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Agromorphological Characterization of 260 Okra Accessions (*Abelmoschus esculentus* L. Moench) in Mali

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Abstract

The lack of suitable varieties is a constraint to okra production in West Africa. This study aimed to assess the magnitude of morphological diversity of 260 accessions of okra (*Abelmoschus esculentus* L. Moench) in Mali. A total of 25 qualitative and quantitative traits, including plant height, number of branches, pod length, and pod yield, were measured under field conditions. Significant variation was observed for all agronomic traits ($p < 0.001$). Yield per hectare ranged from 0.013 to 16.72 t/hectare. The phenotypic coefficient of variation (PCV) was higher than the comparing genotypic coefficient of variation (GCV) for every trait with a close relationship between them, indicating substantial genetic diversity among accessions. Broad sense heritability estimates for major traits were found to be moderate and high ($31 < h^2 < 60$), suggesting that these traits are largely controlled by genetic factors. The pod yield was affected by the incidence of diseases. Principal component analysis (PCA) revealed four distinct clusters, indicating a broad genetic base. These findings provide valuable insights for breeding programs targeting improved okra varieties with enhanced yield and resilience, contributing to sustainable agricultural development in Mali.

Keywords

Morphological Diversity, Genotypic and Phenotypic Coefficient of Variation, PCA, Cluster

1. Introduction

Okra (*Abelmoschus esculentus* L. Moench) is an important traditional vegetable crop cultivated widely in tropical and subtropical regions [1] [2]. Okra originated around Ethiopia and was cultivated by the ancient Egyptians during the 12th century BC when it spread throughout the Middle East and North Africa. [3] Okra grows in regions of low latitude with marked high humidity. It is sensitive to low temperatures and develops poorly below 15˚C [4]. In Mali, okra is significant in food security and income generation. The local variety, namely Gankourouni, is widely grown in most of the rural areas in Mali. It is a staple in many local dishes and is valued for its edible pods rich in fiber, vitamins, and minerals. [5] Despite its economic and nutritional importance, there remains a limited understanding of Mali's genetic diversity and agro morphological characteristics of okra landraces.

Its cultivation in Mali faces several challenges that limit its potential. One of the main issues is the lack of well-adapted, high-yielding varieties that can thrive in Mali's diverse agroecological zones. Local farmers often rely on traditional landraces, which may exhibit wide variability in yield, growth habits, and resistance to pests, diseases, and environmental stress. [6]

Additionally, limited research on the genetic diversity of okra germplasm has hindered the development of improved varieties tailored to local conditions. This lack of characterization makes it difficult to identify varieties with desirable traits such as drought tolerance, early maturation, or improved pod quality. [7] Furthermore, the growing threat of climate change exacerbates the challenge, as erratic rainfall and soil degradation continue to impact okra production.

Another critical issue is the insufficient access to modern agricultural practices and inputs, which limits farmers' ability to improve productivity. Coupled with inadequate knowledge of pest and disease management, these constraints reduce yields and the overall quality of okra in Mali. [8] Addressing these problems requires a combined effort to identify, conserve, and utilize okra varieties with superior agro morphological traits, ultimately supporting food security and livelihoods [9].

Agromorphological characterization, which involves assessing traits such as plant height, pod size, flowering time, and yield components, is a crucial step toward improving crop performance [10] [11]. This study provides vital information for breeding programs aimed to enhance productivity, resilience to environmental stresses, and adaptability to local conditions. This study aims to assess the nature and magnitude of genetic variability, identify the potential genotypes toward yield, and the association between yield and other morphological traits.

2. Material and Method

2.1. Genetic Material

260 okra accessions from the World Vegetable Center gene bank in Tanzania were used in this study.

2.2. Site and Experimental Design

The agro-morphological characterization was carried out in one environment during the 2023 rainy season (Samanko). The Samanko experimental station has clay soil, richer in nutrients and more water-retaining, but heavier to work, especially when dry. It has an average temperature of 27.7˚C. Figure 1 shows rainfall distribution during this characterization period. The trial was implemented following a randomized incomplete block design with three replications. Experimental plots consisted of two 3 m rows with a 75 cm distance between rows and 50 cm between hills within rows.

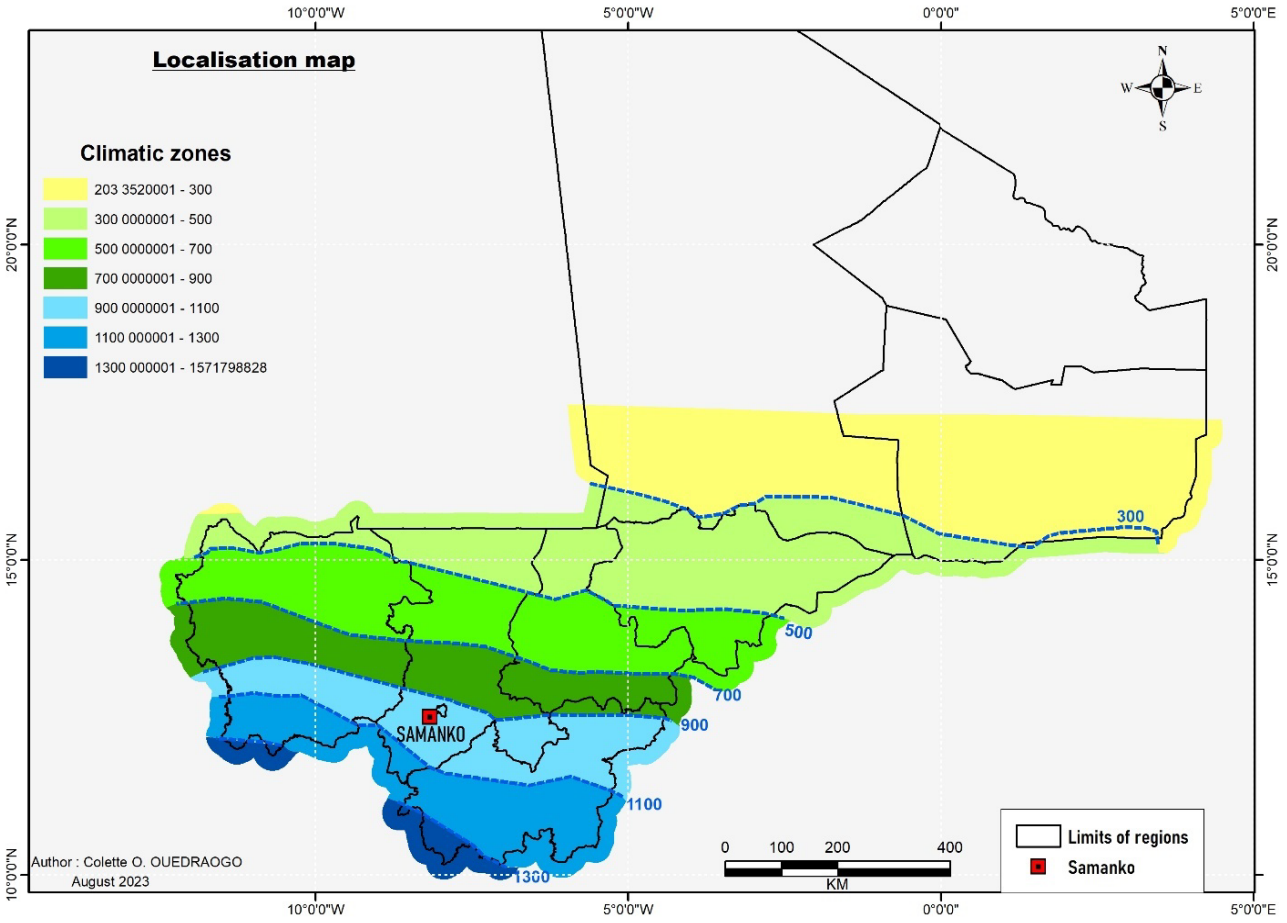


Figure 1. Geographical position of the experimental site with the range of rainfall.

2.3. Field Evaluation and Management

The 260 okra accessions were evaluated for pod yield and components, flowering time, and morphological traits. The seeds of each accession were sown into the two rows after treatment with Apron Star. The seedlings were thinned to 2 plants per hill three weeks after emergence. Mineral fertilization was done according to the required standards, DAP was applied before ridging at a rate of 100 kg/ha and 50 kg/ha of urea (46% N) 45 days after sowing. Two weedings were done, and a phytosanitary treatment was made to protect the plants from pests and diseases to

minimize their impact on the plants. The okra descriptor proposed by WorldVeg was used for characterization. The measurements were focused on yield-relevant traits. The observations for the qualitative characteristics were essentially based on the color, shape, growth habit, pubescence, branching, and persistence of the calyx. Twenty-five (25) quantitative and qualitative traits were used for agro-morphological evaluation. The grain yield and the 50% flowering time were observed on the whole plot, the other traits were measured on three (3) plants randomly selected per line. Plant height was measured in centimeters from the soil to the tip of the panicle. Panicle length was measured in centimeters from the bottom to the tip of the panicle.

2.4. Data Analysis

Data collected were analyzed using a variety of software. The Breeding View software was used to perform the analysis of variance to evaluate the presence of statistically significant differences among genotypes for the traits studied and to obtain the best linear unbiased estimate (BLUES) and the best linear unbiased prediction estimate (BLUP). Two models were used to run the analysis to obtain the BLUEs and BLUPs. In the first model, the genotype was taken as a random factor and the environment as a fixed factor, and in the second model, the genotype was considered fixed. The following formulas were used: Model:

$$Yijk = \mu + Gi + Rj + Bk + B(R) + Eijk$$

where $Yijk$ is the observed value; μ is the population mean; Gi is the effect due to the i-th genotype tested; Rj is the effect due to the j-th replicate; Bk is the effect due to the k-th block; $B(R)$ = interaction effect of the block in the replicate; $Eijk$ is the effect due to the random error.

The genotype factor that was taken as random was used to calculate the predicted values and standard error for each genotype. R software was used to analyze correlation and graphs.

The pod yield was calculated as follows:

$$\mathrm{PY}(\mathrm{g/m2}) = \frac{\mathrm{PW}}{0.75(3+0.6)}$$

where 0.75 = line spacing; 3 = length of the sowing row; 0.6 = 2 borders corresponding to the inter-hill, PY is the pod yield and PW is the pod weight.

Coefficients of genotypic variation (CGV) were calculated according to the method proposed by [12] to allow comparisons of genetic variability of all traits.

$$\mathrm{CVG}(\%) = \frac{\sqrt{(\vartheta g2)}}{\mu} \times 100 \quad \text{and} \quad \mathrm{CVP}(\%) = \frac{\sqrt{(\vartheta p2)}}{\mu} \times 100$$

where $2g\sigma$ is the genotypic variance component, and μ is the overall trial mean.

To obtain the average variance of a difference (aVD) between genotypes, the square root of the standard error of difference (SEd) was estimated and normalized by dividing it by the grand mean of the trial. The broad sense of heritability h^2 was calculated based on the formula of [13].

$$h^2 = 1 - \frac{aVD}{2Vg}$$

with Vg = genetic variance and aVD = average variance of a difference.

A principal component analysis (PCA) was conducted using SPSS software, and the coordinates of the individuals were used to group the accessions through hierarchical ascending classification (HAC). The groups derived from the HAC were characterized by discriminant factor analysis (DFA).

3. Results

3.1. Variability Parameters

The analysis of variance revealed highly significant differences ($p < 0.001$) for all traits among the accessions studied. Large phenotypic variation among the accessions was observed for morphological and pod yield traits, as shown by the range between the minimum and maximum traits. Large variability was observed in the fruits (Figure 2). Yield per hectare ranged from 0.013 to 16.72 t/hectare. In the genetic variability studies (Table 1), the phenotypic coefficient of variation (PCV) was higher than the comparing genotypic coefficient of variation (GCV) for every trait with a close relationship between them, therefore, the environment has a low impact and subsequently, the phenotypic performance of traits ought to be utilized for selection. Moderate and high GCV values were observed for most traits except hypocotyl color, Number of nodes, Persistence of calyx, and Number of locules. Narrow differences between the phenotypic and genotypic coefficient of variation were observed in most of the traits. Among twenty-five traits, twelve traits displayed high heritability (heritability > 60%), five traits showed moderate heritability (31% < h^2 < 60%), and the rest included low heritability < 30%.

Figure 2. Variation of fruits in terms of color, size, pubescence, and length.

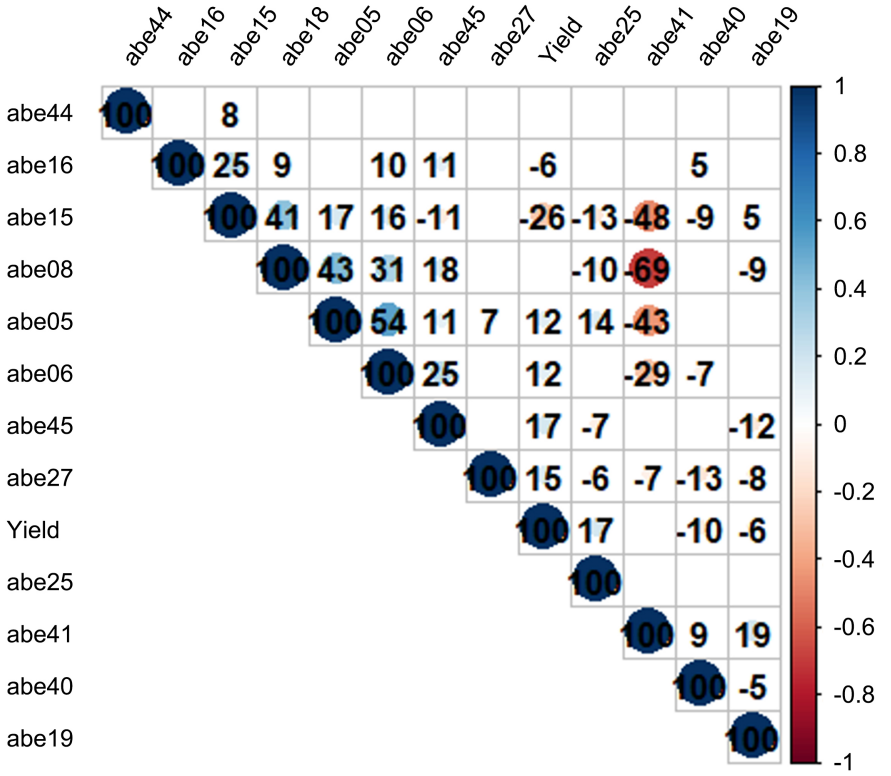
Table 1. Genetic and phenotypic coefficient of variation (GCV & PCV and broad sense of heritability (h^2) for traits.

Traits	Minimum	Meam	Maximum	F	h^2	PCV	GCV
Abe02	0.93	1.05	1.2	<0.001	0.16	0.12	0.09
Abe04	1	1.09	3	<0.001	0.89	0.41	0.31
Abe05	18.25	54.61	151	<0.001	0.7	0.42	0.39
Abe06	2	11.14	24	<0.001	0.45	0.36	0.34
Abe07	1	1.08	3	<0.001	0.87	0.44	0.3
Abe08	17.88	18.99	29.28	<0.001	0.17	0.18	0.13
Abe09	1.14	1.36	1.57	<0.001	0.15	0.2	0.14
Abe10	1	1.24	3	<0.001	0.88	0.47	0.42
Abe11	1	3.5	12	<0.001	0.57	0.42	0.48
Abe12	1	1.74	5	<0.001	0.72	0.33	0.28
Abe13	1	2.03	3	<0.001	0.42	o.42	0.35
Abe14	1	1.85	3	<0.001	0.77	0.33	0.25
Abe15	38	64.05	96	<0.001	0.85	0.32	0.25
Abe16	6.4	7.02	7.86	<0.001	0.03	0.11	0.1
Abe17	1	1.87	3	<0.001	0.91	0.44	0.38
Abe18	1	1.53	2	<0.001	0.72	0.49	0.41
Abe20	1	1.23	3	<0.001	0.95	0.6	0.48
Abe21	1	1	1	<0.001	0.01	0.04	0.001
Abe22	1	1.25	3	<0.001	0.95	0.42	0.35
Abe24	1	2.03	4	<0.001	0.63	0.33	0.27
Abe25	10.29	10.94	13.48	<0.001	0.19	0.54	0.45
Abe26	1	1.55	3	<0.001	0.37	0.6	0.53
Abe27	1	2.31	3	<0.001	0.02	0.2	0.1
Abe28	1	8	15	<0.001	0.9	0.7	0.75
Yield	0.013	2.34	16.72	<0.001	0.38	0.9	0.89

Abe02: Hypocotyl color; Abe03: Cotyledon color; Abe04: Plant growth habit; Abe05: Plant height (cm); Abe06: Number of internodes; Abe07: Branching habit; Abe08: Stem diameter measured at the base (mm); Abe09: Stem pubescence; Abe10: Stem color; Abe11: Leaf shape; Abe12: Leaf color; Abe13: Leaf pubescence; Abe14: Petiole color; Abe15: Flowering date; Abe16: Number of nodes to first flower; Abe17: Corolla color; Abe18: Red color on the base of corolla; Abe19: Number of calyx segments; Abe20: Shape of calyx segments; Abe21: Persistence of calyx segments; Abe22: Position of fruits at the primary stem; Abe23: Date to fruit maturity; Abe24: Fruit color; Abe25: Fruit length (cm); Abe26: Fruit pubescence; Abe27: Number of locules per fruit; Abe28: Fruit type.

3.2. Correlation Analysis

In the present study, the phenotypic correlation coefficient analysis is represented in Figure 3. Fruit length showed a highly significant and negative correlation with stem diameter (−0.69**). Fruit length showed a significant and negative correlation with days to 50% flowering (−0.48*). Fruit length showed a significant and negative correlation with plant height (−0.43*). A positive relationship was observed between plant height and pod yield (0.12). A negative and significant correlation was observed on the one hand between the number of plants attacked by insects and the flowering date and on the other hand between the plant height and the number of plants attacked by insects. The correlation was positive and highly significant for plant height and number of internodes (0.54**), and the correlation was negative and significant for the flowering time and pod yield (−0.26*).



Abe05: Plant height (cm); Abe06: Number of internodes; Abe08: Stem diameter measured at the base (mm); Abe15: Flowering date; Abe16: Number of nodes at first flower; Abe25: Fruit length; Abe27: Number of locules per fruit; Abe41: number of plants attacked by insects; Abe40: Plant sensibility to diseases; Abe19: Number of calyx segments; Abe44: Fruit diameter; Abe45: Plant germination rate.

Figure 3. Relationship between characteristics.

3.3. Principal Component Analysis

The principal component analysis (PCA) is presented in Table 2. This analysis was conducted to assess the extent of variation among the genotypes and to explore their relationships with the observed traits. The first six principal components

have Eigenvalues > 1, contributing to 77.66 percent variation. From the loading of the variables in PC I, it was found that the number of plants attacked by diseases, the stem diameter, the days to 50% flowering, the plant height, and the number of internodes were the dominant features that contributed to 20.67 percent of the total variation. In PCA II, the pod yield and the fruit length exerted a maximum influence, accounting for 12.59 percent of the total variation. The number of branching and locules per fruit were the dominant features in PCA III, accounting for 12.07 percent of the total variation. In PC IV, the number of internodes and germination rate were the dominant features contributing to 11.90 percent of the total variation. PC V and PC VI were influenced by the number of calyx segments and the fruit diameter, which accounted for 10.80 and 9.63 of the total variation, respectively. (Table 3)

Table 2. Eigenvalue and percent variation are explained by the first 5 principal components and correlations between PC scores and quantitative traits.

Traits	PC I	PC II	PC III	PC IV	PC V	PC VI	Eigen Value
Abe45	−0.41	−0.092	0.02	0.634	−0.097	−0.048	2.681
Abe05	0.233	0.338	0.002	0.077	0.079	0.153	1.625
Abe06	0.163	0.245	0.012	0.303	0.234	0.018	1.175
Abe08	0.318	−0.055	0.049	0.055	−0.093	0.03	1.152
Abe15	0.277	−0.225	0.007	−0.142	0.22	−0.153	1.126
Abe19	−0.05	0.075	−0.039	−0.061	0.721	−0.005	1.022
Abe40	−0.023	−0.022	0.603	0.098	0.152	0.23	0.973
Abe27	−0.008	−0.141	−0.584	0.036	−0.107	0.233	0.836
Abe41	−0.342	0.016	0.068	0.108	0.164	0.017	0.711
Abe16	0.031	−0.285	0.077	0.352	0.376	0.116	0.607
Abe44	−0.001	0.024	−0.004	0.048	−0.034	−0.878	0.451
Abe25	−0.021	0.531	0.107	−0.133	0.043	−0.054	0.38
Yield	−0.091	0.309	−0.297	0.225	−0.112	0.022	0.61
Eigen Value	2.68	1.62	1.17	1.15	1.12	1.02	
% of Total Variance Explained	20.67	12.59	12.07	11.90	10.80	9.63	
Cumulative Variation	20.67	33.26	45.33	57.23	68.03	77.66	

Abe05: Plant height (cm); Abe06: Number of internodes; Abe08: Stem diameter measured at the base (mm); Abe15: Flowering date; Abe16: Number of nodes to first flower; Abe19: Number of calyx segments; Abe25: Fruit length (cm); Abe27: Number of locules per fruit; Abe44: Fruit diameter; Abe41: number of plants attacked by insects; Abe40: Plant sensibility to diseases.

Table 3. Relationship between components and variables.

Variables	Components					
	1	2	3	4	5	6
Abe41	0.857					
Abe08	0.827					
Abe15	0.674					
Abe05	0.636					
Abe25		0.701				
Yield		0.512				
Abe40			0.72			
Abe27			0.711			
Abe45				0.835		
Abe06	0.512			0.516		
Abe19					0.817	
Abe16						
Abe44						0.918

Abe05: Plant height (cm); Abe06: Number of internodes; Abe08: Stem diameter measured at the base (mm); Abe15: Flowering date; Abe16: Number of nodes to first flower; Abe19: Number of calyx segments; Abe25: Fruit length (cm); Abe27: Number of locules per fruit; Abe44: Fruit diameter; Abe41: number of plants attacked by insects; Abe40: Plant sensibility to diseases.

3.4. Cluster Analysis

Hierarchical cluster analysis of genotypes based on yield and yield-contributing traits was performed to group the genotypes. A truncation level of 52% results in the structuring of diversity into four distinct groups. (Figure 4) Cluster I contained 150 genotypes, Cluster II had 45 genotypes, Cluster III included 29 genotypes, and Cluster IV consisted of 36 genotypes. Genotypes that are distantly placed exhibit greater diversity, while those nearby are morphologically similar. The maximum intra-cluster distance was observed between genotype 4 and genotype 131 in sub-cluster 1, genotype 164 and genotype 59 in sub-cluster 2, genotype 236 and genotype 110 in sub-cluster 3, and genotype 14 and genotype 220 in sub-cluster 4. The maximum inter-cluster distance was recorded between genotype 4 and genotype 220.

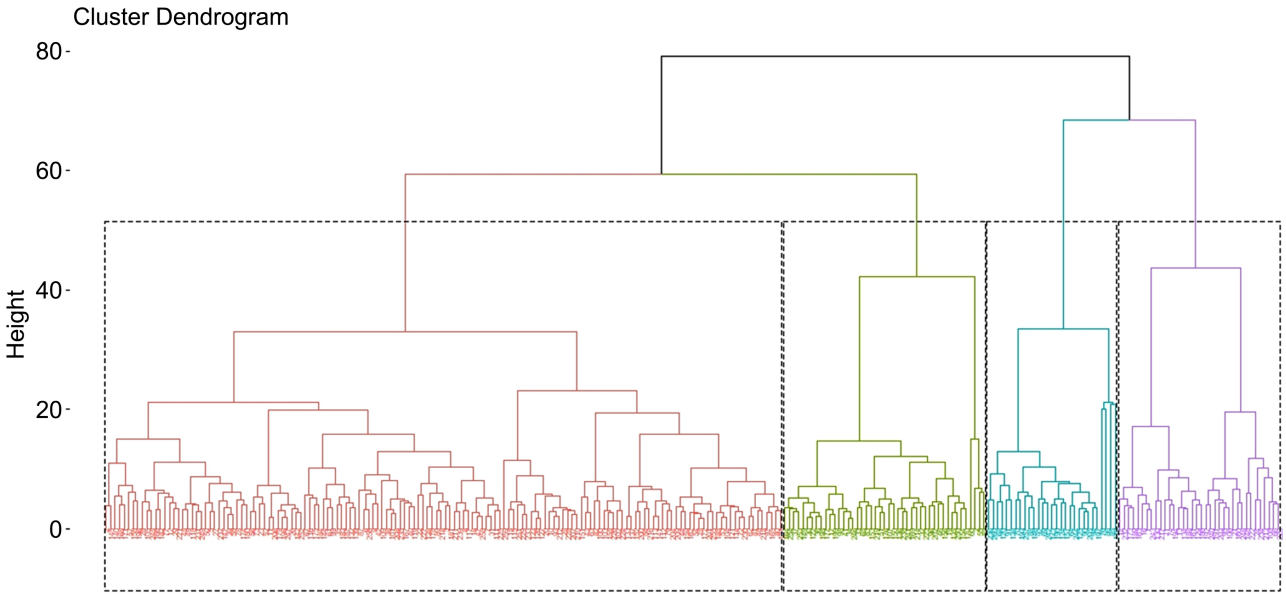


Figure 4. Dendrogram shows the genetic relationship among two thousand and sixty okra accessions.

3.5. Discriminant Factor Analysis

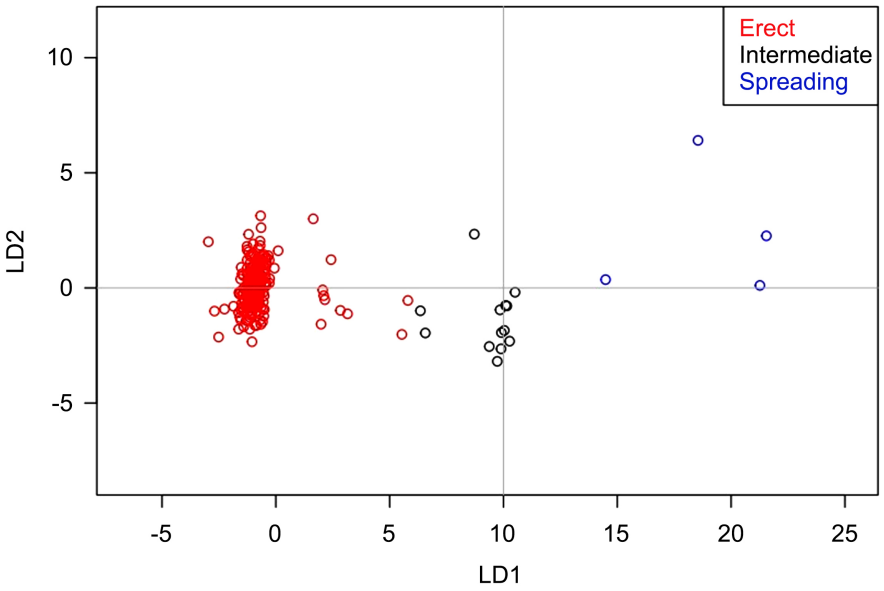


Figure 5. Representation of the accessions derived from the HCA in the discriminant factor analysis plan.

The characterization of the four groups using discriminant factor analysis with the qualitative variable abe4 is shown in **Figure 5**. This analysis clusters the accessions into three groups. Group I, with 243 accessions, exhibits an erect plant growth habit, representing over 93% of the total accessions. Group II includes 13 accessions with an intermediate growth habit, while Group III consists of only 4 accessions with a spreading growth habit. In terms of agronomic performance, the four accessions in Group III—234, 222, 191, and 148—exhibit superior traits: early

maturity, a spreading growth habit, a high number of primary branches, and high pod yield. Their stems are glabrous. Accessions in Groups I and II are tall, have a long growth cycle, long pod, high pod yield, and display erect or intermediate growth habits. However, the agronomic performance of Group I is slightly lower compared to that of Group II.

4. Discussion

4.1. Importance of Genetic Variability

The characterization of 260 okra accessions revealed significant genetic variability, which is critical for breeding and conservation efforts. The study likely measured traits such as plant height, stem diameter, fruit size, pubescence, color, plant growth habit, days to flowering, pod yield, and resistance to pests and diseases. This variability indicates the potential for selecting superior genotypes with desirable traits such as high yield, disease resistance, farmers' preferred traits, and adaptability to diverse environments. In genetic variability studies, the phenotypic coefficient of variation (PCV) was consistently higher than the genotypic coefficient of variation (GCV) for all traits, though the two showed a close relationship. This suggests minimal environmental influence, and phenotypic performance can be effectively used for selection. [14] Moderate to high GCV values were observed for most traits, supporting these findings. These results align with Ranga [15], who reported narrow differences between PCV and GCV for most traits, indicating their relative stability against environmental variation. Moderate to high heritability was exhibited by most of the characteristics, suggesting that the okra improvement through selection based on these traits would be beneficial [7]. Heritability is a good index of the transmission of traits from parents to their offspring [16].

The observed intra-accession variability in okra can be partly attributed to its reproductive mode, which is predominantly autogamous but can exhibit allogamy rates as high as 69% in *Abelmoschus esculentus* [17]. According to [18], allogamy facilitates cross-pollination, leading to natural genetic mixing and significant genetic diversity. The seeds used in this study were accessions collected from farmers, derived from mass selection within populations. Since genetic purity is not a priority for farmers, such practices further promote intra-accession variability. These factors collectively enhance the genetic diversity observed in the accessions.

The observed diversity also suggests that these accessions originate from a wide range of agroecological zones, allowing the identification of specific accessions suited to different climates or regions. Additionally, the genetic variation could be harnessed for hybridization programs to improve okra's overall productivity and resilience to climate change. This diversity is a valuable resource for future breeding programs aimed at enhancing the crop's performance and sustainability [19] [20].

4.2. Potential for Indirect Selection

The pod yield of a crop is a complicated character and is the outcome of the action

and interaction of numerous components. Hence, to develop the elite variety having higher yield or other characteristics, the association of pod yield or weight with other traits must be considered for the breeding program [21]. In the accumulation of an optimum combination of yield-contributing traits in a single genotype, it is essential to know the implication of the interrelationship of various traits [22]. The analysis of the relationship among the pod yield and related traits in the 260 accessions of okra revealed important insights into their genetic and phenotypic correlations. Key traits, such as plant height, pod yield, fruit length, number of plants attacked by insects, and days to flowering, showed significant associations. The negative and significant correlation between the number of plants attacked by diseases and the flowering date suggests that plants that flower earlier tend to experience fewer insect attacks. This could imply that early-flowering plants either escape the peak periods of insect pressure [23] or have developed mechanisms that make them less susceptible during their shorter growth cycle [24].

Similarly, the negative correlation between plant height and disease incidence indicates that shorter plants are more resistant to insects, or at least less frequently attacked, compared to taller plants. This could be due to factors like plant architecture, microclimate effects around the plant canopy, or genetic traits linked to both height and disease resistance. Furthermore, a significant negative correlation was found between flowering time and pod yield, suggesting that earlier-flowering plants tend to produce higher yields.

These correlations are valuable for breeding programs, as they highlight the potential for indirect selection. By targeting easily measurable traits such as plant height, breeders may influence other important traits like pod yield, flowering time, or fruit length. Understanding these relationships can streamline breeding strategies and support the development of superior okra varieties with improved yield, resilience, and adaptability.

4.3. Identification of Elite Groups

The hierarchical ascendance classification of the 260 okra accessions likely grouped the accessions into four main groups based on their phenotypic similarities, providing insight into the underlying population structure. This clustering revealed four distinct groups of accessions, each characterized by specific trait patterns such as plant growth habit, plant height, flowering time, and pod yield. Accessions within the same cluster shared similar traits, suggesting common ancestry or adaptation to similar environments.

This classification is particularly useful for identifying elite groups with desirable traits for breeding. One cluster exhibited early flowering, spreading growth habit, and high pod yield, making it ideal for breeding programs focused on short growing seasons. Another cluster demonstrated high pod yield and larger pod size, which could be prioritized for productivity improvement.

The hierarchical clustering also highlights genetic diversity within the accessions,

suggesting there are ample opportunities for cross-breeding between different clusters to combine favorable traits. The presence of distinct groups indicates the potential for both intraspecific improvement and broadening of the genetic base by introducing new genetic variability into breeding programs.

Ultimately, this classification serves as a guide for selecting parent lines, conserving genetic diversity, and tailoring breeding strategies to enhance desired traits while maintaining overall crop resilience.

5. Conclusion

This study highlights the significant morphological diversity present among the 260 okra accessions in Mali, with substantial genetic variability across key traits such as yield, pod length, and plant height. The moderate to high heritability estimates suggest that these traits are predominantly influenced by genetic factors, making them promising candidates for breeding programs. The identification of four distinct genetic clusters through PCA further supports the potential for developing improved okra varieties. These findings offer a valuable foundation for future breeding efforts aimed at increasing okra yield and resilience, contributing to sustainable agriculture in West Africa.

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Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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