Plant Archives Vol. 25, Supplement 2, 2025 pp. 1215-1220 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org

DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2025.v25.supplement-2.151

EVALUATION AND ASSESSMENT OF GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR YIELD AND QUALITY RELATED TRAITS IN OKRA (*ABELMOSCHUS ESCULENTUS* L. MOENCH)

Govind Maury[1*], Ashish Kumar Singh[2], Aastik Jha[2], Anil Kumar[2], Dhananjay Upadhyay[2], C.N. Ram[2], Priti Patel[3], Rajanikant[1], Brajpal Singh[1], Monu Kumar Chaudhari[1] and Brijesh Patel[4]

[1]Department of Vegetable Science, College of Horticulture and Forestry Acharya Narendra Deva University of Agriculture & Technology, Kumarganj, Ayodhya-224229, Uttar Pradesh, India

[2]Department of Vegetable Science, Acharya Narendra Deva University of Agriculture & Technology, Kumarganj, Ayodhya-224229, Uttar Pradesh, India

[3]Department of Agronomy, College of Agriculture, Acharya Narendra Deva University of Agriculture & Technology, Kumarganj, Ayodhya-224229, Uttar Pradesh, India

[4]Department of Fruit Science, Acharya Narendra Deva University of Agriculture & Technology, Kumarganj, Ayodhya, 224229, Uttar Pradesh, India

*Corresponding author E-mail: govindmauryabhu2017@gmail.com

(Date of Receiving : 07-05-2025; Date of Acceptance : 11-07-2025)

ABSTRACT

The present investigation work entitled at the Main Experiment Station, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology (Narendra Nagar) Kumarganj, Ayodhya (U.P.) 224229 during the Kharif, 2024. using 28 diverse okra genotypes in a Randomized Block Design with three replications. Significant differences among genotypes were observed for all 17 traits, indicating the presence of substantial genetic variability. Traits such as total pod yield, number of seed per pod, pod yield per plant and pod showed high genotypic and phenotypic coefficients of variation. High heritability estimates coupled with high genetic advance as a percentage of the mean were recorded for pod yield per plant, total pod yield, number of seed per plant, titrable acidity, pod length and number of pods per plant, suggesting additive gene action and effectiveness of direct selection. genotypes NDO-23-6, NDO-23-7, NDO-23-8, and NDO-23-9 were found highest in yield then the check variety NDO-10, indicating their potential utility in future breeding programs aimed at yield enhancement. The findings highlight how crucial it is to take use of genetic variety in order to improve okra genetically.

***Keywords* :** okra, genetic variability, heritability, genetic advance, PCV, GCV, yield improvement.

Introduction

The okra [*Abelmoschus esculentus* (L.) Moench.] is also known as Lady's finger. It is a fast growing, erect, herbaceous annual and belong to the family Malvaceae. It has somatic chromosome number 2n=4X=130 and is considered as amphidiploids (Naveed *et al.*, 2009). In Okra, found medicinal properties are associated with genitro-urinary disorders, spermatorrhoea and chronic dysentery. Being an often-cross pollinated crop, the extent of cross-pollination is 4-19 % of which 42.2 % is due to insects attracted by its large attractive flowers and also because of protogyny nature (Kundari *et al.*, 2021). The fruits are harvested when immature and eaten as a vegetable. When making jaggery in India, the dry roots and stems are steeped in water for the entire night to produce mucilage, which is then used to clear the sugarcane juice. The paper business uses fully ripe fruit and stems that contain crude fiber. When eaten raw on an empty stomach every morning, tender fruits boost vitality and nourish the body (Sharma & Kaushik, 2017). It is supposed to be highly beneficial, and those who have renal calculus (a kidney stone) should eat it. It is a great source of iodine, which helps to control goitre. Okra is indigenous to Africa. It is an important fruit vegetable crop of the tropical and subtropical regions of the world. It is grown commercially in India, Turkey, Iran, Yugoslavia, Bangladesh, Afghanistan and Southern United State. India ranks first in the world with 5784.0 thousand tons (72% of the total world production). In India, the total area covered under okra is 498 thousand hectares with the production of 5784 thousand metric tons green fruits, whereas productivity is 11.60 metric tons per hectare (NHB, 2021; FAOSTAT, 2020). In India, okra is commercially grown in the state of Gujarat, Maharashtra, Andhra Pradesh, Uttar Pradesh, Tamil Nadu, Karnataka, Haryana, and Punjab. The present status of Uttar Pradesh reported 351.012 tons per hectare increase from previous year record 347.696 tons per hectare (Anonymous, 2024). In India, Uttar Pradesh comes in fourth rank in okra production.

It has good nutritive value and 100 g edible pod found 88.6 g water, 36 kcal energy, 2.10 g protein, 8.20 g carbohydrate, 0.20 g fat, 1.70 g fiber, 84.00 mg Ca, 90.00 mg P, 1.20 mg Fe, 0.08 mg riboflavin, 0.04 mg thiamin, 0.60 mg niacin and 47.00 mg ascorbic acid (Singh *et al.,* 2014). The high iodine content of fruit is useful in curing goiter disease and also possesses export potential. Okra seed oil is a rich source of linoleic acid, a polyunsaturated fatty acid essential for human nutrition. The dry seed contain 13-22% edible oil and 20-24% protein. Roasted and grinded seeds find their use as coffee substitute (NHB, 2024).

Materials and Methods

The present research work entitled at the Main Experiment Station, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology (Narendra Nagar) Kumarganj, Ayodhya (U.P.) 224229 during the Kharif, 2024. The experimental materials of the present investigation comprise twenty-eight genotypes of okra collected from different places and the germplasm stock maintained in the Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya (U.P). The local high-yielding variety NDO-10 used as a Check variety. The details of the materials are given in Table 1. The experiment was conducted in Randomized Block Design with three replications to assess the performance of twenty-eight genotypes. Each entry was sown in three rows with 3 m, net row length spaced 45 cm with a plant-to-plant spacing of 30 cm in each replication. The experiment was sown on 20 March 2024. All the recommended agronomic packages of practices and plant protection measures were followed to raise a good crop.

Table 1 : List of genotypes and their source of origin

	Name of genotype	**Source of genotype**
1.	NDO-23-1	Local Collection (Ayodhya)
2.	NDO-23-2	Local Collection (Varanasi)
3.	NDO-23-3	Local Collection (Ayodhya)
4.	NDO-23-4	Local Collection (Varanasi)
5.	NDO-23-5	Local Collection (Jaunpur)
6.	NDO-23-6	Local Collection (Kanpur)
7.	NDO-23-7	Local Collection (Kanpur)
8.	NDO-23-8	Local Collection (Jaunpur)
9.	NDO-23-9	Local Collection (Kanpur)
10.	NDO-23-10	Local Collection (Varanasi)
11.	NDO-23-11	Local Collection (Ayodhya)
12.	NDO-23-12	Local Collection (Ayodhya)
13.	NDO-23-13	Local Collection (Ayodhya)
14.	NDO-23-14	Local Collection (Ayodhya)
15.	NDO-23-15	Local Collection (Ayodhya)
16.	NDO-23-16	Local Collection (Jaunpur)
17.	NDO-23-17	Local Collection (Jaunpur)
18.	NDO-23-18	Local Collection (Jaunpur)
19.	NDO-23-19	Local Collection (Kanpur)
20.	NDO-23-20	Local Collection (Kanpur)
21.	NDO-23-21	Local Collection (Kanpur)
22.	NDO-23-22	Local Collection (Lucknow)
23.	NDO-23-23	Local Collection (Varanasi)
24.	NDO-23-24	Local Collection (Varanasi)
25.	NDO-23-25	Local Collection (Varanasi)
26.	NDO-23-26	Local Collection (Varanasi)
27.	NDO-23-27	Local Collection (Varanasi)
28.	NDO-23-28	Local Collection (Varanasi)

Result and Discussion

The analysis of variance for experimental design indicated highly significant differences among all the genotypes for all the seventeen traits viz., days to first flower appearance, days to 50% flowering, days to first harvesting, plant height (cm), internodal length (cm), stem diameter (mm), first pod producing node, pod length (cm), pod diameter (mm), average pod weight (g), number of pod per plant, number of seed per pod, T.S.S (° Brix), Ascorbic acid (mg/100g), Titrable acidity (%), pod yield per plant (g) and total pod yield (q/hac). The mean square due to genotypes indicated the presence of considerable amount of variability in the experimental material, which can be exploited for improvement of fruit yield and yield attributes in okra (Table 2).

Table 2 : Analysis of variance (mean squares) for seventeen characters in okra.

S. No.	Traits	Source of variation		
		D.F.		
		Replication	Treatments	Error
		2	27	54
1.	Days to first flower appearance	1.87	2.58**	1.17
2.	days to 50% flowering	0.46	2.11**	0.79
3.	days to first harvesting	0.87	14.72**	4.21
4.	Plant height (cm)	41.99	193.71**	44.61
5.	Internodal length (cm)	0.117	0.157**	0.062
6.	Stem diameter(mm)	0.251	0.807**	0.341
7.	First pod producing node	0.03	1.57**	0.17
8.	Pod length (cm)	0.01	6.29**	0.48
9.	Pod diameter (mm)	0.12	2.25**	0.88
10.	Average pod weight (g)	0.01	5.55**	0.57
11.	Number of pod per plant	0.01	9.75**	0.82
12.	Number of seed per pod	13.36	149.84**	6.72
13.	T.S.S (° Brix)	0.102	0.372**	0.052
14.	Ascorbic acid (mg/100g)	3.24	5.68**	0.86
15.	Titrable acidity (%)	0.0005	0.0015**	0.0001
16.	Pod yield per plant (g)	249.17	2733.20**	97.10
17.	Total pod yield (q/hac)	5.26	1308.22**	52.07

Coefficients of Variations

Information of the nature and degree of variability present in population helps in selection the desirable characteristics for the success of breeding Programme. Coefficients of Variation used to determine the variability. The phenotypic coefficient of variations was higher than genotypic coefficient of variation for all the characters showing that the environment play an important role in influencing the expression of characters.

The estimates of genotypic and phenotypic coefficients of variations for 28 characters of okra germplasm had been presented in table 4 The estimates of phenotypic coefficients of variations (PCV) were higher than genotypic coefficients of variations (GCV) for all the characters. The highest phenotypic (>15%) as well as genotypic coefficients of variation were observed in case of total pod yield (17.38% and 16.39%) followed by number of seed per pod (17.37% and 16.26%) and pod yield per plant (16.65% and 15.80%). Moderate (10- 15%) estimates of PCV and GCV were estimated for pod length (13.47% and 12.05%) followed by number of pod per plant (13.03% and 11.54%), first pod producing node (12.52% and 10.76%), average pod weight (11.94% and 10.29%) and tritable acidity (11.30% and 10.16%). Lower (<10%) PCV and GCV was found for plant height (9.47% and 6.87%) followed by T.S.S (8.00% and 6.57%), pod diameter (7.30% and 4.27%), ascorbic acid (7.26% and 5.86%), internodal length (6.33% and 3.67%), stem diameter (5.47% and 3.06%), days to first harvesting (5.40% and 3.64%), days to first flower appearance (3.17% and 1.70%) and days to 50% flowering (2.36% and 1.42%).

A similar result was reported by Prakash *et al.* (2022) and Kharat *et al.* (2022).

Heritability and Genetic Advance

Estimates of heritability and genetic advance for different characters has been presented in table 3. The heritability in ranged from 28.76 per cent in case days to first flower appearance to 90.05 per cent for pod yield per plant.

High estimates of heritability (>75%) were recorded for six characters i.e. pod yield per plant (90.05%) followed by total pod yield (88.94%), number of seed per pod (87.65%), tritable acidity (80.85%), pod length (80.10%), number of pod per plant (78.45%), However, moderate heritability (>50% and <75%) were recorded for five characters i.e. average pod weight (74.30%) followed by first pod producing node (73.76%), T.S.S (67.44%), ascorbic acid (65.06%), plant height (52.70) and lower heritability (<50%) was recorded for remaining characters i.e. days to first harvesting (45.38%) followed by days to 50% flowering (35.98%) pod diameter (34.10%), internodal length (33.72%), stem diameter (31.32%), days to first flower appearance (28.76%) estimated in all 6 characters.

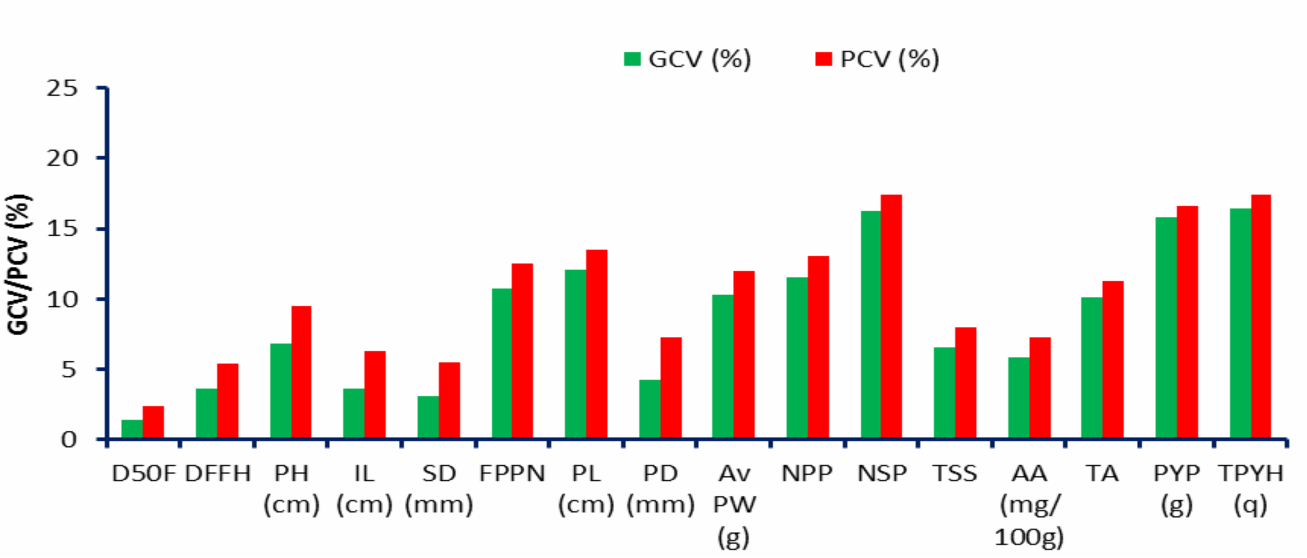

Fig. 1: Genotypic and Phenotypic Coefficient of Variation

Highest value of genetic advance in per cent of mean was shown by total pod yield (31.84). While days to 50% flowering exhibited lowest value (1.75%) for this parameter. The characters which observed very high estimates of genetic advance was pod yield per plant (57.95%) and lowest genetic advance was estimated for tritable acidity (0.04%).

High heritability coupled with high genetic advance in per cent of mean were recorded for pod yield per plant (90.05% and 30.89%), total pod yield (88.94% and 31.84%), number of seed per pod (87.65% and 31.37%), tritable acidity (80.85% and 18.82%), pod length (80.10% and 22.22%), number of pod per plant (78.45% and 21.06%), average pod weight (74.30% and 18.28%), first pod producing node (73.76% and 19.03%), T.S.S (67.44% and 11.11%), ascorbic acid (65.06% and 9.74%), plant height (52.70% and 10.28%), days to first harvesting (45.38% and 5.05%), days to 50% flowering (35.98% and 1.75%), pod diameter (34.10% and 5.13%), internodal length (33.72% and 4.40%), stem diameter (31.32% and 3.53%) and days to first flower appearance (28.76% and 1.88%) indicating that these traits were little influenced by environment. Thus, require low selection intensity for improvement. Its also supported by the finding of Awasthi *et al.* (2022) and Pundir *et al.* (2022).

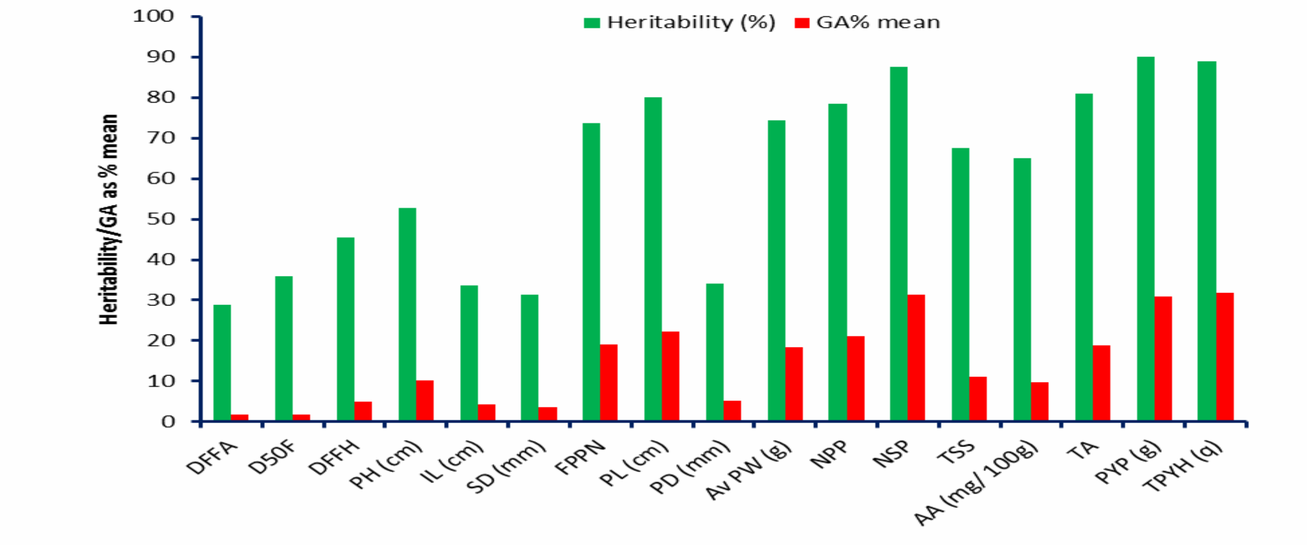

Fig. 2: Heritability and Genetic Advance

Table 3 : Estimates of range, grand mean, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, genetic advance (Ga) and Ga in per cent of mean for seventeen characters in okra germplasm.

Characters	**Mean**	**Min**	**Max**	**GCV (%)**	**PCV (%)**	**Heritability (%)**	**Genetic Advancement 5%**	**Gen. Adv as % of Mean**
Days to first flower appearance	40.40	38.67	42.33	1.70	3.17	28.76	0.76	1.88
days to 50% flowering	46.86	43.67	48.00	1.42	2.36	35.98	0.82	1.75
days to first harvesting	51.45	44.00	54.67	3.64	5.40	45.38	2.60	5.05
Plant height (cm)	102.55	86.99	120.64	6.87	9.47	52.70	10.54	10.28
Internodal length (cm)	4.84	4.44	5.39	3.67	6.33	33.72	0.21	4.40
Stem diameter(mm)	12.88	12.20	14.53	3.06	5.47	31.32	0.45	3.53
First pod producing node	6.35	5.00	7.60	10.76	12.52	73.76	1.21	19.03
Pod length (cm)	11.55	8.10	13.43	12.05	13.47	80.10	2.57	22.22
Pod diameter (mm)	15.82	13.45	17.49	4.27	7.30	34.10	0.81	5.13
Average pod weight (g)	12.51	9.56	15.02	10.29	11.94	74.30	2.29	18.28
Number of pod per plant	14.94	11.51	17.77	11.54	13.03	78.45	3.15	21.06
Number of seed per pod	42.47	32.44	56.42	16.26	17.37	87.65	13.32	31.37
T.S.S (° Brix)	4.97	4.38	5.53	6.57	8.00	67.44	0.55	11.11
Ascorbic acid (mg/100g)	21.62	19.80	24.49	5.86	7.26	65.06	2.11	9.74
Titrable acidity (%)	0.21	0.17	0.27	10.16	11.30	80.85	0.04	18.82
Pod yield per plant (g)	187.58	134.33	241.86	15.80	16.65	90.05	57.95	30.89
Total pod yield (q/hac)	124.85	86.22	161.08	16.39	17.38	88.94	39.75	31.84

Conclusion

The analysis of variance (mean of squares) for seventeen characters were highly significant for the seventeen traits out of seventeen, indicating ample variation among the genotypes. The highest phenotypic (>15%) as well as genotypic coefficients of variation were observed in case of total pod yield (17.38% and 16.39%) followed by number of seed per pod (17.37% and 16.26. Lowest (<10%) PCV and GCV was found for plant height (9.47% and 6.87%) followed by T.S.S (8.00% and 6.57%). High heritability coupled with high genetic advance in per cent of mean were recorded for pod yield per plant (90.05% and 30.89%) and total pod yield (88.94% and 31.84%). Out of 28 genotypes 12 genotypes NDO-23-6 (141.30), NDO-23-7 (161.08), NDO-23-8 (137.54), NDO-23-9 (141.74), NDO-23-11 (158.84), NDO-23-13 (153.69), NDO-23-16 (143.74) and NDO-23-19 (136.83), NDO-23-22 (160.15), NDO-23-25 (126.25), NDO-23-27 (130.12), NDO-23-28 (137.93) were found highest total pod yield then the check variety NDO-10 (126.12) q/ha can be utilized in breeding programmers.

References

Anonymous (2024). Department of Agriculture and Farmers Welfare

Ashraf, A.T.M., Rahman, M.M., Hossain, M.M. and Sarker, U. (2020). Performance evaluation of some selected okra genotypes. *Int. J. Plant Soil Sci*. **32**, 13-20

Awasthi, S., Singh, D.P., Lal, B., Singh, P., Upadhyay, A., Singh, P.K., Kuswaha, C., Pandey, S., Maurya, P.K. and Kumar, A. (2022). Assessment of genetic variability, heritability and genetic advance of okra genotypes [*Abelmoschus esculentus* (L). Moench]. *Assessment.* **53**(04), 7501-7512

Burton, G.W. and De vane, E.W. (1953). Estimating heritability in tall fescue (*Festuca arundiancea*) from replicated clonal material. *Proejtunnien*. **9**, 12-15

FAOSTAT (2020). Food and Agriculture Organization of the United Nations. http$_2$//www.fao.org/faostat (For global okra production statistics and India's contribution)

Hanson, G.H., Robinson, H.F. and Comstock, R.E. (1963). Biometrical studies of yield in segregating population of korean lespedeza. *Agron. J.* **48**, 268-271

Johanson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybean. *Agron. J.* **47**, 314-318

Kharat, M.A., Bhalerao, R.V. and Bhise, D.R. (2022). Genetic variability, heritability, and genetic advance for selection parameters of okra [*Abelmoschus esculents* (L.) Moench] genotype. *The Pharm. Innov. J.* **11**(12), 3718-3723

Kumar, R., Singh, B.D., & Srivastava, K. (2012). Genetic variability, heritability and genetic advance studies in okra (*Abelmoschus esculentus* (L.) Moench). *Veg. Sci.* **39**(1), 82–84

Kundari, 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] for productivity traits. *J. Pharmacogn. Phytochem.* **9**(6), 1574-1576

Mishra, S. P., Singh, A. K., & Singh, A. K. (2018). Estimation of genetic parameters in okra (*Abelmoschus esculentus* (L.) Moench) under Eastern Uttar Pradesh condition. *Int. J. Curr. Microbiol. Appl. Sci.* **7**(6), 2662–2668

Muthusamy, V., Dharmalingam, C., & Thirugnanakumar, S. 2014. Genetic variability and correlation studies in okra (*Abelmoschus esculentus* (L.) Moench). *Electron. J. Plant Breed*. **5**(1), 64–73

Naveed, A., Khan, A.A., Khan, I.A. (2009). Generation mean analysis of water stress tolerance in okra [*Abelmoschus esculentus* (L.) Moench]. *Pak. J. Bot*. **41**, 195-205

NHB (2024). Horticulture Statistics at a Glance-Okra Seed Composition. National Horticulture Board, Ministry of Agriculture, India

NHB (2021). National Horticulture Board, Government of India, Horticultural Statistics at a Glance. http,//nhb.gov.in (For area, production, and productivity data in India)

Panse, V.G., and Sukhatme, P.V. (1984). Statistical methods for agricultural workers. ICAR, pub., New Delhi

Patel, U. K., Patel, K. D., & Patel, A. I. (2015). Genetic variability, heritability and genetic advance in okra (*Abelmoschus esculentus* L. Moench). *Int. J. Agric. Sci.* **11**(1), 130–132

Prakash, G., Halesh, G.K., Jagadeesha, R.C., Ravishankar, K.V., Pitchaimuthu, M. and Shankarappa, K.S. (2022). Studies on genetic variability and character association in okra [*Abelmoschus esculentus* (L.) Moench] for yield and its contributing traits. *The Pharm. Innov. J.* **11**(12), 3639-3664

Pundir, S., Singh, M.K., Alam, K. and Ahmad, M. 2022. To assess the genetic variability, heritability and genetic advance as percent of mean for selection parameters in okra [*Abelmoschus esculentus* (L.) Moench]. *Pharm. Innov.J.* **11**(5), 1963-1968

Sankar, M., & Kumar, M. 2010. Genetic variability and character association in okra (*Abelmoschus esculentus* (L.) Moench). *Madras Agric. J.* **97**(1–3), 44–46

Sharma, P., & Kaushik, P. (2017). Health benefits of okra consumption, A traditional perspective. *J. Ethnopharmacol*. **204**, 68–74

Singh, P., Chauhan, V., Tiwari, B.K., Chauhan, S.S., Simon, S., Bilal, S., and Abidi, A.B. (2014). An overview on okra [*Abelmoschus esculentus* (L.) Moench] and it's importance as a nutritive vegetable in the world. *Int. J. Pharm. Biol. Sci*. **4**(2), 227-233.