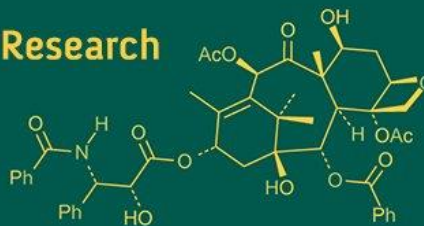


International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2026): 5.29
IJABR 2026; SP-10(8): 1989-1994
www.biochemjournal.com
Received: 02-06-2026
Accepted: 06-07-2026

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Estimates of genetic variability for yield traits in the F₅ and F₆ populations of okra (*Abelmoschus esculentus* L. Moench)

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DOI: <https://www.doi.org/10.33545/26174693.2026.v10.i8Sv.9703>

Abstract

The present investigation was undertaken to assess the magnitude of genetic variability, heritability and genetic advance for yield and yield attributing traits in advanced populations of okra (*Abelmoschus esculentus* L. Moench), comprised of F₅ and F₆ progenies developed from the crosses OK-2017-010 × Pusa Sawani and OK-2017-010 × Varsha Uphar. The study was conducted during *khari* 2024 and 2025 using Randomized Complete Block Design with two replications. Analysis of variance revealed significant differences among the progenies for most of the characters studied, indicating the presence of substantial genetic variability. In the F₅ populations, high genotypic coefficient of variation and phenotypic coefficient of variation were recorded for total yield per plant, number of fruits per plant and number of branches per plant. High heritability coupled with high genetic advance as percent of mean was observed for total yield per plant, number of fruits per plant, plant height, number of nodes on the main stem and number of seeds per fruit, indicating the predominance of additive gene action. Similar trends were observed in the F₆ progenies, where total yield per plant exhibited high GCV (23.74%), PCV (24.50%), heritability (93.94%) and GAM (47.41%). The findings suggested that direct selection for these traits would be effective for improving fruit yield in okra breeding programmes.

Keywords: Okra, genetic variability, GCV, PCV, heritability, genetic advance, advanced population, yield traits

Introduction

Okra (*Abelmoschus esculentus* L. Moench) is an important dicotyledonous vegetable crop widely grown in tropical and subtropical regions of the world. It belongs to the family Malvaceae and has a somatic chromosome number of 2n = 130. Cultivated okra is considered an allopolyploid species evolved through interspecific hybridization between *Abelmoschus tuberculatus* and *Abelmoschus ficulneus*, followed by chromosome doubling (Liu *et al.*, 2024) [18]. The crop is known to have originated in South Asia, Ethiopia and West Africa (Singh and Nigam, 2023) [31]. Among the species of the genus *Abelmoschus*, *Abelmoschus esculentus* L. Moench is the most widely cultivated species for its high nutritional, medicinal, and economic value.

Okra is an erect annual herbaceous plant with a semi-woody stem and hibiscus-like flowers. It is an often-cross-pollinated crop with natural outcrossing ranging from 4 to 19 percent. The crop is well adapted to different agro-climatic conditions and is mainly cultivated for its tender green fruits. India is the leading producer of okra, contributing about 60-63 percent of global production. Major okra-growing states in India include West Bengal, Odisha, Bihar, Madhya Pradesh, Haryana, Andhra Pradesh and Karnataka (Anonymous, 2024) [4].

Okra fruits are highly nutritious and rich in carbohydrates, proteins, dietary fibre, vitamins and minerals. The fruits are excellent sources of vitamins C, B₁, B₆, K and folate, along with minerals such as calcium, potassium and iron. Mature seeds contain considerable amount of oil and crude protein (Simon *et al.*, 2013) [29]. The mucilage present in fruits is used in sugar clarification and paper production, while flavonoids and phytosterols present in okra exhibit antioxidant and cholesterol-lowering properties.

Fruit yield is an important economic trait in okra and is influenced by several component characters such as plant height, number of fruits per plant, fruit length and fruit weight.

Since these traits are quantitatively inherited and influenced by environment, assessment of genetic variability becomes essential for effective selection. Parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance help in understanding the extent of variability present in breeding materials. Advanced generations such as F_5 and F_6 provide good opportunities for identifying stable and superior segregants with desirable yield traits for crop improvement programmes.

Materials and Methods

The experiment for the analysis of genetic variability parameters for yield traits in the F_5 and F_6 populations of okra (*Abelmoschus esculentus* L. Moench) was carried out during *kharif* 2024 and 2025 in the research field of the Department of Biotechnology and Crop Improvement, College of Horticulture, Bengaluru, University of Horticultural Sciences, Bagalkot, Karnataka. The experimental site is situated at an elevation of 930 m above mean sea level at 12°58' North latitude and 77°35' East longitude and falls under the Eastern Dry Zone of Karnataka. The soil of the experimental field was red sandy loam with slightly acidic pH ranging from 6.2 to 6.4.

The research material consisted of F_5 and F_6 populations derived from two biparental crosses, namely OK-2017-010 × Pusa Sawani and OK-2017-010 × Varsha Uphar. The F_5 populations were developed by selfing selected superior F_4 plants and further selfing of selected F_5 progenies generated the F_6 populations. The F_5 and F_6 generations, along with their respective parents and commercial checks, were evaluated in a Randomized Complete Block Design (RCBD) with two replications. The F_5 population consisted of 18 lines, three parents and three checks, while the F_6 population consisted of 14 lines, three parents and one check. Each family was represented by 20 plants with a spacing of 60 cm × 40 cm.

Standard agronomic practices and plant protection measures were followed throughout the crop growth period to raise a healthy crop. Observations were recorded on all plants in the F_5 and F_6 populations for fourteen quantitative traits viz., days to first flowering, days to 50 percent flowering, plant height, number of branches per plant, number of nodes on the main stem, internodal length, number of ridges on fruit surface, fruit diameter, fruit length, stem girth, number of fruits per plant, average fruit weight, number of seeds per fruit and total yield per plant. Plant height was measured from the base to the apex at 90 DAS, while internodal length was measured between the 8th and 9th node at final harvest. The number of branches and nodes were counted at final picking stage.

The data recorded for different traits were subjected to statistical analysis following Randomized Complete Block Design. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated according to Burton and DeVane (1953)^[7]. Heritability in broad sense was calculated following Lush (1940)^[19], while

genetic advance was estimated as per the method suggested by Johnson *et al.* (1955)^[14].

Results and Discussion

The analysis of variance revealed the presence of considerable variation among the progenies of F_5 and F_6 generations derived from the crosses OK 2017-010 × Pusa Sawani and OK 2017-010 × Varsha Uphar for all the characters studied (Tables 1, 2 and 3). Highly significant variation between the genotypes for important yield contributing traits such as plant height, number of nodes, internodal length, number of fruits per plant, average fruit weight, number of seeds per fruit and total yield per plant and significant differences observed for flowering traits, fruit diameter, fruit length, stem girth and number of ridges on fruit surface indicated substantial genetic variability in the populations, thereby providing considerable scope for effective selection and genetic improvement in okra. Similar findings were reported by Reddy *et al.* (2012)^[26], Nwangburuka *et al.* (2012)^[23], Chandra *et al.* (2014)^[8] and Kerure *et al.* (2017)^[15]. The existence of wide variability among the progenies indicated that the parental combinations generated sufficient genetic recombination and segregation for economically important traits. These results agree with the findings reported by Das *et al.* (2012)^[10], Duggi *et al.* (2013)^[11], Patel *et al.* (2014)^[24] and Alam *et al.* (2020)^[3].

The estimates of variability parameters revealed that the phenotypic coefficient of variation (PCV) was slightly higher than the genotypic coefficient of variation (GCV) for all characters across the F_5 and F_6 generations (Tables 4, 5 and 6), indicating the minimal influence of the environment on trait expression and predominance of genetic control. Similar results were reported by Chandra *et al.* (2014)^[8] and Khajuria *et al.* (2016)^[16]. Among the traits studied, high GCV and PCV were consistently observed for total yield per plant, number of fruits per plant, number of branches, number of nodes, average fruit weight and plant height in both F_5 and F_6 generations. In the F_5 generation of OK 2017-010 × Pusa Sawani, total yield per plant recorded high GCV (20.67%) and PCV (21.41%), while in OK 2017-010 × Varsha Uphar the corresponding values were still higher (23.74% and 24.50%). Similarly, the F_6 generation also exhibited high variability for total yield per plant with GCV and PCV values of 19.42 and 20.56 percent, respectively. High variability for these traits indicated greater opportunity for improvement through selection. These observations are consistent with earlier findings reported by Syfullah *et al.* (2018)^[33], Alam *et al.* (2020)^[3], Shwetha *et al.* (2022)^[28] and Nanditha *et al.* (2023)^[21].

Moderate variability was observed for internodal length, fruit length, number of seeds per fruit and stem girth, whereas low GCV and PCV values were recorded for days to first flowering, days to 50 percent flowering and fruit diameter in most generations, indicating comparatively narrow variation for these characters. Similar observations were reported by Sharma *et al.* (2016)^[27], Kumar *et al.* (2020)^[17] and Singh *et al.* (2020)^[30].

Table 1: Analysis of variance among the F₅ progenies of the cross OK 2017-010 × Pusa Sawani in Okra

Source of variation	Replication	Treatment	Error
Degrees of Freedom	1	14	14
Days to first flowering	10.80*	8.18* *	2.16
Days to 50% flowering	6.53	7.70*	2.1
Plant height (cm)	167.48	1164.26* *	57.67
Number of branches	0.02	0.49*	0.18
Number of nodes	0.71	6.30* *	0.43
Internodal length (cm)	0.01	2.54* *	0.23
Number of ridges on the fruit surface	0.12	0.25* *	0.03
Fruit diameter (cm)	0	0.01*	0
Fruit length (cm)	0	1.82* *	0.19
Stem girth (cm)	0	0.13*	0.05
Number of fruits per plant	1.65	44.59* *	0.83
Average fruit weight (g)	0.1	1.40* *	0.27
Number of seeds per fruit	5.82	80.90* *	7.69
Total yield per plant (g)	745.62	12671.12* *	445.52

* and ** Indicate significance at 5 and 1 percent probability level, respectively.

Table 2: Analysis of variance among the F₅ progenies of the cross OK 2017-010 × Varsha Uphar in Okra.

Source of variation	Replication	Treatment	Error
Degrees of Freedom	1	14	14
Days to first flowering	3.33*	8.03* *	0.40
Days to 50% flowering	2.13	7.46* *	0.49
Plant height (cm)	53.16	808.58* *	40.51
Number of branches	0.01	0.51* *	0.10
Number of nodes	0.19*	11.95* *	0.02
Internodal length (cm)	0.00	2.57* *	0.44
Number of ridges on the fruit surface	0.03	0.73* *	0.01
Fruit diameter (cm)	0.03	0.43* *	0.00
Fruit length (cm)	0.01	1.43* *	0.10
Stem girth (cm)	0.00	0.09*	0.03
Number of fruits per plant	0.01	28.88* *	1.63
Average fruit weight (g)	0.01	5.26* *	0.28
Number of seeds per fruit	14.24	127.01* *	22.45
Total yield per plant (g)	0.14	23063.4* *	720.05

* and ** Indicate significance at 5 and 1 percent probability level, respectively.

Table 3: Analysis of variance among the F₆ progenies of the cross OK 2017-010 × Pusa Sawani and OK 2017-010 × Varsha Uphar in Okra

Source of variation	Replication	Treatment	Error
Degrees of Freedom	1	17	17
Days to first flowering	0.44	14.12* *	3.42
Days to 50% flowering	1.78	12.65* *	2.98
Plant height (cm)	1.07	622.62* *	2.10
Number of branches	0.00	0.15* *	8.90
Number of nodes	1.36	7.62* *	6.44
Internodal length (cm)	0.25	2.41* *	3.38
Number of ridges on the fruit surface	0.03	0.19* *	2.25
Fruit diameter (cm)	0.00	0.02* *	2.50
Fruit length (cm)	0.56	2.47* *	5.25
Stem girth (cm)	0.00	0.04* *	2.95
Number of fruits per plant	0.03	21.91* *	3.38
Average fruit weight (g)	1.31	10.09* *	5.92
Number of seeds per fruit	7.11	115.94* *	2.96
Total yield per plant (g)	781.76	13322.70* *	6.74

* and ** Indicate significance at 5 and 1 percent probability level, respectively.

Table 4: Estimates of genetic variability parameters for growth and yield traits among the F₅ progenies of the cross OK 2017-010 × Pusa Sawani.

Characters	Mean	Range		GCV (%)	PCV (%)	h ² bs (%)	GAM (%)
		Min	Max				
Days to first flowering	41.53	39.00	46.00	4.18	5.47	58.25	6.57
Days to 50% flowering	43.93	41.00	47.50	3.81	5.04	57.09	5.93
Plant height (cm)	170.00	136.80	214.20	13.84	14.54	90.56	27.13
Number of branches	2.00	1.13	3.00	19.73	29.07	46.07	27.59
Number of nodes	13.79	10.17	16.60	12.42	13.30	87.2	23.9
Internodal length (cm)	12.06	9.67	13.88	8.90	9.76	83.14	16.72
Number of ridges on the fruit surface	5.52	5.08	6.26	6.04	6.80	78.81	11.05
Fruit diameter (cm)	1.62	1.53	1.71	3.24	4.30	56.82	5.04
Fruit length (cm)	10.95	9.65	12.41	8.22	9.15	80.83	15.23
Stem girth (cm)	1.97	1.44	2.49	10.02	15.19	43.55	13.63
Number of fruits per plant	26.47	16.58	36.00	17.67	18.00	96.37	35.73
Average fruit weight (g)	14.22	12.62	15.81	5.29	6.42	67.84	8.98
Number of seeds per fruit	54.34	38.30	64.68	11.13	12.25	82.64	20.85
Total yield per plant (g)	378.31	220.49	530.17	20.67	21.41	93.21	41.10

GCV: Genotypic Coefficient of Variation	h ² bs: Broad sense heritability
PCV: Phenotypic Coefficient of Variation	GAM: Genetic Advance Percent Mean

Table 5: Estimates of genetic variability parameters for growth and yield traits among the F₅ progenies of the cross OK 2017-010 × Varsha Uphar

Characters	Mean	Range		GCV (%)	PCV (%)	h ² bs (%)	GAM (%)
		Min	Max				
Days to first flowering	41.13	37.50	45.00	4.75	4.99	90.41	9.30
Days to 50% flowering	44.47	41.50	47.50	4.20	4.48	87.66	8.10
Plant height (cm)	173.74	136.80	212.00	11.28	11.86	90.46	22.10
Number of branches	2.46	1.50	3.25	18.40	22.43	67.32	31.10
Number of nodes	16.13	11.90	19.90	15.13	15.16	99.59	31.11
Internodal length (cm)	12.18	9.67	14.23	8.48	10.07	70.84	14.70
Number of ridges on the fruit surface	5.96	5.08	7.15	10.08	10.19	97.84	20.53
Fruit diameter (cm)	2.09	1.55	2.85	22.09	22.18	99.21	45.33
Fruit length (cm)	11.52	10.13	13.30	7.08	7.59	87.17	13.63
Stem girth (cm)	2.06	1.75	2.48	7.83	11.88	43.41	10.63
Number of fruits per plant	28.23	23.50	36.50	13.08	13.83	89.32	25.46
Average fruit weight (g)	15.58	13.96	18.70	10.12	10.68	89.80	19.76
Number of seeds per fruit	58.01	42.44	72.74	12.47	14.90	69.96	21.48
Total yield per plant (g)	445.16	333.73	682.10	23.74	24.50	93.94	47.41

GCV: Genotypic Coefficient of Variation	h ² bs: Broad sense heritability
PCV: Phenotypic Coefficient of Variation	GAM: Genetic Advance Percent Mean

Table 6: Estimates of genetic variability parameters for growth and yield traits among the F₆ progenies of the crosses OK 2017-010 × Pusa Sawani and OK 2017-010 × Varsha Uphar

Characters	Mean	Range		GCV (%)	PCV (%)	H ² bs (%)	GAM (%)
		Min	Max				
Days to first flowering	42.33	39.50	49.00	5.79	6.72	74.19	10.28
Days to 50% flowering	46.17	43.00	52.00	5.02	5.84	73.93	8.90
Plant height (cm)	188.43	163.10	239.70	9.25	9.48	95.10	18.57
Number of branches	1.85	1.20	2.20	13.42	16.10	69.44	23.04
Number of nodes	12.77	10.20	16.90	14.58	15.94	83.69	27.48
Internodal length (cm)	14.02	12.05	15.95	7.46	8.19	82.92	13.99
Number of ridges on the fruit surface	5.27	5.00	6.18	5.61	6.04	86.18	10.73
Fruit diameter (cm)	1.55	1.40	1.69	5.69	6.21	83.84	10.73
Fruit length (cm)	12.03	9.12	13.24	8.46	9.96	72.24	14.81
Stem girth (cm)	1.99	1.69	2.21	6.72	7.34	83.84	12.68
Number of fruits per plant	24.96	20.70	30.90	13.04	13.47	93.70	26.01
Average fruit weight (g)	16.32	11.32	20.10	13.11	14.39	83.06	24.62
Number of seeds per fruit	56.67	41.00	71.00	13.27	13.60	95.26	26.68
Total yield per plant (g)	408.11	286.64	528.56	19.42	20.56	89.25	37.80

GCV: Genotypic Coefficient of Variation	h ² bs: Broad sense heritability
PCV: Phenotypic Coefficient of Variation	GAM: Genetic Advance Percent Mean

High heritability coupled with high genetic advance as percent mean was recorded for several economically important traits across the generations. Total yield per plant exhibited high heritability along with high GAM in all the generations studied. In the F_5 generation of OK 2017-010 × Pusa Sawani, total yield per plant recorded heritability of 93.21 percent with GAM of 41.10 percent, while in the cross OK 2017-010 × Varsha Uphar, heritability recorded was 93.94 percent with 47.41 percent GAM. Similarly, in the F_6 generation, total yield per plant showed heritability of 89.25 percent coupled with GAM of 37.80 percent. These findings indicated the predominance of additive gene action and effectiveness of direct phenotypic selection for improving yield. These findings are in line with the observations of Patro and Ravisankar (2004)^[25], Singh *et al.* (2007)^[32], Barche *et al.* (2014)^[6], Tudu *et al.* (2021)^[34], Awasthi *et al.* (2022)^[5] and Mohammed *et al.* (2022)^[20].

High heritability coupled with high GAM was also observed for number of fruits per plant, plant height, number of nodes, average fruit weight and number of seeds per fruit in both F_5 and F_6 generations, suggesting that these characters were mainly governed by additive gene effects and could be effectively improved through simple selection procedures. Similar findings were reported by Nasit *et al.* (2009)^[22], Adiger *et al.* (2011)^[1], Barche *et al.* (2014)^[6], Jadhav *et al.* (2022)^[12] and Mohammed *et al.* (2022)^[20].

Fruit diameter and number of ridges on fruit surface in the F_5 generation of OK 2017-010 × Varsha Uphar exhibited very high heritability estimates of 99.21 and 97.84 percent, respectively, coupled with high GAM, indicating strong genetic control over these traits. Similarly, plant height and number of seeds per fruit in the F_6 generation recorded high heritability estimates of 95.10 and 95.26 percent, respectively. Similar reports were given by Awasthi *et al.* (2022)^[5], Jadhav *et al.* (2022)^[12] and Singh *et al.* (2020)^[30].

Moderate heritability coupled with moderate GAM was observed for internodal length, fruit length and flowering traits in most generations, indicating the involvement of both additive and non-additive gene action along with environmental influence. Low heritability coupled with low genetic advance was observed for certain traits such as stem girth and fruit diameter in some populations, suggesting limited effectiveness of selection due to environmental effects. Similar findings were reported by Jaiprakashnarayan *et al.* (2006)^[13], Akotkar *et al.* (2010)^[2] and Chaurasiya *et al.* (2010)^[9].

Overall, the present investigation revealed substantial genetic variability among the advanced populations of both the crosses. Traits such as total yield per plant, number of fruits per plant, plant height, number of nodes, average fruit weight and number of seeds per fruit exhibited high heritability coupled with high genetic advance across generations, indicating the predominance of additive gene action and greater scope for improvement through direct phenotypic selection in okra breeding programmes. Similar conclusions were also drawn by Reddy *et al.* (2012)^[26], Kerure *et al.* (2017)^[15], Syfullah *et al.* (2018)^[33], Alam *et al.* (2020)^[3] and Nanditha *et al.* (2023)^[21].

Conclusion

The present investigation on F_5 and F_6 populations derived from the crosses OK 2017-010 × Pusa Sawani and OK 2017-010 × Varsha Uphar revealed significant variability

among the progenies for flowering, growth, fruit and yield traits, indicating ample scope for selection and improvement in okra. High heritability coupled with high genetic advance was observed for important traits such as total yield per plant, number of fruits per plant, plant height, number of nodes, average fruit weight and number of seeds per fruit, suggesting the predominance of additive gene action and effectiveness of direct phenotypic selection. The study identified promising lines with desirable yield contributing traits, which can be further utilized in okra breeding programmes for the development of high yielding varieties.

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