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EVALUATION AND GENETIC VARIABILITY ANALYSIS OF F₄ SEGREGATING POPULATION OF BRINJAL (*SOLANUM MELONGENA* L.) FOR FRUIT YIELD AND BACTERIAL WILT TOLERANCE

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ABSTRACT

The present investigation was conducted during the *rabi* season of 2022-23 at the AICRP on Vegetable Crops, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, India. A total of forty brinjal genotypes comprising thirty-one F₄ segregating populations, eight diverse parents, and one check variety (BB-67) were evaluated in a randomized block design (RBD). The primary objective was to identify superior round-fruited brinjal F₄ segregant(s) with higher fruit yield and tolerance to bacterial wilt. Additional objectives included assessment of genetic variability, estimation of correlation coefficients, path coefficient analysis, and divergence analysis to support future brinjal improvement programmes. Observations on growth, flowering, yield and yield-attributing traits, fruit quality parameters, and reaction to bacterial wilt were recorded and analysed using standard statistical and biometrical methods. Notably, high broad-sense heritability (>60%) and genetic advance (>20% of mean) marked traits like plant height (90.52%, 22.09%), leaf blade length (97.19%, 25.88%), days to first flowering (82.18%, 20.70%), average fruit weight (93.49%, 50.49%), fruits per plant (87.70%, 54.08%) and total yield per plant (68.64%, 21.97%). The presence of significant variability among traits indicated ample scope for direct selection based on plant height, days to first flowering, fruit girth, incidence of bacterial wilt at 90 DAT and total fruit yield plant⁻¹ for the development of high-yielding brinjal varieties. Hybridization between Selection from BBSR-192-1 × BBSR-10-26 or BBSR-10-26 × Selection from BBSR-192-1 is recommended for the development of F₄ hybrids or transgressive segregants. The F₄ segregants BBSR-08-02 × Jammusahi Local, BBSR-195-3 × Selection from BBSR-192-1, BBSR-08-2 × BBSR-192-1, Jammusahi Local × Selection from BBSR-192-1 and BBSR-192-1 × Selection from BBSR-145-1 are recommended for round fruit shape, higher fruit yield plant⁻¹ and tolerance to bacterial wilt under Bhubaneswar, Odisha conditions.

Key words : Brinjal, Round fruited, Bacterial wilt tolerant, Genetic variability, F₄ segregating population.

Introduction

In many regions of the world, brinjal (*Solanum melongena* L.) is referred to as aubergine or eggplant belonging to the family *Solanaceae*. The Indo-Burma region is the centre of origin of this significant vegetable crop (Vavilov, 1928). Due to its wider adaptability and

easy availability, it is also popularly known as “Poor man’s Vegetable”. Brinjal fruits are not only treated as good source of vitamins *viz.*; A, B complex and C but also minerals like calcium, iron and phosphorous. Now-a-days, white brinjal fruits are recommended for treatment against diabetic people primarily due to presence of relatively higher amount of dietary fibres along with other vitamins,

minerals and antioxidants. Overall, the medicinal benefits of brinjal fruits range from helping people lose weight to treating a number of illnesses, such as cholera, bronchitis, gonorrhoea, diabetes, leprosy, skin infections, constipation, asthma, dysuria, dysentery, asthenia and haemorrhoids (Nwodo *et al.*, 2011).

Throughout the world, about 19.24 lakh ha (47.544 lakh acres) area was covered under Brinjal with production of 608.27 lakh tonnes and yield 31615 kg/ha (FAO, 2023). In India, it occupies an area of 7, 47'000 ha with total production of 129, 82'000 MT and productivity of 17.39 t ha⁻¹ (NHB, 2021-22). Odisha ranked second in brinjal production after West Bengal in India during 2023–24, with a total output of 2,198.13/ kilotonnes (17.1% of national production) (Desikheti.com).

One of the most destructive diseases of brinjal, especially in hot and humid tropical regions of the world, is bacterial wilt, which is one of the major biotic stresses (Pitchai *et al.*, 2024). *Ralstonium solanacearum*, a soil-borne pathogen spread by soil, irrigation water, etc., is the bacterium that causes the disease. According to reports, yield loss can reach 100.00% in hot climates. According to estimates, 32.2% of indigenous brinjals, 50.0% of OP/HYVs and 17.8% of hybrids are still grown in India. The prevalence of local types and landraces might be due to regional preference by consumers due to various quality attributes. Odisha represents a rich centre of brinjal diversity and the heterozygous nature of local landraces offers substantial scope for genetic improvement. Out of various colour and shape of the brinjal landraces available, the consumer's preference is with green and round fruits, specifically in the eastern part of the country because due to high temperature the green colour of brinjal fruit does not change and additionally the shelf life is for 4 weeks under normal condition. Thus, in India in general and Odisha in particular, the development of local landrace is essential to the future of brinjal breeding programmes. The fundamental pre-requisite for any programme aimed at improving crops is variability. Genetic indices like as phenotypic and genotypic coefficients of variation, heritability and genetic advancement can be used to separate the total variability found in germplasm into heritable and non-heritable components. The degree of genetic advancement and heritability as a percentage of the mean for that character directly affects how effective selection is to determine the direction of selection and optimize yield in the shortest amount of time, the correlation coefficient between the yield-contributing features must be estimated.

Materials and Methods

The present experiment was carried out during the *rabi* season of 2022-23 at the AICRP on Vegetable Crops, Odisha University of Agriculture & Technology, Bhubaneswar, Odisha. The experiment was laid out in a randomized block design and replicated thrice. The experimental material consisted of eight parents, 31 F₄ segregants and one check variety, BB-67 (Table 1). All the genotypes were subjected to the same standard package of practices required to raise healthy crops. The assigned experimental area was completely ploughed and divided into 80 plots, each measuring 2.7 m × 1.2m with plant spacing of 60cm × 45cm.

Five plants from each treatment and replication, excluding border crops, were randomly selected and tagged for recording all the observations pertaining to vegetative, flowering, yield and yield attributing characters along with biochemical parameters. Vegetative growth parameters like plant height, land spread, number of primary branches plant⁻¹, leaf blade length, leaf blade width and leaf area and flowering parameters like days to first flowering, days to 50% flowering, number of flowers cluster⁻¹, total fruit yield plant⁻¹ and plot⁻¹ were observed. Likewise, fruit parameters like fruit length, fruit girth, average fruit weight and number of fruits plant⁻¹ and percentage of bacterial wilt incidence were also recorded. Many biochemical parameters were also assessed. The total soluble solids (TSS) contents of the fruit samples were calculated using a hand refractometer with a range of 0-32°Brix. Volumetric calculations were used to determine the ascorbic acid content of the fruit samples (Sadasivam and Balasubramanian, 1987). The total sugar content in fruits was determined using Fehling's A and B solution. To identify the distinctions between the various traits, the variance for each was examined and subjected to analysis using the randomized block design analysis method (Panse and Sukhatme, 1967).

Results and Discussion

The results of the analysis of variance (ANOVA) showed significant differences for all the 21 traits under investigation, clearly demonstrating the existence of trait variability and providing a better basis for future brinjal improvement programmes. With the exception of the incidence of bacterial wilt at 90 DAT (73.26%), the degree of experimental precision during the current study was approximately 10.00% for all traits, which adequately demonstrated that the precision of the field experiment was within the acceptable normal limit. Analysis of variance (ANOVA) revealed significant differences among the 40 genotypes for all traits (P<0.01), except

Table 1 : List of F₄ Segregants, parents and check variety used in the experiment.

S. no.	Notations	Crosses/ Parents/Hybrid Checks	Name of the Genotypes (F ₄ segregants /Parents/ Hybrid Checks)
1	V1	1 × 2	BBSR-08-2 × BBSR-10-25
2	V2	1 × 3	BBSR-08-2 × Jammusahi Local
3	V3	1 × 4	BBSR-08-2 × BBSR-10-26
4	V4	1 × 5	BBSR-08-2 × BBSR-195-3
5	V5	1 × 6	BBSR-08-2 × BBSR-192-1
6	V6	1 × 7	BBSR-08-2 × Selection from BBSR-192-1
7	V7	1 × 8	BBSR-08-2 × Selection from BBSR-145-1
8	V8	1 × 10	BBSR-08-2 × BBSR-09-5
9	V9	2 × 4	BBSR-10-25 × BBSR-10-26
10	V10	2 × 5	BBSR-10-25 × BBSR-195-3
11	V11	2 × 6	BBSR-10-25 × BBSR-192-1
12	V12	2 × 7	BBSR-10-25 × Selection from BBSR-192-1
13	V13	2 × 8	BBSR-10-25 × Selection from BBSR-145-1
14	V14	2 × 10	BBSR-10-25 × BBSR-09-5
15	V15	3 × 4	Jammusahi Local × BBSR-10-26
16	V16	3 × 6	Jammusahi Local × BBSR-192-1
17	V17	3 × 7	Jammusahi Local × Selection from BBSR-192-1
18	V18	3 × 8	Jammusahi Local × Selection from BBSR-145-1
19	V19	4 × 5	BBSR-10-26 × BBSR-195-3
20	V20	4 × 6	BBSR-10-26 × BBSR-192-1
21	V21	4 × 7	BBSR-10-26 × Selection from BBSR-192-1
22	V22	4 × 8	BBSR-10-26 × Selection from BBSR-145-1
23	V23	4 × 10	BBSR-10-26 × BBSR-09-5
24	V24	5 × 6	BBSR-195-3 × BBSR-192-1
25	V25	5 × 7	BBSR-195-3 × Selection from BBSR-192-1
26	V26	5 × 10	BBSR-195-3 × BBSR-09-5
27	V27	6 × 8	BBSR-192-1 × Selection from BBSR-145-1
28	V28	6 × 10	BBSR-192-1 × BBSR-09-5
29	V29	7 × 8	Selection from BBSR-192-1 × Selection from BBSR-145-1
30	V30	7 × 10	Selection from BBSR-192-1 × BBSR-09-5
31	V31	8 × 10	Selection from BBSR-145-1 × BBSR-09-5
32	V32	S1	BBSR-08-2(Bhadrak Local)
33	V33	S2	BBSR-10-25(Chhatia Local Selection)
34	V34	S3	JammusahiLocal
35	V35	S4	BBSR-10-26(Chhatia Local Selection)
36	V36	S6	BBSR-192-1(Salepur Local Selection)
37	V37	S7	SelectionfromBBSR-192-1
38	V38	S8	SelectionfromBBSR-145-1
39	V39	S10	BBSR-09-5(SelectionfromBBSR-195-3, which has been selectedfromChhatiaLocal)
40	V40	CHECK	BB-67(Andharua Local Selection)

bacterial wilt incidence at 90 days after transplanting (DAT) ($P < 0.05$).

Vegetative Growth parameters

Vegetative traits exhibited wide variability, which is crucial for assessing plant vigour and adaptability in brinjal breeding programmes. Plant height ranged from 47.20 cm (BBSR-10-25 × BBSR-195-3) to 73.65 cm (BBSR-08-02 × BBSR-10-25), with a mean of 57.34 cm. The segregant BBSR-08-02 × BBSR-10-25 was significantly taller, statistically at par with BBSR-08-2 × BBSR-195-3 (69.70 cm) and BBSR-08-2 × Selection from BBSR-192-1 (70.25 cm). Number of primary branches per plant varied from 3.60 (BBSR-08-2 × BBSR-09-5) to 6.20 (BB-67), with a mean of 4.93, with several segregants (e.g., BBSR-10-25 × Selection from BBSR-192-1) showing parity with the check variety. Plant spread E-W (63.03-83.73 cm, mean 73.93 cm) and N-S (63.13-83.91 cm, mean 74.15 cm) peaked in BBSR-10-25 × Selection from BBSR-145-1 and BBSR-08-2 × BBSR-10-26, respectively. Leaf blade length (9.04-16.47 cm, mean 11.41 cm), width (4.90-7.65 cm, mean 6.33 cm) and area (136.25-170.66 cm², mean 152.03 cm²) showed significant variation (Graph 1). The extensive range of vegetative traits observed underscores their significant breeding potential, as taller plants with greater spread often contribute to higher biomass and yield potential, and identification of superior vegetative growth parameter will definitely contribute more towards higher fruit yield and yield attributing parameters. Similar significant variations with respect to vegetative traits have also been reported by Khorbragade *et al.* (2019) and Tripathy *et al.* (2025).

Flowering parameters

Flowering traits indicated earliness in specific genotypes, which is an important parameter for shortening the crop cycle and escaping late-season stresses. Days to first flowering ranged from 35.00 (BBSR-10-25) to 56.00 (BBSR-08-2 × BBSR-10-26), mean 45.03 days, with

Table 2 : Mean performance of 40 brinjal genotypes including F₄ segregants, parents and check on vegetative growth parameters.

S. no.	Genotypes	PH	PBP	PS(EW)	PS(NS)	LBL	LBW	LA
01.	BBSR-08-2 × BBSR-10-25	73.65	5.10	68.24	69.21	12.89	7.35	162.79
02.	BBSR-08-2 × Jammusahi Local	64.15	4.50	74.35	68.70	13.46	6.95	154.88
03.	BBSR-08-2 × BBSR-10-26	65.00	4.80	79.77	83.91	15.52	7.55	165.01
04.	BBSR-08-2 × BBSR-195-3	69.70	3.70	80.92	79.35	11.70	6.00	170.66
05.	BBSR-08-2 × BBSR-192-1	58.75	4.10	78.92	76.62	11.56	6.15	162.29
06.	BBSR-08-2 × Selection from BBSR-192-1	70.25	4.20	70.41	64.78	11.92	6.55	151.34
07.	BBSR-08-2 × Selection from BBSR-145-1	67.25	4.60	72.36	65.85	12.40	6.10	157.63
08.	BBSR-08-2 × BBSR-09-5	64.75	3.60	68.70	63.55	13.20	6.65	166.78
09.	BBSR-10-25 × BBSR-10-26	55.40	3.80	73.63	72.25	10.72	5.80	152.37
10.	BBSR-10-25 × BBSR-195-3	47.20	3.90	70.57	68.40	11.39	5.40	161.98
11.	BBSR-10-25 × BBSR-192-1	48.25	4.20	65.84	63.13	12.37	6.70	159.70
12.	BBSR-10-25 × Selection from BBSR-192-1	54.50	5.30	69.75	72.38	11.53	5.90	162.82
13.	BBSR-10-25 × Selection from BBSR-145-1	58.75	5.30	83.73	81.79	11.80	5.20	157.49
14.	BBSR-10-25 × BBSR-09-5	59.59	5.00	66.55	69.59	11.13	5.90	162.91
15.	Jammusahi Local × BBSR-10-26	58.85	5.60	79.30	76.06	12.04	4.90	152.99
16.	Jammusahi Local × BBSR-192-1	52.70	5.10	70.00	79.84	11.87	6.05	152.53
17.	Jammusahi Local × Selection from BBSR-192-1	50.15	4.50	65.68	71.04	10.60	6.05	148.69
18.	Jammusahi Local × Selection from BBSR-145-1	51.40	5.20	78.10	72.32	10.88	7.65	151.26
19.	BBSR-10-26 × BBSR-195-3	52.20	5.00	76.28	73.68	10.78	5.80	149.31
20.	BBSR-10-26 × BBSR-192-1	52.20	5.10	79.03	80.24	10.98	6.20	142.72
21.	BBSR-10-26 × Selection from BBSR-192-1	47.55	4.80	72.75	78.32	9.98	4.90	157.28
22.	BBSR-10-26 × Selection from BBSR-145-1	53.30	4.30	78.65	80.20	11.49	7.60	152.69
23.	BBSR-10-26 × BBSR-09-5	57.20	4.90	71.25	73.49	11.42	6.15	151.98
24.	BBSR-195-3 × BBSR-192-1	58.70	5.20	63.90	76.59	10.94	6.50	151.86
25.	BBSR-195-3 × Selection from BBSR-192-1	55.45	5.50	80.35	71.04	11.90	6.50	148.05
26.	BBSR-195-3 × BBSR-09-5	66.60	5.50	63.03	71.73	11.23	6.80	156.16
27.	BBSR-192-1 × Selection from BBSR-145-1	48.95	5.40	78.33	79.18	11.61	7.05	148.12
28.	BBSR-192-1 × BBSR-09-5	51.05	5.50	78.95	78.35	10.49	6.20	144.88
29.	Selection from BBSR-192-1 × Selection from BBSR-145-1	52.55	5.10	82.18	79.80	10.78	6.50	144.87
30.	Selection from BBSR-192-1 × BBSR-09-5	60.40	5.50	72.83	75.18	10.78	7.05	147.47
31.	Selection from BBSR-145-1 × BBSR-09-5	52.45	4.60	80.28	78.35	9.90	5.85	138.65
32.	BBSR-08-2	53.45	5.40	72.48	80.70	9.77	6.20	141.50
33.	BBSR-10-25	66.30	5.50	71.70	68.32	10.99	6.30	147.55
34.	Jammusahi Local	59.30	5.50	83.10	75.57	9.08	6.75	143.99
35.	BBSR-10-26	56.90	5.60	64.95	77.81	9.04	6.60	143.90
36.	BBSR-192-1	58.90	5.70	72.55	65.10	10.08	5.50	136.25
37.	Selection from BBSR-192-1	55.30	5.00	74.25	76.90	16.47	6.00	141.72
38.	Selection from BBSR-145-1	55.10	4.90	80.38	79.99	10.47	6.20	141.38
39.	BBSR-09-5	53.00	4.60	74.03	81.35	9.63	6.15	140.26
40.	BB-67 (Check)	56.55	6.20	69.13	65.48	11.90	7.45	156.52
	Grand mean	57.34	4.93	73.93	74.15	11.41	6.33	152.03
	SE(m)±	1.48	0.35	1.74	2.76	0.17	0.28	4.04
	CV (%)	3.65	9.95	3.33	5.27	2.17	6.27	3.76

PH: Plant height at final harvest (cm); **PBP:** No. of primary branches plant⁻¹; **PS (EW):** Plant spread (EW); **PS (NS):** Plant Spread (NS); **LBL:** Leaf blade length (cm); **LBW:** Leaf blade width (cm); **LA:** Leaf area (cm²).

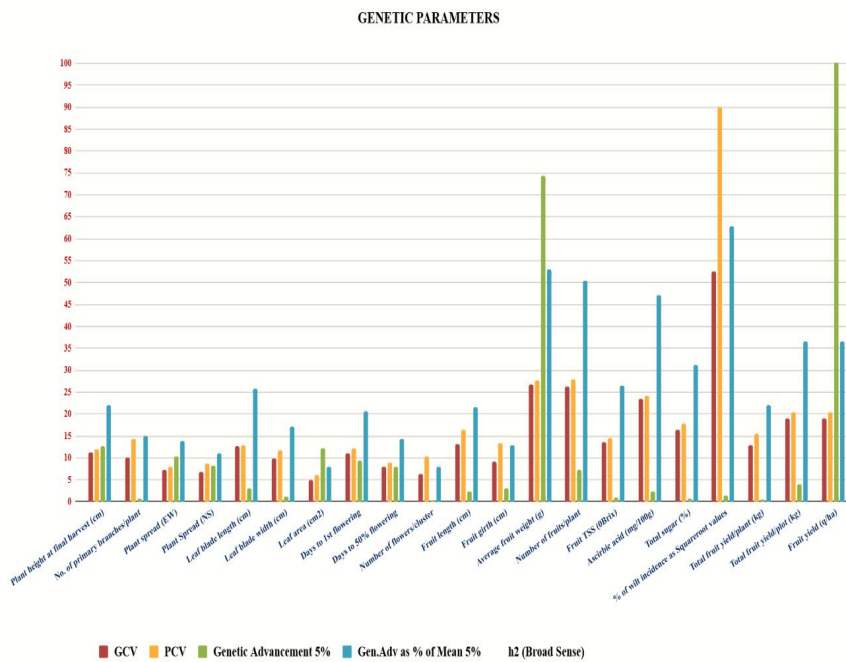


Fig. 1 : Genetic parameters of the population.

segregants like BBSR-10-26 × BBSR-192-1 (39.50 days) statistically at par with the earliest parent. Days to 50% flowering varied from 43.50 (BBSR-10-26 × Selection from BBSR-145-1) to 66.50 (Jammusahi local × Selection from BBSR-145-1), mean 56.30 days. Number of flowers per cluster ranged from 3.10 (BBSR-08-2 × BBSR-09-5) to 4.80 (BBSR-192-1 × BBSR-09-5), mean 4.09. The study also revealed that the F₄ segregant namely, BBSR-10-26 × Selection from BBSR-145-1 recorded earlier in days to attend 1st flowering (37.50 DAS) and 43.50 to attend the 50% flowering. Hence, the particular F₄ segregant, BBSR-10-26 × Selection from BBSR-145-1 may be recommended as early genotype either for commercial cultivation or will be used as male parent for induction of earliness in future brinjal breeding improvement programme. Similar reports on significant variations in days to 1st flowering and 50% flowering in brinjal have already been reported by Saha *et al.* (2014); Umesh *et al.* (2018); Khobragade *et al.* (2019); Sharma *et al.* (2024). The early flowering segregants may confer the added advantage of enhancing fruit set by aligning with optimal environmental conditions, as previously demonstrated by Patel *et al.* (2023).

Fruit Yield attributing parameters

In this study emphasis have been made for identification of significantly lower fruit length with correspondingly higher fruit girth was considered for development of brinjal genotype (s) of more or less round fruit shape. Fruit length ranged from 7.55 cm (BBSR-09-5) to 13.92 cm (Selection from BBSR-192-1), mean 10.66

cm. Fruit girth varied from 14.50 cm (BB-67) to 27.68 cm (Jammusahi local × Selection from BBSR-192-1), mean 22.82 cm *statistical parity* were recorded with highest value of 27.68 in brinjal F₄ segregants viz., BBSR-08-02 × BBSR-10-25, Selection from BBSR-192-1, BBSR-08-2 × BBSR-10-26, BBSR-08-2 × BBSR-195-3, BBSR-08-2 × BBSR-192-1, BBSR-08-2 × Selection from BBSR-192-1, BBSR-08-2 × Selection from BBSR-145-1, Jammusahi local × Selection from BBSR-145-1, BBSR-10-26 × BBSR-195-3, BBSR-10-26 × BBSR-09-5, BBSR-195-3 × BBSR-192-1, BBSR-195-3 × Selection from BBSR-192-1, BBSR-192-1 × Selection from BBSR-145-1, Selection from BBSR-192-1 × Selection from BBSR-145-1, Selection from BBSR-192-1 × BBSR-09-5, Selection from BBSR-145-1 × BBSR-

09-5. Average fruit weight was 77.26 g (BBSR-08-2) to 226.03 g (BBSR-10-26), mean 140.13 g, with BBSR-10-26 × BBSR-195-3 statistically at par with the maximum. Fruits per plant ranged from 8.15 to 24.80, mean 14.30, with BBSR-10-26 × Selection from BBSR-192-1 yielding 20.30 fruits. The result also showed that due to continuous selection of brinjal fruits in segregating population to develop the round fruited type most of F₄ segregants showed lower fruit length as compared to their respective parents. The inheritance pattern of average fruit weight of brinjal have also been reported by Vethamoni and Pranetha (2016), Khorbragade *et al.* (2019).

Bacterial Wilt incidence

Bacterial wilt incidence at 90 DAT ranged from 0.00% (e.g., BBSR-08-2 × Jammusahi Local, BBSR-08-2, Jammusahi Local, BBSR-10-26, BB-67) to 25.00% (BBSR-195-3 × BBSR-09-5), mean 2.15%, indicating tolerance in several segregants (Table 1.3). The results of the study showed better resistance to bacterial wilt by F₄ segregating population under sick plot condition might be due to inheritance of resistance / tolerance from parent to progenies. Similar inheritances have also been reported by several scientists in brinjal (Ashupriya, 2022). The low incidence in selected genotypes highlights the success of screening in a hot spot, consistent with recent studies on bacterial wilt resistance in brinjal by Salunkhe *et al.* (2024).

Quality and Yield attributes

Quality traits showed variability essential for

Table 3 : Mean performance of 40 brinjal genotypes including F_4 segregants, parents and check on incidence of bacterial wilt.

S. no.	Genotypes	Incidence of bacterial wilt at 90 DAT
01.	BBSR-08-2 × BBSR-10-25	12.50(3.98)
02.	BBSR-08-2 × Jammusahi Local	0.00(0.50)
03.	BBSR-08-2 × BBSR-10-26	12.50(3.98)
04.	BBSR-08-2 × BBSR-195-3	0.00(0.50)
05.	BBSR-08-2 × BBSR-192-1	0.00(0.50)
06.	BBSR-08-2 × Selection from BBSR-192-1	4.15(1.94)
07.	BBSR-08-2 × Selection from BBSR-145-1	0.00(0.50)
08.	BBSR-08-2 × BBSR-09-5	4.15(1.94)
09.	BBSR-10-25 × BBSR-10-26	0.00(0.50)
10.	BBSR-10-25 × BBSR-195-3	12.50(3.00)
11.	BBSR-10-25 × BBSR-192-1	0.00(0.50)
12.	BBSR-10-25 × Selection from BBSR-192-1	12.50(3.98)
13.	BBSR-10-25 × Selection from BBSR-145-1	12.50(3.00)
14.	BBSR-10-25 × BBSR-09-5	16.66(4.58)
15.	Jammusahi Local × BBSR-10-26	12.48(3.98)
16.	Jammusahi Local × BBSR-192-1	8.33(2.54)
17.	Jammusahi Local × Selection from BBSR-192-1	0.00(0.50)
18.	Jammusahi Local × Selection from BBSR-145-1	0.00(0.50)
19.	BBSR-10-26 × BBSR-195-3	0.00(0.50)
20.	BBSR-10-26 × BBSR-192-1	12.48(3.98)
21.	BBSR-10-26 × Selection from BBSR-192-1	4.15(1.94)
22.	BBSR-10-26 × Selection from BBSR-145-1	12.50(3.98)
23.	BBSR-10-26 × BBSR-09-5	12.48(3.98)
24.	BBSR-195-3 × BBSR-192-1	0.00(0.50)
25.	BBSR-195-3 × Selection from BBSR-192-1	0.00(0.50)
26.	BBSR-195-3 × BBSR-09-5	25.00(5.50)
27.	BBSR-192-1 × Selection from BBSR-145-1	0.50(1.00)
28.	BBSR-192-1 × BBSR-09-5	4.15(1.94)

*Table 3 continued...***Table 3 continued...**

29.	Selection from BBSR-192-1 × Selection from BBSR-145-1	16.66(4.58)
30.	Selection from BBSR-192-1 × BBSR-09-5	4.15(1.94)
31.	Selection from BBSR-145-1 × BBSR-09-5	8.33(2.54)
32.	BBSR-08-2	0.00(0.50)
33.	BBSR-10-25	8.33(2.54)
34.	Jammusahi Local	0.00(0.50)
35.	BBSR-10-26	0.00(0.50)
36.	BBSR-192-1	12.50(3.00)
37.	Selection from BBSR-192-1	4.15(1.94)
38.	Selection from BBSR-145-1	4.15(1.94)
39.	BBSR-09-5	16.66(4.58)
40.	BB-67 (Check)	0.00(0.50)
	Grand mean	2.15
	SE(m)±	1.11
	CV (%)	73.26

Figures in the parenthesis indicate the corresponding square root values.

nutritional breeding. Fruit TSS ranged from 2.50 to 4.70 °Brix, mean 3.61, highest in Jammusahi Local except F_4 segregants, BBSR-192-1 × Selection from BBSR-145-1 and Jammusahi local × BBSR-10-26 where *statistical parity* were observed. Ascorbic acid content was 2.75-7.70 mg/100g, mean 5.02, peaking in BBSR-10-26 × Selection from BBSR-192-1. Total sugar ranged from 1.60% to 3.11%, mean 2.23%, maximum in Selection from BBSR-145-1. Similar observations for fruit quality in brinjal have also been reported by Mistry *et al.* (2014) and Ashupriya (2022). Yield per plant ranged from 1.19 kg (BB-67) to 2.05 kg (BBSR-10-26 × BBSR-09-5), mean 1.63 kg. Yield per plot was 7.10-16.83 kg, mean 11.00 kg, and q/ha was 219.14-519.44, mean 339.64, both peaking in the F_4 segregant, Jammusahilocal × BBSR-10-26 recorded significantly highest fruit yield than rest of genotypes and was statistically at par with F_4 segregant, BBSR-10-26 × Selection from BBSR-145-1.

Genetic variability

Significantly better performance in F_4 segregant might be due to inheritance of major fruit yield attributing traits with high heritability coupled with GA. The entire fruit yield attributing traits might be transmitted from parents to respective progenies in turn producing superior genotypes at F_4 segregating population due to

Table 4 : Mean performance of 40 genotypes of brinjal including F₄ segregants parents and check on fruit quality traits.

S. no.	Genotypes	Fruit TSS content (°Brix)	Fruit ascorbic acid content (mg 100g ⁻¹)	Total sugar content of fruits (%)
01.	BBSR-08-2 × BBSR-10-25	3.65	6.70	1.96
02.	BBSR-08-2 × Jammusahi Local	4.10	5.65	1.82
03.	BBSR-08-2 × BBSR-10-26	3.90	4.20	2.24
04.	BBSR-08-2 × BBSR-195-3	3.40	5.05	2.94
05.	BBSR-08-2 × BBSR-192-1	3.35	4.10	1.60
06.	BBSR-08-2 × Selection from BBSR-192-1	2.75	3.45	1.95
07.	BBSR-08-2 × Selection from BBSR-145-1	3.20	4.40	1.98
08.	BBSR-08-2 × BBSR-09-5	3.20	7.10	1.85
09.	BBSR-10-25 × BBSR-10-26	2.90	4.60	2.43
10.	BBSR-10-25 × BBSR-195-3	3.90	4.00	2.22
11.	BBSR-10-25 × BBSR-192-1	3.40	5.30	2.60
12.	BBSR-10-25 × Selection from BBSR-192-1	4.20	5.40	2.04
13.	BBSR-10-25 × Selection from BBSR-145-1	3.35	5.30	2.08
14.	BBSR-10-25 × BBSR-09-5	4.00	4.75	2.21
15.	Jammusahi Local × BBSR-10-26	4.35	5.45	1.82
16.	Jammusahi Local × BBSR-192-1	3.35	3.15	2.95
17.	Jammusahi Local × Selection from BBSR-192-1	3.90	5.00	2.61
18.	Jammusahi Local × Selection from BBSR-145-1	3.70	3.15	2.25
19.	BBSR-10-26 × BBSR-195-3	4.25	4.25	2.00
20.	BBSR-10-26 × BBSR-192-1	3.20	4.45	2.18
21.	BBSR-10-26 × Selection from BBSR-192-1	4.00	7.70	1.83
22.	BBSR-10-26 × Selection from BBSR-145-1	3.90	6.70	2.38
23.	BBSR-10-26 × BBSR-09-5	2.50	4.30	2.05
24.	BBSR-195-3 × BBSR-192-1	2.90	6.50	2.19
25.	BBSR-195-3 × Selection from BBSR-192-1	3.45	5.50	2.20
26.	BBSR-195-3 × BBSR-09-5	4.10	5.00	1.91
27.	BBSR-192-1 × Selection from BBSR-145-1	4.45	5.45	1.90
28.	BBSR-192-1 × BBSR-09-5	3.60	4.50	2.83
29.	Selection from BBSR-192-1 × Selection from BBSR-145-1	4.00	4.75	2.04
30.	Selection from BBSR-192-1 × BBSR-09-5	3.50	7.40	1.87
31.	Selection from BBSR-145-1 × BBSR-09-5	4.10	6.55	2.78
32.	BBSR-08-2	4.10	4.45	1.85
33.	BBSR-10-25	3.60	3.85	2.65
34.	Jammusahi Local	4.70	5.65	2.35
35.	BBSR-10-26	2.90	4.35	2.37
36.	BBSR-192-1	2.85	2.75	2.46
37.	Selection from BBSR-192-1	3.40	3.65	2.88
38.	Selection from BBSR-145-1	3.40	6.60	3.11
39.	BBSR-09-5	3.70	4.55	1.99
40.	BB-67 (Check)	3.30	5.20	1.74
	Grand mean	3.61	5.02	2.23
	SE(m) ±	0.13	0.19	0.11
	CV (%)	4.92	5.37	6.93

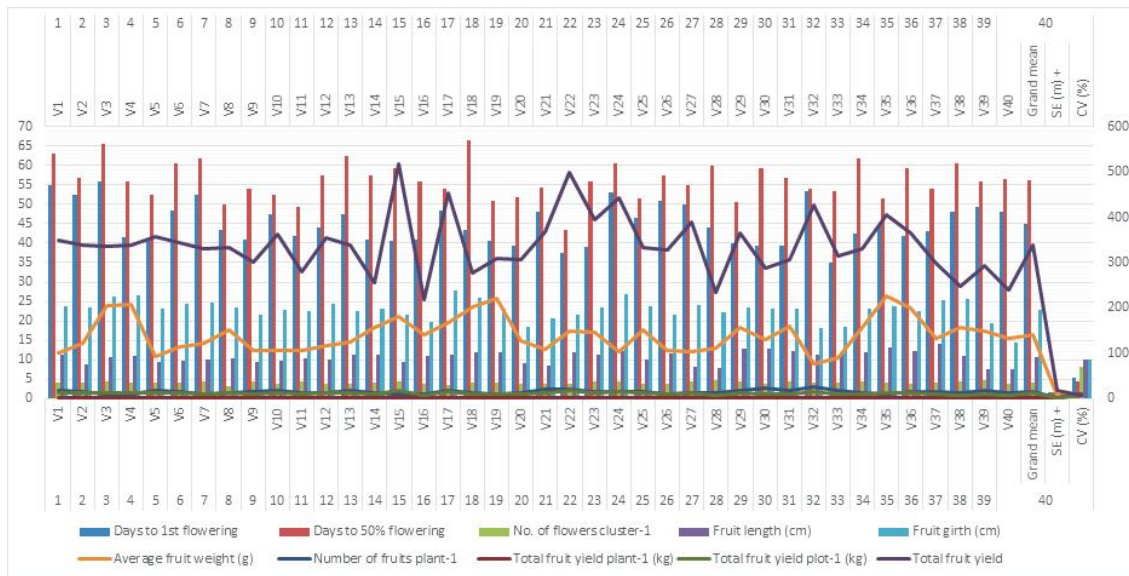


Fig. 2 : Mean performance of 40 brinjal genotypes including F_4 segregants, parents and check variety on flowering parameters, Fruit yield attributing traits & fruit yield.

accumulation of more desirable gene recombinants during the process of intensive selection pressure. The high yield in these segregants aligns with heterosis studies for wilt tolerance by Datta *et al.*, 2021; Ashupriya, 2022; Tripathy *et al.* (2025).

Phenotypic coefficients of variation (PCV) exceeded genotypic coefficients (GCV) for all traits, reflecting environmental influences. High GCV and PCV (>20%) were observed for average fruit weight (26.65%/27.56%), Number of fruits plant⁻¹(26.17%/27.95%), ascorbic acid (23.43%/24.04%) and Bacterial wilt incidence (%) (52.44%/90.10%), indicating strong potential for selection. Similar observations were also reported by scientists in brinjal (Konyak *et al.*, 2020; Chithra *et al.*, 2021; Kumar *et al.*, 2022; Ashupriya, 2022). High broad-sense heritability (>60%) was recorded for several traits, *viz.*: plant spread (N-S) (62.52%), leaf area (62.91%), fruit length (63.74%), total fruit yield plant⁻¹ (68.64%), leaf blade width (70.97%), days to 50% flowering (77.52%), days to 1st flowering (82.18%), plant spread (E-W) (82.98%), total fruit sugar content (84.93%), number of fruits plant⁻¹ (87.70%), fruit TSS content (88.45%), plant height at final harvest (90.52%), average fruit weight (93.49%), fruit ascorbic acid content (95.01%) and leaf blade length (97.19%) coupled with genetic advance as percent mean (GA as % of mean >20%) for key yield components *viz.*: days to 1st flowering (20.70), fruit length (21.57), total fruit yield plant⁻¹ (21.97), plant height at final harvest (22.09), leaf blade length (25.88), fruit TSS (26.38), total fruit sugar content (31.25), fruit ascorbic acid content (47.05), number of fruits plant⁻¹ (50.49), average fruit weight (53.08) and incidence of bacterial

wilt at 90 DAT (62.87) in an increasing trend. The high heritability and GA as % of mean for these traits suggest additive gene action, enabling effective phenotypic selection as reported in recent brinjal variability studies by Bende *et al.* (2023) and Singh *et al.* (2025). Such parameters are vital for breeding wilt-tolerant varieties, where environmental interactions play a role in disease expression.

Correlation Coefficient analysis

Genotypic correlation coefficients were generally higher than phenotypic ones, indicating strong genetic associations influenced by environment. Fruit yield per plant showed positive significant correlations with days to first flowering (0.352 genotypic, 0.353 phenotypic), fruit girth (0.269, 0.265), fruit girth ($g=0.269, p=0.265$), yield per plot ($g=0.259, p=0.261$), and yield q/ha ($g=0.259, p=0.261$). Positive but non-significant correlations were observed with plant height, plant spread (N-S), leaf area, and bacterial wilt incidence. Bacterial wilt incidence showed non-significant correlations with all traits, including a positive link with yield per plant ($g=0.203, p=0.201$), likely due to rigorous selection for tolerance in the sick plot. This is corroborated by recent insights into bacterial wilt in brinjal by Rao *et al.* (2024), emphasizing selection pressure in hot spots. Fruit quality traits like total soluble solids (TSS), ascorbic acid, and total sugar showed varied correlations. TSS had positive correlations with plant spread (E-W) (0.247, 0.249), while ascorbic acid correlated with number of fruits per plant (0.263, 0.261). Total sugar showed positive correlations with fruit length (0.244, 0.250) and negative with leaf area (-0.244, -0.257). These align with Sivasankarreddy *et al.* (2020),

Table 5 : Direct and indirect effects of component traits on yield in 40 F₄ segregants including parents and check variety of brinjal.

Traits	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
1	0.198	-0.011	-0.025	-0.054	0.065	0.042	0.067	0.046	0.074	-0.010	0.024	0.031	-0.001	-0.032	-0.044	0.004	-0.031	0.020	0.000	0.000	0.218
2		0.101	0.003	0.008	-0.018	0.009	-0.031	0.004	0.026	0.001	0.013	-0.028	0.004	-0.010	0.013	-0.004	-0.012	0.010	-0.002	-0.002	-0.115
3			0.161	0.077	0.000	-0.011	-0.028	-0.035	0.018	0.029	-0.011	0.002	0.037	0.002	0.040	0.004	0.016	-0.011	-0.005	-0.005	-0.075
4				0.064	-0.008	-0.003	-0.016	-0.002	0.001	0.012	0.004	0.004	0.009	0.005	0.012	0.005	0.010	0.008	0.008	0.008	0.036
5					-0.177	-0.036	-0.070	-0.039	-0.015	0.021	0.000	-0.035	0.011	0.040	0.014	0.015	0.004	-0.011	0.011	0.011	0.103
6						-0.041	-0.004	-0.007	-0.001	0.000	-0.001	-0.001	-0.001	0.001	-0.001	-0.004	0.005	0.003	0.005	0.005	-0.053
7							0.125	0.022	0.010	-0.028	-0.022	0.014	-0.011	-0.024	0.000	0.021	-0.032	0.006	-0.001	0.001	0.148
8								0.361	0.147	0.042	-0.083	0.059	-0.075	-0.003	0.030	0.046	-0.097	-0.014	0.035	0.035	0.353
9									-0.255	-0.050	0.003	-0.059	-0.019	0.054	0.004	0.023	0.004	-0.012	0.056	0.056	0.080
10										-0.082	0.008	-0.007	-0.001	0.014	-0.009	0.010	-0.015	0.000	0.012	0.012	-0.029
11											-0.222	-0.087	-0.073	-0.015	0.012	0.014	-0.056	-0.023	-0.025	-0.025	-0.095
12												0.465	0.143	-0.094	-0.008	0.023	0.087	-0.021	0.077	0.077	0.265
13													-0.188	0.081	-0.004	0.034	-0.043	0.001	-0.009	-0.009	-0.148
14														0.106	0.004	0.028	-0.028	0.003	0.031	0.031	0.080
15															-0.181	-0.042	0.026	-0.019	-0.024	-0.024	-0.154
16																-0.382	0.064	-0.013	-0.070	-0.070	-0.164
17																	-0.046	0.002	0.013	0.013	-0.197
18																		0.267	0.012	0.012	0.201
19																			0.228	0.228	0.261
20																				-0.091	0.261
21																					1.000

1. PH: Plant height at final harvest (cm); **2. PBP:** No. of primary branches plant⁻¹; **3. PS(EW):** Plant spread (EW); **4. PS(NS):** Plant spread (NS); **5. LBL:** Leaf blade length (cm); **6. LBW:** Leaf blade width (cm); **7. LA:** Leaf area (cm²); **8. DFF:** Days to 1st flowering; **9. DFPF:** Days to 50% flowering; **10. NFC:** Number of flowers cluster⁻¹; **11. FL:** Fruit length (cm); **12. FG:** Fruit girth (cm); **13. AFW:** Average fruit weight (g); **14. NFP:** Number of fruits plant⁻¹; **15. TSS:** Fruit TSS (0Brix); **16. AA:** Ascorbic acid (mg/100g); **17. TS:** Total sugar (%); **18. BW:** % of wilt incidence; **19.** Total fruit yield plant⁻¹ (kg)

Ashupriya (2022) and recent updates by Ramesh *et al.* (2024).

Number of fruits per plant negatively correlated with leaf blade length (g=-0.227, p=-0.228) and average fruit weight (g=-0.427, p=-0.431), indicating a trade-off often seen in yield components. Average fruit weight positively correlated with plant spread E-W (g=0.223, p=0.227), fruit length (g=0.323, p=0.328) and fruit girth (g=0.312, p=0.308). Fruit girth positively correlated with days to 50% flowering (g=0.223, p=0.231) and fruit length (g=0.377, p=0.391), but negatively with primary branches (g=-0.266, p=-0.278). Fruit length negatively correlated with days to first flowering (g=-0.230, p=-0.229). These results align with correlation studies in brinjal by Ashupriya (2022) and recent findings by Patel *et al.* (2023), where yield was positively linked to girth for round-fruited types.

Days to 50% flowering positively correlated with plant height (g=0.372, p=0.374), primary branches (g=0.249, p=0.252), and days to first flowering (g=0.406, p=0.374). Days to first flowering correlated with plant height (g=0.231, p=0.230) and leaf blade length (g=0.221, p=0.221). Leaf area positively correlated with plant height (g=0.342, p=0.340) and leaf blade length (g=0.395, p=0.397), but negatively with primary branches (g=-0.296, p=-0.308) and plant spread N-S (g=-0.258, p=-0.248). Plant spread N-S correlated with plant spread E-W (g=0.481, p=0.479), but negatively with plant height (g=-0.276, p=-0.274). Leaf blade length correlated with plant height (g=0.327, p=0.326). Similar correlations between vegetative

Table 6 : Composition of D² based genetic diversity of 40 genotypes of brinjal including F₄ segregants, parents and check.

Cluster Group	No. of Genotypes	List of Genotypes
1 Cluster	34	BBSR-10-25×Selection from BBSR-192-1, BBSR-10-25×BBSR-09-5,BBSR-195-3 × BBSR-09-5, BBSR-08-2 × Selection from BBSR-145-1,BBSR-195-3 × Selection from BBSR-192-1, BBSR-10-25 × Selection from BBSR-145-1, BBSR-10-26 × BBSR-192-1, BBSR-10-25 × BBSR-10-26, Selection from BBSR-192-1 × Selection from BBSR-145-1, BBSR-10-25 × BBSR-195-3, BBSR-09-5, BBSR-08-2 × BBSR-192-1, BBSR-10-26 × BBSR-09-5, BBSR-08-2 × Selection from BBSR-192-1, BBSR-10-25 × BBSR-192-1, BBSR-192-1 × Selection from BBSR-145-1, Jammusahi local × Selection from BBSR-192-1, BBSR-192-1 × BBSR-09-5, BBSR-10-26 × BBSR-195-3, BB-67, Jammusahi Local× BBSR-192-1, BBSR-145-1, Selection from BBSR-145-1 × BBSR-09-5, BBSR-08-2, BBSR-10-26 × Selection from BBSR-145-1, BBSR-10-25, BBSR-195-3 × BBSR-192-1, Jammusahi Local× BBSR-10-26, BBSR-08-2 × Jammusahi Local, Selection from BBSR-192-1 × BBSR-09-5, BBSR-08-2 × BBSR-195-3, BBSR-08-02 × BBSR-10-25, Jammusahi Local× Selection from BBSR-145-1&Jammusahi Local
2 Cluster	1	BBSR-192-1
3 Cluster	1	BBSR-08-2×BBSR-09-5
4 Cluster	1	BBSR-10-26 × Selection from BBSR-192-1
5 Cluster	1	BBSR-10-26
6 Cluster	1	BBSR-08-2×BBSR-10-26
7 Cluster	1	Selection fromBBSR-192-1

and flowering traits have been noted by Tripathy (2021) and elaborated in recent heritability studies by Bende *et al.* (2023).

Path analysis

Path analysis revealed direct and indirect effects on fruit yield per plant. Positive direct effects were from fruit girth (0.465), days to first flowering (0.361), wilt incidence (0.267), yield per plot (0.228), plant height (0.198), plant spread E-W (0.161), leaf area (0.125), fruits per plant (0.106), primary branches (0.101), and plant spread N-S (0.064). Negative direct effects included total sugar (-0.046), flowers per cluster (-0.082), leaf blade width (-0.141), leaf blade length (-0.177), TSS (-0.181), average fruit weight (-0.188), fruit length (-0.222), days to 50% flowering (-0.255), and ascorbic acid (-0.382) (Table 1.8). Similar findings of positive direct effect of fruit yield plant⁻¹ in brinjal have also been reported by Konyak *et al.* (2020); Gurve *et al.* (2020). The residual effect (0.500) suggests unaccounted traits influencing yield. The positive direct effect of fruit girth on yield emphasizes its role in round-fruited breeding, consistent with path analyses in recent heterosis studies by Kumar *et al.* (2024). Wilt incidence's positive direct effect, though counterintuitive, may reflect tolerant genotypes maintaining yield, as discussed in breeding reviews by Salunkhe *et al.* (2024).

Genetic Divergence

Mahalanobis D² analysis grouped genotypes into

seven clusters. Cluster I included 34 genotypes (most F₄ segregants, parents and check), while Clusters II-VII were monotypic. Maximum inter-cluster distance was between Clusters V and VII (1138.27), followed by IV and VII (953.69) and II and III (822.07), clearly demonstrated that genotypes in the cluster can be used as parent in future hybridization programme followed by selection either at F₁ stage or in subsequent segregating generation for producing high yielding variety. The results of the present study are well corroborated with findings of earlier scientists *viz.* Mohanty *et al.* (2021); and Ashupriya (2022). Cluster I showed the highest intra-cluster distance (191.60), reflecting diversity due to natural and artificial selection. Cluster means highlighted superiority: Cluster I for TSS (3.65 °Brix); Cluster II for primary branches (5.70), fruits per plant (15.95), and yield per plant (1.78 kg); Cluster III for leaf area (166.78 cm²) and earliest 50% flowering (50 days); Cluster V for fruit length (8.48 cm) and ascorbic acid (7.70 mg/100g); Cluster VI for heaviest fruits (226.03 g), zero wilt incidence, highest plot yield (13.19 kg), and q/ha (406.94); Cluster VII for plant height (65.00 cm), plant spread (79.77 cm E-W, 83.91 cm N-S), leaf blade width (7.55 cm), flowers per cluster (4.48), and fruit girth (25.24 cm); Cluster IV for leaf blade length (16.47 cm), earliest first flowering (47 days) and total sugar (2.88%). Yield per plant (12.22%), average fruit weight (10.30%), fruits per plant (10.20%), fruit girth (7.20%), and days to first

Table 7 : Inter and intra cluster distance of 40 genotypes brinjal including F₄ segregants, parents and check.

<i>Cluster Distances</i>							
	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7
Cluster 1	191.60	317.82	354.62	310.71	392.02	416.62	551.77
Cluster 2		0.00	822.07	728.03	200.26	632.91	691.53
Cluster 3			0.00	229.12	734.64	486.66	643.03
Cluster 4				0.00	608.40	791.55	953.69
Cluster 5					0.00	798.44	1138.27
Cluster 6						0.00	306.15
Cluster 7							0.00

flowering (6.38%) contributed 46.30% to divergence, emphasizing their role in selection. Cluster means showed superiority in specific traits. Cluster V (BBSR-10-26) exhibited highest yield (406.94 q ha⁻¹) and zero bacterial wilt incidence, while Cluster VII (Selection from BBSR-192-1) was earliest in flowering. Total fruit yield per plant contributed most to divergence (12.22%), followed by average fruit weight (10.30%). These results corroborate with Dash *et al.* (2020), Mohanty *et al.* (2021) and Ashupriya (2022).

The clustering pattern, with Cluster I dominating, indicates shared genetic backgrounds among local landraces, similar to divergence in brinjal in recent assessments by Singh *et al.* (2025). High inter-cluster distances suggest crosses involving Clusters V, VI, and VII could enhance variability and wilt tolerance. Superior segregants like BBSR-10-26 × BBSR-09-5 and Jammusahi local × BBSR-10-26 represent valuable germplasm for breeding programmes, offering significant potential for genetic improvement of yield, nutritional quality and bacterial wilt tolerance in brinjal.

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