in beverages: Reference

series in phytochemistry. Cham: Springer; 2023b. p. 1–37.

- Kumar, A., Misra, S. C., Singh, Y. P., Chauhan, B. P. S. (1985). Variability and correlation studies in triticale, *Journal of Maharashtra Agricultural Universities* 1985. 10: 273-275.
- Lahai, P.M., Aikpokpodion, P.O., Norman, P.E., Kamanda, I., Conteh, A.R. (2025). Morphological Characterization and Genetic Diversity Analysis of Cacao (*Theobroma cacao* L.) Genotypes from Sierra Leone. *American Journal of Plant Sciences*, 16, 903-922. https://doi.org/10.4236/ajps.2025.167061
- Lavoie, A., Thomas, E., Olivier, A. (2023). Local working collections as the foundation for an integrated conservation of *Theobroma cacao* L. in Latin America. *Front. Ecol. Evol*. 2023. 10:1063266. doi: 10.3389/fevo.2022.1063266
- Oyekale, A.S. (2022). Determinants of cocoa farmers’ compliance with agrochemical safety precautions in Ogun and Osun States, Nigeria. *Toxics*. 10 (8):454. https:// doi. org/ 10. 3390/ toxic s1008 0454.
- Siva-Subramanian, S. Menon, M. (1973). Heterosis and inbreeding depression in rice. *Madras Agricultural Journal*, 1973. 60: 1139.
- Sunpress (2025). Cocoa industry 2025- key concerns that can influences the cocoa industry. Sunbelt Global Concept, weekly bulletin; Issue 35
- Toker, G. (2004). Estimate of broad sense heritability for yield and yield criteria in faba bean (Vicia faba L.). *Hereditas*. 40:222-225.

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