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PCA-driven Insights into Hybrid-Parent Performance in Okra [*Abelmoschus esculentus* (L.) Moench.]

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Authors' contributions

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

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ABSTRACT

Aims: The study aimed to evaluate genetic diversity and identify trait relationships among okra (*Abelmoschus esculentus* L. Moench) F1 hybrids and their parental lines using principal component analysis (PCA). It sought to uncover key traits contributing to yield variability and to support breeding efforts by identifying superior hybrids and combining parents suited to Sudanese agro-ecologies.

Study Design: The study used a line × tester mating design involving 10 parental lines and their 21 resulting F1 hybrids. Multivariate statistical tools, including PCA and hierarchical clustering, were

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employed to assess trait variability, relationships, and genotype grouping based on multiple morphological and yield-related parameters.

Place of Study: The research was conducted at the demonstration farm of the Faculty of Agriculture, University of Al Zaeim Al Azhari, located in Khartoum North, Sudan.

Methodology: Eleven agronomic traits were recorded, including plant height, number of fruits per plant, yield per plant, and others. Data were analyzed using analysis of variance and principal component analysis. The first four principal components were extracted, and their eigenvalues, trait loadings, and correlations were studied. Standardized Euclidean Distance and Ward's method were used for hierarchical clustering to group genotypes based on similarity.

Results & Discussion: Substantial phenotypic variation was observed, with yield per plant (CV = 21.2%), fruit fresh weight (18.9%), and number of lateral branches (16.3%) showing the highest variability. PCA revealed four principal components explaining 71.85% of the total variance. PC1 (27.48%) was highly associated with yield traits, while PC2 (22.14%) captured architectural and earliness traits. PC3 and PC4 explained structural variation. Cluster analysis grouped genotypes into four major clusters. Sinnar-derived hybrids formed a compact, high-yielding group, indicating superior combining ability. Clemson crosses exhibited wide variability and heterotic potential, while Hjerat lines showed genetic divergence useful for broadening the gene pool.

Conclusion: Principal Component Analysis (PCA) effectively revealed genetic diversity and key trait associations among okra hybrids and their parental lines. Sinnar was identified as a superior parent for yield improvement, while other testers contributed distinct and complementary traits. These findings support the use of PCA for trait prioritization and the selection of promising hybrid-parent combinations, ultimately facilitating the development of improved okra cultivars adaptable to Sudanese and similar agro-ecological environments.

Keywords: Abelmoschus esculentus; principal component analysis; hybrid performance; yield traits; parental line selection; okra breeding.

1. INTRODUCTION

Okra [*Abelmoschus esculentus* (L.) Moench], a warm-season vegetable crop of tropical and subtropical origin, is widely grown across Asia, Africa, and the Middle East for its edible immature pods, nutritional value, and medicinal uses. Rich in vitamins A, C, and K, as well as calcium, magnesium, and mucilage, okra contributes significantly to food and nutritional security, especially in low-income communities (Dhankhar et al., 2022). Globally, okra is cultivated on over two million hectares, with India, Nigeria, and Sudan among the top producers (FAOSTAT, 2022). In Sudan, okra is one of the most popular traditional vegetables, cultivated under both irrigated and rain fed conditions and consumed in fresh and dried forms. Despite its importance, yield levels remain low due to limited genetic improvement, poor seed systems, and a lack of systematic breeding strategies. Most farmers grow local landraces that are genetically diverse but largely uncharacterized, with little data available on hybrid performance or parent-hybrid relationships.

To address these challenges, hybridization programs have been initiated to develop improved cultivars with better yield, quality, and adaptability. However, the selection of promising hybrids and parents requires a deeper understanding of the genetic architecture of yield and morphological traits. Most of these traits are quantitatively inherited, complex, and highly influenced by environmental factors, making direct phenotypic selection difficult. In this context, Principal Component Analysis (PCA) offers a powerful multivariate statistical approach to unravel the underlying structure of trait variability, reduce data dimensionality, and reveal hidden patterns of trait association. PCA transforms correlated traits into a set of orthogonal principal components that capture the maximum variance, thereby facilitating genotype classification and trait prioritization. Its application in crop breeding has proven effective in identifying trait combinations that explain most of the variability, simplifying the selection process and supporting genetic improvement.

In okra breeding, PCA can also be used to explore the clustering of hybrids about one or both of their parents, providing insights into genetic relationships, heterosis, and transgressive segregation (Ranga et al., 2022; Haq et al., 2023). However, despite its utility, the application of PCA in okra breeding remains limited in Sudan, especially in studies comparing hybrids with their parental lines. This gap restricts breeders' ability to exploit the full potential of multivariate analysis for selection and cultivar development. Therefore, this study was conducted to analyze the morphological and yield-related variation in okra hybrids and their parents using Principal Component Analysis to provide insight into genetic diversity, determine the relative contribution of each trait to total variation, examine the clustering patterns of hybrids near one or both parents and identify superior hybrids based on multivariate trait performance. The findings are expected to inform selection strategies and support ongoing efforts to enhance okra breeding efficiency and genetic gain in Sudan and similar agro-ecological regions.

2. MATERIALS AND METHODS

The present investigation was conducted at the demonstration farm of the Faculty of Agriculture at the University of Al Zaeim Al Azhari, located in Khartoum North. A total of ten genetically diverse parental lines of okra were crossed using the line × tester method developed by Kempthorne in 1957. Seven lines, namely HSD 1835, HSD1834, HSD1839, HSD 2543, HSD 2482, HSD 1840, and HSD 2550, were used as female lines, while Sinnar, Hjerat, and Clemson Spineless served as male lines/testers.

The crossing was performed in standard crossing blocks, with emasculation and pollination conducted before flower opening. Standard procedures for emasculation and pollination were followed, utilizing a cutter, forceps, tags, and paper bags. In total, twenty-one F1 hybrids, along with the ten parental lines, were arranged in a Complete Randomized Block Design (CRBD) with three replications. Each plot consisted of three ridges, extending three meters. The spacing adopted was 75 cm between ridges and 30 cm between plants.

Observations on the number of days to flowering were recorded on a plot basis, noting the time from the sowing date to the onset of flowering. Additionally, plant height (cm), fruit length (cm), number of nodes per plant, number of lateral branches, number of fruits per plant, fruit dry weight (g), fruit fresh weight (g), number of seeds per fruit, and yield per plant (g) were recorded as averages from ten randomly selected plants in each plot across the three replicates. The weight of the hundred-seed count (g) was measured using a sensitive balance.

Data were analyzed using Analysis of Variance (ANOVA) as described by Gomez and Gomez (1984) through the online software package Grapes 1.1.0, developed by Gopinath et al. (2021) at Kerala Agricultural University. Additionally, Principal Component Analysis (PCA) was performed to assess trait divergence, variability, and genotype clustering, as outlined by Pearson (1901) and Hotelling (1933). Trait-based clustering among genotypes was examined by Ward (1963), a hierarchical clustering method. The differences in scales or units across variables (traits) were adjusted using the Standardized Euclidean Distance formula, suggested by Gower (1966) and Kaufman & Rousseeuw (1990).

3. RESULTS AND DISCUSSION

3.1 Trait Variability

Table 1 presents the descriptive statistics for 11 morphological and yield-related traits among okra genotypes. The results indicate considerable phenotypic variation, which is essential for effective selection in breeding programs. For instance, plant height ranged from 23.2 cm to 45.6 cm (mean = 31.15 cm), and yield per plant ranged from 12.1 g to 27.0 g (mean = 20.29 g). The coefficient of variation (CV %) was notably high for yield per plant (21.2%), fruit fresh weight (18.9%), and number of lateral branches (16.3%), suggesting these traits are more influenced by genetic diversity and thus valuable for selection. In contrast, days to flowering exhibited a low CV (2.8%), indicating this trait was relatively stable across genotypes.

3.2 Eigenvalue Structure and Total Variation

Table 2 summarizes the eigenvalues and variance explained by each principal component. The first four principal components (PC1 to PC4) had eigenvalues >1 and jointly accounted for 71.85% of the total variation. The first principle component PC1 (27.48%) was the most influential, followed by PC2 (22.14%), PC3 (11.83%), and PC4 (10.39%). This pattern indicates that the first four components effectively summarize the multidimensional data and can be used to classify genotypes and interpret trait interrelationships. The drop in eigenvalues after PC4 supports retaining these components for further biological interpretation, consistent with the report by Idehen & Ola, (2021) on the Kaiser criterion (Kaiser, 1960).

Table 1. Descriptive statistics of morphological and yield traits in okra hybrids and their parents

Variance	**Number of days to flowering**	**Number of lateral branches**	**Plant height (cm)**	**Number of nodes per plant**	**Fruit length (cm)**	**Number of fruits per plant**	**Fruit dry weight(g)**	**Fruit fresh weight(g)**	**Number of seeds per fruit**	**Weight of hundred-seeds(g)**	**Yield per plant (g)**
Minimum	41.700	4.300	23.200	6.700	3.600	3.000	0.400	3.900	35.300	3.900	12.100
Maximum	48.000	8.300	45.600	11.000	5.800	6.000	0.600	5.500	64.700	6.300	27.000
Mean	45.603	5.958	31.145	8.677	4.713	4.539	0.497	4.848	49.339	5.116	20.294
Standard error mean	0.230	0.174	0.947	0.229	0.106	0.154	0.011	0.061	1.273	0.104	0.774
Standard deviation	1.278	0.971	5.270	1.274	0.593	0.859	0.060	0.342	7.087	0.580	4.308
Coefficient of variation %	2.8	16.3	16.9	14.7	12.6	18.9	12.2	7.1	14.4	11.3	21.2

Across various okra studies, PC1 alone explained a significant portion of the total variance. The first principle component (PC1) values reported ranged from (25.38%- 42.50%) was recorded in several works (Das et al., 2022; Mohammed et al., 2022; Kenaw et al., 2023; Abhilash et al., 2023). This confirms and is in lieu of the result obtained in this study.

Several researchers have reported that the first four principal components (PCs) effectively summarize multidimensional data, classify genotypes, and interpret trait interrelationships in okra (Dos Santos et al., 2013; Das et al., 2022; Idehen & Ola, 2021; Murtadha et al., 2023; Abhilash et al., 2023; Kenaw et al., 2023; Syfullah et al., 2025). The first four PCs frequently account for over 60% and sometimes up to 85% of the total variation (Murtadha et al., 2023; Mohammed et al., 2022; Kenaw et al., 2023; Nwangburuka et al., 2011). In Nigeria, Olayiwola et al. (2021) found the first four PCs accounted for 80% of the total variation, with PC1 having the highest discriminatory power. Another report from India by Ranga, et al. (2021) recorded as high as 84.28% cumulative variance across the first four PCs.

3.3 Contribution of Traits to Principal Components

Table 3 details the percentage contribution of each trait to the first eight PCs. Yield per plant followed by number of fruits per plant (22.31%), had the highest contribution to PC1 (25.75%), confirming its role as a primary determinant of genetic divergence among the studied genotypes. The specific trait identified as the highest contributor to PC1 varies from one study to another depending on the specific germplasm, traits measured, and environmental conditions of the study. However, yield-related traits such as "yield per plant," "pod yield," or "fruit yield per hectare" are consistently highlighted as major, and often the highest, contributors to PC1 in many investigations (Badiger et al., 2018; Ranga, et al., 2021; Idehen & Ola, 2021; Mohammed et al., 2022; Kenaw et al., 2023; Abhilash et al., 2023). Other major contributors to PC1 included the number of seeds per fruit (19.07%), and fruit dry weight (14.92%). This indicates that PC1 largely represents yield performance and associated reproductive traits. Consensus from the sources indicates that yield performance and associated reproductive traits (such as number of fruits/pods per plant, fruit/pod yield, fruit/pod length, fruit/pod weight, and seed weight) are generally major, and often the most influential, contributors to the first principal component in genetic diversity analyses of okra. This makes PC1 a crucial indicator for identifying superior genotypes for breeding programs aimed at improving yield (Ranga et al., 2022; Yadav et al., 2024). PC2 was dominated by days to flowering (25.01%) and the number of lateral branches (23.87%), suggesting that it represents a dimension of plant architecture and earliness. Several studies indicate that PC2 is significantly influenced by, or largely loaded with a combination of plant architectural traits (e.g., plant height, branching) and earliness traits (e.g., days to flowering, days to maturity), often alongside important reproductive or yield components (Idehen & Ola, 2021; Ranga, et al.,2021; Mohammed et al., 2022).The third principle component (PC3) captured variation in plant height (27.17%) and fruit fresh weight (37.14%), while PC4 was mainly explained by fruit length (34.98%) and number of nodes per plant (25.87%).

Table 2. Eigenvalues and variance explained by principal components for morphological and yield traits in okra

Principle components	Eigen value	percentage of variance	Cumulative variance percentage
PC1	3.023	27.48	27.48
PC2	2.436	22.142	49.622
PC3	1.301	11.83	61.452
PC4	1.143	10.394	71.846
PC5	0.728	6.615	78.461
PC6	0.689	6.266	84.727
PC7	0.607	5.52	90.247
PC8	0.379	3.446	93.694
PC9	0.361	3.284	96.978
PC10	0.24	2.186	99.164
PC11	0.092	0.836	100

Table 3. Percentage contributions of variables on principal components (PC1–PC8) in okra

Variables	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Number of days to flowering	0.923	25.009	1.697	2.647	0.048	16.644	2.155	0.011
Number of lateral branches	0.496	23.875	5.416	7.331	5.275	4.296	1.815	18.74
Plant height (cm)	0.044	12.308	27.173	15.277	0.342	6.156	4.247	7.805
Number of nodes per plant	0.758	17.802	0.352	25.869	18.454	2.614	0.121	10.892
Fruit length (cm)	2.142	9.819	1.701	34.975	0.095	26.181	7.075	4.083
Number of fruits per plant	22.314	0.564	0.348	4.334	6.8	0.163	18.071	16.002
Fruit dry weight(g)	14.924	2.285	7.276	0	15.317	12.083	17.544	18.246
Fruit fresh weight(g)	3.652	1.154	37.141	5.742	33.185	3.164	3.612	0.517
Number of seeds per fruit	19.072	4.1	0.052	2.58	0.147	21.28	1.277	9.424
Weight of hundred-seeds(g)	9.927	1.628	18.137	1.17	18.558	2.838	33.566	13.572
Yield per plant (g)	25.749	1.455	0.708	0.076	1.779	4.579	10.517	0.707

3.4 Trait–Principal Component Correlations

Table 4 provides the correlation coefficients between each trait and the first eight PCs. High correlations between a trait and a PC indicate the trait's influence on that component. Yield per plant showed a strong positive correlation with PC1 (r = 0.882), followed by number of fruits per plant (r = 0.821) and number of seeds per fruit (r = 0.759), reinforcing their contribution to PC1 variation and their relevance for yield improvement.

Days to flowering were strongly negatively correlated with PC2 (r = -0.780), reflecting variation in earliness among genotypes. This aligns with the findings of Abhilash et al. (2023), which demonstrate strong positive correlations between the number of fruits per plant and fruit yield per plant with Principal Component 1 (PC1). Additionally, recorded strong positive correlations for earliness with Principal Component 2 (PC2), which includes days to first flowering, days to 50% flowering, and days to the first fruit harvest.

Plant height and fruit fresh weight had substantial contributions to PC3, with respective correlations of −0.595 and 0.695 respectively. Fruit length was negatively correlated with PC4 (r = -0.632), and nodes per plant had a positive association (r = 0.544), defining structural variation in this axis. These patterns affirm that PCA not only reduces data complexity but also identifies trait combinations that most influence genotype classification, which is critical in early-generation selection (Singh & Pandey, 2024).

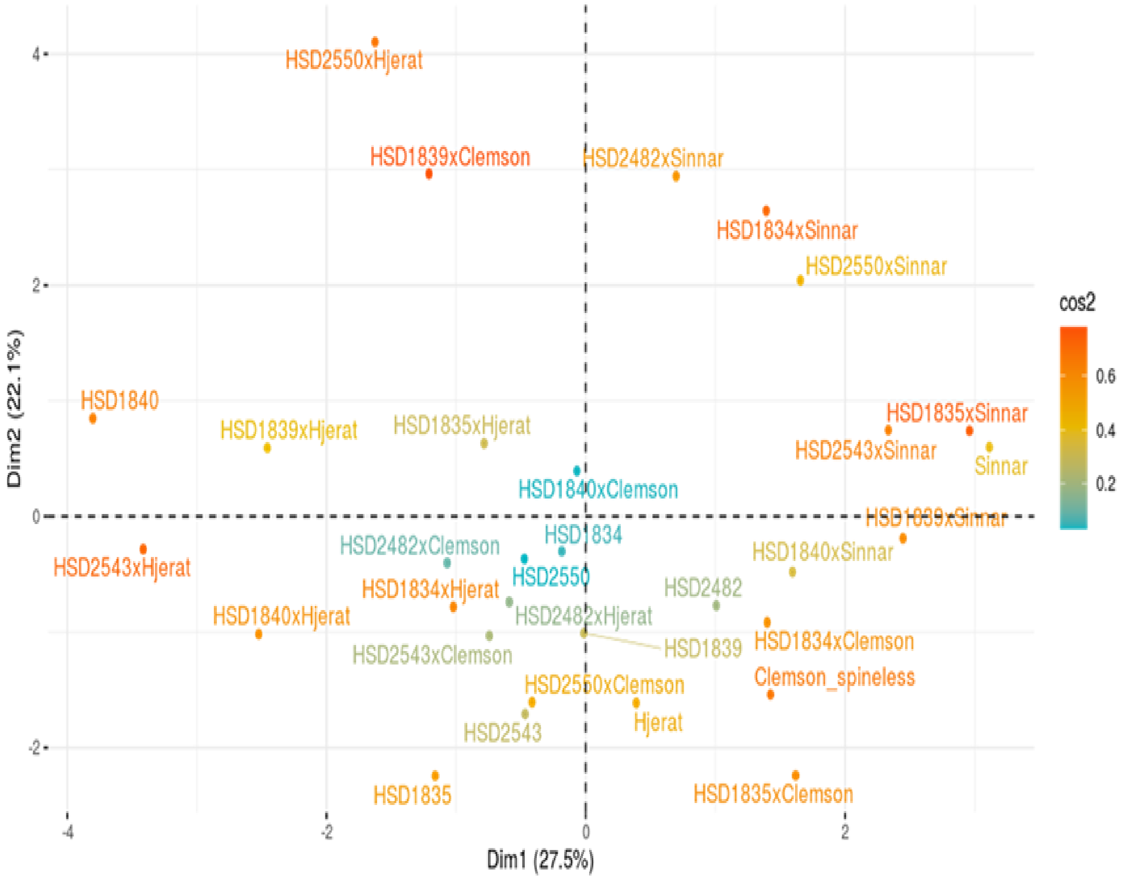

Fig. 1. Principal component analysis bi-plot (PC1- PC2) of Okra hybrids and parental lines

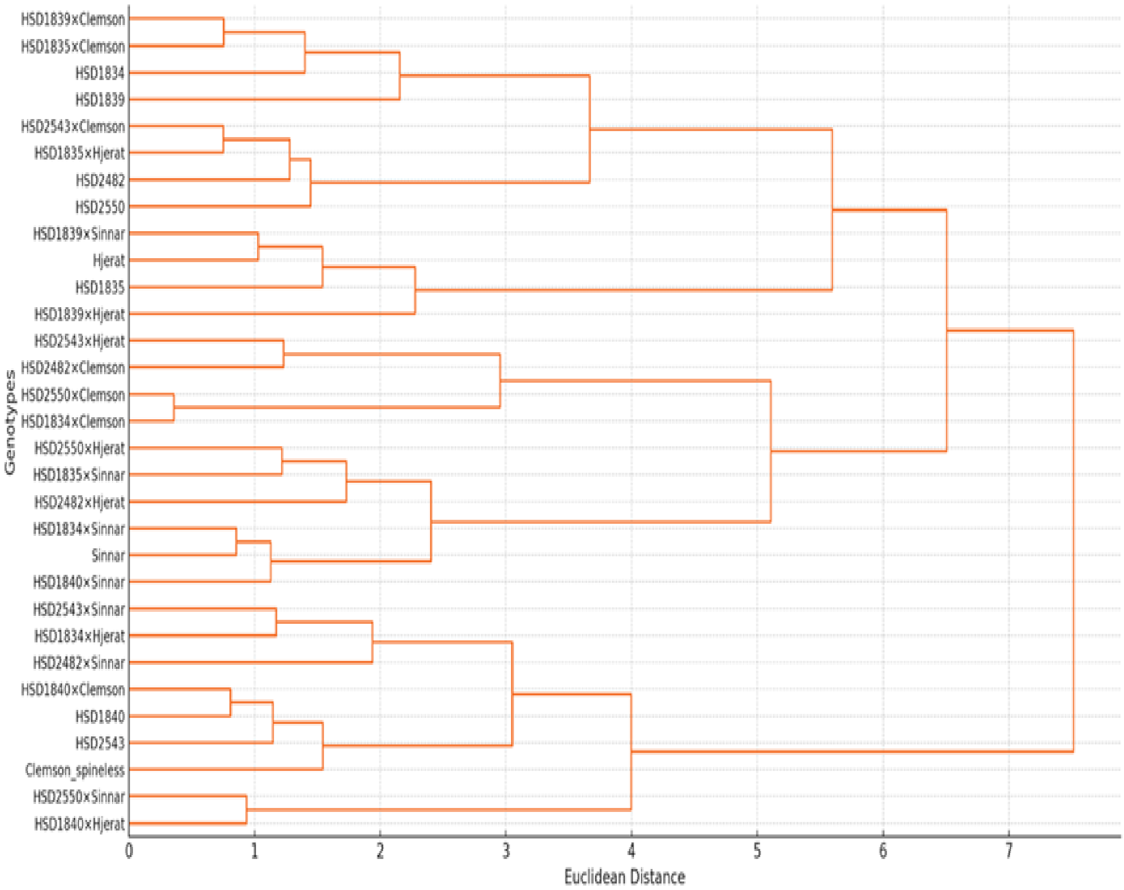

Fig. 2. Cluster dendrogram of okra genotypes using PCA scores

Table 4. Trait–Principal component correlation matrix (PC1–PC8) for okra genotypes

Variables	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Number of days to flowering	0.167	-0.78	-0.149	0.174	0.019	0.339	-0.114	0.006
Number of lateral branches	-0.122	0.763	0.265	0.289	-0.196	-0.172	0.105	0.267
Plant height (cm)	0.036	0.548	-0.595	-0.418	0.05	-0.206	-0.161	-0.172
Number of nodes per plant	-0.151	0.658	0.068	0.544	0.366	0.134	0.027	-0.203
Fruit length (cm)	0.254	0.489	0.149	-0.632	-0.026	0.425	0.207	0.124
Number of fruits per plant	0.821	0.117	-0.067	0.223	-0.222	0.034	-0.331	0.246
Fruit dry weight(g)	0.672	-0.236	0.308	-0.001	-0.334	-0.289	0.326	-0.263
Fruit fresh weight(g)	0.332	-0.168	0.695	-0.256	0.491	-0.148	-0.148	0.044
Number of seeds per fruit	0.759	0.316	0.026	0.172	-0.033	0.383	0.088	-0.189
Weight of hundred-seeds(g)	0.548	-0.199	-0.486	0.116	0.367	-0.14	0.451	0.227
Yield per plant (g)	0.882	0.188	-0.096	-0.029	0.114	-0.178	-0.253	-0.052

3.5 Cluster and Bi-plot Analysis of Okra Hybrids and their Parents

Fig. 1 shows the Bi-Plot (PC1-PC2) for Okra Hybrids and Parental Lines, while Fig. 2 displays the cluster dendrogram of Okra Genotypes using PCA scores. Both figures illustrate the clustering pattern of okra hybrids and their parental lines identifying four clustering groups. Group A includes the High-Yielding Sinnar Hybrids, HSD2482×Sinnar, HSD1834×Sinnar, HSD1835×Sinnar HSD2550×Sinnar, and Sinnar. These hybrids form a tight cluster, indicating Sinnar's strong combining ability for yield traits.

Group B comprises the Clemson-Derived Diverse Hybrids, including HSD1839×Clemson, HSD1835×Clemson, and HSD1834×Clemson. These genotypes are widely separated, reflecting higher variability and heterotic expression. Group C include the divergent Hjerat Lines and Late Maturing Genotypes, which Include HSD1839×Hjerat, HSD2543×Hjerat, HSD1835, and HSD1840. These are genetically divergent, showing unique trait profiles possibly suited for genetic base broadening. Group D represent the core cluster of stable lines that Includes HSD1839, HSD2482, HSD2550, and Hjerat. These genotypes display moderate trait values and genetic stability. The dendrogram confirms PCA findings and highlights Sinnar-derived hybrids for yield improvement. Hjerat and Clemson contribute to broader trait diversity, suggesting their value in heterotic group development. The core genotypes may be used as standard checks or donor parents. The results align with previous work on these hybrids reporting significant heterosis for yield and yield components for these hybrid combinations HSD2482×Sinnar, HSD1834×Sinnar, HSD1835×Sinnar HSD2550×Sinnar, (Abdalla & ElKamil, 2025a). The role of sinner as a parent has also been highlighted and recommended as a parent in several studies (Abdalla & AlKamal, 2025b).

4. CONCLUSION

The Principal Component Analysis (PCA) of morphological and yield traits in okra hybrids and their parental lines revealed significant genetic diversity and trait relationships critical for breeding programs. The first four principal components (PC1–PC4) cumulatively explained 71.85% of the total variation, with PC1 (27.48%) primarily associated with yield-related traits such as yield per plant, number of fruits per plant, and seeds per fruit, highlighting their importance for selection. PC2 (22.14%) was linked to earliness (days to flowering) and plant architecture (lateral branches), while PC3 and PC4 captured structural traits like plant height, fruit length, and node number. Hierarchical clustering and biplot analysis grouped the genotypes into four distinct clusters. The high-yielding Sinnar hybrids (HSD2482×Sinnar, HSD1834×Sinnar, HSD1835×Sinnar HSD2550×Sinnar). These findings confirm Sinnar as a superior parent for yield enhancement. This research supports the development of improved cultivars for enhanced productivity and food security. Future work should integrate genomic data to validate clustering patterns and expand trait evaluations across diverse environments to further refine breeding strategies.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

The author(s) hereby declare that generative AI technologies and digital tools, including Grammarly Version 1.2.169.1689, released June 19, 2025 and Zotero 7.0.19, were used solely for reference management, proofreading, and language editing. All content and ideas presented in the manuscript were entirely generated by the authors, without AI assistance in writing or data interpretation.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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