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ASSESSMENT OF GENETIC VARIABILITY FOR QUANTITATIVE TRAITS IN F_3 GENERATION OF OKRA (*Abelmoschus esculentus* L. MOENCH)

Vaishnavi R. Naktode[1], D.K. Zate[1], Subhash Kumar[1], S.M. Umate[1], A.H. Rathod[2] and F.S. Khan[3]

[1]Department of Genetics and Plant Breeding, College of Agriculture, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani- 431 402, Maharashtra, India.

[2]Quality Seed Production Unit, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani-431 402, Maharashtra, India.

[3]Department of Entomology, College of Agriculture, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani-431 402, Maharashtra, India.

*Corresponding author E-mail : vaishnavinaktode2002@gmail.com

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ABSTRACT

The genetic improvement of okra (*Abelmoschus esculentus* (L.) Moench) depends largely on the amount of variability available within segregating generations. The objective of this study was to estimate the genetic variability, broad-sense heritability and genetic advance for 11 quantitative characters in the F_3 progenies of okra to determine appropriate selection parameters for increasing yield. 84 single-plant selection (SPS) progenies obtained from 15 bi-parental crosses and two commercial checks were evaluated in randomized block design with two replications in the Kharif season (2025-26). The analysis of variance showed significant ($P < 0.01$) genotypic variation in all the studied traits, thereby suggesting a high degree of genetic diversity. The phenotypic coefficient of variation (PCV) values were only slightly higher than the genotypic coefficient of variation (GCV), which suggests a high genetic control with low environmental effect on the expression of the characters. Interestingly, the number of branches per plant had the highest GCV (37.89%) and PCV (38.66%). Estimates of broad-sense heritability (h^2_{bs}) for most of the characters were extremely high (>60%), ranging from 90.51% for fruit diameter and 96.04% for number of branches per plant. In addition to this, high heritability along with high genetic advance as a proportion of the mean (GAM > 20%) was recorded for branches per plant, plant height, internode length, and fruit yield. It is apparent from these data that there is a predominance of additive gene action for these traits and therefore early generation phenotypic selection would be extremely efficient for selection of better homozygous recombinants and developing high-yielding okra cultivars.

Key words : Okra, *Abelmoschus esculentus*, F_3 generation, Genetic variability, Heritability, Genetic advance.

Introduction

Okra (*Abelmoschus esculentus* (L.) Moench), belongs to the Malvaceae family. It is indigenous to Africa, though some wild varieties of okra have been found in India. It is an annual, fast-growing herb and the tender fruits of the plant are often used as vegetables. Okra is among the major fruit vegetables of the world's tropical and subtropical zones. Cultivation of okra in India takes place primarily in the states of Gujarat, Maharashtra, Andhra Pradesh, Uttar Pradesh, Madhya Pradesh, West Bengal, Assam, Rajasthan, Tamil Nadu, Karnataka, Haryana and Punjab. In India, okra is grown in the plains on an area of 509 thousand hectares, with an annual production of 6095 thousand tonnes (NHB, 2019).

The range of chromosome numbers present in this crop is found to be from 2n = 72 to 2n = 132; the genetic constitution of 2n = 132 chromosome numbers has been reported to be dominant in its wild variety. It is an example of a self-incompatible crop where cross-pollination naturally takes place in the range of 4-18%. The fruit is in the form of a capsule, which could be light green in colour or sometimes red in colour. It is oblong-shaped, having longitudinal furrows and is pointed at the end, having a beak. Its size ranges between 10-30 cm. It is very nutritious, having a high content of vitamins, calcium, potassium and fibers.

It can be seen that one of the primary foundations of any effective plant breeding program is genetic variability in the germplasm (Awasthi *et al*., 2022). Segregating generations, particularly F_2 and F_3 generations, serve as an important source of transgressive segregants and the creation of novel genotypes through recombination. The study of the F_3 generation is essential due to the higher degree of homozygosity compared to F_2 generations; thus, estimation of genetic parameters is made with increased precision (Naik *et al*., 2024).

It is extremely important to split the phenotypic variability into genetic and environmental components to understand the inheritance pattern of particular traits (Al-Jibouri *et al*., 1958). Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and environmental coefficient of variation (ECV) are the basic indicators of variability (Chavan *et al*., 2019). However, variability per se is not sufficient for success in the selection process. Broad-sense heritability estimates, along with genetic progress, were found to be highly accurate predictors of the genetic progress that could be achieved through selection (Johnson *et al*., 1955 and Priyanka *et al*., 2019). Additive traits can be selected at an early generation, whereas non-additive traits require delayed selection or appropriate mating designs.

Materials and Methods

Experimental material and Site

The field experiment was carried out in the Quality Seed Production (QSP) Unit, Vasantrao Naik Marathwada Krishi Vidyapeeth (VNMKV), Parbhani (19° 16' N lat., 76° 47' E long., 409.0 m MSL) in the *Kharif* season of 2025-26. The germplasm used for this investigation included 84 SPSs (F_3 generation) obtained from fifteen crosses of okra (Table 1). Parbhani Kranti and Pusa Sawani, two commercially grown cultivars, served as the control standards.

Experimental Design and Crop management

A Randomized Block Design (RBD) with two replications was used in conducting the experiment. The seeds were manually dibbled in a crop spacing of 60 cm × 30 cm using a gross plot size of 1.2 m × 3.0 m. Standard agronomic practices and natural selection criteria (lack of intensive chemical control for pests) were strictly adhered to in order to achieve uniformity of plant expression.

Data were collected from five randomly selected competing plants from each treatment replication. Calculation of days to 50% flowering was done on a whole-plot basis.

Table 1 : Details of the genetic material involved in the investigation.

S. no.	Name of Crosses	No. SPS	Checks
1.	EC 305653 × IC 4328	5	Parbhani Kranti
2.	IC 3340 × IC 3302C	9	Pusa Sawani
3.	EC 305609 × Parbhani Kranti	6	
4.	IC 3340 × Parbhani Kranti	8	
5.	EC 305609 × IC 3302	6	
6.	IC 9856C × Parbhani Kranti	5	
7.	IC 305613 × IC 293590	5	
8.	EC 305653 × IC 293590	5	
9.	IC 3769A × Parbhani Kranti	6	
10.	EC 305664 × IC 293590	5	
11.	EC 305612 × Punjab-8	5	
12.	IC 3769A × IC 3302	5	
13.	EC 305612 × Parbhani Kranti	5	
14.	EC 305653 × Parbhani Kranti	5	
15.	IC 3340C × IC 4507	4	

Quantitative Traits recorded: Days to 50% flowering, plant height (cm), number of branches per plant, number of fruits per plant, days to first harvest, fruit length (cm), fruit diameter (cm), fruit weight (g), internode length (cm), and fruit yield per plant (g) and marketable fruit yield (g)

Statistical analysis

The quantitative data collected during the experiment was statistically analyzed using ANOVA based on the randomized block design (RBD).

The different variance components were estimated based on the methodological procedures advocated by Burton and DeVane (Fisher, 1972). For instance, the genotypic variance $\left(\sigma_g^2\right)$ was computed as (MST – MSE)/ *r*, where MST denotes the mean square due to treatments or genotypes, MSE represents the mean sum of squares for error and *r* is the number of replications. The environmental variance $\left(\sigma_e^2\right)$ was equated to the error mean square (MSE), while the phenotypic variance $\left(\sigma_p^2\right)$ was derived as the sum of the genotypic and environmental variances $\left(\sigma_g^2 + \sigma_e^2\right)$.

Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), and Environmental Coefficient of Variation (ECV) were also computed using the method of Burton and DeVane (Fisher, 1972). These measures were computed through expressing the standard deviation of each trait as a

percentage of the general mean $(\overline{X})$ for each trait, formulated as $GCV = 100 \times \left(\sqrt{\sigma_g^2} / \overline{X}\right)$, $PCV = 100 \times \left(\sqrt{\sigma_p^2} / \overline{X}\right)$ and $ECV = 100 \times \left(\sqrt{\sigma_e^2} / \overline{X}\right)$.

Broad-sense heritability () was estimated as the proportion of genotypic variance relative to the total phenotypic variance, expressed as a percentage: $h_{bs}^2 = 100 \times \left(\sigma_g^2 / \sigma_p^2\right)$.

The genetic advance (GA) anticipated with the assumption of 5% selection intensity was calculated using the methods developed by Lush (1940) and by Johnson *et al*. (1955) and was defined as $GA = K \times \sigma_p \times h_{bs}^2$, where K = 2.06 represents the selection differential at a 5% selection intensity, σ_p is the phenotypic standard deviation and h_{bs}^2 is the broad-sense heritability measured as a proportion. The genetic advance as a percentage of the mean (GAM) was calculated using the following equation: $100 \times \left(GA / \overline{X}\right)$. The combined estimation of heritability and genetic advance was used in order to evaluate the prospects of selection for the analyzed traits.

In addition, when fruit weight data were available, the marketable fruit yield (MFY) was calculated in percent according to the following equation: MFY = 100 × [Weight of healthy fruit per plant/Weight of healthy fruit + Weight of damaged fruit)].

Results and Discussion

Analysis of Variance (ANOVA)

ANOVA indicated significant differences (P<0.01) between the 86 genotypes in all 11 quantitative traits (Table 1). This indicates considerable genetic variability in the selected F_3 progenies and shows great promise for genetic improvement of yield and its attributes (Chavan *et al*., 2019).

Mean Performance and Range

Wide variations have been observed in the mean performance of the F_3 selections (Table 2) and are comparable with those obtained in segregating generations of okra. There were wide differences in days to 50% flowering (44.50 – 52.00 days; mean = 48.53), wherein some of the selections, like IC 3340C × IC 4507-3, were found to have more earliness than the checks. The second parameter, where wide variation exists, is plant height (58.70 – 130.77 cm). Similar findings also reported by Janarthanan and Sundaram (2021), Shivaramegowda *et al.* (2016), Reddy *et al.* (2022).

It is to be mentioned here that the number of fruits per plant, one of the important components of yield, exhibited high variability, with values ranging from 14.70 - 18.25. High variability also existed in fruit yield per plant (229.63 – 347.77 g). Although the check variety Parbhani Kranti recorded the highest yield (347.77 g), there were F_3 selections from crosses such as EC 305612 × Parbhani Kranti-3 (343.04 g) and IC 3340C × Parbhani Kranti-5 (341.67 g) with comparable yield levels. Such

Table 2 : Analysis of Variance (Mean Sum of Squares) for Quantitative Traits in F_3 Generation of Okra.

S. no.	Source of Variation	Replication	Treatment	Error	F Ratio
	Degrees of freedom	1	85	85	(85, 85)
	Mean Sum of Squares				
1.	Days to 50% flowering	10.75	4.38**	2.16	2.02
2.	Plant height (cm)	4.84	492.85**	38.87	12.68
3.	Number of branches per plant	0.0002	0.21**	0.004	49.54
4.	Number of fruits per plant	9.73	1.43**	0.29	4.86
5.	Number of days to first harvest	0.15	2.03**	0.78	2.59
6.	Length of fruit (cm)	1.67	2.74**	0.22	12.22
7.	Diameter of fruit (cm)	0.00	0.019**	0.0009	20.08
8.	Weight of fruit (gm)	0.14	4.65**	0.38	12.08
9.	Internodal length (cm)	0.60	1.54**	0.13	11.74
10.	Fruit yield per plant (gm)	87.15	1965.43**	449.35	8.19
11.	Marketable fruit yield (gm)	173.95	215.43**	26.30	4.37

* and ** Significant at 5% and 1% levels of significance.

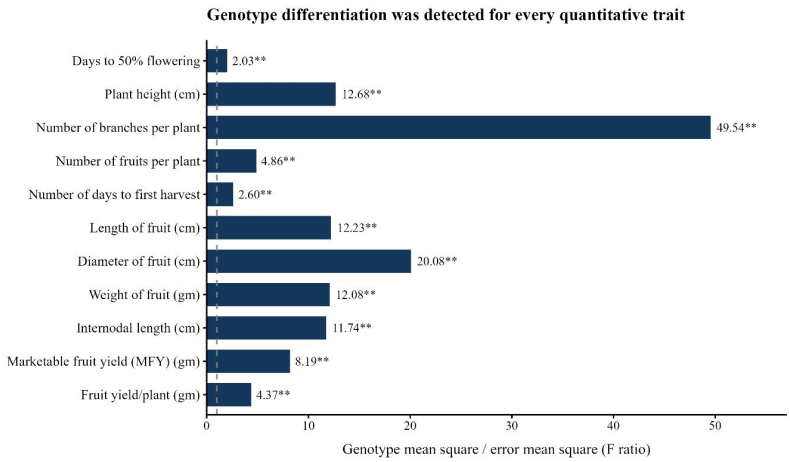


Fig. 1 : F-ratios (genotype mean square divided by error mean square) illustrating the degree of genotype differentiation for eleven quantitative traits in the F_3 generation of okra. Asterisks (**) denote high statistical significance at the 1% level ($P < 0.01$).

Table 3 : Mean, Range and Minimum/Maximum performance for Quantitative traits.

Trait	Minimum	Maximum	Mean±SEm	C.D. at 5%
Days to 50%flowering	44.50	52.00	48.53 ± 1.04	2.92
Plant height (cm)	58.70	130.77	93.73 ± 4.41	12.39
No. of branches/plant	0.20	1.58	0.84 ± 0.05	0.13
No. of fruits/plant	14.70	18.25	16.14 ± 0.38	1.07
Days to first harvest	52.50	57.00	55.51 ± 0.62	1.75
Length of fruit (cm)	10.60	16.65	14.45 ± 0.33	0.94
Diameter of fruit (cm)	1.71	2.22	1.93 ± 0.02	0.06
Weight of fruit (g)	12.90	20.40	17.19 ± 0.44	1.23
Internodal length (cm)	4.28	8.52	6.41 ± 0.26	0.71
Fruit yield/plant (g)	229.63	347.77	290.22 ± 14.98	42.14
Marketable fruit yield (%)	55.58	100.00	77.82 ± 3.63	10.19

transgressive segregants for yield components provide excellent prospects for selection (Awasthi *et al*., 2022 and Shiri *et al*., 2025).

Genotypic, Phenotypic and Environmental variance and Genetic parameters

Assessment of genetic variation is the very first prerequisite for every breeding program. Variability parameters of eleven quantitative characters have been provided in Table 3.

Phenotypic and Genotypic variance (σ^2p and σ^2g)

Generally, phenotypic variance (σ^2p) was slightly higher than genotypic variance (σ^2g) in all the characters considered in the study. This shows that the environment plays a role in the manifestation of these traits (Shiri *et al*., 2025).

Phenotypic and Genotypic Coefficient of variation (PCV and GCV)

Estimation of higher variability of GCV and PCV (>20%) was seen in the traits of number of branches per plant (GCV = 37.89%, PCV = 38.66%). These higher variations show a significant scope for genetic improvement of these traits by simple selection (Alam *et al*., 2020). Moderate variability was seen in traits of plant height, internodal length and marketable fruit yield (10-20%). Whereas low variability (<10%) was seen in fruit yield per plant, weight of fruit, length of fruit, diameter of fruit, number of fruits per plant, days to 50% flowering and number of days to first harvest. Lower variability of these traits shows that improvement can be done by hybridization to create more variability or selection for a longer time period (Priyanka *et al*., 2018). The general estimation of these variability parameters is in accordance with the basic principles mentioned by Burton and DeVane (1953) and Al-Jibouri *et al*. (1958).

Environmental Coefficient of Variation (ECV)

The Environmental Coefficient of Variation (ECV) precisely measures the modifying influence of the environment. ECV estimates were considerably high for ECV estimates were very low (<5%) for phenological and physical fruit traits such as number of days to first harvest (1.59%), fruit diameter (1.59%) and days to 50% flowering (3.03%). Overall, the narrow difference between PCV and GCV for most yield-attributing traits suggests that they are primarily governed by genetic factors, and selection based on phenotype would be highly rewarding.

Heritability (h^2bs)

The heritability estimates give information about the amount of total variance that can be attributed to genetic variation (Lush, 1940). The heritability estimates were found to be relatively high for 9 out of the 11 traits, ranging from $h^2 > 60\%$. The trait having the highest heritability was number of branches per plant (96.04%), followed by diameter of fruit (90.51%), plant height (85.38%), length of fruit (84.88%), weight of fruit (84.71%), internodal length (84.31%), marketable fruit yield (78.24%), number of fruits per plant (65.89%), and fruit yield per plant (62.78%). Moderate heritability was observed in the number of days to first harvest (44.44%) and days to 50% flowering (33.92%). Similar high heritability estimates for yield components in segregating

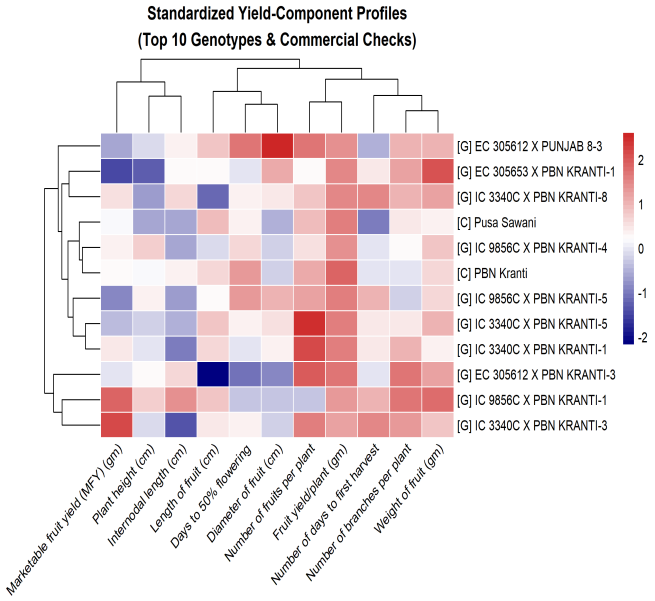


Fig. 2 : Hierarchical clustering and heatmap of standardized yield-component profiles comparing the top 10 F_3 genotypes with two commercial checks (Parbhani Kranti and Pusa Sawani). The colour gradient from blue to red represents standardized trait values from lowest to highest, highlighting trait synergies in transgressive segregants.

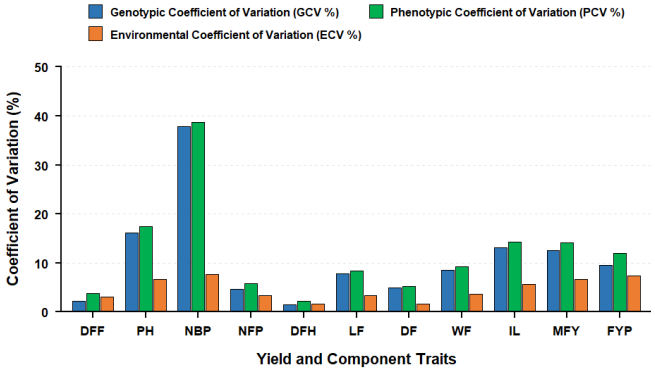


Fig. 3 : Genotypic, phenotypic and Environmental coefficients of variation for yield and its components in the F_3 generation of Okra.

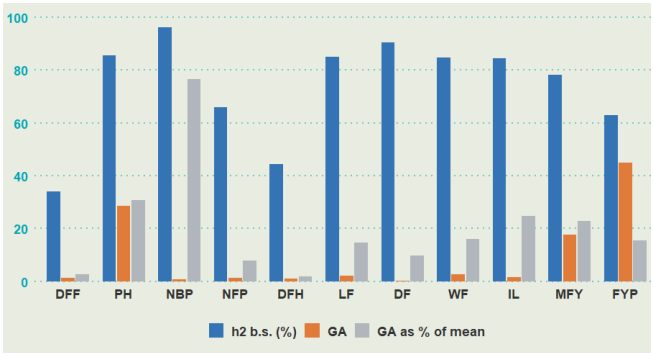


Fig. 4 : Heritability (h^2), genetic advance (GA) and genetic advance as % of mean (GA %) in the F_3 generation of Okra.

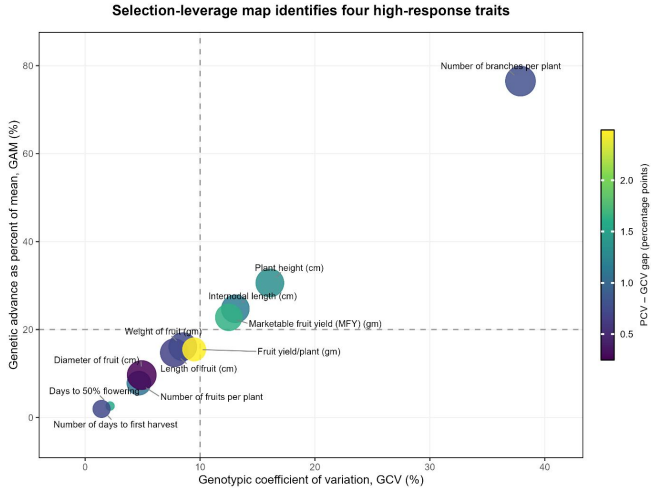


Fig. 5 : Selection-leverage map plotting Genetic Advance as a percentage of Mean (GAM) against the Genotypic Coefficient of Variation (GCV) for all evaluated traits. The dashed lines represent optimal thresholds (GCV > 10%, GAM > 20%). Bubble size and the corresponding color gradient represent the gap between Phenotypic and Genotypic Coefficients of Variation (PCV – GCV gap), indicating the magnitude of environmental influence on trait expression.

Table 4 : Genotypic and Phenotypic Variances and Genetic parameters.

S. no.	Character	Variance Components			CVs (%)		
		σ^2_g	σ^2_e	σ^2_p	GCV	PCV	ECV
1	Days to 50% flowering	1.109	2.162	3.271	2.17	3.73	3.03
2	Plant height (cm)	226.991	38.866	265.857	16.07	17.40	6.65
3	Number of branches per plant	0.102	0.004	0.106	37.89	38.66	7.69
4	Number of fruits per plant	0.569	0.295	0.863	4.67	5.76	3.36
5	Number of days to first harvest	0.624	0.781	1.405	1.42	2.14	1.59
6	Length of fruit (cm)	1.257	0.224	1.481	7.76	8.42	3.28
7	Diameter of fruit (cm)	0.009	0.0009	0.010	4.92	5.17	1.59
8	Weight of fruit (gm)	2.133	0.385	2.518	8.49	9.23	3.61
9	Internodal length (cm)	0.703	0.131	0.833	13.07	14.23	5.64
10	Marketable fruit yield (MFY)(gm)	94.567	26.299	120.866	12.50	14.13	6.59
11	Fruit yield/plant (gm)	758.041	449.347	1207.388	9.49	11.97	7.30

Table 5 : Genetic parameters.

S. no.	Character	h^2_{bs} (%)	Genetic Advance	
			GA	GAM
1	Days to 50% flowering	33.92	1.26	2.60
2	Plant height (cm)	85.38	28.68	30.60
3	Number of branches per plant	96.04	0.64	76.49
4	Number of fruits per plant	65.89	1.26	7.81
5	Number of days to first harvest	44.44	1.09	1.95
6	Length of fruit (cm)	84.88	2.13	14.73
7	Diameter of fruit (cm)	90.51	0.19	9.65
8	Weight of fruit (gm)	84.71	2.77	16.11
9	Internodal length (cm)	84.31	1.59	24.72
10	Marketable fruit yield (MFY) (gm)	78.24	17.72	22.77
11	Fruit yield/plant (gm)	62.78	44.94	15.48

generations of okra have been reported by Chavan *et al*. (2019), Bhavidoddi and Kantharaju (2021) and Awasthi *et al*. (2022).

Genetic Advance and Genetic advance as percentage of Mean (GAM)

In view of the fact that heritability cannot solely serve as an absolute criterion for predicting genetic progress, its estimation in conjunction with GAM (Johnson *et al*., 1955) is very reliable. High heritability values associated with high GAM (>20%) were obtained for the number of branches per plant (76.49%), plant height (30.60%), internodal length (24.72%), and marketable fruit yield (22.77%). The above data clearly demonstrate that these characters are governed by additive gene action. This would mean that phenotypic mass selection or progeny selection for these characters in the initial segregating generations would be very effective. It is also consistent with the suggestions made by Alam *et al*. (2020), Naik *et al*. (2024) and Shiri *et al*. (2025). However, some traits like fruit yield per plant have shown high heritability (62.78%) and moderate GAM (15.48%), which can suggest the presence of non-additive gene action, suggesting that selection for this trait might be deferred to later generations.

Conclusion

The current study has successfully proven the presence of significant genetic variation among the F*f* generation of okra studied. Plant morphological characteristics (plant height, number of branches, and internodal length) showed very little difference between PCV and GCV, high heritability in the broad sense and high genetic advance as a percentage of the mean. This has provided evidence of dominance of fixable additive gene effects, suggesting that phenotype-based individual and family selections would be effective enough in isolating homozygous recombinants in future generations.

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Conflict of interest : The authors hereby declare that there is no conflict of interest regarding the publication of this paper.

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