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Assessment of Genetic Variability and Heritability in Okra [*Abelmoschus esculentus* (L.) Moench.] Genotypes

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ABSTRACT

Okra is a nutritionally and economically important crop, yet its genetic potential is underexploited due to limited knowledge of variability among genotypes. This study aimed to assess genetic variability, heritability, and genetic advance in okra to identify key traits for targeted improvement. This comprehensive analysis examined genetic variation across 25 okra genotypes, alongside the check variety Arka Anamika, to pinpoint advantageous characteristics for advanced breeding programs targeting yield optimization and quality enhancement. Executed during summer 2019 at Horticultural Research Centre (H.N.B. Garhwal University), the trial utilized a triple-replicated randomized complete block design (RCBD) to maximize experimental reliability. Statistical analysis of 15 agronomic and biochemical traits included evaluations of phenotypic/genotypic variation of coefficients (PCV/GCV), broad-sense heritability (h^2) and genetic advancement metrics (GA, GAM). The key outcome revealed marked genetic differentiation in key characteristics like number of primary branches, total soluble solids content, seed yield per fruit, and physiological loss demonstrated high GCV/PCV ratios and high heritability with high genetic gains. These findings highlighted additive genetic effects, making these traits optimal for traditional phenotypic selection. Conversely, chlorophyll content, leaf length and petiole diameter showed moderate to low heritability and genetic gain, suggesting environmental susceptibility or epistatic genetic regulation that may necessitate biotechnological interventions like CRISPR-based editing or transcriptomic profiling to bypass traditional breeding constraints. The research underscored the untapped genetic reservoir within existing okra germplasm, offering an actionable framework for crop improvement. High-heritability traits warrant immediate selection protocols, while polygenic characteristics could benefit from integrated genomic selection models or haplotype-based breeding.

Keywords: Genetic gain, Genetic variability, Crop improvement, Genetic advance, Heritability, Okra, Quality traits.

INTRODUCTION

Okra [*Abelmoschus esculentus* (L.) Moench.], popularly known as lady's finger, is a highly valued warm-season vegetable crop renowned for its broad spectrum of nutritional, economic and medicinal properties (Baghel *et al,* 2022; Joshi *et al,* 2025a). This species is recognized by a plethora of regional names, such as bhindi in Hindi, vendakkai in Tamil, bhendi in Marathi and gumbo in the southern United States and is a member of the Malvaceae family (Joshi *et al,* 2020; Sharma *et al,* 2022). Its tender, immature pods are prized for their culinary versatility, being consumed in fresh, boiled, fried, pickled, or dried forms, thereby underscoring its significance in both domestic cuisine and commercial food processing (Joshi *et al,* 2021; Petropoulos *et al,* 2022; Singh *et al,* 2023). The crop's remarkable adaptability to diverse agro-ecological conditions and its relatively brief growth cycle make it an attractive option for both smallholder and commercial farming enterprises (Kumar and Joshi, 2024; Joshi *et al,* 2025b).

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The genus *Abelmoschus* comprises between six and fifteen species, exhibiting considerable morphological and physiological diversity (Ray *et al,* 2022). Of these, *A. esculentus* is the most widely cultivated, while *A. caillei* a natural amphidiploid, is predominantly grown in the humid zones of West Africa. Wild relatives such as *A. manihot*, *A. moschatus* and *A. ficulneus* serve as valuable reservoirs of genetic diversity, offering traits that can be leveraged in breeding programs to enhance resistance to various biotic and abiotic stresses (Singh *et al,* 2023). The genetic richness present within and among these species provides a robust foundation for the advancement of improved cultivars through both conventional and molecular breeding methodologies.

Nutritionally, okra is distinguished by its low caloric content and high levels of moisture and dietary fiber, factors that support digestive health and glycemic regulation. The pods are also notable sources of essential vitamins, including A (beta-carotene), C, K, and several B-complex vitamins, as well as minerals such as calcium, potassium, magnesium, manganese, phosphorus, and iron (Gemede *et al,* 2015). The mucilage, primarily composed of polysaccharides, is recognized for its beneficial effects on gastrointestinal health and blood glucose management. Furthermore, okra is rich in phytochemicals, including flavonoids, polyphenols, and antioxidants, which impart a range of therapeutic properties, such as anti-diabetic, anti-inflammatory, antibacterial, and cholesterol-lowering effects (Karmakar *et al,* 2022). In addition to its nutritional merits, okra holds considerable industrial significance. The mucilage is widely utilized as a natural thickener, stabilizer, and emulsifier in the food, pharmaceutical, and cosmetic industries. Okra seeds, which constitute 15-20% of pod weight, are a valuable source of oil rich in unsaturated fatty acids, particularly linoleic and oleic acids, making them suitable for nutraceutical and biodiesel applications.

The lignocellulosic fibers derived from okra stems are being explored as sustainable raw materials for the paper and textile sectors. Moreover, the development of processed okra products, such as dehydrated flakes, powders, and canned pods, enhances shelf life, adds value, and opens new avenues for agribusiness and export (Petropoulos *et al,* 2022). Despite its widespread cultivation and multifaceted applications, okra remains relatively underutilized in advanced breeding and genomic research. The narrow genetic base of most cultivated varieties poses a significant constraint to genetic improvement. Contemporary breeding programs require a comprehensive evaluation of genetic diversity, using morphological, biochemical, and molecular markers to identify superior genotypes with enhanced yield, resilience, and quality traits (Sharma *et al,* 2022; Singh *et al,* 2023). The development of robust, high-yielding, and climate-resilient cultivars is essential to satisfy the escalating global demand for nutritious vegetables. The present study seeks to assess the genetic variability among selected okra genotypes, with a focus on yield and quality-related traits. Identification of promising genotypes will facilitate the breeding of superior hybrids and contribute to the sustainability of okra production systems.

MATERIALS AND METHODS

This study was undertaken during the summer cropping season of 2019 at the Horticultural Research Centre, located within the North Terrace Valley adjacent to the Alaknanda River. The experimental site lies at geographic coordinates 78°47'30" E longitude and 30°13'9" N latitude, elevated approximately 540 meters above mean sea level (MSL), within the Lesser Himalayan zone. The location experiences a subtropical highland climate characterized by notable diurnal temperature fluctuations, which are favourable for horticultural research. Maximum temperatures reached up to 42.16°C, whereas minimum temperatures declined to 20.7°C. Relative humidity exhibited a wide range, varying from 11.76% to 95.41%, indicative of the humid subtropical conditions prevalent in the region. Precipitation was limited, with peak rainfall recorded in July, averaging 0.158 mm, consistent with the onset of the regional summer monsoon. These environmental parameters were meticulously recorded throughout the crop growth cycle to examine their influence on genotype performance.

The experimental material comprised twenty-five okra genotypes, with one standard check cultivar, Arka Anamika, which functioned as a benchmark for comparative analysis. The cultivars evaluated included: Agri Bahar, Chanda, Hisar Naveen, Hisar Unnat, Kashi Kranti, Kashi Mohini, Kashi Pragati, Kashi Vibhuti, Kaveri, King Bhindi, LC-1 through LC-6 series, Lucky-666, Parbhani Kranti, Punjab-8, Pusa A-4, Pusa Sawani, Super Anamika, VL Bhindi-2, Vandana-241, and Varsha Uphar. A randomized complete block design (RCBD) with three replications was implemented to minimize experimental variability and enhance the precision of results. Each genotype was cultivated in discrete plots, and uniform agronomic practices were consistently applied across

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all treatments to mitigate confounding factors. Within each replicate, five vigorous plants per genotype were randomly chosen, tagged, and monitored for detailed phenotypic observations. Data on yield and quality traits were systematically recorded from these selected plants, and mean values were calculated to represent genotype performance.

For data analysis, initial data organization was carried out using Microsoft Excel, while advanced statistical analysis was performed with SPSS version 26. The phenotypic variance (PCV) and genotypic variance (GCV) were estimated, partitioning the total observed variation into genetic and environmental components (Lush, 1940). The extent of genetic variability was quantified using the Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV), both expressed as percentages (Burton and DeVane, 1953). These parameters provide insights into the relative contributions of genetic and environmental factors to trait expression. The magnitude of variability was categorized as low (0–10%), moderate (11–20%), or high (>20%) (Sivasubramanian and Madhavamenon, 1973), facilitating identification of traits with substantial genetic variability, which serve as essential targets for selection in breeding programs. Broad-sense heritability (h^2b), representing the proportion of phenotypic variance attributable to genetic causes (Hansen *et al,* 1956), was estimated. Heritability values were stratified into low (0–50%), moderate (51–70%), and high (>70%) categories, enabling evaluation of the reliability of phenotypic selection. Genetic advance (GA), indicating the expected improvement from selection under ideal conditions (Johnson *et al,* 1955), was also determined. Genetic advance as percent of mean (GAM) was calculated to normalize genetic gain relative to the trait mean, and classified into low (0–10%), moderate (11–20%), and high (>20%) categories. These metrics collectively provide a predictive framework for the potential genetic progress achievable through selection.

RESULTS AND DISCUSSION

Genetic variability

The genetic variability parameters, including the phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability (h^2), genetic advance and genetic advance as a percentage of the mean, across all 15 evaluated traits, are summarized in Table 1. The comparative analysis of PCV and GCV provided a detailed understanding of the extent of variability present within the studied germplasm. Notably, for all traits assessed, the PCV values consistently exceeded the corresponding GCV values. However, in most instances, the disparity between PCV and GCV was minimal, aligning with findings reported by Prakash *et al* (2011), Khajuria *et al* (2015), Chandramouli *et al* (2016) and Kerure *et al* (2017) in okra. This close proximity between PCV and GCV suggests that environmental influences on the expression of these traits are relatively minor, implying that the observed variation is predominantly governed by genetic factors. The magnitude of both coefficients varied across traits, ranging from low to moderate or high, which underscores the considerable genetic diversity inherent in the experimental material. Such diversity is crucial, as it provides a robust foundation for effective selection and breeding strategies aimed at crop improvement.

Genotypic and phenotypic coefficient of variation

The phenotypic variability observed among the evaluated okra genotypes for various traits is a manifestation of the interplay between genetic constitution and environmental influences. While environmental variance is inherently non-heritable and, therefore, not amenable to selection, the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are valuable tools for quantifying total trait variability and discerning the relative contributions of genetic and environmental components (Badiger *et al,* 2017). These parameters facilitate the identification of traits governed primarily by genetic factors, which are critical for effective selection in crop improvement programs.

In the present investigation, traits such as the number of primary branches per plant (GCV: 33.54%; PCV: 34.20%), exhibited high levels of both GCV and PCV. The narrow gap between genotypic and phenotypic variances for these traits indicates a minimal influence of environmental factors and suggests a predominance of additive gene action. Consequently, these traits present substantial potential for genetic improvement through direct phenotypic selection. Similar trends have been reported in earlier studies by Khajuria *et al* (2015), Chandramouli *et al* (2016), Deepanshu and Shamd (2017), Kerure *et al* (2017) and Kumari *et al* (2019) affirming the genetic stability of these attributes.

Moderate levels of variability were recorded for traits such as number of seeds per fruit (GCV: 17.94%; PCV: 19.17%), total soluble solids (GCV:

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13.30%; PCV: 13.93%), seed index (GCV: 10.43%; PCV: 12.99%) and ash content (GCV: 10.34%; PCV: 12.96%). The moderate divergence between GCV and PCV in these parameters reflects a balanced influence of genotypic and environmental components, indicating partial heritability and a moderate response to selection. These findings align with the results of by Khajuria *et al* (2015), Chandramouli *et al* (2016) and Badiger *et al* (2017).

Conversely, several traits exhibited low GCV and PCV values, including stem girth (GCV: 8.45%; PCV: 9.03%), number of ridges per fruit (GCV: 5.79%; PCV: 6.38%), ascorbic acid content (GCV: 5.71%; PCV: 6.59%), petiole diameter (GCV: 4.78%; PCV: 7.42%), fruit diameter (GCV: 4.59%; PCV: 5.46%), chlorophyll content (GCV: 3.23%; PCV: 6.50%), leaf length (GCV: 2.61%; PCV: 5.14%) and moisture content (GCV: 1.51%; PCV: 1.94%). These results suggest that such traits are predominantly influenced by environmental factors, thereby limiting their scope for genetic enhancement through conventional selection. These outcomes are consistent with the findings of Ahmad *et al* (2015) who also noted low heritable variation for similar parameters. Additionally, traits such as physiological loss exhibited a relatively high PCV (20.85%) and a moderate GCV (18.47%) indicating a significant environmental effect. Similarly, flesh thickness showed a moderate PCV (11.11%) but a low GCV (7.74%), further emphasizing environmental predominance in its expression and limiting the expected genetic gain. Overall, traits characterized by high GCV and PCV values with minimal differential between them are most suitable for direct selection, as they are predominantly governed by genetic variability. Such traits hold promise for enhancing selection efficiency and achieving meaningful genetic progress (Ahmad *et al,* 2015; Khajuria *et al,* 2015; Chandramouli *et al,* 2016; Badiger *et al,* 2017; Kerure *et al,* 2017; Kumari *et al,* 2019).

Heritability

Heritability constitutes a cornerstone of quantitative genetics and plant breeding, representing the proportion of total phenotypic variance attributable to genetic variance. While the genotypic coefficient of variation (GCV) quantifies the magnitude of genetic diversity within a population, it does not differentiate between genetic and environmental contributions to phenotypic expression. Consequently, the integration of heritability estimates with GCV and genetic advance provides a more robust framework for evaluating the effectiveness of selection and the potential for genetic gain (Burton and DeVane, 1953). High heritability, when coupled with high GCV and high genetic advance, typically reflects the predominance of additive gene effects, suggesting that such traits are amenable to improvement through direct phenotypic selection (Johnson *et al,* 1955).

In the present investigation, broad-sense heritability estimates across the studied traits ranged from 24.67% to 96.22%, highlighting considerable variability in the degree of genetic control. Traits exhibiting high heritability (>70%) included the number of primary branches per plant, total soluble solids, stem girth, number of ridges per fruit, physiological loss, ascorbic acid content, and fruit diameter. These high heritability values imply that genetic variance constitutes the dominant source of phenotypic variation for these traits, rendering them ideal candidates for selection-based breeding strategies. These findings are in alignment with earlier research by Patel *et al* (2014), Ahmad *et al* (2015), Chandramouli *et al* (2016) and Kumari *et al* (2019) who similarly documented high heritability in okra for comparable traits, underscoring their relevance in genetic enhancement programs. For instance, the number of primary branches per plant demonstrated high GCV along with high heritability, suggesting that this trait is primarily governed by additive gene action, and thus offers substantial promise for improvement via simple selection protocols. Similarly, traits such as ascorbic acid content and stem girth, which are crucial for fruit quality and consumer acceptability, showed high heritability, indicating their amenability to improvement through conventional selection methods. Moderate heritability (51-70%) was recorded for traits such as seed index, ash content, pedicel diameter, moisture content and petiole length, reflecting a balanced contribution of genetic and environmental factors. While selection is still feasible for these traits, the realized genetic gain may be moderate and environmental variation could obscure underlying genetic effects. These observations are consistent with prior findings by Goswami *et al* (2012) and Umesh *et al* (2013), who emphasized the necessity for multi-environment evaluation to ensure stability and consistency of trait expression under variable growing conditions.

In contrast, traits such as flesh thickness, petiole diameter, leaf length and chlorophyll content exhibited low heritability (<50%), suggesting a predominant influence of environmental factors and/or non-additive gene effects. For example, chlorophyll

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content, a trait sensitive to fluctuations in light, water, and nutrient regimes, showed particularly low heritability, indicating that its phenotypic expression is highly plastic and less genetically determined. Such traits are less responsive to direct phenotypic selection and may benefit from precision breeding approaches, such as marker-assisted selection, genomic selection, or environment-specific breeding strategies. Previous studies by Goswami *et al* (2012), Shaikh *et al* (2013) and Kerure *et al* (2017) support these conclusions, recommending more advanced breeding methodologies for traits with substantial environmental sensitivity. Moreover, the relationship between heritability and genetic advance provides additional insights into the underlying genetic architecture of traits. Traits with high heritability but low genetic advance, such as fruit diameter, may be governed predominantly by non-additive gene effects or epistasis, thereby necessitating breeding strategies such as recurrent selection or heterosis breeding. Conversely, traits that exhibit both high heritability and high genetic advance, such as yield per plant and number of branches, are indicative of additive gene action and are thus ideal for direct and effective phenotypic selection. In conclusion, the combined assessment of heritability, genotypic coefficient of variation (GCV), and genetic advance provides a comprehensive framework for differentiating traits that can be effectively improved through direct phenotypic selection from those that necessitate more sophisticated breeding approaches. This integrative analysis is vital for developing strategic and efficient selection methodologies, thereby enhancing the overall success and genetic gains in okra improvement programs.

Genetic advance

Genetic advance, when interpreted in conjunction with heritability, serves as a critical indicator of the potential success of selection strategies within a breeding program. In the current investigation, the highest genetic advance as a percentage of the mean was observed for the number of seeds per fruit (22.51%), signifying substantial scope for genetic improvement. This high genetic advance, paired with elevated heritability, suggests that the trait is predominantly controlled by additive gene action, making it highly responsive to direct phenotypic selection, a finding consistent with the results reported by Kumawat *et al* (2022). In contrast, flesh thickness exhibited the lowest genetic advance (0.18%), indicating minimal potential for improvement. This may be attributed to strong environmental influence or a predominance of non-additive gene effects, as noted by Yadav *et al* (2020), thereby reducing the efficiency of direct selection for this trait.

Traits such as number of primary branches per plant, number of seeds per fruit, total soluble solids and physiological loss exhibited both high heritability and high genetic advance, making them excellent candidates for direct selection. These traits are likely governed by additive genetic effects, offering substantial potential for improvement through conventional breeding methods. These findings are corroborated by earlier studies conducted by Goswami *et al* (2012), Mishra *et al* (2015), Deepanshu and Shamd (2017) and Kumari *et al* (2019) affirming their value as reliable selection indices in okra breeding programs. As emphasized by Panse and Sukhatme (1984), high heritability must be interpreted alongside genetic advance to accurately predict the effectiveness of selection, as high heritability alone does not necessarily indicate additive gene action. Traits showing high heritability but low genetic advance, such as fruit diameter, are likely influenced by non-additive gene effects, reducing the efficiency of simple phenotypic selection. For such traits, breeding approaches like recurrent selection, heterosis breeding, or marker-assisted selection may be more effective.

Moreover, certain traits such as stem girth, number of ridges per fruit, total soluble solids and ascorbic acid exhibited high heritability combined with moderate genetic advance. According to Chandramouli *et al* (2016), this pattern indicates the involvement of both additive and non-additive genetic components, suggesting that while selection can be moderately effective, more refined strategies may be required for sustained genetic gains. Overall, the integration of genetic advances with heritability provides a more comprehensive framework for identifying superior traits for selection in okra. This approach enhances selection efficiency by enabling breeders to distinguish traits with high genetic potential from those heavily influenced by environmental variation or complex gene action, thereby facilitating the development of improved okra cultivars with desirable agronomic and nutritional traits.

Genetic advance over mean (GAM)

The genetic gain observed across various traits in the present study ranged from low to high (2.42% to 67.78%), underscoring the diverse genetic mechanisms influencing trait expression and the

Table 1: Estimates of phenotypic and genotypic coefficients of variation, heritability, genetic advance, and genetic advance over mean for growth and yield traits in okra.

Sr. No.	Character	Mean	Range	Coefficients of Variation		Heritability (%)	GA	GA as % of the mean
				GCV (%)	PCV (%)			
1.	Number of primary branches per plant	5.59	3.80-11.47	33.54	34.20	96.22	3.79	67.78
2.	Stem girth (mm)	36.67	26.22-42.34	8.45	9.03	87.57	5.97	16.28
3.	Petiole diameter (mm)	6.47	5.57-7.13	4.78	7.42	41.44	0.41	6.33
4.	Leaf length (cm)	21.33	19.75-22.76	2.61	5.14	25.86	0.58	2.74
5.	Fruit diameter (mm)	15.71	14.37-18.26	4.59	5.46	70.49	1.25	7.93
6.	Number of ridges per fruit	5.19	5.00-6.00	5.79	6.38	82.42	0.56	10.83
7.	Flesh thickness (mm)	1.59	1.27-1.99	7.74	11.11	48.61	0.18	11.12
8.	T.S.S (^{0}Brix)	10.86	8.07-13.90	13.30	13.93	91.20	2.84	26.17
9.	Ascorbic acid (mg/100g)	17.30	15.40-19.16	5.71	6.59	74.92	1.76	10.18
10.	Chlorophyll content (SPAD)	57.83	54.05-63.08	3.23	6.50	24.67	1.91	3.30
11.	Ash content (%)	9.73	7.41-11.54	10.34	12.96	63.60	1.65	16.98
12.	Moisture content	90.36	86.60-92.40	1.51	1.94	60.53	2.18	2.42
13.	Physiological loss	4.94	3.33-7.00	18.47	20.85	78.45	1.66	33.69
14.	Number of seeds per fruit	65.10	44.73-86.80	17.94	19.17	87.58	22.51	34.58
15.	Seed index	6.36	4.84-7.62	10.43	12.99	64.45	1.10	17.25

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differential effectiveness of selection. Notably, high genetic gains were recorded for number of primary branches per plant (67.78%), number of seeds per fruit (34.58%), physiological loss (33.69%) and total soluble solids (26.17%). The substantial genetic gains for these traits, especially when paired with high heritability estimates, strongly indicate the predominance of additive gene action. This genetic architecture enhances their responsiveness to selection, rendering these traits highly amenable to genetic improvement in okra. These findings are consistent with previous studies that have documented similar trends (Shaikh *et al,* 2013; Patel *et al,* 2014; Ahmad *et al,* 2015; Mishra *et al,* 2015; Deepanshu and Shamd, 2017), reaffirming the utility of these traits as reliable selection targets in breeding programs. Traits exhibiting moderate genetic gains, such as seed index (17.25%), ash content (16.98%), stem girth (16.28%), flesh thickness (11.12%), number of ridges per fruit (10.83%), and ascorbic acid (10.18%), suggest a more complex inheritance pattern involving both genetic and environmental components. While selection for these traits can yield genetic progress, the rate of improvement may be less pronounced compared to traits with higher genetic gains. This pattern reflects findings by Ahmad *et al* (2015) and Chandramouli *et al* (2016), who noted that moderate genetic gains often necessitate more refined breeding approaches or environmental management for optimal selection efficiency.

Conversely, traits such as pedicel diameter (9.43%), petiole diameter (6.33%), chlorophyll content (3.30%), leaf length (2.74%), and moisture content (2.42%) demonstrated low genetic gains, suggesting that these traits are significantly influenced by environmental factors or governed by non-additive genetic variance. The limited scope for improvement through direct phenotypic selection diminishes their utility as primary selection criteria. Similar observations have been reported by Kerure *et al* (2017), who emphasized the necessity of alternative breeding strategies, such as genotype-by-environment interaction studies or molecular approaches, to improve the selection response for traits with inherently low genetic gains. Overall, the observed variation in genetic gain underscores the importance of trait-specific strategies in okra improvement. Prioritizing traits with high genetic gain and heritability ensures more efficient selection, whereas traits with low gain may require integrated or indirect approaches to achieve meaningful genetic advancement.

CONCLUSION

This study revealed substantial genetic variability among twenty-five okra genotypes across key yield and quality traits. High GCV, PCV, heritability, and genetic advance for traits like number of primary branches per plant, total soluble solids, seeds per fruit and physiological loss indicate the

predominance of additive gene action, making them ideal for improvement through direct phenotypic selection. Traits with moderate variability, such as ash content and seed index, may benefit from multi-environment trials for stable expression, while those with low heritability and genetic gain, like chlorophyll content and petiole diameter require advanced breeding tools such as marker-assisted or genomic selection. High genetic advance over the mean in certain traits further supports their utility in breeding programs targeting yield and quality enhancement. The findings underscore the importance of tailored breeding strategies, conventional for heritable traits and molecular for complex ones. This work provides a valuable foundation for developing improved and high-performing okra cultivars, contributing to future food and nutritional security.

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