OPEN ACCESS
International Journal of Agriculture and Sustainable Development
IJASD

Inter-Relational Grouping and Genetic Diversity Estimates of Adaptable Okara *(Abelmoschus esculentus L.)*

Zunaira Akbar[1], Asma Mehboob[1], Amna Saghir Aasi[2], Umaira Akbar[3], Umar Farooq[6], Arbaz Hassan[4*], Maria Anjum[5], Zaryab Hassan[6], Nusrat Parveen[7]
[1]Plant Breeding and Genetics, University of Agriculture, Faisalabad
[2]Centre of Agricultural Biochemistry and Biotechnology, University of Agriculture, Faisalabad
[3]National Institute of Food Science and Technology, University of Agriculture, Faisalabad
[4]Maize Research Station, Ayub Agricultural Research Institute, Faisalabad
[5]Vegetable Research Institute, Ayub Agricultural Research Institute, Faisalabad
[6]Maize and Millets Research Institute, Yusaf Wala, Sahiwal
[7]Vegetable Research Institute, Ayub Agricultural Research Institute, Faisalabad
*** Correspondence:** Hassanarbaz40@gmail.com

Citation | Akbar. Z, Mehboob. A, Aasi. A. S, Akbar. U, Farooq. U, Hassan. A, Anjum. M, Hassan. Z, Parveen. N, "Inter-Relational Grouping and Genetic Diversity Estimates of Adaptable Okara (Abelmoschus esculentus L.)", IJASD, Vol. 08 Issue. 02 pp 211-226, May 2026

Received | March 05, 2026 **Revised |** March 28, 2026 **Accepted |** March 31, 2026 **Published |** April 08, 2026.

The vegetable crop known as okra (Abelmoschus esculentus L.) is a prominent one that is grown all over the world. Frequently called the "ideal villager's vegetable," it provides a wealth of vitamins, minerals, and elements that support general human health. Okra, a member of the Malvaceae family, is produced and consumed in a variety of ways, and because of its declining yields, breeders must work to create new varieties that can significantly increase and stabilize production. A study was carried out at the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, to evaluate the genetic diversity of okra. In the experiment, 12 distinct okra genotypes were assessed to determine their yield patterns and associated attributes during the 2023 kharif season using a randomized complete block design (RCBD) with three replications. Data were collected for plant height, number of nodes, number of fruits, fruit length, fruit diameter, petiole length, internodal distance, stem diameter, fresh weight, dry weight, and number of seeds. Highly significant differences ($P \leq 0.01$) were observed among genotypes for all studied traits, indicating the presence of substantial genetic variability. Phenotypic variance (PV) was only slightly higher than genotypic variance (GV) for all traits, while environmental variance (EV) remained very low, demonstrating strong genetic control. For example, plant height showed GV and PV values of 227.86 and 234.21, respectively, while number of seeds exhibited GV and PV values of 37.09 and 38.12, respectively. Fruit diameter displayed a significantly positive correlation with stem diameter (r = 0.5492**) and plant height (r = 0.5283**), whereas number of nodes showed a strong positive association with number of fruits (r = 0.7796**) and zero nodal distance (r = 0.7032**). Fresh weight was highly associated with dry weight (r = 0.9781**) and stem diameter (r = 0.8274**). Principal component analysis revealed that the first three principal components accounted for 84.05% of the total variability, with PC1 alone contributing 40.65% of the variation. Cluster analysis grouped the 12 genotypes into four distinct clusters at a 66.67% similarity index, indicating broad genetic diversity among the germplasm. Among the tested genotypes, PBG-OKRA-69 outperformed others for plant height, node count, fruit number, and fruit diameter, while PBG-OKRA-28 showed superior performance for stem diameter, fresh weight, and dry weight. These genotypes may be effectively utilized in future breeding programs aimed at improving yield and adaptability in Okra.

Keywords: Okra, Diversity in Okra, Clustering, PCA, ANOVA

Introduction:

Okra (Abelmoschus esculentus L.) is one of the most widely cultivated vegetable crops due to its wide adaptability, nutritional richness, medicinal value, and year-round market demand. It belongs to the family Malvaceae and is considered an important vegetable crop in tropical and subtropical regions. Okra pods are rich in vitamins, minerals, dietary fiber, antioxidants, and bioactive compounds that contribute significantly to human nutrition and health. Recent studies highlighted the pharmacological importance of okra due to its antioxidant, anti-diabetic, antimicrobial, and anti-inflammatory properties, making it an important functional food crop [1][2]. Okra seeds also contain high-quality proteins and essential amino acids comparable to soybean, which further enhances its nutritional and industrial value [3].

Globally, the demand for nutritionally rich vegetables is increasing due to rapid population growth and changing climatic conditions. Therefore, improving yield stability and adaptability in okra has become an important objective of modern breeding programs. Recent advances in okra research emphasized the importance of exploiting genetic variability for the development of climate-resilient and high-yielding cultivars [4]. Genetic diversity provides the foundation for crop improvement because it enables breeders to select desirable genotypes with superior agronomic performance and adaptability under varying environmental conditions [5].

Fruit yield in okra is a complex quantitative trait influenced by several morphological and physiological characteristics including plant height, stem diameter, number of fruits, fruit length, and biomass accumulation. Studies conducted during the last few years demonstrated that these traits are strongly associated with yield performance and can be effectively utilized for indirect selection in breeding programs [6][7]. Correlation and variance component analyses are particularly useful for understanding the relationship among yield-associated traits and determining the extent of genetic and environmental influences on trait expression [8].

Recent developments in multivariate statistical analyses such as principal component analysis (PCA) and cluster analysis have improved the efficiency of germplasm characterization and parental selection in okra breeding. These approaches help identify genetically diverse genotypes and determine the contribution of individual traits toward total variability [9][10]. PCA and clustering methods are now widely used to classify okra germplasm into distinct genetic groups for efficient hybridization and selection strategies [3][4].

Despite the economic and nutritional importance of okra, limited information is available regarding the comprehensive evaluation of locally adaptable germplasm under Faisalabad agro-climatic conditions. Moreover, environmental influence often masks true genetic variability, making it difficult to distinguish superior genotypes based solely on phenotypic performance. Therefore, integrated evaluation using variance components, correlation studies, PCA, and cluster analysis is necessary to identify genetically stable and high-performing okra genotypes suitable for future breeding programs.

Although molecular markers provide high-resolution estimates of genetic diversity, morpho-agronomic characterization remains a practical and effective approach for evaluating phenotypic variability, adaptive performance, and economically important traits under field conditions, particularly in preliminary breeding and germplasm evaluation studies.

Novelty of the Study:

Although previous studies have reported variability and trait associations in okra, limited research has integrated variance component analysis, correlation analysis, principal component analysis, and cluster analysis simultaneously for locally adaptable Pakistani okra germplasm. The present study quantified genotypic, phenotypic, and environmental variances for important yield-related traits and identified genetically stable genotypes with superior agronomic performance. Furthermore, the integration of PCA and dendrogram-based clustering enabled precise grouping of genetically diverse germplasm and identification of promising genotypes such as PBG-OKRA-69 and PBG-OKRA-28 for future hybridization and selection programs under Faisalabad conditions.

Objectives:

To evaluate genetic variability among okra genotypes for morphological and yield-related traits.

To estimate genotypic, phenotypic, and environmental variance components for important quantitative traits.

To determine the association among yield and related traits through correlation analysis.

To assess genetic diversity and genotype grouping using principal component and cluster analyses.

To identify superior and adaptable okra genotypes for future breeding programs.

Materials and Methods:

The research was performed at the vegetable research area of the Department of Plant Breeding and Genetics, University of Agriculture Faisalabad. The research material consisted of 13 genotypes collected from the department (Table 1). The experiment was managed during the normal okra sowing season in 2023. The research was sown in the randomized complete block design (RCBD) with 3 replications for each variety. The recommended plant-to-plant distance (30 cm) and row-to-row distance (90 cm) were maintained. At the time of sowing, two seeds per hole were sown with the help of a dibbler and later thinned to one seedling per hole after emergence. The experimental population was kept under normal condition from sowing to maturity. Moreover, Standard agronomic practices were followed throughout the experiment. (Figure 1). At maturity stage, three well-guarded plants from each line were selected to record the data of the characteristics mentioned below:

Table 1. List of Okra genotypes

Serial No.	Genotype	Serial No.	Genotype
1	NARALI	7	PBG-OKRA-72
2	CLENSON SPINELESS	8	PBG-OKRA-69
3	PBG-OKRA-2011	9	PBG-OKRA-30
4	PBG-OKRA-48	10	PBG-OKRA-18-1
5	PBG-OKRA-20-13	11	PBG-OKRA-51
6	PBG Okra 21	12	PBG-OKRA-28
13	SUPER GREEN		

Experimental Conditions and Crop Management:

The experiment was conducted during the kharif season of 2023 at the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. The experimental field had well-prepared loamy soil with good drainage and uniform fertility. Before sowing, the field was ploughed, levelled, and divided into experimental blocks according to RCBD layout. The crop was grown under normal field conditions of Faisalabad, characterized by warm temperature and seasonal rainfall during the okra growing period. Irrigation was applied immediately after sowing and subsequently at regular intervals according to crop requirement and prevailing weather conditions to avoid moisture stress. Recommended agronomic practices were followed throughout the crop season. Fertilizer was applied according to standard okra production recommendations, including basal application before sowing and nitrogen supplementation during vegetative growth. Weeds were controlled manually when required, while pest and disease management practices were applied according to field observation to maintain a healthy crop stand. The experiment continued from sowing until final fruit harvesting, and data were recorded at maturity from three randomly selected guarded plants from each genotype in each replication. These details were included to improve reproducibility and clarify the environmental and management conditions under which the genotypes were evaluated (Figure. 1).

Data Recording:

At maturity, 3 plants from each replication were selected for estimation of the data for the following morphological traits.

Plant Height (cm):

Plant height was measured with a meter rod as measuring tape size of 400 cm. plant height was measured till the tip of the stalk from soil bottom stem. Three representative plants selected for data recording and after data recording average data was used for next procedure. The average height per plant was estimated for the statistical analysis.

Number of Nodes (cm):

Total number of nodes on the main stem of okra plant were counted starting from ground level to tip of the plant and the results were future evaluated for statistical analysis.

Number of Fruits:

Number of fruits was counted from first picking to last picking from bottom to tip. Number of Fruit was counted manually and data was recorded. After complete harvesting average of every picking was done and were used for further statistical analysis.

Fruit Length (cm):

Three plants were selected from each replication and their fruit length was measured. Length of fruit was measured by using meter rod as well measuring tape. length of fruit was measured without its pedicel length to tip of the fruit.

Diameter of Fruit (cm):

Three plants from each replication were selected and their fruit diameter was measured by using the measuring tape and vernier caliper and their average was noted in the note book for further analysis.

Stem Diameter (cm):

Stem diameter was recorded for three plants from each replication with the help of vernier caliper and measuring tape. Average data was perfectly noted in the notebook for the further analysis.

Inter nodal Distance (cm):

Inter nodal distance was noted with the help of measuring tape. Two nodes of each three plants from each replication were selected to measure inter-nodal distance. The average data was recorded in the notebook for next analysis.

Fresh Weights of Fruit (gm.):

Representative healthy fruits were selected and their fresh weight was recorded one by one with the help of the scientific weight balance without any error. Weight of each fruit from each plant was noted. An average of fruit weight was recorded for the future analysis.

Dry weight of Fruit (gm):

After recording the fresh weight, fruits were dried under sunlight for 2–3 days to dry. After that dried fruit was weighed at electric scientific weighing balance without any error. Same as done in fresh weight average of each fruit weight was taken for the future analysis.

Number of seed/ fruits:

After recording the dry weight each selected fruit of selected plant was open to remove the seeds one by one separately. After removal of the seeds number of seeds were counted and then average number of seeds were recorded for the future statistical analysis.

Statistical Analyses:

Analysis of variance of the collected quantitative traits data was done by using statistics 8.1 as described by [11]. The correlation coefficient was evaluated by the formula as explained by [12]. Characters showing significant differences were taken under consideration for the least significant difference (LSD) mean comparison test [13]. Principal component analysis was also computed by using R software [14] and cluster analysis by using Minitab as given by [15].

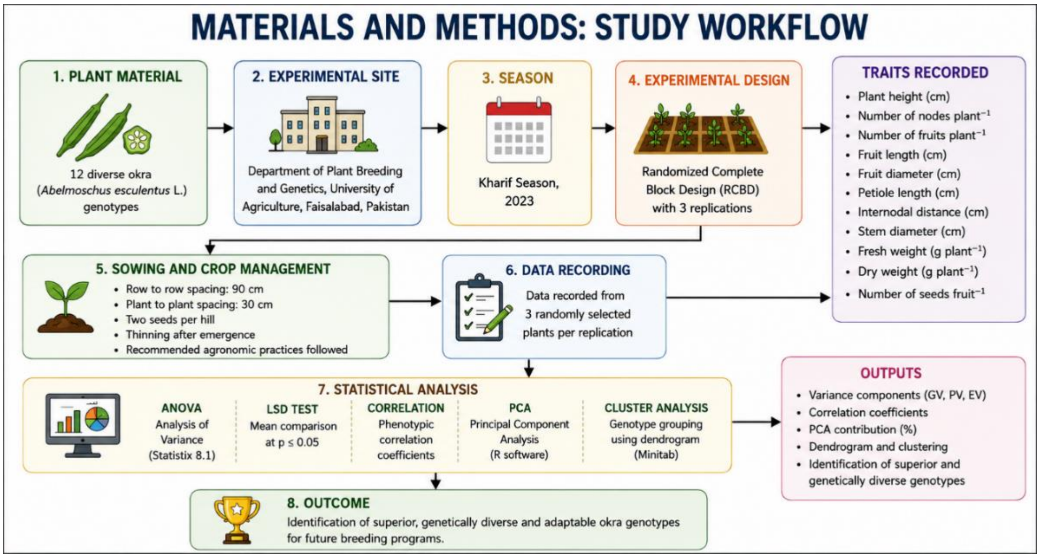


Figure 1. Flowchart of Experimental Materials and Methodology for Genetic Diversity Analysis in Okra

Results and Discussion:

The analysis of variance shows that the mean sum of squares (MSS) due to genotypes is highly significant ($P \leq 0.01$) for all studied traits, including plant height, number of nodes, number of fruits, fruit length, fruit diameter, petiole length, internal diameter (ID), ZND, stem diameter, fresh weight, dry weight, and number of seeds. This indicates the presence of substantial genetic variability among okra genotypes for all morphological and yield-related traits. Such highly significant differences confirm that the experimental material is suitable for selection and genetic improvement (Table 2).

A deeper insight comes from partitioning total phenotypic variance (PV) into genotypic variance (GV) and environmental variance (EV). Across all traits, PV is only slightly higher than GV, while EV remains very low. For instance, in plant height, GV (227.86) is very close to PV (234.21), with a minimal environmental variance (1.96). This trend is consistent across other traits such as number of nodes (GV = 29.04; PV = 30.39; EV = 1.25), fruit diameter (GV = 0.07; PV = 0.08; EV ≈ 0.00), and number of seeds (GV = 37.09; PV = 38.12; EV = 1.03). The narrow difference between GV and PV suggests that most of the observed variation is genetic rather than environmental (Table 2)

From a breeding perspective, this is a critical outcome. When GV is close to PV and EV is negligible, it implies high heritability in the broad sense, meaning that phenotypic selection will be effective. Traits like fruit diameter, dry weight, and stem diameter show extremely low environmental influence, indicating strong genetic control and stability across conditions. These traits are ideal candidates for direct selection in early generations.

Yield-related traits such as number of fruits, fresh weight, dry weight, and number of seeds also exhibit strong genetic control, though slightly more environmental influence compared to purely morphological traits. Still, the relatively small EV values indicate that environmental noise is limited, and selection based on phenotype would reliably reflect genotype performance.

The Least Significant Difference (LSD) values further support practical selection. Traits such as plant height (LSD = 5.02), number of seeds (3.12), and number of nodes (2.10) have moderate LSD values, meaning that only reasonably large differences among genotypes are statistically meaningful. In contrast, traits like fruit diameter (0.04), petiole length (0.04), and dry weight (0.02) have very small LSD values, indicating high precision of measurement and the ability to detect even minor differences among genotypes. This enhances the reliability of selection decisions for these traits.

An important observation is the consistency between variance components and LSD values. Traits with low environmental variance generally show smaller LSD values, reinforcing the idea that these traits are less influenced by experimental error and more genetically controlled. For example, fruit diameter and dry weight combine low EV with very small LSD, making them highly dependable for selection.

Overall, the results indicate that all studied traits in okra are under strong genetic control with minimal environmental interference. This suggests that selection based on phenotypic performance will be highly effective, particularly for traits with very low EV and small PV–GV differences. Traits such as fruit diameter, dry weight, stem diameter, and number of seeds emerge as key selection targets due to their stability and genetic determination. Meanwhile, traits like plant height and number of nodes, although slightly more influenced by environment, still show sufficient genetic variability to be improved through selection.

In conclusion, the dataset demonstrates a favorable genetic architecture for okra improvement, where high variability, strong genetic control, and reliable statistical separation collectively support efficient breeding and selection strategies.

Table Analysis of variance and variance components for morphological and yield-related traits in okra genotypes

The present study revealed highly significant genotypic differences ($P \leq 0.01$) for all evaluated traits in okra, indicating the presence of substantial genetic variability among the tested genotypes. Such significant variation is a fundamental requirement for effective selection and genetic improvement in crop breeding programs. Similar findings have been widely reported in recent okra studies, where significant differences among genotypes for yield and morphological traits confirmed the existence of exploitable genetic diversity [16].

The variance component analysis further showed that phenotypic variance (PV) was only slightly higher than genotypic variance (GV) for all traits, while environmental variance (EV) remained very low. This indicates that most of the observed variation was genetically controlled rather than environmentally influenced. For example, traits such as plant height, number of nodes, and number of seeds showed a very narrow difference between GV and PV, suggesting strong genetic control over their expression. Similar patterns have been reported in okra germplasm where low environmental influence and high genotypic contribution confirmed the reliability of phenotypic selection [6].

Traits such as fruit diameter, dry weight, and stem diameter exhibited extremely low environmental variance, indicating strong genetic stability and minimal environmental disturbance. Such traits are generally considered highly heritable and are ideal for direct selection in breeding programs. Recent studies have also emphasized that traits with low environmental variance and high genetic control show greater response to selection and are useful for varietal improvement [17]. This confirms that these traits can be effectively exploited for genetic gain in okra improvement programs.

Yield-related traits, including number of fruits, fresh weight, dry weight, and number of seeds, also exhibited strong genetic control with minimal environmental influence. This suggests that additive gene effects are likely important in the expression of these traits. Similar conclusions have been drawn in recent studies where yield components in okra showed moderate to high heritability and significant genetic advance, making them suitable for selection-based breeding approaches [18].

The relatively small environmental variance across all traits further supports the stability of trait expression under the experimental conditions. Studies have shown that when environmental variance is low, phenotypic performance becomes a reliable indicator of genotypic potential, which significantly improves the efficiency of selection in breeding programs.

The Least Significant Difference (LSD) values obtained in this study further validate the reliability of the observed differences among genotypes. Traits with lower LSD values, such as fruit diameter and dry weight, indicate higher experimental precision and greater sensitivity in detecting differences among genotypes. This is consistent with previous studies where lower error variance improved the reliability of mean comparisons in okra trials [19][20].

From a breeding perspective, the combination of high genotypic variance, low environmental variance, and significant mean differences indicates that most traits are under strong genetic control. This suggests that phenotypic selection will be highly effective, particularly in early generations. Recent advances in okra breeding also highlight that traits with high genetic control and stability can be improved efficiently through conventional selection methods, with additional gains possible through molecular breeding approaches [9].

Furthermore, the presence of substantial variability in both vegetative and reproductive traits suggests that the studied germplasm possesses broad genetic potential. This variability is crucial for developing improved okra cultivars with higher yield and better adaptability. Maintaining and utilizing such genetic diversity is essential for long-term breeding success and resilience against environmental challenges.

MSS=mean sum of squares, GV=genotypic variance PV= Phenotypic variance EV= environmental variance, ID= Internodal distance, ZND= zero nodal distance

For plant height (a), noticeable variation is evident among genotypes, with some showing distinctly higher growth while others remain comparatively shorter. This suggests differential genetic potential for vegetative vigor, which is an important determinant of biomass production and yield potential. Genotypes with greater plant height generally indicate stronger vegetative growth, though extremely tall plants may also require lodging management considerations.

In number of nodes (b), moderate variability is observed. Certain genotypes exhibit a higher node count, which is directly associated with increased branching potential and reproductive site availability. Genotypes with fewer nodes may reflect compact growth habits, which can be advantageous for high-density planting systems.

The number of fruits per plant (c) shows relatively strong variation among genotypes. A few genotypes clearly outperform others, indicating superior reproductive efficiency and better sink formation capacity. This trait strongly contributes to final yield differences and is a key selection criterion in okra improvement programs.

For fruit length (d), moderate variability is present. Some genotypes exhibit longer fruits, while others produce comparatively shorter fruits. This variation reflects underlying genetic differences affecting fruit development and may also be associated with market preference depending on fruit type (processing vs fresh consumption).

In fruit diameter (e), variation is relatively less pronounced compared to fruit number traits, although some genotypes still show slightly thicker fruits. This suggests partial genetic control with relatively stable expression across environments, though selection for uniform fruit size remains important for commercial quality.

The petiole length (f) shows moderate differences among genotypes. Longer petioles may contribute to better canopy architecture and light interception, whereas shorter petioles may indicate compact growth habits. This trait indirectly influences photosynthetic efficiency and plant spacing adaptability.

For internodal distance (g), variability is clearly visible, with some genotypes exhibiting elongated internodes while others remain compact. Longer internodes often correspond to taller, more open plant architecture, while shorter internodes are typically associated with dwarf or semi-dwarf growth types, which are preferred in high-density cultivation.

The zero nodal distance (h) also shows variation among genotypes, indicating differences in basal stem development and early vegetative growth patterns. Genotypes with lower values may exhibit more compact early growth, which can be beneficial for mechanical stability.

In stem diameter (i), moderate to high variation is observed. Genotypes with thicker stems generally possess stronger mechanical support and improved resistance to lodging, while thinner stems may indicate weaker structural strength but potentially higher resource allocation to reproductive growth.

Finally, fresh weight (j) demonstrates appreciable variation among genotypes, reflecting differences in overall biomass accumulation. Genotypes with higher fresh weight indicate better overall vigor and assimilate production, which ultimately contributes to yield potential.

The present study evaluated a set of okra genotypes for important morpho-physiological and yield-related traits, including plant height, number of nodes, and number of fruits, fruit morphology, vegetative architecture, and biomass accumulation. The observed significant variability across all traits reflects a broad genetic base among the tested genotypes, which is essential for effective selection and genetic improvement in okra breeding programs. Similar levels of variation have been widely reported in okra germplasm, indicating that yield and related traits are highly polygenic and influenced by genotype × environment interactions.

Substantial variation was observed for plant height, node number, petiole length, internodal distance, and stem diameter. These traits collectively define plant architecture and influence light interception, assimilate distribution, and ultimately productivity. Genotypes showing greater plant height and higher node numbers generally indicate enhanced vegetative vigor and higher photosynthetic capacity. However, excessive elongation may lead to inefficient assimilate partitioning or lodging susceptibility, particularly under high-input conditions.

Internodal distance varied notably among genotypes, indicating contrasting growth habits ranging from compact to elongated types. Compact genotypes are often preferred in modern okra breeding due to their suitability for high-density planting and improved resource-use efficiency. Similar architectural variation has been linked to adaptive growth responses under different environmental conditions, particularly drought and heat stress environments where compact phenotypes often perform better [21][22].

Stem diameter variation further supports differential biomass allocation strategies. Genotypes with thicker stems tend to exhibit improved mechanical strength, enhanced vascular transport capacity, and greater resilience against environmental stress. Such traits are particularly important under abiotic stress conditions where structural stability contributes to yield maintenance.

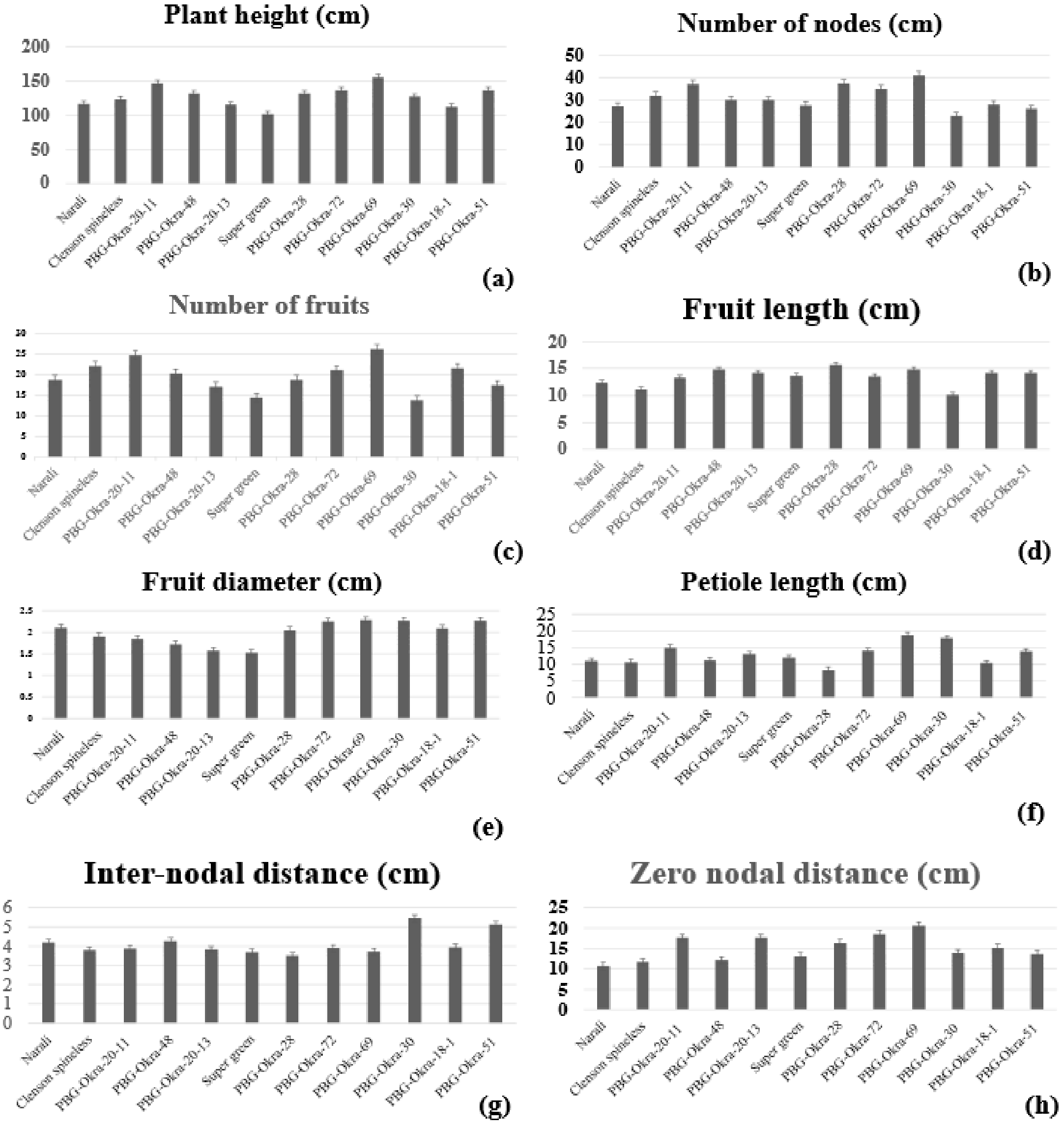
Marked variability was recorded in number of fruits per plant, fruit length, and fruit diameter, which are primary determinants of yield potential. Among these, the number of fruits per plant showed the highest level of differentiation among genotypes, indicating strong genetic control and high selection efficiency for this trait. This aligns with previous findings where fruit number per plant was identified as one of the most heritable and yield-contributing traits in okra.

Fruit size traits (length and diameter) also exhibited moderate variability, reflecting differential sink strength and assimilate partitioning efficiency. Larger fruit size is often associated with improved market value, but may be negatively correlated with fruit number due to trade-offs in resource allocation. This source–sink relationship is a key consideration in okra yield optimization strategies.

Fresh weight variation among genotypes indicates significant differences in overall biomass production and physiological efficiency. Genotypes with higher fresh weight likely possess superior photosynthetic capacity, better water uptake, and improved metabolic activity. Such genotypes are typically more resilient under favorable as well as stress conditions, making them valuable for breeding programs targeting yield stability.

The observed variability also confirmed the presence of exploitable genetic diversity, which is essential for selection gain in breeding programs. Recent studies emphasize that such diversity, when combined with multivariate selection approaches, can significantly enhance genetic improvement efficiency in okra.

From a breeding perspective, traits such as number of fruits per plant, stem diameter, and internodal distance should be prioritized due to their high variability and strong contribution to yield expression. Genotypes exhibiting favorable combinations of these traits can be considered promising candidates for hybrid development and varietal improvement. Additionally, compact genotypes with high fruit load may be particularly useful for modern intensive cultivation systems.



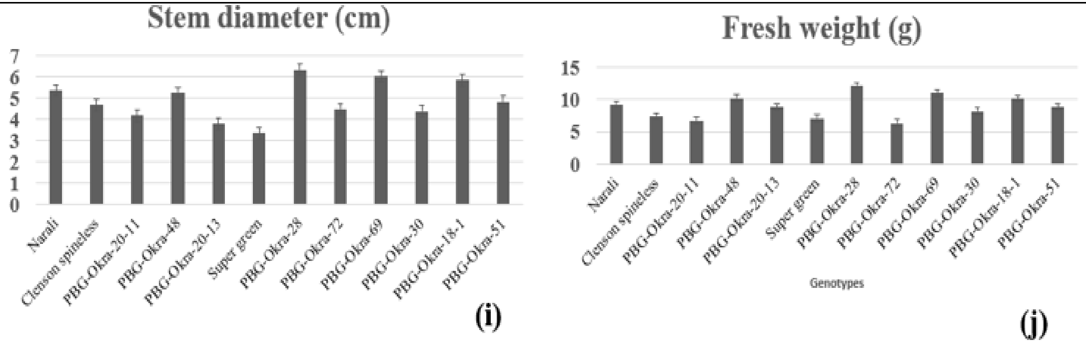


Figure 2. Mean data presented for different yield related characters show genetic diversity in the okra

Correlation analysis:

The phenotypic correlation analysis revealed that plant height showed a positive and significant association with number of nodes, number of fruits, fruit diameter, petiole length, and zero-nodal distance, whereas it exhibited a non-significant relationship with fruit length, internodal distance, fresh weight, dry weight, and number of seeds. Similar positive associations of plant height with yield and related traits have also been reported by [23][24][25], confirming consistency with previous findings Figure 2.

Number of fruits per plant showed a significant positive correlation with plant height, number of nodes, zero-nodal distance, and stem diameter, while it was negatively associated with internodal distance. Comparable positive associations between plant height and yield components have also been reported by [25][24][23].

Fruit length exhibited a significant positive correlation with number of nodes, zero-nodal distance, stem diameter, fresh weight, dry weight, and number of seeds, while it showed a negative association with internodal distance and non-significant relationships with other traits. [26] Also reported a positive significant association of fruit length with number of seeds and fresh weight.

Fruit diameter showed a negative correlation with fruit length and a non-significant association with some traits, while it was positively and significantly correlated with plant height, petiole length, internodal distance, and stem diameter. Similar findings were reported by [27], who observed positive correlations of fruit diameter with plant height and stem diameter.

Petiole length showed a positive significant correlation with plant height, fruit diameter, internodal distance, and zero-nodal distance, while it showed a negative significant correlation with fruit length, stem diameter, fresh weight, dry weight, and number of seeds. In contrast, [28] reported negative associations of internodal length and node number with fruit traits such as fruit length and fruit weight.

Internodal distance showed positive correlations with fruit diameter and petiole length, whereas it exhibited negative associations with plant height, number of nodes, and number of fruits, fruit length, and zero-nodal distance. It showed non-significant relationships with other traits. [28] Also reported similar negative associations of internodal traits with yield components.

Zero-nodal distance showed positive significant correlations with plant height, number of nodes, number of fruits, fruit length, and petiole length, while it showed a negative significant association with internodal distance.

Stem diameter showed a strong positive and significant correlation with plant height, number of nodes, number of fruits, fruit length, fruit diameter, zero-nodal distance, fresh weight, dry weight, and number of seeds, while it was negatively and non-significantly associated with petiole length and internodal distance. Similar results were reported by [29][30], where stem diameter was positively associated with several yield-related traits.

Fresh weight exhibited a positive significant correlation with fruit length, stem diameter, dry weight, and number of seeds, while it showed a negative non-significant correlation with most other traits. [31] Also reported positive associations of fruit weight with fruit length and fruit girth.

Dry weight showed a positive significant correlation with fruit length, stem diameter, fresh weight, and number of seeds, while it was negatively and non-significantly associated with petiole length and internodal distance. Similar results were reported by [31], who observed positive correlations of fruit weight with fruit length and girth.

Number of seeds showed a positive significant correlation with fruit length, stem diameter, fresh weight, and dry weight, while it exhibited negative non-significant associations with petiole length and internodal distance. These findings are in agreement with [27][26], who reported strong positive correlations of fruit weight and fruit length with seed number and fruit traits.

Plant Height (PH), Number of nodes (NON), Number of fruits (NOF), Fruit length (FL), Fruit Diameter (FD), Petiole length (PL), Inter-Nodal distance (IND), Zero-nodal distance (ZND), Stem diameter (SD), Fresh weight (FW), Dry weight (DW), Number of seeds (NOS) very closely meaning that there was more similarity between these two genotypes.

Table 2 Genotypic mean square, genotypic variance, phenotypic variance, environmental variance, and least significant difference (LSD) for growth and yield traits in okra.

Sr No	Parameters	MSS (Genotypes)	GV	PV	EV	LSD value for comparison
1	Plant height	689.93**	227.86	234.21	1.96	5.02
2	number of Nodes	88.35**	29.04	30.39	1.25	2.10
3	Number of Fruits	42.09**	2.56	2.63	0.07	1.50
4	Fruit length	7.75**	2.56	2.63	0.07	0.75
5	Fruit Diameter	0.22**	0.07	0.08	0.00	0.04
6	Petiole Length	28.27**	9.34	9.60	0.26	0.04
7	ID	1.05**	0.35	0.36	0.01	0.20
8	ZND	28.21**	9.32	9.58	0.26	0.03
9	Stem Diameter	2.49**	0.83	0.85	0.02	0.25
10	Fresh weight	9.76**	3.22	3.31	0.09	0.12
11	Dry weight	2.42**	0.80	0.82	0.02	0.02
12	No of seeds	112.92**	37.09	38.12	1.03	3.12

Table 3. Correlation analysis for 12 genotypes for different yield related parameters in okra

Variables	P.H	NON	NOF	FL	FD	PL	IND	ZND	SD	FW	DW	Nos
P.H	**1****											
NON	0.6569**	**1****										
NOF	0.6668**	0.7796**	**1****									
FL	0.1952NS	0.5054**	0.2885ns	**1****								
FD	0.5283**	0.0743ns	0.2184ns	-0.1614ns	**1****							
PL	0.5536**	0.0935ns	0.1473ns	-0.2916ns	0.3876*	**1****						
IND	0.0614NS	-0.6984*	-0.4856*	-0.4991*	0.4308**	0.417*	**1****					
ZND	0.5743**	0.7032**	0.4841**	0.4222*	0.2076NS	0.491**	-0.3482*	**1****				
SD	0.3746*	0.3739*	0.4523**	0.4153*	0.5492**	-0.2121ns	-0.1417ns	0.1122ns	**1****			
FW	0.144ns	0.2188ns	0.1258ns	0.5813**	0.1934ns	-0.2414ns	-0.1259ns	0.0864ns	0.8274**	**1****		
DW	0.1738ns	0.1987ns	0.1515ns	0.542**	0.277ns	-0.1953ns	-0.0765ns	0.05ns	0.8662**	0.9781**	**1****	
NOS	0.1868ns	0.1705ns	0.2194ns	0.5672**	0.2227ns	-0.2418ns	-0.0566ns	0.0089ns	0.8299**	0.9577**	0.9411**	**1****

Principal component analysis (PCA):

PCA served as the foundation for multivariate data analysis using projection techniques. In order to identify trends, jumps, clusters, and outliers, it is crucial to describe a multivariate data table as a smaller number of variables (summary indices). The links between observations and variables as well as those within the variables may be revealed by this overview.

According to the analysis, the first five principal components i.e. PC1, PC2, PC3, PC4, and PC5, have the eigenvalues of 4.8782, 2.9216, 2.2865, 8.5207, and 4.1770 respectively are greater than 1 and their contribution to cumulative variability is around 94.65. A total cumulative variability of 84.05% was explained by the first three principal components i.e. PC1, PC2, PC3 whereas each component contributes to cumulative variability of 40.65, 64.99 and 84.05 percent, respectively (Figure. 3).

All the traits as vectors on the graph can be seen by observing the biplot in the Principal Component Analysis. The length of a character shows the variation contributed by that character.PBG-OKRA-18-1 is the best performing for the Fresh weight and dry weight, PBG-OKRA-51 is best performing for the inter-nodal distance, PBG-OKRA-72 is best performing for the petiole length and PBG-OKRA-48 is best performing for fruit length.

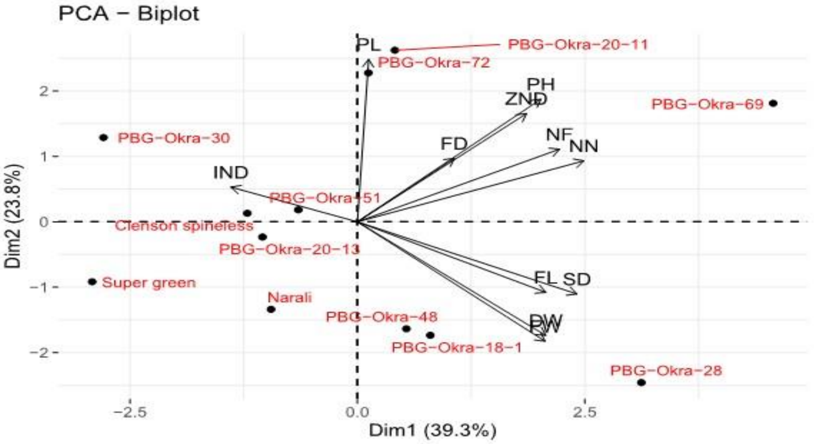


Figure 3. Principal component biplot showing variability among okra genotypes.

Cluster Analysis:

The ability to identify the accessions with different levels of similarity can be assessed with the help of cluster analysis using a dendrogram. Cluster analysis exhibited that significant variation was present in genotypes since 12 genotypes were grouped into 4 clusters on the basis of the 66.67% similarity index Table 3. Clusters provide information about genetic diversity (Figure. 4).

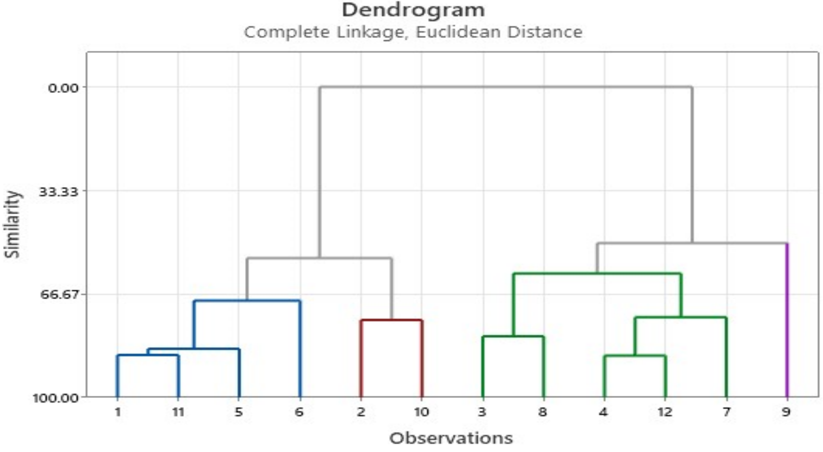


Figure 4. Dendrogram based on Euclidean distance

The dendrogram was calculated based on the Euclidean distance by the average linkage between groups. Cluster III is the biggest one having 5 genotypes. Cluster I, II and IV consisted of 4, 2 and 1 genotypes respectively. Cluster III is the biggest one among all and consisted of PBG-OKRA-21, PBG-OKRA-48, PBG-OKRA-28, PBG-OKRA-72 and PBG-OKRA-51 while cluster I have 4 genotypes as follows NARALI, PBG-OKRA-20-13, SUPER GREEN and PBG-OKRA-18-1. CLENSON SPINELESS and PBG-OKRA-30 falls in cluster II, PBG-OKRA-69 falls in cluster IV. The average and maximum distance from the centroid in the case of cluster III were 10.97 and 13.87, respectively Figure 4. According to [32], cluster analysis isolates genotypes into clusters that show great homogeneity both within and between clusters. The landraces' distribution pattern into four clusters provided evidence of their variety. This finding supports the assertions made by [33] and [5] that a sizable number of clusters had only one genotype of okra.

References:

[1] ABM Sharif Hossain, Mekhled M. Alenazi, "Seedless okra pod, chlorophyll, vitamin C and mineral content development using plant growth regulator in vitro and in vivo culture," *Cell. Mol. Biol. (Noisy-le-grand).*, vol. 69, no. 13, pp. 53–58, 2023, doi: 10.14715/cmb/2023.69.13.8.

[2] Renu Yadav, Sarika Jaiswal, "Potentials of genotypes, morpho-physio-biochemical traits, and growing media on shelf life and future prospects of gene editing in tomatoes," *Front. Genome Ed.*, vol. 5, 2023, doi: https://doi.org/10.3389/fgeed.2023.1203485.

[3] "Genetic architecture of yield and its component in okra (Abelmoschus esculentus L. Moench)." Accessed: May 23, 2026. [Online]. Available: https://www.researchgate.net/publication/277186243_Genetic_architecture_of_yield_and_its_component_in_okra_Abelmoschus_esculentus_L_Moench

[4] Sanket J. More, K.N. Chaudhari, "Genotype x Environment Interaction and Stability Analysis for Earliness, Seed Yield and Fruit Yield in Okra Using the Additive Main Effect and Multiplicative Interaction (AMMI)," *Int. J. Curr. Microbiol. Appl. Sci.*, vol. 7, no. 3, pp. 373–383, 2018, doi: 10.20546/ijcmas.2018.703.043.

[5] D. Muluken, M. Wassu, and G. Endale, "Variability, Heritability and Genetic Advance in Ethiopian Okra [Abelmoschus esculentus (L.) Monech] Collections for Tender Fruit Yield and Other Agro-morphological Traits," *J. Appl. Life Sci. Int.*, vol. 4, no. 1, pp. 1–12, Jan. 2016, doi: 10.9734/JALSI/2016/19483.

[6] A. Behera *et al.*, "Assessment of Genetic Variability and Trait Association in Okra (Abelmoschus esculentus L. Moench)," *J. Adv. Biol. Biotechnol.*, vol. 28, no. 6, pp. 431–447, Jun. 2025, doi: 10.9734/JABB/2025/V28I62409.

[7] "Genetic Variability, Heritability and Genetic Advance studies in Genotypes of Okra [(Abelmoschus esculentus (L.) Moench]." Accessed: May 23, 2026. [Online]. Available: https://www.researchgate.net/publication/330634199_Genetic_Variability_Heritability_and_Genetic_Advance_studies_in_Genotypes_of_Okra_Abelmoschus_esculentus_L_Moench

[8] "Studies on genetic variability, heritability and genetic advance in Okra [Abelmoschus esculentus (L.) Moench.]." Accessed: May 23, 2026. [Online]. Available: https://www.researchgate.net/publication/349320343_Studies_on_genetic_variability_heritability_and_genetic_advance_in_Okra_Abelmoschus_esculentus_L_Moench

[9] Maria Doroteia Campos, Maria do Rosário Félix, "High throughput sequencing unravels tomato-pathogen interactions towards a sustainable plant breeding," *Hortic. Res.*, vol. 8, 2021, [Online]. Available: https://pmc.ncbi.nlm.nih.gov/articles/PMC8325677/

[10] H. A. Agrama *et al.*, "Genetic structure associated with diversity and geographic

distribution in the USDA rice world collection," *Nat. Sci.*, vol. 2, no. 4, pp. 247–291, Apr. 2010, doi: 10.4236/NS.2010.24036.

[11] R. G. D. Steel, J. H. Torrie, "Principles and procedures of statistics, a biometrical approach.," *CABI Databases*, 1981, [Online]. Available: https://www.cabidigitallibrary.org/doi/full/10.5555/19810721475

[12] D. R. Dewey and K. H. Lu, "A Correlation and Path-Coefficient Analysis of Components of Crested Wheatgrass Seed Production1," *Agron. J.*, vol. 51, no. 9, pp. 515–518, Sep. 1959, doi: 10.2134/AGRONJ1959.00021962005100090002X.

[13] K. M., "The Design of Experiments," *Nat. 1947 1604075*, vol. 160, no. 4075, pp. 775–775, Dec. 1947, doi: 10.1038/160775A0.

[14] K. P. F.R.S., "LIII. On lines and planes of closest fit to systems of points in space," *London, Edinburgh, Dublin Philos. Mag. J. Sci.*, vol. 2, no. 11, pp. 559–572, Nov. 1901, doi: 10.1080/14786440109462720.

[15] R. Scitovski, K. Sabo, F. Martínez-Álvarez, and Š. Ungar, "Cluster Analysis and Applications," *Clust. Anal. Appl.*, pp. 1–271, Jan. 2021, doi: 10.1007/978-3-030-74552-3/SAVE-RESEARCH.

[16] Khursheed Alam, Manoj Kumar Singh, "Genetic variability, heritability and genetic advance for selection parameters of genotypes in okra (Abelmoschus esculentus (L.) Moench)," *Int. J. Chem. Stud.*, vol. 8, no. 6, pp. 1016–1022, 2020, doi: 10.22271/chemi.2020.v8.i6o.10896.

[17] A. V. Mohite and R. V. Gurav, "Induced mutation using gamma rays in okra (Abelmoschus esculentus (L.) Moench)," *J. Appl. Hortic.*, vol. 21, no. 3, pp. 205–208, 2019, doi: 10.37855/JAH.2019.V21I03.35.

[18] "Heterosis and combining ability for yield traits in okra (Abelmoschus esculentus L.)." Accessed: May 23, 2026. [Online]. Available: https://www.researchgate.net/publication/278741490_Heterosis_and_combining_ability_for_yield_traits_in_okra_Abelmoschus_esculentus_L

[19] K. Satish, A.V. Agalodiya, "Combining Ability for Yield and Its Attributing Traits in Okra [Abelmoschus esculentus (L.) Moench]," *Int. J. Curr. Microbiol. Appl. Sci.*, vol. 6, no. 9, pp. 1944–1954, 2017, doi: 10.20546/ijcmas.2017.609.238.

[20] Iveren Blessing Iorliam, Barnabas Achakpa Ikyo, "Application of Machine Learning Techniques for Okra Shelf Life Prediction," *J. Data Anal. Inf. Process.*, vol. 9, no. 3, pp. 136–150, 2021, doi: 10.4236/jdaip.2021.93009.

[21] Samikshya Bhattarai, Joshua T. Harvey, "Exploring Morpho-Physiological Variation for Heat Stress Tolerance in Tomato," *Plants*, vol. 10, no. 2, p. 347, 2021, [Online]. Available: https://pmc.ncbi.nlm.nih.gov/articles/PMC7918821/

[22] Veronica Conti, Marco Romi, "Morpho-Physiological Classification of Italian Tomato Cultivars (Solanum lycopersicum L.) According to Drought Tolerance during Vegetative and Reproductive Growth," *Plants*, vol. 10, no. 9, p. 1826, 2021, doi: https://doi.org/10.3390/plants10091826.

[23] K. Syfullah *et al.*, "Genetic Variability, Heritability, Character Association and Morphological Diversity in Okra (Abelmoschus esculentus L. Moench)," *Int. J. Plant Soil Sci.*, vol. 25, no. 6, pp. 1–11, Dec. 2018, doi: 10.9734/IJPSS/2018/45828.

[24] O. B. B. D. Aminu, "Varietal Performance And Correlation of Okra Pod Yield And Yield Components," *Bangladesh J. Plant Breed. Genet.*, vol. 29, no. 1, 2017, doi: 10.3329/bjpbg.v29i1.33703.

[25] "Correlation And Path Analyses For Fruit Yield And Its Component Traits In Okra." Accessed: May 23, 2026. [Online]. Available: https://www.researchgate.net/publication/315382773_Correlation_And_Path_Analyses_For_Fruit_Yield_And_Its_Component_Traits_In_Okra_Abelmoschus_Esculent

us_L_Moench_Genotypes
[26] Khajuria, R. K. Sharma, "Variability studies in Okra (Abelmoschus esculentus L. Moench)," *Electron. J. Plant Breed.*, vol. 7, no. 2, p. 226, 2016, doi: 10.5958/0975-928X.2016.00031.4.
[27] "Genetic variability and heritability in cultivated okra [Abelmoschus esculentus (L.) Moench]." Accessed: May 23, 2026. [Online]. Available: https://www.researchgate.net/publication/274421262_Genetic_variability_and_heritability_in_cultivated_okra_Abelmoschus_esculentus_L_Moench
[28] "Implication of multivariate analysis in breeding to obtain desired plant type of okra (Abelmoschus esculentus L. Moench)." Accessed: May 23, 2026. [Online]. Available: https://www.researchgate.net/publication/342977535_Implication_of_multivariate_analysis_in_breeding_to_obtain_desired_plant_type_of_okra_Abelmoschus_esculentus_L_Moench
[29] "Characterization of Okra (Abelmoschus esculents [L.] Moench) Accessions for Agronomic Traits in Assosa District, North Western Ethiopia." Accessed: May 23, 2026. [Online]. Available: https://www.researchgate.net/publication/391738403_Characterization_of_Okra_Abelmoschus_esculents_L_Moench_Accessions_for_Agronomic_Traits_in_Assosa_District_North_Western_Ethiopia
[30] Medagam Thirupathi Reddy, Kadiyala Hari Babu, "Correlation and path coefficient analysis of quantitative characters in okra [Abelmoschus esculentus (L.) Moench.]," *Int. J. Chem. Stud.*, vol. 8, no. 6, pp. 206–208, 2020, doi: 10.22271/chemi.2020.v8.i6c.10771.
[31] L. B. Thulasiram, S. R. Bhople, "Correlation and path analysis studies in okra," *Electron. J. Plant Breed.*, vol. 8, no. 2, p. 620, 2017, doi: 10.5958/0975-928X.2017.00094.1.
[32] D. B. Jaynes, T. C. Kaspar, T. S. Colvin, and D. E. James, "Cluster analysis of spatiotemporal corn yield patterns in an Iowa field," *Agron. J.*, vol. 95, no. 3, pp. 574–586, May 2003, doi: 10.2134/AGRONJ2003.5740;CTYPE:STRING:JOURNAL.
[33] Zate DK, Rathod AH, Faria S Khan and Shelke Supriya, "Genetic divergence studies in okra (Abelmoschus esculentus (L.) Moench)," *Int. J. Res. Agron.*, vol. 7, no. 7, pp. 41–47, 2024, [Online]. Available: https://www.agronomyjournals.com/archives/2024/vol7issue7S/PartA/S-7-6-82-721.pdf