Plant Archives Vol. 25, Supplement 2, 2025 pp. 448-452 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-2.054

ASSESSMENTS OF GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE IN BRINJAL (*SOLANUM MELONGENA* L.)

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(Date of Receiving : 21-03-2025; Date of Acceptance : 02-06-2025)

ABSTRACT

Brinjal (*Solanum melongena* L.) is a vital solanaceous vegetable crop with significant genetic variability, offering potential for horticultural trait improvement. This study, conducted during the Rabi season of 2023–2024 at Acharya Narendra Deva University of Agriculture and Technology, aimed to assess genetic variability, heritability, and genetic advance among 27 genotypes using a randomized block design. Seventeen agronomic traits were evaluated, and statistical parameters such as phenotypic and genotypic coefficients of variation (PCV & GCV), broad-sense heritability (h^2), and genetic advance were calculated. High heritability estimates were observed for most traits, indicating strong genetic control, while traits like fruit yield exhibited considerable genetic advance, suggesting additive gene action. The findings provide valuable insights into selection strategies for brinjal improvement, supporting future breeding programs aimed at enhancing yield and quality traits.

***Keywords* :** genetic variability, heritability, genetic advance, PCV, GCV, heritability, gene action.

Introduction

Brinjal (*Solanum melongena* L.) is one of the important solanaceous vegetable crops. Brinjal is a versatile crop adapted to various agro-climatic regions of India and can be grown all over the year. The family Solanaceae includes it. 11,309 thousand hectares were used for vegetable agriculture in India in 2022–2023, yielding 212,548 thousand metric tons of vegetables. Merely 681 thousand hectares were planted to brinjal, which added 12,972 thousand metric tons to the country's vegetable production. (NHB, 2022-23). It is grown mainly for its tender and immature fruits utilised in culinary preparations. Fruits serve as rich source of nutrients in terms of carbohydrates, proteins, fibre and vitamins like thiamine, niacin and folacin as well as minerals like calcium, iron, potash, zinc, copper and manganese. Besides various parts of the plants are used in preparing decoction for curing ailments such as diabetes, leprosy, cholera, asthenia and haemorrhoids. Further, it is proven in ISM as cure to heart disease and control blood pressure (Okon *et al*., 2010, Bidyalaxmi Devi and Kanaujia, 2020). There is substantial spectrum of genetic variability existing in this crop. Because of its rich genetic diversity there is scope for improvement of various horticultural traits (Gavade and Ghadege, 2015). variance. Knowledge on the structure of the genetic variability within ecotypes of a region is of great help to draft programs for character improvement (Rathi *et al.*, 2011). High heritability alone is not sufficient to make effective selection in segregating generations, unless information is provided for considerable amount of genetic advance. Genetic advance which indicates the improvement in the mean genotypic values of the superior families over the base population helps the breeders to select the progenies in the earlier generation (Sidhya *et al.*, 2014).

Material and Methods

The present investigation conducted during Rabi season of 2023–2024, at the Main Experiment Station, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar, Kumarganj, Ayodhya (U.P.) India.

The experimental site is geographically, falls under humid, sub-tropical climate and is located in between 24.470 and 26.560 N latitude and 82.120 and 83.980 E longitude at an altitude of 113 m above the mean sea stratum in the Gangetic alluvial plains of Eastern Uttar Pradesh. The soil of experimental site was sandy loam with average fertility level with pH in the range of 7.5-8.5. A randomized block design with three replications was used to assess twenty-seven distinct genotypes were collected from ANDUAT, Kumarganj, Ayodhya (Table 1). Six weeks old healthy seedlings were transplanted into the main field in two-row plots, each measuring three meters. Ten plants per genotype were allowed in each replication, with plant spacing kept at 60 × 50 cm.

Table 1: List of genotypes and their source of origin

S.No.	Genotype	Source of origin
1	NDB-23-16	A.N.D.U.A.&T, Ayodhya (U.P.)
2	NDB-23-17	A.N.D.U.A.&T, Ayodhya (U.P.)
3	NDB-23-18	A.N.D.U.A.&T, Ayodhya (U.P.)
4	NDB-18-1	A.N.D.U.A.&T, Ayodhya (U.P.)
5	NDB-18-2	A.N.D.U.A.&T, Ayodhya (U.P.)
6	NDB -23-2	A.N.D.U.A.&T, Ayodhya (U.P.)
7	NDB-15-27	A.N.D.U.A.&T, Ayodhya (U.P.)
8	NDB-23-19	A.N.D.U.A.&T, Ayodhya (U.P.)
9	NDB-23-20	A.N.D.U.A.&T, Ayodhya (U.P.)
10	NDB-23- 21	A.N.D.U.A.&T, Ayodhya (U.P.)
11	Pant Rituraj	G.B.P.U.A.T., Pant Nagar (U.K.)
12	NDB-19-1	A.N.D.U.A.&T, Ayodhya (U.P.)
13	NDB-19-2	A.N.D.U.A.&T, Ayodhya (U.P.)
14	NDB-19-3	A.N.D.U.A.&T, Ayodhya (U.P.)
15	NDB-19-4	A.N.D.U.A.&T, Ayodhya (U.P.)
16	NDB-2 (Check)	A.N.D.U.A.&T, Ayodhya (U.P.)
17	NDB-19-6	A.N.D.U.A.&T, Ayodhya (U.P.)
18	NDB-19-7	A.N.D.U.A.&T, Ayodhya (U.P.)
19	NDB-19-8	A.N.D.U.A.&T, Ayodhya (U.P.)
20	NDB-19-9	A.N.D.U.A.&T, Ayodhya (U.P.)
21	BR-14	A.N.D.U.A.&T, Ayodhya (U.P.)
22	IVBL-22	A.N.D.U.A.&T, Ayodhya (U.P.)
23	IVBL-31	A.N.D.U.A.&T, Ayodhya (U.P.)
24	IVBL-24	A.N.D.U.A.&T, Ayodhya (U.P.)
25	IVBL-27	A.N.D.U.A.&T, Ayodhya (U.P.)
26	IVBL-30	A.N.D.U.A.&T, Ayodhya (U.P.)
27	IVBL-28	A.N.D.U.A.&T, Ayodhya (U.P.)

In order to ensure good crop growth, the cultivation followed the guidelines and tactics that were recommended. Five randomly chosen plants from each plot were taken into consideration for recording observations for seventeen different features. Phenotypic and genotypic coefficient of variation (Burton, 1952), heritability (Lush, 1940), and genetic advance as per cent of mean (Robinson *et al.*, 1949) were calculated. The ratio of genotypic variation to total phenotypic variance was used to calculate the broad-sense heritability (h^2) for each characteristic. Each trait's genetic progress estimates were derived using the formula proposed by (Johnson *et al.* 1955).

Results and Discussion

The mean sum of squares for seventeen characters in genotypes of brinjal is presented in table 2. Analysis of variance revealed highly significant differences among genotypes for all seventeen characters. The results pertaining to mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (h^2) and expected genetic advance as per cent of mean (GAM) for all the seventeen characters.

Table 2: Analysis of variance (ANOVA) for growth and yield characters in brinjal

S. N.	Traits	Mean squares		
		Replicate	**Treatments**	**Error**
		2	**26**	**52**
1	Days of 1st flowering	10.95	56.30**	5.70
2	Days of 50% flowering	11.78	57.81**	7.36
3	Days to first fruit harvest	5.70	56.24**	11.86
4	Polar fruit length (cm)	0.55	17.48**	0.97
5	Equatorial fruit Diameter (cm)	0.152	1.101**	0.063
6	Length of pedicle (cm)	0.023	1.271**	0.166
7	No of primary branches	0.022	0.485**	0.043
8	Plant height (cm)	16.37	106.69**	19.67
9	No of Fruit per cluster	0.071	1.054**	0.058
10	Average Five fruit weight (g)	9.89	293.17**	20.65
11	No of Fruit per plant	0.63	13.95**	2.00
12	TSS	0.188	0.547**	0.049
13	Ascorbic Acid	0.07	11.36**	0.05
14	Dry matter (g)	0.085	1.436**	0.039
15	Phenol content (mg/100 gm)	0.008	0.230**	0.033
16	Total fruit yield per plant (kg)	0.0004	0.517**	0.033
17	Total fruit yield (q/ha)	23.40	3613.44**	249.55

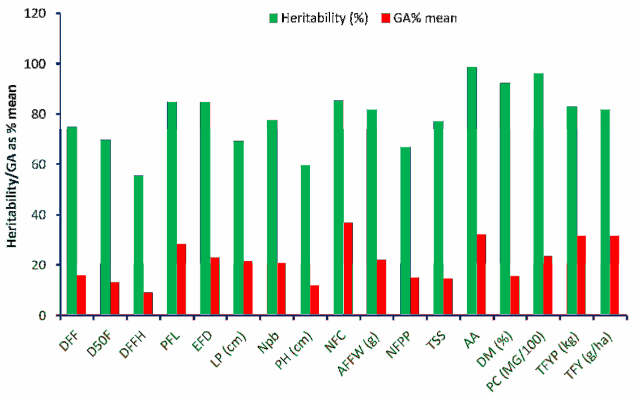
The phenotypic variance ranged from 8.04 to 18.87, and the lowest variance was recorded for Days of first fruit harvest and the maximum was recorded for Number of fruits per cluster, followed by Total fruit yield (q/ha) and Total fruit yield per plant (kg). The genotypic coefficient of variance (GCV) ranged from 5.99 to 19.29. High GCV was observed for Number of fruits per cluster followed by Total fruit yield (q/ha) and Total fruit yield per plant (kg), whereas the lowest GCV was recorded in Days of first fruit harvest. The investigation revealed that the genotypic variation was high as compared to the phenotypic variation for all the traits studied, indicating the influence of environment. This result is in accordance with the reports of Vaishya *et al.* (2017) and Sujin *et al.* (2017).

Table 3: General mean, range and PCV, GCV, heritability and genetic advance for various growth and yield characters in brinjal

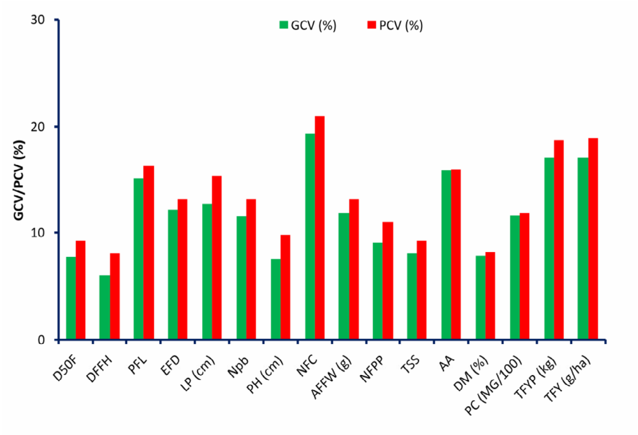
Characters	Mean	Min	Max	Heritability broad sense (%)	Genetic advance	GA% mean	GCV (%)	PCV (%)
Days of first flowering	45.65	32.33	57.67	74.75	7.31	16.02	9.00	10.41
Days of 50% flowering	52.88	40.33	65.67	69.57	7.05	13.33	7.76	9.30
Days of first fruit harvest	64.19	52.33	77.67	55.50	5.90	9.20	5.99	8.04
Polar fruit length (cm)	15.57	9.87	18.63	85.08	4.46	28.64	15.07	16.34
Equatorial fruit diameter(cm)	4.84	3.57	5.70	84.68	1.12	23.04	12.16	13.21
Length of Pedicle (cm)	4.76	3.70	6.23	69.00	1.04	21.83	12.76	15.36
Number of primary branches	3.32	2.73	4.13	77.41	0.70	20.98	11.58	13.16
Plant height (cm)	71.11	60.34	80.30	59.58	8.56	12.04	7.57	9.81
Number of fruits per cluster	2.99	1.63	3.77	85.11	1.09	36.66	19.29	20.91
Average five fruit weight (g)	80.19	62.21	98.29	81.48	17.72	22.10	11.88	13.17
Number of fruits per plant	22.13	17.80	25.53	66.61	3.36	15.16	9.02	11.05
TSS	5.02	4.20	5.77	77.19	0.74	14.70	8.12	9.24
Ascorbic acid (mg/100g)	12.23	9.42	15.47	98.65	3.97	32.46	15.87	15.98
Dry matter (%)	8.66	7.27	9.80	92.26	1.35	15.59	7.88	8.20
Phenol content (MG/100)	2.36	1.86	2.77	96.38	0.56	23.58	11.66	11.88
Total fruit yield per plant (kg)	2.36	1.63	2.93	83.05	0.75	31.92	17.00	18.65
Total fruit yield (q/ha)	196.19	134.72	247.41	81.80	62.39	31.80	17.07	18.87

High estimates for both PCV and GCV were obtained for Number of fruits per cluster in the present study. Moderate estimates of PCV and GCV were recorded for Polar fruit length (cm), Equatorial fruit diameter(cm), Length of Pedicle (cm), Number of primary branches, Number of fruits per cluster, Average five fruit weight (g), Number of fruits per plant. Ascorbic acid (mg/100g), Phenol content (MG/100), Total fruit yield per plant (kg), Total fruit yield (q/ha). Such findings are in conformity with the reports of Patel *et al.* (2015), Suranjna *et al.* (2017), and Parvati *et al.* (2018).

In the present study, almost all the characters exhibited high heritability, which ranged from 55.50 to 98.65 per cent. The characters included plant height, days to 50% flowering, number of flowers per cluster, number of fruits per cluster, days to first harvest, Average fruit weight, fruit length, fruit diameter, number of fruits per plant and fruit yield per plant. Heritability along with genetic advance as per cent of mean would be helpful in assessing the nature of gene action. In the present study, the characters namely Days of first flowering, Days of 50% flowering, Polar fruit length (cm), Equatorial fruit diameter(cm), Length of Pedicle (cm), Number of primary branches, Number of fruits per cluster, Average five fruit weight (g), Number of fruits per plant, TSS, Ascorbic acid (mg/100g), Dry matter (%), Phenol content (mg/100), Total fruit yield per plant (kg), Total fruit yield (q/ha) showed high estimates of heritability and genetic advance as per cent of mean which may be ascribed to the predominance of additive gene action (Verma *et al.*, 2018). Days of first fruit harvest and Plant height (cm) showed high heritability and low genetic advance as per cent of mean, which indicated that the expression of these characters was governed by non-additive genes. Above research is in accordance with the findings of Vaishya *et al.* (2017) and Mangai *et al.* (2017).



Graph 1: Percentage of heritability and genetic advance



Graph 2: Percentage of GCV and PCV

Conclusion

The present study revealed substantial genetic variability among brinjal (*Solanum melongena* L.) genotypes, providing a strong basis for selection and genetic improvement. High heritability estimates coupled with significant genetic advance in key yield-related traits suggest the predominance of additive gene action, making direct selection effective for improvement. Traits such as the number of fruits per cluster, total fruit yield per plant, and total fruit yield per hectare exhibited high genotypic and phenotypic coefficients of variation, indicating substantial scope for enhancement through breeding programs. The results underscore the importance of exploiting genetic diversity to develop high-yielding and quality-enhanced brinjal varieties, supporting sustainable vegetable production in diverse agro-climatic conditions. These findings serve as a valuable resource for breeders aiming to optimize productivity and fruit quality in brinjal cultivation.

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