



Plant Archives

Journal homepage: <http://www.plantarchives.org>DOI Url : <https://doi.org/10.51470/PLANTARCHIVES.2025.v25.no.2.320>

GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE ANALYSIS IN F_2 SEGREGATING POPULATIONS FOR YIELD AND ITS CONTRIBUTING TRAITS IN OKRA (*ABELMOSCHUS ESCULENTUS* L. MOENCH)

V.R. Khandebharad^{1*}, R.A. Patil² and S.P. Pole³¹Department of Horticulture (Vegetable Science), College of Agriculture, Latur - 413 512, VNMKV Parbhani, Maharashtra, India.²Department of Horticulture, College of Agriculture, Dharashiv - 413 501, VNMKV, Parbhani, Maharashtra, India.³Oilseeds Research Station, Latur - 413 512, VNMKV, Parbhani, Maharashtra, India.*Corresponding author E-mail : vrkhandebharad@gmail.com

(Date of Receiving-26-07-2025; Date of Acceptance-30-09-2025)

ABSTRACT

A field experiment titled “Genetic studies and inbreeding depression in F_2 generation of selected crosses in Okra (*Abelmoschus esculentus* (L.) Moench)” was carried out during the *kharif* season of 2024 and the *summer* season of 2025 at the Oilseeds Research Station, Latur-413512, Maharashtra, India. The crossing and selfing programme were conducted during *kharif* 2024 and the experiment was conducted during *summer* 2025. This study aimed to assess the genetic variability, heritability, genetic advance and trait correlations of yield and its related characteristics in F_2 populations of three crosses along with their respective parental lines and F_1 . Six parents and F_1 were evaluated following a randomized block design with three replications while the F_2 generations of three crosses; Arka Anamika $\times$ IC-42464 (Cross-I), Konkan Bhindi $\times$ IC-42470 (Cross-II) and Arka Abhay $\times$ IC 42472 (Cross-III) were evaluated without replication as segregating F_2 generations were involved. Significance variability observed for ten quantitative characters in F_2 populations of okra. The PCV and GCV were moderate to high for all the characters except fruit length and fruit weight in F_2 population of C-I; Fruit yield per plant in F_2 population of C-II and internodal length, fruit diameter and number of nodes per plant in F_2 population of C-III. High heritability coupled with moderate to high genetic advance as a percentage of mean (GAM) was observed for traits like number of nodes per plant, fruit diameter, fruit yield per plant, days to flowering and internodal length in F_2 population of C-I; fruit length, internodal length, number of primary branches per plant and fruit weight in F_2 population of C-II and plant height, fruit weight, number of fruits per plant and fruit yield per plant in F_2 population of C-III which indicated lower environmental influence on these traits and indicating strong additive genes action. Simple and early selection schemes would be effective for the improvement of these traits. For certain traits like fruit length and fruit weight in F_2 population of C-I: plant height in F_2 population of C-II and fruit diameter in F_2 population of C-III where high heritability was observed but with limited genetic progress simple selection may not be advantageous. The finding of these traits valuable as inbred lines in a hybrid development programme contributing to genetic diversity and potential improvements in hybrid vigour.

Key words : Okra, Genetic variability, Heritability, Genetic advance, Yield and quality.

Introduction

Vegetables are considered as ‘protective supplementary foods’ because they are rich in minerals, vitamins, and essential amino acids that are vital for the proper functioning of the human metabolic process. Okra (*Abelmoschus esculentus* [L.] Moench) is a significant

vegetable crop propagated from seeds, primarily cultivated in tropical and subtropical regions globally. It belongs to the Malvaceae family with a chromosome number $2n=130$ and amphidiploids in nature. This crop can thrive both in home gardens and on large scale commercial farms. It is a versatile crop with a broad range of adaptability, owing to its ease of cultivation, short

duration, high export potential, and suitability to diverse environmental conditions and soil types (Priyanka *et al.*, 2018).

The green, non-fibrous fruits of okra which round seeds are harvested while still immature, before fiber develops and are consumed as a vegetable. Okra can be used in various culinary dishes, while its leaves are consumed similarly to spinach in some African cultures. Additionally, the roots and stems are utilized in purifying cane juice for producing jaggery or brown sugar (Chauhan, 1972). The greenish-yellow oil derived from okra seeds is viewed as an alternative to edible oil noted for its richness in oleic acid and linoleic acid. It also possesses substantial nutritional value containing vitamin C (30 mg/100 g), vitamin A (20 mg/100 g), zinc (6 mg/100 g), β -carotene (300 μ g/100 g) and folic acid (300 μ g/100 g). with its high dietary fiber content, low calorie count and abundance of minerals such as Ca, P, K and Mg okra is a valuable addition to human nutrition. It is known to be a good iodine source and acts as a diuretic to ease gastric discomfort largely due to its high polysaccharide content that creates a mucilaginous texture.

In terms of commercial farming okra is extensively grown in West Africa, India, Southeast Asia, the Southern United States, Brazil and Turkey. In India, key states for okra production include Uttar Pradesh, Assam, Bihar, Orissa, Maharashtra, West Bengal and Karnataka. Among all vegetables cultivated in India, okra is grown over an area of 562 (000 Ha) yielding an annual production of 7694 (000 MT) (Anonymous, 2024). Specifically, In Maharashtra, okra is cultivated across 12.29 (000 Ha) resulting in a production of 123.69 (000 MT) (Anonymous, 2024). Okra holds considerable export potential, contributing approximately 13% to the total export of fresh vegetables.

Increase in demand and the area under cultivation necessitates development of improved varieties in this crop. Improvement of the crop for yield and yield attributing characters depends upon variability present in crop and breeding method used. Genetic variability is prerequisite for any successful breeding programme. The variability that is present naturally in population was considered enough for crop improvement. Lack of useful variability necessitates the creation of variability through different means like hybridization or hybridization followed by selection in segregating population is very useful. The degree to which the environment influences character expression and the potential for improvement following selection are both determined by heritability and genetic

advancement. The F_2 generation is critical for success of the breeding programme, as there are more chances of recovering superior recombinants in advanced generations (Hallur *et al.*, 2017).

Materials and Methods

The experimental material in the present study consisted five contrasting parental lines viz., Arka Anamika, Konkan Bhindi, Arka Abhay, IC-42464, IC-42470, IC-42472 obtained from various sources as indicated in Table 1. The F_1 progeny of three crosses viz., Arka Anamika $\times$ IC-42464 (Cross-I), Konkan Bhindi $\times$ IC 42470 (Cross-II) and Arka Abhay $\times$ IC-42472 (Cross-III) hereafter referred to as C-I, C-II and C-III respectively along with their parental line were sown during *kharif* season of 2024 at Oilseeds Research Station, Latur. The crosses were developed by mating the contrasting parents viz., Arka Anamika $\times$ IC-42464, Konkan Bhindi $\times$ IC-42470 and Arka Abhay $\times$ IC-42472. The seeds of parents and F_2 were produced by selfing while fresh F_1 seeds were developed by hand emasculation followed by pollination. The experiment was conducted at Oilseeds Research Station, Latur during Summer season of 2025. The parents and their respective F_1 's were sown in separate blocks with three replications and the F_2 population sown without replication. Each entry of Parents and F_1 was sown in a single row of three-meter length with a row-to-row spacing of 60 cm and plant-to-plant spacing of 30 cm in each replication. Each row accommodated ten plants. The parents and hybrids were evaluated following randomized block design with three replications and the F_2 population was unreplicated. The experiment was sown on 23 January 2025. All the recommended agronomic packages of practices and necessary plant protection measures were followed to raise a good crop. The observation recorded following standard procedures from five plants per parent and hybrid cross. The mean of these five plants was considered for statistical analysis. With respect to F_2 , observations were recorded on 158 plants in C-I, 143 plants in C-II and 142 plants in C-III on the ten characters viz., days to flowering, plant height (cm), internodal length (cm), number of nodes per plant, number of primary branches per plant, fruit length(cm), fruit diameter (cm), fruit weight (g), number of fruits per plant, fruit yield per plant (g). Variances for all the characters under study was worked out by using the formula of Panse and Sukhatme (1985). The Parameters of variability were calculated as per formula given by Burton and De Vane (1953). Heritability in broad sense and Genetic advance, Genetic advance as per cent of mean was determined as per formula given

by Hanson *et al.* (1956) and Johnson *et al.*, (1955).

Results and Discussion

The mean, range, phenotypic and genotypic coefficient of variation, heritability and genetic advance as per cent of mean for 10 traits are presented in Table 1 and Fig. 1a, 1b for population Arka Anamika $\times$ IC-42464 (C-I), Table 2 and Fig. 2a, 2b for population Konkan Bhindi

$\times$ IC-42470 (C-II), Table 3 and Fig. 3a, 3b for population Arka Abhay $\times$ IC-42472 (C-III). In the present study, all three crosses exhibited substantial variability for most traits with minimal environmental influence as indicated by small differences between GCV and PCV emphasizing the strong genetic control over trait expression.

Table 1 : Estimates of Range, mean, Genotypic and phenotypic coefficient of variation (GCV and PCV), heritability, genetic advance and genetic advance as per cent of mean for fruit yield and yield attributing traits in F_2 population of Arka Anamika $\times$ IC-42464 in okra.

S. no.	Characters	Range		Mean $\pm$ SEM of F_2	GCV (%)	PCV (%)	Heritability h^2 (bs) (%)	Genetic advancement	Genetic advance % Mean GAM (%)
		Min	Max						
1.	Days to Flowering	36	56	46.05 $\pm$ 0.42	6.1	6.1	99.62	9.9	12.5
2.	Plant height (cm)	17	81	43.68 $\pm$ 1.20	4.7	4.8	96.16	9.6	9.5
3.	Internodal length (cm)	1.78	8.7	4.80 $\pm$ 0.13	12.0	12.8	87.63	1.5	23.2
4.	Number of Nodes per Plant	6	22	12.76 $\pm$ 0.23	17.2	17.3	98.10	4.6	35.0
5.	Number of primary branches per plant	0	3	1.41 $\pm$ 0.06	12.0	12.3	95.22	5.3	24.1
6.	Fruit length (cm)	4.5	19	11.41 $\pm$ 0.19	4.4	4.7	87.75	9.4	8.4
7.	Fruit diameter (cm)	1	2	1.29 $\pm$ 0.01	13.0	13.1	98.38	8.0	26.5
8.	Fruit weight (g)	9.25	27	15.33 $\pm$ 0.23	4.2	4.5	90.42	3.6	8.3
9.	Number of fruits per Plant	1	17	6.65 $\pm$ 0.22	10.0	10.9	83.72	6.0	18.9
10.	Fruit yield per plant (g)	12	320.4	101.41 $\pm$ 3.84	12.5	13.6	84.98	10.0	23.8

Table 2 : Estimates of Range, Mean, Genotypic and phenotypic coefficient of variation (GCV and PCV), heritability, genetic advance and genetic advance as per cent of mean for fruit yield and yield attributing traits in F_2 population of Konkan Bhindi $\times$ IC-42470 in okra.

S. no.	Characters	Range		Mean $\pm$ SEM of F_2	GCV (%)	PCV (%)	Heritability h^2 (bs) (%)	Genetic advancement	Genetic advance % Mean GAM (%)
		Min	Max						
1.	Days to Flowering	40	59	44.58 $\pm$ 0.47	29.34	14.50	87.80	9.80	26.23
2.	Plant height (cm)	5	71	38.10 $\pm$ 1.15	0.77	9.83	82.90	1.49	16.79
3.	Internodal length (cm)	1.8	7.4	4.09 $\pm$ 0.11	19.82	17.60	83.90	7.70	30.43
4.	Number of Nodes per Plant	4	24	12.87 $\pm$ 0.25	3.23	17.67	98.00	3.63	35.67
5.	Number of primary branches per plant	0	4	1.48 $\pm$ 0.07	1.78	14.29	95.80	2.63	28.21
6.	Fruit length (cm)	2	18.3	12.96 $\pm$ 0.21	36.38	23.22	89.50	11.12	42.79
7.	Fruit diameter (cm)	1	1.8	1.30 $\pm$ 0.01	21.33	13.46	67.20	6.39	18.63
8.	Fruit weight (g)	8	23	12.52 $\pm$ 0.22	9.39	8.84	91.70	5.79	16.70
9.	Number of Fruits per Plant	1	22	8.13 $\pm$ 0.25	71.50	8.72	78.00	13.59	14.01
10.	Fruit yield per plant (g)	20	306	102.95 $\pm$ 4.12	1.93	3.83	64.70	1.85	5.11

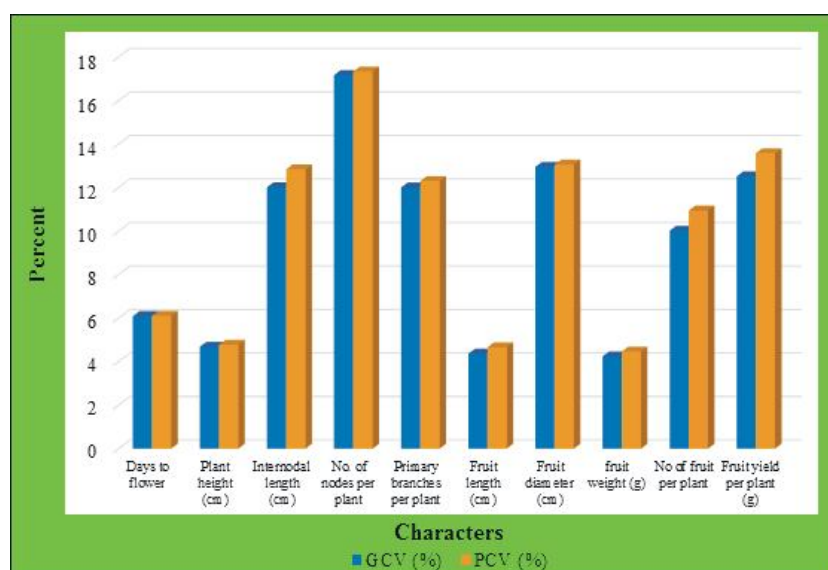


Fig. 1a : Genotypic coefficient of variation and Phenotypic coefficient of variation in F_2 population of okra cross Arka Anamika × IC-42464.

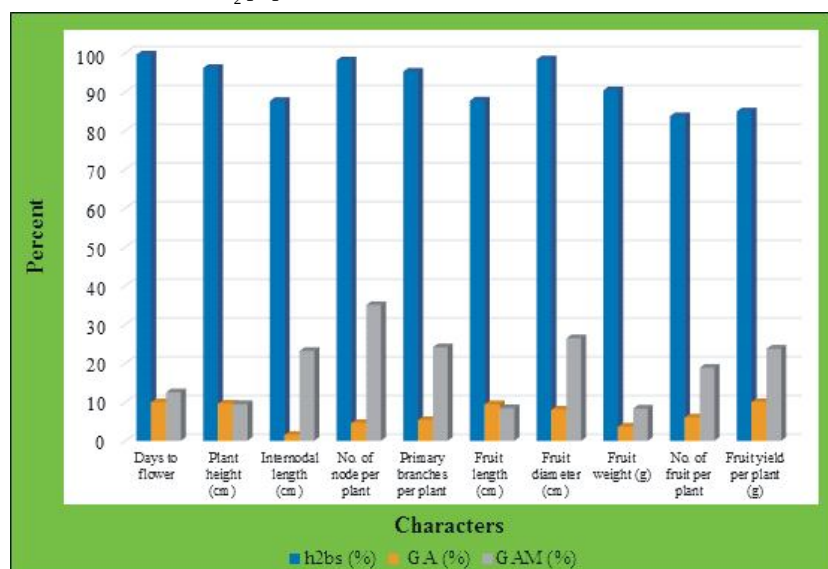


Fig. 1b : Heritability, Genetic advance and percent mean of genetic advance in F_2 population of okra cross Arka Anamika × IC-42464.

F_2 population of cross Arka Anamika × IC-42464

The F_2 population of the cross Arka Anamika × IC-42464 exhibited moderate to high genotypic and phenotypic variability for most traits. High heritability coupled with moderate to high genetic advance as a percentage of mean was observed for traits like number of nodes per plant, fruit diameter and fruit yield per plant indicating the predominance of additive gene effects. Traits such as days to flowering and internodal length also showed promising selection potential due to high heritability and moderate genetic advance as per cent of mean. However, traits like fruit length and fruit weight showed limited genetic variability and low genetic advance as per cent of mean suggesting less effectiveness through

direct selection. In F_2 Population of C-I the genotypic and phenotypic coefficients of variation (GCV and PCV) for days to flowering were both 6.1% showing that environmental effect on this trait were minimal. The traits exhibited very high heritability (99.62%) and a moderate genetic advance as a percentage of the mean (GAM 12.5%). This suggests that days to flowering is largely controlled by additive gene effects making direct selection a promising approach for improvement. Plant height showed moderate GCV (4.7%) and PCV (4.8%) indicating low environmental influence. With a high heritability of 96.16%, but a low GAM (9.5%) the trait appears to be influenced by non-additive gene effects which may limit the effectiveness of direct selection. Internodal length showed a moderate GCV (12.0%) and a slightly higher PCV (12.8%) and high heritability (87.63%) combined with a GAM of 23.2% suggests that this trait is primarily governed by additive gene effects making it responsive to selection. Number of nodes per plant exhibited high GCV (17.2%) and PCV (17.3%) along with very high heritability (98.10%) and a GAM of 35.0%. These values indicate significant genetic variability and additive gene control suggesting that direct selection would be highly effective. Number of primary branches per plant showed moderate GCV (12.0%) and PCV (12.3%) with high heritability (95.22%) and GAM of 24.1%. These results suggest that selection could be effective though minor environmental influences may exist. Fruit length recorded low GCV (4.4%) and PCV (4.7%) with high heritability (87.75%) but a low GAM (8.4%). This indicates limited genetic variability and possible non-additive gene effects reducing the effectiveness of selection. Fruit diameter also showed moderate GCV (13.0%) and PCV (13.1%) with very high heritability (98.38%) and a GAM of 26.5%. The close GCV and PCV values indicate minimal environmental impact and the high heritability and GAM suggest that selection would be effective. Fruit weight showed low GCV (4.2%) and PCV (4.5%) indicating limited genetic variability. Despite high heritability (90.42%) the low GAM (8.3%) suggests non-additive gene effects making selection less effective. Number of fruits per plant showed moderate GCV (10.0%) and PCV

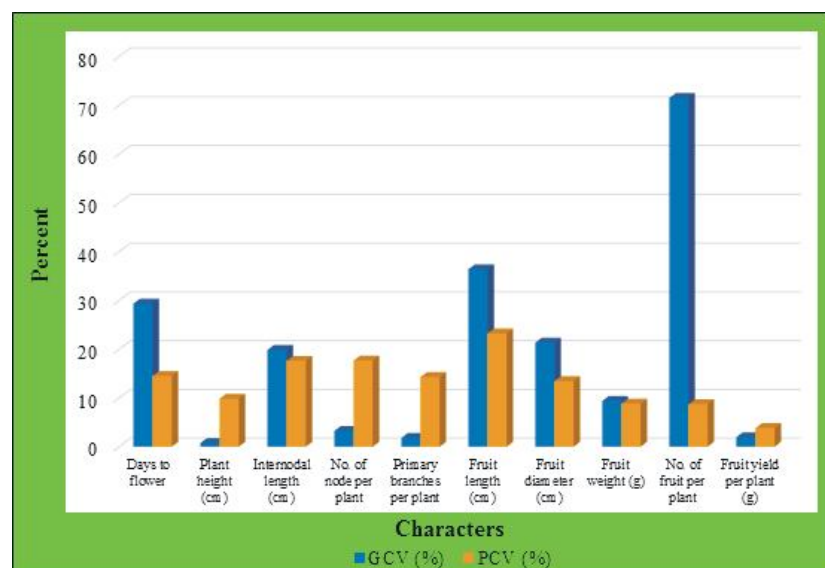


Fig. 2a : Genotypic coefficient of variation and Phenotypic coefficient of variation in F_2 population of okra cross Kokan Bhindi × IC-42470.

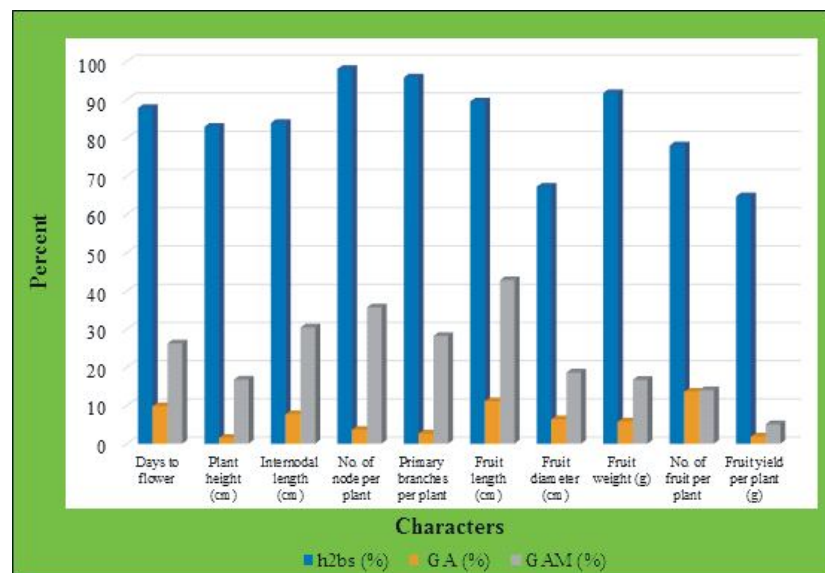


Fig. 2b : Heritability, Genetic advance and percent mean of genetic advance in F_2 population of okra cross Kokan Bhindi × IC-42470.

(10.9%) with high heritability (83.72%) and a moderate GAM (18.9%). This indicates that additive gene effects dominate and selection could improve this trait. Fruit yield per plant exhibited moderate to high variability with a GCV of 12.5% and a PCV of 13.6%. The high heritability (84.98%) and GAM (23.8%) suggest that additive gene effects are significant making selection a viable strategy for improvement. Similar result was noted by Badiger *et al.* (2017) found high heritability coupled with high genetic advance for internodal length indicating additive gene action. Akotkar *et al.* (2010) reported high GCV, PCV, heritability and genetic advance for the number of fruiting nodes indicating additive gene control. Pachiyappan and Saravana (2013) also observed high PCV and GCV for

the number of nodes per plant in F_2 generation crosses. Jindal *et al.* (2010) found high heritability coupled with high genetic advance for number of primary branches per plant suggesting additive gene effects. Guddadamath *et al.* (2011a) noted high heritability and GAM for average fruit weight. Sharma *et al.* (2016) reported low GCV and PCV values for fruit weight suggesting a low response to selection. Pal *et al.* (2010) reported high heritability for the number of fruits per plant in both F_1 and F_2 generations. Pachiyappan and Saravannan (2016) also found high PCV, GCV and heritability coupled with high genetic advance for fruit yield per plant.

F_2 population of cross Kokan Bhindi × IC-42470

The F_2 population of the cross Kokan Bhindi × IC-42470 demonstrated considerable variability for several traits especially fruit length, internodal length and number of primary branches per plant which showed high heritability and genetic advance as a percentage of mean indicating effectiveness of selection. Fruit weight also exhibited high heritability and moderate genetic advance as a percentage of mean showing potential for improvement. However, traits like plant height and number of nodes per plant were highly influenced by the environment as shown by the wide gap between GCV and PCV despite high heritability. Fruit yield per plant recorded low genetic variability and heritability indicating limited scope for improvement through

selection. In F_2 population of C-II days to flowering showed high genotypic coefficient of variation (GCV) of 29.34% and a moderate phenotypic coefficient of variation (PCV) of 14.50% indicating significant genetic diversity with high heritability (87.80%) and a strong genetic advance as a percentage of the mean of 26.23% this trait is likely influenced by additive gene effects making direct selection effective for improvement. The GCV for plant height was very low (0.77%) while the PCV was much higher (9.83%) suggesting a strong environmental impact. Despite high heritability (82.90%) and GAM (16.79%) were moderate pointing to non-additive gene effects. Direct selection may not be the best approach for this trait. Internodal length showed high GCV (19.82%) and PCV (17.60%) along with high heritability (83.90%)

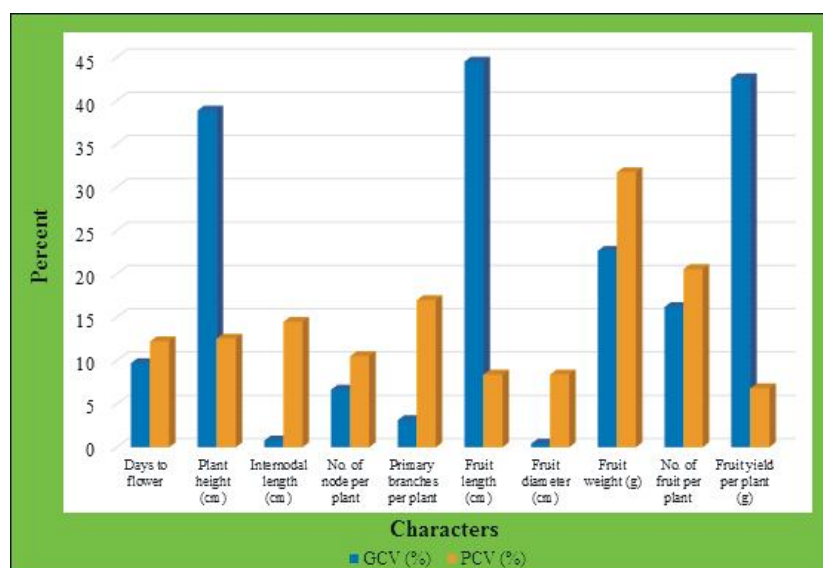


Fig. 3a : Genotypic coefficient of variation and Phenotypic coefficient of variation in F_2 population of okra cross Arka Abhay × IC-42472.

and GAM (30.43%). These values suggest that additive gene effects control this trait and selection could lead to good improvement. Number of nodes per plant trait showed a low GCV (3.23%) and a moderate PCV (17.67%) indicating significant environmental influence. Although heritability was very high (98.00%) the GAM was moderate (35.67%) suggesting that direct selection may have limited effectiveness. However, these results align with that the high heritability alone does not guarantee high genetic gain if the genetic advance is not also high as environmental factors can still play a significant role as indicated by the discrepancy between GCV and PCV. Number of primary branches per plant showed low GCV (1.78%) and a moderate PCV (14.29%) showing environmental variation. High heritability (95.80%) and moderate GAM (28.21%) suggest a mix of additive and non-additive gene effects. Fruit length exhibited very high GCV (36.38%) and PCV (23.22%) with high heritability (89.50%) and a very high GAM (42.79%). These indicate strong additive genetic control making selection highly effective for improving this trait. Fruit diameter trait showed a moderate GCV (21.33%) and low PCV (13.46%) suggesting limited environmental influence with moderate heritability (67.20%) and low GAM (18.63%) non-additive gene effects may play a role and advanced breeding strategies might be needed for improvement. Fruit weight showed moderate GCV (9.39%) and PCV (8.84%), which were close indicating minimal environmental impact high heritability (91.70%) and moderate GAM (16.70%) suggest additive gene effects and good potential for genetic improvement. Number of fruits per plant trait showed a very high GCV (71.50%) and a low PCV

(8.72%) indicating high genetic variability and low environmental influence. However, moderate heritability (78.00%) and low GAM (14.01%) suggest that direct selection may not yield strong results. Fruit yield per plant showed low GCV (1.93%) and PCV (3.83%) indicating limited variability and strong environmental influence with relatively low heritability (64.70%) and very low GAM (5.11%) selection may not lead to quick improvements. The similar results were obtained by Kudari *et al.* (2021) noted high heritability and GAM for days to first flowering indicating additive gene effects. Shanthakumar and Salimath (2010) reported high heritability coupled with high genetic advance for days to first flowering indicating additive gene action and effective selection. Guddadamath *et al.* (2011a) found high

heritability and GAM for plant height indicating its potential for crop improvement. Beerasha *et al.* (2024) observed high PCV and GCV for internodal length in F_2 population across different crosses with high heritability and genetic advance suggesting strong additive gene action. Kumar *et al.* (2020) found fruit length to have comparatively higher values of PCV, GCV, heritability and genetic advance revealing additive gene effects.

F_2 population of cross Arka Abhay × IC-42472

The F_2 population of Arka Abhay × IC-42472 displayed high genotypic variability and heritability for several traits including plant height, fruit weight, and number of fruits per plant suggesting strong additive gene action. Fruit yield per plant also exhibited very high GCV and heritability along with good genetic advance as a percentage of mean indicating its suitability for selection. In contrast traits like internodal length, fruit diameter and number of nodes per plant showed low GCV and genetic advance as a percentage of mean highlighting the influence of non-additive gene effects and environmental factors limiting the scope for direct improvement through selection. In the F_2 population of C-III the genotypic coefficient of variation (GCV) was 9.71% and the phenotypic coefficient of variation (PCV) was 12.22% for days to flowering both at moderate levels suggesting some environmental influence on this trait. Heritability was moderate at 63.60% with a genetic advance as a percentage of mean (GAM) of 16.01%. This indicates a reasonable potential for improvement through selection with additive gene effects playing a partial role. Plant height showed high GCV of 38.86% and a moderate PCV of 12.53% pointing to significant genetic diversity.

Table 3 : Estimates of Range, Mean, Genotypic and phenotypic coefficient of variation (GCV and PCV), heritability, genetic advance and genetic advance as per cent of mean for fruit yield and yield attributing traits in F₂ population of Arka Abhay x IC-42472 in okra.

S. no.	Characters	Range		Mean± SEM of F ₂	GCV (%)	PCV (%)	Heritability h ² (bs) (%)	Genetic advancement	Genetic advance % Mean GAM (%)
		Min	Max						
1.	Days to Flowering	39	60	46.53 ± 0.48	9.71	12.22	63.60	4.08	16.01
2.	Plant height (cm)	5	85	47.67 ± 1.32	38.86	12.53	92.90	11.93	23.97
3.	Internodal length (cm)	1.8	8.5	4.92 ± 0.13	0.78	14.47	80.90	1.47	24.12
4.	Number of Nodes per Plant	4	26	13.76 ± 0.28	6.63	10.51	35.30	1.87	7.64
5.	Number of primary branches per plant	0	4	1.77 ± 0.08	3.13	16.97	94.30	3.43	32.96
6.	Fruit length (cm)	5.5	20	11.77 ± 0.23	44.50	8.39	87.80	12.07	15.17
7.	Fruit diameter (cm)	1	1.9	1.40 ± 0.01	0.41	8.40	55.80	0.74	9.66
8.	Fruit weight (g)	9.2	28	13.68 ± 0.25	22.67	31.74	84.60	8.30	55.31
9.	Number of Fruits per Plant	1	22	8.13 ± 0.27	16.19	20.57	89.50	7.42	37.95
10.	Fruit yield per plant (g)	20	306	109.20 ± 4.45	42.59	6.80	92.40	12.42	12.94

Heritability was very high at 92.90% and the GAM was also high at 23.97% suggesting that additive gene effects are dominant. This makes plant height a promising trait for improvement through selection. Internodal length showed GCV very low at 0.78%, while the PCV was moderate at 14.47% indicating a strong environmental influence. Heritability was high at 80.90% but the GAM was moderate at 24.12%. This suggests that direct selection may have limited success due to possible dominance or epistatic gene effects. Moderate GCV (6.63%) and PCV (10.51%) were recorded for number of nodes per plant showing some environmental influence. However, heritability was low at 35.30% and the GAM was also low at 7.64% indicating limited potential for improvement through selection. Non-additive gene effects or environmental factors may play a significant role. Number of primary branches per plant showed the GCV was low at 3.13% while the PCV was moderate at 16.97% suggesting a strong environmental impact. Heritability was high at 94.30% and the GAM was also high at 32.96% indicating that additive gene effects are prominent despite low genetic variation. Selection for this trait could be effective. Fruit length showed very high GCV of 44.50% and a low PCV of 8.39% were observed reflecting substantial genetic variation. Heritability was high at 87.80% but the GAM was moderate at 15.17% suggesting some influence of non-additive gene effects. Fruit diameter GCV was very low at 0.41% with a moderate PCV of 8.40% indicating significant

environmental influence. Heritability was moderate at 55.80% and the GAM was low at 9.66% suggesting that selection may not be highly effective due to non-additive gene effects. Fruit weight showed high GCV (22.67%) and PCV (31.74%) were observed along with high heritability (84.60%) and a very high GAM (55.31%). These values suggest strong additive gene effects and excellent potential for genetic improvement through selection. Number of fruits per plant showed high GCV (16.19%) and PCV (20.57%) indicating significant genetic variation with some environmental influence. High heritability (89.50%) and GAM (37.95%) suggest that additive gene effects are dominant making this trait suitable for improvement through direct selection. Fruit yield per plant showed very high GCV (42.59%) and a moderate PCV (6.80%) were recorded indicating strong genetic control with some environmental influence. Heritability was very high at 92.40% and the GAM was high at 12.94% suggesting that additive gene effects predominate. This trait shows good potential for improvement through selection. These findings align with previous reports by Shiri *et al.* (2024) observed low to moderate heritability for days to anthesis, days to 50% flowering, and days to first picking indicating a greater degree of environmental control for these traits. Nwangburuka *et al.* (2012) reported high GCV, broad-sense heritability and genetic advance for plant height suggesting additive gene effects. Shanthakumar and Salimath (2010) also found high heritability coupled with

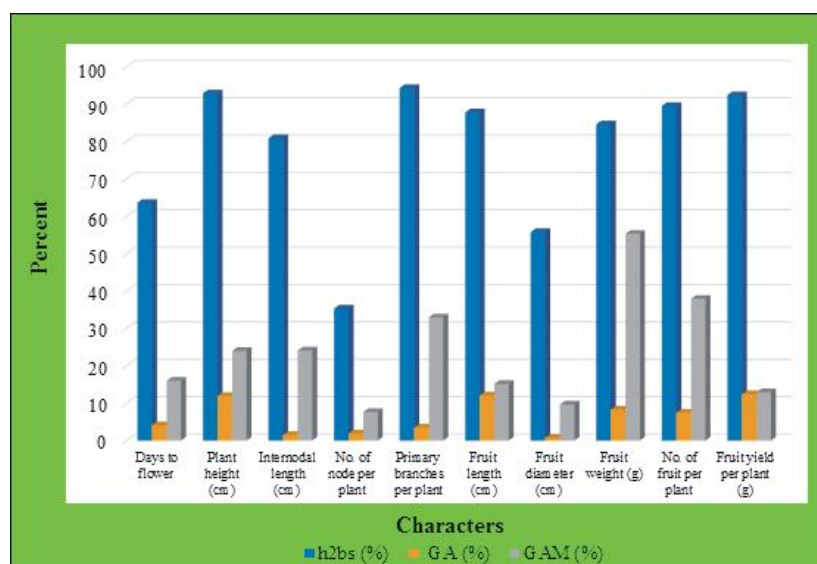


Fig. 3b : Heritability, Genetic advance and percent mean of genetic advance in F_2 population of okra cross Arka Abhay × IC-42472.

high GAM for number of primary branches per plant indicating additive gene action. Guddadamath *et al.* (2011a) found high heritability and GAM for number of branches per plant. Pal *et al.* (2010) observed width of fruit to have moderate heritability in F_1 and F_2 generations. Awadhes *et al.* (2016) found fruit diameter to have the lowest GCV and PCV among the traits studied. Prakash and Pitchaimuthu (2010) observed high GCV and PCV for average fruit weight. Shanthakumar and Salimath (2010) reported high heritability coupled with high GAM for fruit weight indicating additive gene action. Pachiyappan and Saravannan (2016) observed high PCV and GCV and high heritability coupled with high GAM for fruit weight. Sravanthi (2017) reported high GCV and PCV with high heritability and genetic advance per cent of mean for number of fruits per plant suggesting improvement through direct selection. Nwangburuka *et al.* (2012) reported high GCV, broad-sense heritability and genetic advance for pod weight per plant and pod yield per plant suggesting additive gene effects. Thulasiram *et al.* (2017) observed high heritability and genetic advance for yield per plant indicating ample scope for improvement through direct selection.

Conclusion

The result of the current study revealed that all three crosses exhibited substantial variability for most traits with minimal environmental influence as indicated by small differences between GCV and PCV emphasizing the strong genetic control over trait expression. Crosses that produced higher variability can be effectively utilized in okra improvement for the development of superior genotypes. Traits like fruit yield, number of fruits per plant,

fruit weight and plant height showed high broad-sense heritability making them suitable for improvement through direct selection especially when coupled with high genetic advance as a percentage of the mean. The F_2 population of cross Arka Anamika × IC-42464 showed high heritability and GAM for number of nodes per plant and fruit diameter indicate effective selection potential. Fruit yield per plant showed good variability and heritability making it a suitable trait for improvement. Fruit length and fruit weight exhibited low genetic variability limiting response to selection. The F_2 population of cross Kokan Bhindi × IC-42470, fruit length and internodal length showed very high GCV, heritability and GAM supporting effective selection. Traits such as plant height and

number of nodes per plant were heavily influenced by environment despite high heritability. fruit yield per plant showed low genetic variability and heritability suggesting poor selection response. The F_2 population of cross Arka Abhay × IC-42472, fruit weight and plant height showed high GCV, heritability and GAM indicating strong additive gene effects. Fruit yield per plant showed excellent variability and high selection potential. Traits like internodal length and fruit diameter showed low GCV and GAM limiting scope for direct improvement. Thus, we should focus on those yield attributing characters which is giving higher response of high estimates of heritability along with high genetic advance. The selected segregating lines can be advanced to the F_3 and subsequent generations and evaluated under diverse agro-climatic conditions and over multiple seasons for the development of high-yielding okra varieties.

Acknowledgement

The author gratefully acknowledges the guidance and support of Dr. S.P. Pole, Junior Breeder, Oilseeds Research Station, Latur for his valuable suggestions and encouragement during the course of this research. The facilities provided by the Oilseeds Research Station, Latur, are also sincerely acknowledged.

References

- Akotkar, P.K., De D.K. and Pal A.K. (2010). Genetic variability and diversity in okra (*Abelmoschus esculentus* L. Moench). *Elect. J. Plant Breed.*, **1**(4), 393–398.
- Anonymous (2024). National Horticulture Board, Ministry of Agricultural and Farmers Welfare, Government of India, Statistics, Area and Production of Horticulture crops, (2nd Advanced Estimates), 360-361.

- Badiger, M., Pitchaimuthu M. and Pujer P. (2017). Genetic variability, heritability, genetic advance and correlation studies among quantitative traits in okra (*Abelmoschus esculentus* (L.) Moench). *Glob. J. BioSci. Biotechnol.*, **6**(2), 314–319.
- Beerasha, H.K., Halesh G.K., Dhananjaya M.V., Pitchaimuthu M., Hanchinamani C.N. and Ravishankar K.V. (2024). Genetic variability analysis in F₂ segregating populations for yield and its contributing traits in okra (*Abelmoschus esculentus* (L.) Moench). *Int. J. Adv. Biochem. Res.*, **SP-8**(7), 517–524.
- Burton, G.W. and De Vane E.H. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agron. J.*, **45**(10), 478–481.
- Chauhan, D.V.S. (1972). *Vegetable production in India* (3rd Edn.) published by Ram Prasad. Sons, Agra, 28–30.
- Guddadamath, S.H.D., Mohankumar and Salimath P.M. (2011a). Genetic analysis of segregating populations for yield in okra (*Abelmoschus esculentus* (L.) Moench). *Karnataka J. Agricult. Sci.*, **24**(2), 114–117.
- Hallur, R.H., Shantappa T. and Jagadeesha R.C. (2017) Studies on genetic variability in segregating populations of okra and their character association. *Res. J. Environ. Sci.*, **10**(1), 71–74.
- Hanson, G., Robinson H.F. and Comstock R.E. (1956). Biometrical studies on yield in segregating population of Korean Lespedeza. *Agron. J.*, **48**, 268–274.
- Jindal, S.K., Arora D. and Ghai T.R. (2010). Variability studies for yield and its contributing traits in okra. *Elect. J. Plant Breed.*, **1**(6), 1495–1499.
- Johnson, H.W., Robinson H.F. and Comstock R.E. (1955). Estimates of genetic and environmental variability in soybean. *Agron. J.*, **47**, 314–318.
- Kudari, G.B., Hanchinamani C.N., Hadimani H.P., Satish D., Bhavidoddi A. and Kantharaju V. (2021). Assessment of genetic variability in F₂ populations of okra (*Abelmoschus esculentus* (L.) Moench). *J. Pharmacog. Phytochem.*, **9**(6), 1574–1576.
- Kumar, Y., Singh V.B., Gautam S.K., Kumar V. and Singh V. (2020). Studies on genetic variability, heritability and genetic advance for fruit yield and its contributing traits in okra (*Abelmoschus esculentus* L. Moench). *Pharma Innov. J.*, **9**(10), 351–354.
- Nwangburuka, C.C., Denton O.A., Kehinde O.B., Ojo D.K. and Popoola A.R. (2012). Genetic variability and heritability in cultivated okra (*Abelmoschus esculentus* (L.) Moench). *Spanish J. Agricult. Res.*, **10**(1), 123–129.
- Pachiyappan, R. and Saravana (2013). Studies on variability in certain intervarietal crosses of okra (*Abelmoschus esculentus* (L.) Moench). *Int. J. Plant Sci.*, **8**(1), 67–69.
- Pachiyappan, R. and Saravanan K. (2016). Studies on genetic variability and correlation for fruit yield and fruit quality characters of okra. *Asian J. Horticult.*, **11**(1), 101–104.
- Pal, M.K., Singh B., Kumar R. and Singh S.K. (2010). Genetic variability, heritability and genetic advance in okra (*Abelmoschus esculentus* (L.) Moench). *Environ. Ecol.*, **28**(1A), 469–471.
- Panse, V.G. and Sukhatme P.V. (1985). *Statistical Methods for Agricultural Workers*, Indian Council of Agriculture Research, New Delhi.
- Prakash, K. and Pitchaimuthu M. (2010). Nature and magnitude of genetic variability and diversity studies in okra (*Abelmoschus esculentus* L. Moench). *Elect. J. Plant Breed.*, **1**(6), 1426–1430.
- Priyanka, V.M., Reddy T., Begum H., Sunil N. and Jayaprada M. (2018). Studies on genetic variability, heritability and genetic advance in genotypes of okra (*Abelmoschus esculentus* (L.) Moench). *Int. J. Curr. Microbiol. Appl. Sci.*, **7**(5), 401–411.
- Shanthakumar, G. and Salimath P.M. (2010). Studies on variability, heritability and genetic advance for fruit yield and its component traits in early segregating generation in bhendi (*Abelmoschus esculentus* (L.) Moench). *Indian J. Plant Gen. Resources*, **23**(3), 296–302.
- Shiri, T., Gaurav S.S., Singh S.K. and Jain S. (2024). Study of genotypic and phenotypic variation in F₂ segregating generation of okra (*Abelmoschus esculentus* (L.) Moench). *Agricultural Science Digest*.
- Sravanthi, U. (2017). Studies on variability, heritability and genetic advance in okra (*Abelmoschus esculentus* (L.) Moench). *Int. J. Curr. Microbiol. Appl. Sci.*, **6**(10), 1834–1838.
- Thulasiram, L.B., Bhople S.R., Srikanth M. and Nayak R.B. (2017). Genetic variability and heritability studies in okra (*Abelmoschus esculentus* (L.) Moench). *Plant Archives*, **17**(2), 907–910.