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RESEARCH ARTICLE

Assessment of genetic variability, heritability and genetic advance in brinjal (*Solanum melongena* L.)

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Abstract

Brinjal breeding lines of the F_3 population (IC0598430 X CARI 1) were evaluated to estimate variability, heritability and genetic advance for different characters. Moderate PCV and GCV values were recorded for stem diameter, fruit weight and yield per plant. At the same time, low PCV and GCV were found for plant height, days to 50 % flowering, fruit length, fruit width, fruit length breadth ratio, fruit pedicel length, fruit pedicel diameter, number of branches per plant and number of fruits per plant. High heritability coupled with high genetic advance was recorded for fruit weight and yield per plant exhibiting that the traits are controlled by additive gene action. Therefore, direct selection may be followed for improving brinjal yield by examining these characters. In the grouping of the F_3 population into immune, highly resistant, resistant, moderately resistant, susceptible and highly susceptible as per the percentage of bacterial wilt disease incidence (PDI), all the lines understudy reported to be highly resistance.

Keywords

brinjal; *Solanum melongena*; bacterial wilt resistance; PCV; GCV; heritability; genetic advance as a percentage of the mean

Introduction

Brinjal (*Solanum melongena* L.) is a solanaceous vegetable with chromosome number 2n=2x=24. It is a perennial vegetable but commercially grown as an annual crop. It is native to India and widely grown during the summer and winter seasons. Because of its highest production potential and availability to consumers, it is often referred as poor man's vegetable. It is essentially a tropical and sub-tropical crop which is grown extensively in India, Bangladesh, Pakistan, China, Japan and Philippines (1). In India, brinjal occupies an area of 7.5 lakh ha with an annual production of 127.78 lakh tonnes and the productivity stands at 17.04 tonnes per ha. Major brinjal producing states are Odisha, Bihar, Karnataka, West Bengal, Andhra Pradesh, Telangana, Maharashtra and Uttar Pradesh. Odisha has grown over an area of annual production of 21.3 lakh tonnes and productivity of 16.90 tonnes per ha (2).

Assessing F_3 population of the IC0598430 X CARI 1 cross for traits like bacterial wilt disease resistance and other horticultural characteristics is crucial for developing more resilient and high-yielding varieties. Studying interfamily variability in the F_3 population can provide valuable insights into the genetic diversity present in these populations. Understanding how different traits manifest across generations can help the breeders in easy selection of desirable characteristics and also in managing disease susceptibility.

The success of any crop improvement program heavily relies on the extent and nature of genetic variability within the breeding materials available to the plant breeder. Variability serves as a fundamental necessity for any crop improvement initiatives. The overall variability within germplasm can be categorized into heritable and non-heritable components, discerned through genetic parameters such as phenotypic and genotypic coefficients of variation, heritability and genetic advancement. The efficacy of selection is directly linked to the levels of heritability and genetic advance expressed as a percentage of the mean for each trait (3).

Understanding genetic information, gained through the analysis of genetic diversity and relationships within and among species, is crucial for the effective use and preservation of plant genetic resources. With these considerations in mind, the present research aims to investigate genetic variability, heritability and genetic advance as a percentage of mean among various quantitative traits of brinjal.

Materials and Methods

The experiment was carried out at Central Horticultural Experiment Station (ICAR-IIHR), Aiginia, Bhubaneswar, Odisha from 2021-2022. The site is located at 20015' N latitude, 85053' E longitude and 25.5 m above mean sea level. The hybridization programme was initiated with the cross IC0598430 × CARI-1 (CARI 1 is the resistant parent and to incorporate bacterial wilt resistance IC0598430 was selected as female parent) and the F_3 population was evaluated for the characters like bacterial wilt resistance, plant height, stem diameter, days to 50 % flowering, number of branches per plant, fruit length, fruit width, fruit length to breadth ratio, fruit pedicel length, fruit pedicel diameter, number of fruits per plant, fruit weight and yield per plant.

Bacterial wilt incidence in each F_4 family was estimated and these were classified into 5 different groups based on percent disease incidence as given (4). Each line was categorized based on a 0-5 scale [0-Immune (No wilt symptoms); 1- Highly Resistant/HR (0.00-20.00 % plants wilted); 2- Moderately resistant/ MR (21.00-40.00 % plants wilted); 3- Moderately susceptible/ MS (41.00- 60.00 % plants wilted); 4- Susceptible/ S (61.00-80.00 % plants wilted); 5- Highly susceptible/ HS (More than 80 % plants wilted)].

The bacterial wilt Percentage Disease Incidence (PDI) of advanced breeding lines of all populations were calculated (5).

Bacterial wilt PDI (%) =

$$\frac{\text{Number of dead plants due to bacterial wilt disease}}{\text{Total number of plants transplanted}} \text{ X 100}$$

The mean performance of the F_4 population was analyzed for interfamily variability studies. Genetic parameters of variability viz., phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2) and genetic advance as percent mean (GAM), were estimated for different characters.

The GCV and PCV were computed according to the formula given (6).

$$\mathrm{PCV} = \frac{\sqrt{\text{Phenotypic variance (PV)}}}{\mathrm{X}}$$

$$\mathrm{GCV} = \frac{\sqrt{\text{Genotypic variance (GV)}}}{\mathrm{X}}$$

X = Population mean

Heritability in broad sense (h^2) was calculated according to the method suggested (7).

$$Heritability = \frac{Vg}{Vp} X\ 100$$

Where, Vg and Vp are genotypic and phenotypic variance respectively.

Genetic advance was calculated by using the formula given (8) was used.

Genetic advance = $h^2 \times K \times \sqrt{Vp}$

Where, K - Standard selection differential which is 2.06 at 5 % selection intensity and $\sqrt{Vp}$ - Phenotypic standard deviation of F_4.

The statistical calculations of phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance as a percentage mean for all the traits under study were carried out by the help of general Rshiny based analysis platform empowered by statistics (Augmented RCBD) developed (9).

Results and Discussion

Results obtained from the evaluation of lines of F_3 generation for bacterial wilt resistance, growth and yield parameters are discussed.

Analysis of variance

The analysis of variance shows clear differences between treatments, the check and progenies in various plant traits and yield. Treatments lead to better results in stem diameter, flowering time and yield compared to the check. Progenies also perform better than the check in some areas, but they don't beat the treatments in yield. The study emphasizes the importance of experimental setup in understanding these findings. Overall, treatments seem effective and there's potential for improving crop productivity with progenies (Table 1).

Table 1. Analysis of variance for various characters (mean sum of squares) of F_3 population (IC0598430X CARI 1).

	Treatment	Check	Progenies	Progenies vs. Check	Block	Residuals
Plant height	0.086	1.309*	0.036	1.269*	0.006	0.021
Stem diameter	0.068*	0.022	0.00*	0.002	0.000	0.002
Days to 50 % flowering	0.046*	0.180*	0.041*	0.126*	0.008	0.002
Fruit length	0.020	0.236*	0.016	0.003	0.002	0.006
Fruit width	0.008*	0.065*	0.006	0.042*	0.001	0.000
Fruit length width ratio	0.004	0.006	0.004	0.014	0.001	0.001
Fruit pedicel length	0.013	0.006	0.011	0.092*	0.000	0.004
Fruit pedicel diameter	0.008	0.012	0.007	0.025	0.001	0.006
No. of branches per plant	0.008	0.017	0.015	0.134*	0.001	0.006
No. of fruits per plant	0.025	0.141*	0.017	0.306*	0.003	0.002
Fruit weight	1.052	6.941*	0.892	2.884*	0.015	0.083
Yield per plant	14.202*	3.206*	11.619*	149.196*	0.016	0.071

*Significance at 0.05 %

Bacterial wilt resistance

The experiment showed that CARI-1 and IC0598430, the resistant parents, demonstrated a survivability rate of 96.00 % and 92.13 %, contrasting to the susceptible check Pusa Purple Long displayed an average survival percentage 4 % respectively.

The grouping of the F_4 population of (IC0598430 X CARI 1) as per the percentage of bacterial wilt disease incidence (PDI) are presented in Table 2. The resistance recorded for the lines of F_3 population may be due to the presence of polyphenolic compounds like tannic acid (TA), epigallocatechin gallate (EGCG) and resveratrol in lines. This result was in corroboration with another study (10).

Phenotypic coefficient of variation (PCV) and Genotypic coefficient of variation (GCV)

In the present study, the variation that existed among the population of F_3 resulting from the cross between IC0598430 and CARI 1 was estimated as coefficients of variation. The data on PCV and GCV for different traits is presented in Table 3.

In the present investigation, the phenotypic coefficient of variation (PCV) ranged from 4.57 % (plant height) to 16.30 % (fruit yield per plant). The PCV values were slightly higher than the corresponding GCV values across all traits, indicating a potential influence of environmental factors on trait expression due to line-environment interactions. This finding aligns with previous studies (11-13).

Table 2. Grouping of F_3 population of (IC0598430 X CARI 1) as per disease reaction to bacterial wilt.

Scale	Advanced breeding lines/ Recombinant Inbred Lines (RILs)	Disease Reaction
0	-	Immune
1	IC0598430XC1-1, IC0598430XC1-5, IC0598430XC1-7, IC0598430XC1-9, IC0598430XC1-10, IC0598430XC1-11, IC0598430XC1-12, IC0598430XC1-15, IC0598430XC1-16, IC0598430XC1-19, IC0598430XC1-20, IC0598430XC1-21, IC0598430XC1-24, IC0598430XC1-25, IC0598430XC1-26, IC0598430XC1-28, IC0598430XC1-29, IC0598430XC1-34, IC0598430XC1-37, IC0598430XC1-38, IC0598430XC1-39, IC0598430XC1-41, IC0598430XC1-42, IC0598430XC1-44, IC0598430XC1-47, IC0598430XC1-49, IC0598430XC1-50, IC0598430XC1-51, IC0598430XC1-52, IC0598430XC1-53, IC0598430XC1-54, IC0598430XC1-55, IC0598430XC1-56, IC0598430XC1-58, IC0598430XC1-59, IC0598430XC1- 60, IC0598430XC1-62, IC0598430XC1-64, IC0598430XC1-65, IC0598430XC1-68, IC0598430XC1-72, IC0598430XC1-73, IC0598430XC1-74, IC0598430XC1-75, IC0598430XC1-76, IC0598430XC1-79, IC0598430XC1- 80	Highly Resistant
2	IC0598430XC1 32	Resistant
3	-	Moderately Resistant
4	-	Susceptible
5	-	Highly Susceptible

Table 3. Range, mean, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) and genetic advance as a percentage of mean (GAM) estimates of various characters of F_3 population (IC0598430X CARI 1).

Sl. No.	Characters	Range	Mean	GCV (%)	PCV (%)	h^2 (%)	GAM
1	**Plant height**	42.30-80.00	53.56	2.95	4.57	41.48	3.91
2	**Stem diameter**	14.40-52.50	17.64	10.88	11.05	97.01	22.11
3	**Days to 50 % flowering**	37.00-58.00	48.33	4.99	5.10	95.59	10.06
4	**Fruit length**	6.50-13.90	10.68	5.37	6.75	63.29	8.82
5	**Fruit width**	5.60-9.00	6.92	4.94	5.09	94.23	9.89
6	**Fruit length width ratio**	0.80-2.30	1.57	6.73	8.28	65.99	11.27
7	**Fruit pedicel length**	2.40-5.60	4.10	7.75	9.35	68.83	13.27
8	**Fruit pedicel diameter**	3.00-6.00	4.69	5.41	7.01	59.64	8.62
9	**No. of branches per plant**	5.30-8.50	6.23	4.81	4.99	28.91	9.76
10	**No. of fruits per plant**	3.50-9.00	6.72	8.30	8.78	89.43	16.19
11	**Fruit weight**	101.30-291.50	186.23	11.47	12.04	90.65	22.53
12	**Yield per plant**	588.00-2378.00	1258.76	16.25	16.30	99.39	33.43

GCV and PCV magnitudes were categorized as low (< 10 %), moderate (10-20 %) and high (> 20 %) (14). For traits such as plant height, number of branches per plant, days to 50 % flowering, fruit length, fruit width, fruit length to width ratio, fruit pedicel length, fruit pedicel diameter and number of fruits per plant in the F_3 population, both PCV and GCV values were reported as low. While, medium PCV and GCV were reported in the traits like stem diameter, fruit weight and yield per plant.

These results are in conformity with findings of earlier works of the scientists for plant height (1, 12, 15-19), for number of branches per plant (20-21), for days to 50 % flowering (12, 17-19, 21-27), for fruit length and fruit width and fruit breadth ratio (15, 18) and for number of fruits per plant in brinjal (28-30). The genetic analysis indicated that both PCV and GCV were moderate for yield per plant and fruit weight, suggesting potential for improvement through selection. These results closely align with those reported by (25, 31).

All the parameters under study exhibited slight differences between PCV and GCV values. The narrow difference between PCV and GCV implied their relative resistance to environmental variation, suggesting that genetic factors were predominantly responsible for the expression of these attributes and that selection could be made effectively on the basis of phenotypic performance. This result was in consonance with another study (32).

Heritability (h^2) and Genetic advance as percentage mean (GAM)

Relying solely on the genotypic coefficient of variation makes it challenging to discern the proportions of variation attributable to heritable and non-heritable factors within a population (1). To better understand this, incorporating estimates of heritability and genetic advance, as a percentage of the mean, would provide valuable insights (13). These additional parameters aid in assessing the type of gene action involved.

Heritability was categorized into 3 levels: low (below 30 %), medium (30 % - 60 %) and high (above 60 %), while genetic advance (as a percentage of mean) was classified as low (<10 %), moderate (10 % - 20 %) and high (>20 %) (8). In the present investigation, heritability ranged from 28.91 % (number of branches per plant) to 99.39 % (yield per plant) and genetic advance as a percentage of mean ranged from 3.91 % (plant height) to 33.43 % (yield per plant). The results on heritability and genetic advance in percent of the mean of the present investigation have been presented in Table 3.

High heritability (>60 %) estimates along with high genetic advance as percent mean (>20 %) were recorded for fruit weight and yield per plant. Similar findings are also reported by several investigators (1, 18, 20, 21, 25, 30, 33-44). High heritability (>60 %) and moderate genetic advance as percent mean (10-20 %) were recorded for days to 50 % flowering, fruit length breadth ratio, fruit pedicel length and number of fruits per plant. The results align with the findings of another study (45) for days to 50 % flowering and for number of fruits per plant (46-48).

High heritability (>60 %) and low genetic advance as a percentage mean (<10 %) were recorded for fruit length, fruit width, fruit pedicel diameter. Similar findings were also reported by several investigators (17). Medium heritability (30-60 %) and low genetic advance as a percentage mean (<10 %) were recorded for plant height (49).

The high heritability indicates that the characters are less influenced by the environment. High heritability with low genetic advance reveals the major role of non-additive gene action in the transmission of the character. High heritability with moderate genetic advance over mean indicates high influence of favorable environment rather than the genotype. Heritability with high genetic advance shows the major role of additive gene action of those characters (fruit weight and yield per plant) would be improved through simple selection (18).

Conclusion

The evaluated brinjal breeding lines demonstrated a spectrum of resistance, ranging from resistant to highly resistant reactions to bacterial wilt disease. These lines exhibited PCV and GCV values ranging from low to medium, moderate to high heritability values and low to high genetic advance percentages relative to the mean for all studied traits.

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Authors' contributions

All authors, including VAK, participated in the conception and design of the analysis. VAK was responsible for data collection, experiment execution, data analysis and article writing. All authors read and approved the manuscript.

Compliance with ethical standards

Conflict of interest: The authors assert that they have no conflict of interest in this research.

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