

DOI: <http://doi.org/10.53550/EEC.2025.v31i03s.029>

Study of Genetic Variability, Heritability and Genetic Advance in okra [*(Abelmoschus esculentus* L.) Moench]

S. Neeraja^{*1}, J. Srinivas² and Veena Joshi³

^{1,2}Department of Vegetable Science, SKLTGHU, Mojerla, Telangana, India

³Department of Fruit Science, SKLTGHU, Rajendranagar, Hyderabad Telangana, India

(Received 16 November, 2024; Accepted 11 January, 2025)

ABSTRACT

Studies on genetic variability, heritability and genetic advance were carried out with thirty-seven genotypes of okra using randomized block design (RBD) with three replications. In the present study the high genetic variability observed for the characters, i.e. number of primary branches, internodal length, number of locules per fruit, number of seeds per fruit, number of fruits per plant, fruit yield per plant, chlorophyll content and indicates the significance of these characters to be used for selecting superior genotypes. High heritability coupled with high genetic advance as per cent of mean indicates operation of additive gene action which was observed in characters *viz.*, plant height, number of primary branches per plant, internodal length, days to 50 % flowering, fruit length, fruit diameter, number of locules per fruit, number of seeds per fruit, number of fruits per plant, fruit yield per plant, seeds weight per fruit, seedling length, seedling dry weight, vigour index I, vigour index II and chlorophyll content.

Key words: Okra, Genotypes, Genetic variability, Heritability and Genetic advance.

Introduction

Okra (*Abelmoschus esculentus* L.) is an annual herbaceous plant that belongs to the family "Malvaceae" having a somatic chromosome number of $2n=130$ and is considered to be an amphidiploid (Siemonsmo, 1982). It is generally known as 'bhendi' or lady's finger in India. Okra is an often cross-pollinated crop, an extent of 20 per cent out-crossing by insects was reported, which renders a considerable amount of variability (Patil, 1995). It is the best vegetable and is widely cultivated in temperate, tropical, and subtropical regions of the world. It is a costly vegetable produced in India for its tender fruits.

India, the world's largest producer of okra, accounts for roughly 72.9 per cent of global okra production. Okra is grown on an area of 526 hectares in India and contributes 3.9 per cent of nation's total vegetable production. Its annual production is 6,505 million tonnes, and its productivity is 11.90 metric tonnes per hectare. Okra is 11.90 metric tonnes per hectare. Okra is grown on 10,881 hectares in Telangana, with an annual output of 55,054 tonnes per year. The major okra producing states are Andhra Pradesh, West Bengal, Bihar, Orissa, Gujarat, Jharkhand, Karnataka and Tamil Nadu (NHB, 2021).

(¹M.Sc. Scholar, ²Assistant Professor, ³Associate Professor)

Tender fruits of okra are used as vegetable or culinary preparation as sliced and fried pieces. The leaves are sometimes used as cattle feed. The ripe seeds are roasted, grinded and used as a substitute for coffee. It is also used for thickening soups and gravies, because of its high mucilage content. Okra fruits are also sliced for sun drying or canning or pickling for off season use. It has good nutritive value *viz.* 86.10 per cent water, 2.20 per cent protein, 0.02 per cent fat, 9.70 per cent carbohydrate, 1.0 per cent fibre and 0.80 per cent ash (Saifullah and Rabbani, 2009) and also rich in vitamin C (30 mg / 100 g), Calcium (90 mg / 100 g) and iron (1.5 mg / 100 g) (Pal *et al.*, 1952).

Materials and Methods

The present experiment was conducted at the PG research block in department of Vegetable Science, College of Horticulture, Mojerla, Wanaparthy district, Sri Konda Laxman Telangana state Horticultural university, Mulugu, Siddipet, Telangana during *Rabi*, 2021-2022. The monthly mean maximum temperature ranged from 24.9 °C to 32.4 °C with an average of 30.50 °C while the monthly mean minimum temperature ranged from 12.7 °C to 21.4 °C with an average of 17.5 °C during the crop growth period. Relative humidity for enoon and afternoon fluctuated between 86% to 90% and 38% to 71% respectively. Rainfall received during the crop growth period. The monthly mean sunshine hours varied from 3.3 to 8.2 with an average of 5.6 hours per day and mean evaporation ranged from 2.8 to 5.1 mm with an average of 4.1 mm per day. The mean wind speed ranged from 2.8 to 11.2 km hr⁻¹ with an average of 5.4 km hr⁻¹. At all stages of the crop growth the weather was congenial for growth and development of okra crop during *rabi*- 2021-22.

Source of Seed Materials

The 37 genotypes of okra were collected from NBPGR, Regional station, New Delhi. IC33823, IC33853, IC34124, IC39132, IC39133, IC39134, IC39135, IC39136, IC39137, IC39143, IC40289, IC42451, IC42456, IC42464, IC42470, IC42472, IC42484, IC42490, EC329362, EC329364, EC329365, EC329366, EC329367, EC329368, EC329369, EC329370, EC329371, EC329372, EC329384, EC329384, EC329406, EC329418, EC329420, EC329421, EC329422, EC329423, Kashi Lalima (Check), IIVR, Varanasi and Arka Anamika (Check)

IIHR, Bangalore the data was recorded on following parameters.

Results and Discussion

Estimating variability in a population is an effective tool for the breeder to design the selection procedures more accurately for identifying superior genotypes. Variability helps to choose the potential genotype, since it indicates the extent of recombination for implementing effective selection. The magnitude of phenotypic and genotypic coefficients of variation has been assessed to know the real worth of the source material.

Genotypic coefficient of variation would be a useful tool for assessing variability since it depends upon the heritable portion of the total variability (Allard, 1960). Heritability estimates give a measure of transmission of characters from one generation to another, thus giving an idea of heritable portion of variability and enabling the plant breeder to isolate the crop's elite genotype. The heritability expresses the portion of total variances attributed to the average effect of genes and determines the degree of resemblance between parents and offspring. It also expresses the reliability of phenotypic values as a guide to the breeding value.

Heritability in broad sense is the portion of genotypic variance to phenotypic variance, which indicates the relative success of selection. It is useful in the selection of elite genotypes from diverse genetic population. High heritability estimates help select superior genotypes based on performance of quantitative characters. In the present study, the heritability in broad sense was found to be high for all the characters. High heritability estimates indicate the presence of large number of fixable additive genes and hence these traits can be improved by selection.

Heritability coupled with genetic advance is an important selection parameter. Johnson *et al.* (1955) reported that heritability along with genetic gain is more useful than the heritability alone, in predicting the resultant effect for selecting the best individuals. He categorized the heritability values, as the values greater than 60 per cent indicate the high heritability, the values ranged between 30 to 60 per cent indicate the moderate heritability, while the values less than 30 per cent indicate the low heritability. Similarly, the values greater than 20 per cent indicate high genetic advance, the values ranged between 10 to 20 per cent indicate moderate genetic

advance, while the values less than 10 per cent indicate low genetic advance.

The simple measure of variability like mean, range and the major components of variability such as phenotypic and genotypic coefficients of variation (PCV and GCV), heritability in broad sense (h^2b), genetic advance and genetic advance as % of mean were furnished in Table 1. All the nineteen characters under study exhibited high variability as evident from the estimates of mean, range, coefficients of variation, heritability and genetic advance.

For plant height high phenotypic and genotypic variances (75.56 and 74.64) respectively coupled with moderate PCV (17.17 %) and moderate GCV (17.06 %) recorded. This trait showed high heritability (98.8 %), moderate genetic advance (17.68) and high GA as per cent mean (34.94%). Similar results for plant height were reported by Alam *et al.* (2020). Sharma *et al.* (2020). and Bello *et al.* (2015).

This trait number of primary branches showed low phenotypic and genotypic variances (0.815 and 0.777 respectively) with more PCV (29.83 %) and more GCV (29.12 %). High heritability (95.2 %), high genetic advance (58.545) and high GA as per cent mean (58.545 %) estimates were recorded for this trait. Similar results for number of primary branches per plant were reported by Bello *et al.* (2015).

With respect to internodal length, low phenotypic and genotypic variance (1.41 and 1.38 respectively), high PCV (32.52 %) and high GCV (32.20 %), high heritability (98.2 %), low genetic advance (2.40) and high GA as % of mean (65.682 %) estimates were observed.

Days to 50% flowering showed high phenotypic and genotypic variances (23.48 and 23.31 respectively) with moderate PCV (11.09 %), moderate GCV (11.05 %), high heritability (99.3 %), low genetic advance (9.91) and high GA as per cent of mean (22.69 %) estimates were noticed for days to 50 % flowering. Similar results for days to 50% flowering were reported by Ramgiry *et al.* (2017). Alam *et al.* (2020).

For this fruit length character, low phenotypic and genotypic variances (2.13 and 2.09 respectively) was observed with moderate PCV and GCV (11.59 % and 11.49% respec-

Table 1. Estimation of variability, heritability and genetic advance as per cent of mean for nineteen characters in thirty-seven genotypes of okra

S. No.	Characters	Range		Mean	Variance		PCV (%)	GCV (%)	h^2 (%)	Genetic Advance	GA as % of mean
		Minimum	Maximum		Phenotypic	Genotypic					
1	Plant height	35.7267	71.2767	50.6250	75.564	74.643	17.171	17.066	98.8	17.689	34.941
2	Number of primary branches	1.6333	5.5333	3.026	0.815	0.777	29.839	29.121	95.2	1.772	58.545
3	Internodal length	1.3633	5.9367	3.6574	1.415	1.387	32.522	32.202	98.2	2.402	65.682
4	Days to 50 % flowering	36.2667	54.9667	3.6574	23.484	23.316	11.096	11.056	99.3	9.911	22.694
5	Fruit length	9.8367	15.2467	12.6005	2.136	2.097	11.599	11.493	98.2	2.956	23.459
6	Fruit diameter	1.2467	2.4267	1.5000	0.058	0.044	16.078	14.039	76.2	0.379	25.251
7	Days to 1 st picking	38.6567	58.2633	47.2421	20.244	20.184	9.524	9.510	99.7	9.241	19.561
8	Number of locules per fruit	4.2400	10.4567	6.0661	2.622	2.521	26.695	26.177	96.2	3.208	52.877
9	Number of seeds per fruit	19.7333	65.9000	50.4369	128.379	124.58	22.465	22.130	97.0	22.652	44.911
10	Number of fruits per plant	17.6867	52.8967	33.3043	78.003	77.349	26.519	26.407	99.2	18.041	54.171
11	Fruit yield per plant	0.1560	0.4447	0.2674	0.004	0.004	22.902	22.381	95.5	0.120	45.058
12	Seeds weight for fruit	2.1967	4.8373	3.5334	0.345	0.324	16.631	16.121	94.0	1.137	32.192
13	Test weight	50.7333	75.8333	63.3432	40.969	36.570	10.105	9.547	89.3	11.770	18.581
14	Germination (%)	65.9667	96.4667	86.3723	51.665	48.094	8.322	8.029	93.1	13.783	15.958
15	Seedling length	7.4767	13.7933	10.1800	2.328	2.279	14.989	14.829	97.9	3.076	30.221
16	Seedling dry weight	0.0207	0.0381	0.0297	0.000	0.00	16.931	16.038	89.7	0.009	31.294
17	Vigour index I	514.08	1225.76	881.496	24318.0	23456.4	17.691	17.374	96.5	309.860	35.152
18	Vigour index II	1.3692	3.4743	2.5797	0.279	0.257	20.483	19.653	92.1	1.002	38.843
19	Chlorophyll content	0.1433	1.9533	0.7150	0.119	0.119	48.296	48.162	99.4	0.707	98.938

tively). High heritability (98.2 %), low genetic advance (2.9) and high GA as percent mean (23.45 %) were also recorded. Similar results for fruit length were reported by Archana *et al.* (2015). Raval *et al.* (2018).

This fruit diameter character recorded low phenotypic and genotypic variances (0.058 and 0.044 respectively) with moderate PCV (16.07 %) and moderate GCV (14.039 %) values, high heritability (76.2 %), low genetic advance (0.37) and high GA as per cent of mean (25.25 %). Similar results for fruit diameter were reported by Chandramouli *et al.* (2016). Sharma *et al.* (2020).

Days to 1st picking showed moderate phenotypic and genotypic variances (20.24 and 20.18) along with low PCV (9.52 %) and low GCV (9.51 %) were recorded for this trait. The character also showed high heritability (99.7 %), low genetic advance (9.24) as well as moderate GA as percent mean (19.56 %).

Concerning number of locules per fruit, low phenotypic (2.62) and low genotypic (2.52) variances, high PCV (26.69 %) and high GCV (26.17 %), high heritability (96.2 %), low genetic advance (3.208) and high GA as per cent mean (52.87 %) estimates were observed for this trait.

This number of seed per fruit character exhibited high phenotypic and genotypic variances of 128.37 and 124.58 respectively with high PCV (22.46 %) and high GCV (22.13 %). The high heritability (97.0 %), high genetic advance (22.65) and high GA as per cent mean (44.91 %) were also reported for this trait. Similar results for number of seeds per fruits were reported by Adeoluwa and Kehinde (2011); Mazid *et al.* (2013) and Ramgiri *et al.* (2017).

Number of fruits per plant showed high phenotypic and genotypic variances (78.00 and 77.34 respectively) with high PCV (26.51 %) and high GCV (26.407 %). High heritability (99.2 %), moderate genetic advance (18.04) and high GA as per cent mean (54.17 %) estimates were also recorded for this trait. Similar results for number of fruits per plant were reported by Sharma *et al.* (2020).

This fruit yield per plant trait showed low phenotypic and genotypic variances (0.004 and 0.004 respectively) with high PCV (22.90 %) and high GCV (22.38 %). High heritability (95.5 %), less genetic advance (0.120) and high GA as per cent mean (45.05 %) estimates were observed for this trait. Similar results for fruit yield per plant were reported by Archana *et al.* (2015). Chandramouli *et al.* (2016). Verma *et al.* (2018).

Seed weight per fruit showed low phenotypic and genotypic variances (0.345 and 0.324 respectively) with moderate PCV (16.631 %), moderate GCV (16.121 %), high heritability (94.0 %), low genetic advance (1.137) and high GA as per cent of mean (32.192 %) estimates were observed for seed weight per fruit.

Test weight showed high phenotypic (40.96) and high genotypic variances (36.57) were registered for test weight, less PCV (10.10 %) and less GCV (9.54 %). This trait showed high values for heritability (89.3 %), moderate genetic advance (11.77) and moderate GA as per cent mean (18.58 %). Similar results for test weight were reported by Koundinya *et al.* (2013).

Germination showed high phenotypic (51.66) and genotypic variances (48.09) were recorded for germination percent, low PCV (8.32 %) and low GCV (8.02 %). This trait showed high values for heritability (93.1 %), moderate genetic advance (13.78) and moderate GA as per cent mean (15.95 %).

This seedling length character recorded low phenotypic and genotypic variances of 2.32 and 2.27 respectively with moderate PCV (14.98 %) and moderate GCV (14.82 %) values. The high heritability (97.9 %), low genetic advance (3.07) and high GA as per cent mean (30.22%) were also recorded.

Seedling dry weight low phenotypic and genotypic variances were 0.00 and 0.00 respectively with moderate PCV (16.93 %) and moderate GCV (16.03 %), high heritability (89.7 %), low genetic advance (0.009) and high GA as per cent mean (31.29 %) were recorded.

Vigour index I showed high phenotypic and genotypic variances of 24318.02 and 23456.42 with moderate PCV (17.69 %) and GCV (17.37 %) respectively noticed for vigour index I. The high heritability (96.5 %), high genetic advance (309.86) and high GA as per cent mean (35.15 %) were also recorded.

For vigour index II, low phenotypic and genotypic variances of 0.279 and 0.257 respectively with high PCV (20.48 %) and moderate GCV (19.653%), high heritability (92.1 %), low genetic advance (1.002) and high GA as per cent mean (38.84 %) were registered.

Chlorophyll content showed low phenotypic and genotypic variances of 0.119 and 0.119 with high PCV (48.29 %) and GCV (48.16 %) respectively were observed. The high heritability (99.4 %), low genetic advance (0.707) and high GA as per cent mean (98.93 %) were also noticed.

The study revealed that PCV was higher than the corresponding GCV for all the characters indicating that all characters had interacted with environment to some degree. In the present study the high genetic variability observed for the characters, i.e. number of primary branches, internodal length, number of locules per fruit, number of seeds per fruit, number of fruits per plant, fruit yield per plant, chlorophyll content and indicates the significance of these characters to be used for selecting superior genotypes.

High PCV and GCV estimates were recorded for number of primary branches, internodal length, number of locules per fruit, number of seeds per fruit, number of fruits per plant, fruit yield per plant and chlorophyll content. The difference between PCV and GCV values were minimum, indicating that the traits under study were less influenced by environment and these characters could be improved by following phenotypic selection.

High heritability coupled with high genetic advance as per cent of mean indicates operation of additive gene action which was observed in characters viz., plant height, number of primary branches per plant, internodal length, days to 50 % flowering, fruit length, fruit diameter, number of locules per fruit, number of seeds per fruit, number of fruits per plant, fruit yield per plant, seeds weight per fruit, seedling length, seedling dry weight, vigour index I, vigour index II and chlorophyll content.

Hence, directional selection for these traits in genetically diverse material could be effective for desired genetic improvement. Moderate genetic advance as percent of mean with high or moderate heritability suggests the action of both additive and non additive genes thereby favorable influence of environment in the expression. The same was reported in case of days to 1st picking, test weight and germination percent.

Genetic advance which estimates the degree of gain in a trait obtained under a given selection pressure is an important parameter that guides the breeder in choosing a selection programme (Hamdi *et al.*, 2003). High heritability and high genetic advance for a given trait indicates that, it is governed by additive gene action and consequently provides the most effective condition for selection.

Hence, the breeder should adopt suitable breeding methodology to utilize both additive and non-additive gene effects simultaneously, since varietal and hybrid development will go a long way in the breeding programmes.

Conclusion

In the present study, high heritability coupled with high genetic advance as per cent of mean was observed for all the characters studied and positive significant correlation along with positive direct effects were observed for plant height, number of fruits per plant, number of seeds per fruit and chlorophyll content and these findings need to be validated in the subsequent generations for the improvement of these traits through direct selection.

Acknowledgements

The authors express sincere thanks to J. Srinivas and Veena Joshi, I am highly thankful to COH, Mojerla, SKLTGHU, for providing all facilities to complete this endeavour.

Conflict of interest: None.

References

- Adeoluwa, O.O. and Kehinde, O.B. 2011. Genetic variability studies in West African okra (*Abelmoschus caillei*). *Agriculture and Biology Journal of North America*. 2(10): 1326-1335.
- Alam, K., Singh, M.K., Kumar, M., Singh, A., Kumar, V., Ahmad, M. and Keshari, D. 2020. Genetic variability, heritability and genetic advance for selection parameters of genotypes in okra (*Abelmoschus esculentus* (L.) Moench). *IJCS*. 8(6): 1016-1022.
- Allard, R.W. 1960. Principles of plant breeding. *John Wiley Sons*. New York, p. 485.
- Archanaa, M., Mishra, H.N., Senapati, N. and Tripathy, P. 2015. Research Note Genetic variability and correlation studies in Okra (*Abelmoschus esculentus* (L.) Moench). *Electronic Journal of Plant Breeding*. 6(3): 866-869.
- Bello, O. B., Aminu, D., Gambo, B.A., Azeez, A.H., Lawal, M., Agbolade, J.O. and Abdulhamid, U.A. 2015. Genetic diversity, heritability and genetic advance in okra [*Abelmoschus esculentus* (L.) Moench]. *Bangladesh J. Pl. Breed. Genet.* 28(2): 25-38.
- Chandramouli, B., Shrihari, D., Rao, A.D. and Rao, M.P. 2016. Studies on genetic variability, heritability and genetic advance in okra [*Abelmoschus esculentus* (L.) Moench] genotypes. *Plant Archives*. 16(2): 679-682.
- Hamdi, A., El-Chareib, A.A., Shafey, S.A. and Ibrahim, M.A.M. 2003. Genetic variability, heritability and expected genetic advance for earliness and seed yield from selections in Lentil. *Egyptian Journal of Agriculture Research*. 81(1): 125-137.
- Johnson, H.W., Robinson, H.F. and Comstock, R.S. 1955. Estimation of Genetic and Environmental Variability

- ity in Soyabean. *Agron. J.* 41: 314-318.
- Koundinya, A.V.V., Dhankhar, S.K. and Yadav, A.C. 2013. Genetic variability and divergence in okra (*Abelmoschus esculentus*). *The Indian Journal of Agricultural Sciences.* 83(6): 685-688.
- Mazid, A., Mohd, S.M.S.A., Mohrir, M.N. and Jadhav, R.S. 2013. Genetic variability, heritability and genetic advance in okra (*Abelmoschus Esculentus* L. Moench.). *Electronic Journal of Plant Breeding.* 4(3): 1255-1257.
- National Horticulture Board (NHB). (2020-2021). *Indian Horticulture Database*, Gurgoan, New Delhi.
- Pal, B.P., Singh, H.B. and Swarup, V. 1952. Taxonomic Relationship and Breeding Possibilities of Species of okra [*Abelmoschus esculentus* (L.) Moench] *Biotech.Gaz.* 113:455 - 464.
- Patil, Y. B. 1995. *Studies on Genetic Divergence, Heterosis and Combining Ability in okra* [*Abelmoschus Esculentus* (L.) Moench]. Ph.D. Thesis. Univ. Agric. Sci. Dharwad.
- Ramgiry, M., Barholia, A.K. and Mishra, P. 2017. Studies on genetic variability, heritability and genetic advance in okra (*Abelmoschus esculentus* (L.) Monech). *Trends in Biosciences.* 10(2): 941-944.
- Raval, V., Patel, A., Rathod, S., Sumita, Z., Vashi, J.M. and Chaudhari, B. 2018. Genetic variability, heritability and genetic advance studies in okra (*Abelmoschus esculentus* (L.) Moench). *International Journal of Chemical Studies.* 6(3): 3319-3321.
- Saifullah, M. and Rabbani, M.G. 2009. Evaluation and Characterization of okra (*Abelmoschus esculentus* (L.) Moench.) Genotypes. *Saarc J. Agric.* 7(1): 91- 98.
- Sharma, T., Bahadur, V. and Prasad, V.M. 2020. Study on genetic analysis for yield and its components and YVMV resistance in okra [*Abelmoschus esculentus* (L.) Moench]. *IJCS.* 8(6): 1418-1424.
- Siemonsmo, J.S. 1982. West African okra. Morphological and Cytological Indications for The Existence of Amnatural Amphiploid of *Abelmoschus esculentus* (L.) Moench and *A. Manihot* (L.) Medikus. *Euphytica.* 31(1): 241- 252.
- Verma, V., Singh, B., Singh, M.K. and Singh, S.K. 2018. Studies on genetic variability, heritability and genetic advance in Okra [*Abelmoschus esculentus* (L.) Moench.]. *Journal of Pharmacognosy and Phytochemistry.* 7(4): 1114-1115.