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Enhancing breeding strategies for selection of yield and yield-attributing traits in brinjal through analysis of genetic variability parameters

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Abstract

The present research investigation was carried out to estimate the genetic variability parameters among 42 genotypes of brinjal at Horticulture Research Centre, SVPUA & T, Meerut (U.P.), India, during 2 consecutive *Kharif* seasons 2022 and 2023, using a 3-replication randomized complete block design. According to the analysis of variance, all the characteristics under study exhibited sufficient variability. For each character, it was found that the Phenotypic Coefficient of Variations (PCV) was greater than the related Genotypic Coefficient of Variations (GCV). For the characteristics of fruit yield per plot, fruit yield/ha, fruit yield/plant, fruit weight, fruit length, number of fruits/plant, fruit girth, pedicle length and number of primary branches, it was discovered that both GCV and PCV were high. High heritability estimates were observed for all traits under study. The fruit yield per ha, fruit yield per plot, fruit yield per plant, fruit weight, fruit length, number of fruits per plant, fruit girth, pedicle length, number of primary branches and plant height were shown to have the highest genetic improvements as a percentage of the mean. As additive gene action controls these characteristics, direct selection is the better method for enhancing these traits genetically.

Keywords

breeding strategies; brinjal; genetic advance; genetic variability; heritability

Introduction

Brinjal belongs to the Solanaceae family and typically exists as a diploid with a chromosome count of 2n=2x=24. However, despite efforts to cultivate polyploid varieties with chromosome numbers of 2n=36 and 48, these variants have not shown significant economic relevance. The crop is native to India and Sri Lanka. *Solanum* is a genus of nearly 2000 species, including both tuber- and non-tuber-bearing forms. Examples of the non-tuber-bearing group are *Solanum melongena*, *S. torvum*, *S. nigrum*, *S. macrocarpon, S. ferox* and *S. aethiopicum*. A wild type of brinjal with deeply variegated leaves, *S. sisymbrifolium*, is considered the ancestral species of *S. melongena* (1).

The plant is an annual herbaceous type that can have self-contained or 2-5 flowers clustered on each stem, depending on the variety. Flowers are typically complete, actinomorphic and hermaphrodite, with a 5-lobed gamosepalous calyx and a 5-lobed gamopetalous corolla with undulate to incurved margins. The flowers can be divided into 4 categories based on style length: Long (each style element is split at 1 or 2 other sizes), Medium (found to have this intermediate size), Semi-short and Pseudo-Short (or sub-pseudo short). The fruit-setting rate of long-styled flowers

(70%-85%) is high because the ovary matures as a large fruit. The rate of medium-styled flowers (12%-55%) is lower than that of long-styled flowers because the ovary starts to develop only as small-medium size; however, fruit setting is partial in the short-styled flowers and there is no fruit at all in other types with stigmas that are too small and underdeveloped (2).

It is easily cultivated in almost all parts of India except at higher altitudes. Orissa, West Bengal, Bihar, Uttar Pradesh, Madhya Pradesh, Andhra Pradesh, Maharashtra, Gujarat and Karnataka are the major brinjal-growing states. Brinjal thrives in a warm, long growing season, with the main crop grown in autumn -winter. The optimal fruit set occurs at temperatures between 15.5 °C and 21.1 °C, with high temperatures above 35 °C during spring-summer reducing production (3). Round varieties are susceptible to frost and set fruit at lower temperatures, whereas long-fruited varieties are more frost-tolerant and can set fruit at higher temperatures (4)

The success of a breeding program depends on the extent and magnitude of variability existing in the germplasm. Generally, the GCV and PCV are measured to study this variability. Yield is a complex characteristic controlled by several yield-contributing components and is highly influenced by environmental factors; consequently, estimates of heritability are useful. The effectiveness of selecting genotypes is based on heritability. Genetic advance (GA) denotes the improvement over the base population that can potentially be made from selection for a characteristic. An improvement in yield and quality of brinjal is typically achieved by selecting the genotypes with desirable character combinations existing in nature or through hybridization. Considering the aforementioned facts, the current investigation aims to estimate the genetic variability parameters among 42 genotypes for the selection of traits that can be incorporated into future breeding programmes.

Materials and Methods

An experiment was carried out with 42 genotypes of brinjal during 2 consecutive *Kharif* seasons of 2022–2023 at the Horticulture Research Center, SVPUA&T, Meerut (U.P.), India. In the state of Uttar Pradesh, Meerut is located in the agro-climatic plain zone and semi-arid area. Seedlings were raised in rays with coco peat and vermicompost (2:1) under intensive care, achieving a high survival percentage at the college of Horticulture net house during June and were transplanted in the third week of July. Seedlings of each genotype were transplanted on 15 cm raised ridges at a spacing of 60×45 cm and were evaluated in randomized block design (RBD) with 3 replications. The recommended intercultural practices were applied to ensure healthy crop growth and development. During each replication, observations were carried out on 5 randomly chosen plants of each genotype for various traits, including the number of primary branches, fruit length (cm), number of fruits/ plant, days to 50% flowering, plant height (cm), fruit weight (g), fruit girth (cm), pedicle length (cm), 1000 seed weight (g), fruit yield/ plant (kg), fruit yield/plot (kg/ha) and fruit yield/ha (ton/ha).

A statistical analysis was carried out on the average data for each attribute across the 3 replications. The GCV and PCV, variances and frequency distributions and the genetic advance were determined according to previously described methods (5, 6 & 7).

Results and Discussion

The analysis of variance

For each trait, an analysis of variance was carried out to test the significance among genotypes (8, 9). The character-wise mean performance of 42 genotypes and the range of variance among several traits are presented in Table 1. Significant variations among the genotypes for every character examined in both seasons were found through the variance analysis, indicating that there is sufficient variability.

The mean genotype performance

Early crop yield is the most desirable attribute and the days to 50% flowering are one of the most significant factors used to determine a genotype's earliness. The genotypes Pusa Ankur, Utkal Madhuri and RCMBL-04-04 took the minimum days for 50% flowering and were considered the earliest bearers. The yield is mostly influenced by the shape and size of the fruit, which also affects fruit weight. The longest fruits were produced by the genotypes Pusa Purple Long and Punjab Sadabhar. For the trait of fruit girth, the highest value was reported by the genotypes Kashi Green Round and Kashi Uttam. The maximum fruit weight has been recorded in Pant Rituraj and Kashi Green Round. The number of fruits per plant is one of the most desirable factors that significantly contribute to production. The maximum number of fruits per plant has been exhibited by the genotypes Pusa Purple Cluster and Punjab Bharpur. Yield is generally considered an economic parameter and higher yield will always remain one of the main breeding objectives in all crop breeding programs. In the present investigation, the genotypes with the maximum fruit yield per plant, fruit yield per plot and fruit yield per hectare were Utkal Madhuri and Kashi Green Round. Therefore, the results obtained in this investigation suggest that there is sufficient variability among the genotypes that may be utilized as promising parent lines in hybridization programs. These findings align with the previous studies that reported significant variation in the traits studied (10, 11, 12, 13)Their results indicate that key characteristics such as days to 50% flowering, fruit length, fruit weight, fruit girth, number of fruits per plant and overall fruit yield per plant, plot and hectare are critical for selecting the best genotypes in breeding programs.

Variability parameters

The variability parameters such as PCV, GCV, heritability and genetic advance are presented in Table 2. A corresponding higher PCV was displayed by all the traits as compared to GCV, indicating a slight influence of the environment in governing these traits. Environmental factors, such as soil quality, climate and cultivation practices, can introduce significant variability in phenotypic expression. In contrast, GCV reflects only the genetic contribution to variation. Therefore, the PCV often exceeds the GCV due to the additional variance introduced by environmental factors. GCV and PCV were observed to be high for the traits such as fruit yield per plot (43.11% and 43.44%), fruit yield per ha (43.14% and 43.39%), fruit yield per plant (41.55% and 41.92%), fruit weight (38.12% and 38.46%), fruit length (37.80% and 38.21%), number of fruits per plant (35.48% and 35.96%), fruit girth (28.48% and 28.97%), pedicle length (27.80% and 28.88%) and number of primary branches (20.63% and 21.11%). These results indicate the existence of large genetic variability and illustrating the potential for effective selection for the given characters. Previous studies reported higher values of GCV and PCV for traits such as the number of fruits per

Table 1. Mean performance (pooled season 2022 and 2023)

Sl. No.	Treatments	Plant height (cm)	Days to 50% flowering	No. of primary branches	Fruit length (cm)	Fruit girth (cm)	Pedicle length (cm)	Fruit weight (g)	No. of fruits per plant	1000 seed weight (g)	Fruit yield per plant (kg)	Fruit yield per plot (kg/ha)	Fruit yield per ha (ton/ha)
1	Kashi Green Round	77.673	61.417	6.943	7.963	9.7	3.263	160.14	14.697	3.303	2.46	20.09	24.8
2	Kashi Modak	121.887	55.337	9.663	6.867	6.81	2.43	81.583	12.8	3.66	1.167	9.723	12.00
3	Kashi Himani	95.857	59.643	8.147	11.07	5.62	3.25	88.443	15.56	3.23	1.487	12.38	15.287
4	Kashi Prakash	96.87	59.357	7.487	12.57	4.187	3.65	66.96	16.613	2.853	1.233	9.89	12.21
5	Pant Rituraj	62.773	58.363	6.513	8.067	7.52	4.247	181.617	11.827	2.883	2.3	17.63	21.777
6	Kashi Taru	105.99	56.35	9.39	17.62	4.503	5.013	81.077	21.06	3.61	1.84	14.10	17.41
7	Kashi Uttam	102.947	58.01	8.5	6.45	8.213	2.607	100.977	11.837	3.283	1.33	11.06	13.653
8	Pusa Ankur	82.29	43.63	7.333	9.193	6.043	5.047	112.077	15.13	2.72	1.817	13.69	16.91
9	Punjab Barasati	68.157	57.223	4.457	13.1	4.187	2.457	78.707	15.997	3.463	1.397	10.60	13.093
10	PR-5	73.037	54.513	4.663	8.17	7.927	3.68	150.59	9.09	3.537	1.497	11.47	14.163
11	CH-215	99.937	61.303	8.07	7.28	7.693	4.11	161.37	9.497	3.463	1.65	12.65	15.62
12	CHBR-2	100.99	61.687	9.457	7.74	6.733	4.39	117.61	10.24	3.81	1.327	10.15	12.533
13	DBL-24	75.49	61.333	5.92	12.79	3.937	5.683	106.233	18.72	3.14	2.113	16.53	20.407
14	Pusa Upkar	84.547	66.047	9.177	8.7	6.947	4.217	141.347	14.053	2.887	2.13	16.75	20.687
15	RCMBL-04-04	70.897	53.033	4.793	15.75	5.34	3.12	130.213	17.52	3.247	2.417	17.74	21.903
16	Utkal Madhuri	97.047	51.737	5.903	17.94	5.117	4.17	132.017	19	3.467	2.657	19.88	24.547
17	Swarnamani	96.29	57.23	4.313	7.067	7.037	5.117	120.307	11.43	3.79	1.517	11.35	14.023
18	Punjab Sadabhar	70.39	68.973	8.977	19.94	3.877	4.353	90.797	20.777	3.523	2.01	15.05	18.58
19	Navina	71.19	57.643	8.25	9.28	4.623	3.143	80.863	11.027	3.337	1.023	7.477	9.233
20	Gulabi	87.873	58.537	9.023	16.29	3.607	5.443	70.37	22.22	3.4	1.697	12.42	15.33
21	EC 305048	81.49	64.15	8.09	9.27	3.167	6.07	53.497	9.993	3.77	0.66	4.93	6.087
22	EC305118	75.303	64.22	6.817	8.317	7.027	4.193	121.047	7.723	3.45	1.05	7.873	9.717
23	EC305121	104.083	62.37	9.253	10.73	5.527	6.34	80.707	11.843	3.413	1.077	8.04	9.927
24	EC316226	65.397	66.15	6.483	6.133	4.77	3.323	58.133	11.353	3.64	0.78	5.69	7.027
25	EC316275	81.457	69.263	6.283	7.92	5.16	4.183	62.677	13.087	3.183	0.943	6.86	8.467
26	EC316284	91.703	67.05	7.273	10.26	4.733	6.067	83.213	11.277	3.86	1.047	7.65	9.45
27	EC316297	82.19	64.367	7.217	7.26	4.637	4.037	60.863	7.997	3.267	0.62	4.54	5.607
28	EC384619	62.367	68.79	8.283	11.22	4.683	4.097	87.273	9	3.57	0.88	6.42	7.933
29	EC393239	75.95	70.533	6.493	7.09	5.74	4.16	65.803	10.903	3.25	0.843	6.17	7.623
30	EC467271	74.277	71.273	8.903	8.12	6.48	3.207	80.16	11.837	3.847	1.093	8.01	9.897
31	EC467272	75.18	65.32	6.907	12.22	4.61	6.323	61.153	7.743	3.247	0.597	4.34	5.36
32	IC090915	59.657	62.58	7.34	10.21	4.93	4.147	79.407	8.017	3.75	0.777	5.82	7.187
33	IC090942	84.807	68.08	9.38	8.533	4.33	5.16	50.93	12.22	3.397	0.743	5.30	6.55
34	IC090966	97.39	61.16	8.907	14.18	4.66	7.037	63.71	9.533	3.83	0.727	5.3	6.543
35	IC099670	85.687	66.963	8.56	4.107	4.51	5.48	48.847	13.403	3.267	0.793	5.77	7.12
36	IC099676	101.193	66.43	9.803	11.37	4.17	5.85	66.653	13.447	3.713	1.013	7.4	9.137
37	IC099703	84.51	60.623	8.403	10.74	5.52	5.083	94.893	18	3.767	1.82	13.31	16.44
38	Pant Samrat	66.317	61.363	7.723	17.04	3.79	6.69	88.69	16.297	2.98	1.59	12.43	15.347
39	Punjab Bharpur	77.017	56.543	10.15	7.00	3.79	2.46	29.373	26.273	3.423	0.89	6.97	8.61
40	Pusa Purple Cluster	84.44	61.063	5.563	14.73	3.10	2.56	56.053	30.06	3.13	1.797	14.98	18.497
41	Pusa Purple Long	66.293	71.537	5.387	21.09	3.05	4.497	82.277	14.43	3.24	1.337	11.07	13.663
42	Local Long	88.643	74.613	8.46	7.267	5.82	4.107	61.22	11.227	3.347	0.67	4.45	5.493
	Mean	83.51	62.04	7.59	10.68	5.33	4.39	90.24	13.92	3.4	1.35	10.33	12.76
	CV	4.79	4.54	4.47	5.61	5.31	5.19	5.11	5.83	2.41	5.55	5.31	4.65
	SEm	2.31	1.63	0.2	0.35	0.16	0.13	2.66	0.47	0.05	0.04	0.32	0.34
	CD at 5%	6.5	4.58	0.55	0.97	0.46	0.37	7.49	1.32	0.13	0.12	0.89	0.96
	CD at 1%	8.61	6.07	0.73	1.29	0.61	0.49	9.93	1.75	0.18	0.16	1.18	1.28
	Minimum	59.66	43.63	4.31	4.11	3.06	2.43	29.37	7.72	2.72	0.6	4.34	5.36
	Maximum	121.89	74.61	10.15	21.09	9.7	7.04	181.62	30.06	3.86	2.66	20.09	24.8

plant, fruit length, fruit girth, fruit weight, yield per plot and yield per ha (8, 11, 12, 13). The moderate values of GCV and PCV were depicted for plant height (16.80% and 17.47%). Earlier findings found a moderate magnitude of GCV and PCV for plant height, which strongly supported our findings (11, 13). However, days to 50% flowering (10.53%) showed a moderate PCV, while in the case of GCV, it exhibited the lowest value (9.50%). The researcher also reported a moderate PCV value; however, in the case of GCV, it exhibited the lowest value (11).The trait 1000 seed weight showed the lowest GCV and PCV (8.47% and 8.81%), indicating the presence of less genetic variability for this characteristic among the studied genotypes, thereby limiting the chance of further crop improvement through selection for this trait.

Heritability refers to the heritable portion of genetic variance. The reliability of phenotypic variance is dependent on the heritability estimates of a specific trait. Thus, high heritability indicates a significant relationship between genotype and phenotypic variations and facilitates the effective selection of a trait (10). Table 2 and Fig. 1 gives an estimate of GA, genetic advance as a mean percentage (GAM) and average heritability (h^2). During the pooled analysis, the heritability estimates were found to be high (>60.00%) for all the traits, namely plant height (92.47%), days to 50% flowering (81.39%), number of primary branches (95.50%), fruit length (97.84%), fruit girth (96.64%), pedicle length (96.63%), fruit weight (98.23%), number of fruits per plant (97.37%), 1000 seed weight (92.53%), fruit yield/plant (98.24%), fruit yield/plot (98.50%) and fruit yield/ha (98.85%). High heritability values suggest that the characters being studied are minimally influenced by environmental factors in their expression. Consequently, plant breeders can use straightforward selection methods based on the phenotype of these characters, ultimately enhancing the genetic background of these traits. Studies reported high h^2 values for the traits in different solanaceous crops, which supports our findings (2, 12,14).

Genetic advance is measured as the improvement in the mean genotypic value of selected families over the base population and determines the expected genetic gain under selection for a particular trait in the base population. The results showed that maximum genetic advance as a percent of the mean was detected for fruit yield per ha (88.36%), fruit yield/plot (88.15%), fruit yield/ plant (84.83%), fruit weight (77.83%), fruit length (77.01%), number of fruits/plant (72.13%), fruit girth (57.67%), pedicle length (56.29%), number of primary branches (41.53%) and plant height (33.27%). Previous studies observed maximum value of genetic advance as a % of the mean, suggesting the presence of high additive genetic variance; hence, selection can be done effectively for these traits (12, 13, 15). The traits, specifically days to 50% flowering (17.65%) and 1000 seed weight (16.79%), revealed moderate genetic advance as a % of the mean, indicating non-additive gene action. Studies also found moderate genetic advance as a % of the mean for days to 50% flowering in their findings (8, 11). Most traits in the current study exhibited higher h^2 with moderate to low genetic advance, suggesting that further selection is required to improve these traits. A higher h^2 with low to moderate genetic advance as a % of the mean indicated the influence of non-additive gene action (dominance or epistasis) in governing these traits (16). These traits cannot be improved through simple selection; therefore, breeders might employ methods such as diallel selective mating or reciprocal recurrent selection.

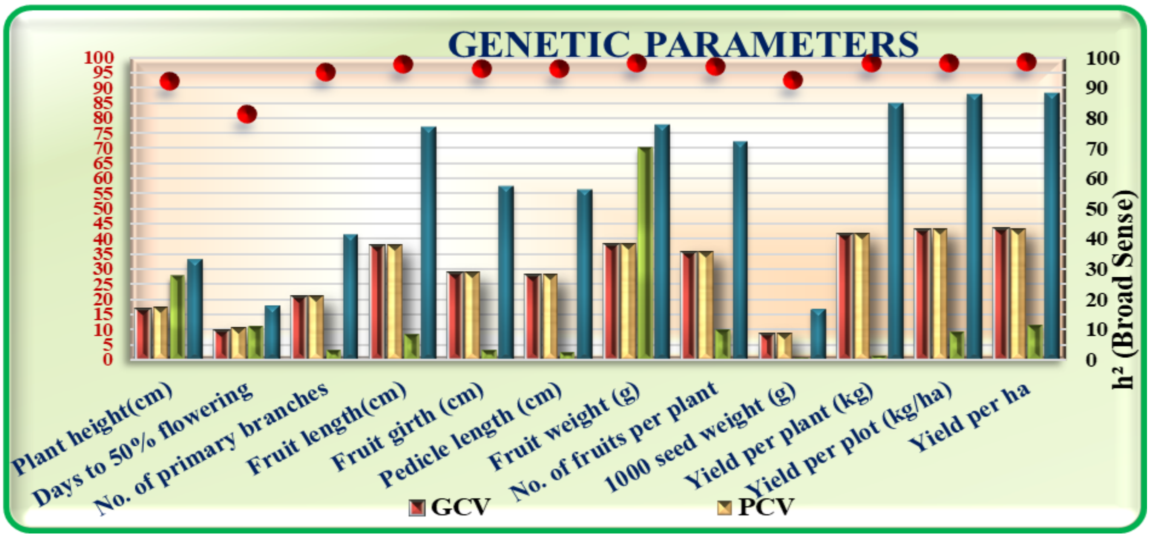

Fig. 1. Genotypic and phenotypic parameters graph.

Table 2. Genotypic and phenotypic variability parameters (pooled season 2022 and 2023)

Sl. No.	Genetic parameters	GCV	PCV	h^2 (Broad sense)	GA	GAM
1	Plant height (cm)	16.80	17.47	92.476	27.79	33.27
2	Days to 50% flowering	9.50	10.53	81.391	10.95	17.65
3	No. of primary branches	20.63	21.11	95.506	3.15	41.53
4	Fruit length (cm)	37.80	38.21	97.846	8.23	77.01
5	Fruit girth (cm)	28.48	28.97	96.646	3.07	57.67
6	Pedicle length (cm)	27.80	28.28	96.633	2.47	56.29
7	Fruit weight (g)	38.12	38.46	98.235	70.23	77.83
8	No. of fruits per plant	35.48	35.96	97.371	10.04	72.13
9	1000 seed weight (g)	8.47	8.81	92.539	0.57	16.79
10	Fruit yield per plant (kg)	41.55	41.92	98.246	1.15	84.83
11	Fruit yield per plot (kg/ha)	43.11	43.44	98.506	9.11	88.15
12	Fruit yield per ha (ton/ha)	43.14	43.39	98.852	11.27	88.36

Conclusion

The main objective of the study was to observe significant variation, heritability and genetic advance as a % of the mean for different traits of genotypes. We found significant genetic variability for the studied traits. High heritability and genetic advance as a % of the mean confirmed that selection could effectively improve traits to increase brinjal yield. In this study, it was found that higher PCV was exhibited by all the traits compared to GCV, indicating a slight influence of the environment in governing these traits. GCV and PCV were observed to be high for the traits such as fruit yield per plot, fruit yield per ha, fruit yield per plant, fruit weight, fruit length, number of fruits per plant, fruit girth, pedicle length and number of primary branches. This showed the existence of large genetic variability and illustrated effective selection for the given characters. Heritability estimates were found to be high (> 60.00%) for all the traits, namely fruit yield per plot, fruit yield per ha, fruit yield per plant, fruit weight, fruit length, number of fruits per plant, fruit girth, pedicle length and number of primary branches. High heritability values suggest that the characters being studied are minimally influenced by environmental factors in their expression. A higher h^2 with low to moderate genetic advance as a % of the mean indicates the effect of the environment on the expression of particular traits. The traits that exhibit high genotypic value (>20%), along with high heritability and genetic advance, should be prioritized for direct selection. Specifically, fruit yield per ha, fruit yield per plot, fruit yield per plant, fruit weight, fruit length, number of fruits per plant, fruit girth, pedicle length, number of primary branches and plant height demonstrate high genotypic coefficients of variation and phenotypic coefficients of variation, heritability and genetic advance. Therefore, these traits should be selected for the crop improvement programme in brinjal.

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Authors' contributions

RJ and VK drafted the manuscript. NK, SP and RS participated in the sequence alignment. RJ and VK participated in the design of the study and performed the statistical analysis. GS, SR, SG and BS conceived the study and participated in its design and coordination. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interest to declare.

Ethical issues: None

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