



OPEN Exploring heterosis, dominance effect, and genetic control in Brinjal (*Solanum melongena* L.) landraces

Barsha Tripathy^{1,2}, P. Tripathy², J. Jyothsna³, G. S. Sahu², S. K. Dash², Meenakshi Badu⁴, Subrat Kumar Mahapatra⁵ & Gyana Ranjan Rout⁶✉

Brinjal (*Solanum melongena* L.) is an important warm-season vegetable with immense antioxidant potential. The present study aims to identify superior high-yielding plants with round fruits and tolerance to bacterial wilt through heterosis breeding. This study evaluated 52 brinjal genotypes, including 48 local landraces collected from eastern India, emphasizing the state of Odisha and four released varieties. The selection process focused on variations in both quantitative and qualitative traits and examined genetic variability, heritability, and genetic advance for yield and yield-contributing traits. The Shannon-Wiener diversity index (H') had an overall mean value of 0.733, with significant variations observed in fruit length-to-breadth ratio, leaf blade color, fruit shape, and petiole color. The estimated h^2 BS for each tested attribute varied from 64.90 to 98.17%, showing that all traits were highly heritable. Based on multivariate analysis, nine parents with different genetic backgrounds were selected among 52 genotypes of diverse origins for breeding study. To ascertain the degree of heterosis, dominance reaction, combining ability and gene action for 12 quantitative features crossed in a diallel fashion without reciprocals to develop 36 F_1 hybrids. Average fruit weight (79.46%) had the highest degree of significant heterobeltiosis in the desired directions, followed by fruit yield per plant (71.61%), plant spread (58.07%), primary branches per plant (56.25%), and days to 1st flowering (-32.72%). No dominance to over-dominance effects was involved in the inheritance of fruit yield and yield-attributing traits. Four landraces (Selection from BBSR-192-1, BBSR-192-1, BBSR-08-2, and BBSR-195-3) were identified as promising general combiners for fruit yield and yield-attributing traits. Overall, based on *per se* performance, heterotic response as well as estimates of combining ability, the four important crosses namely, BBSR-08-2 X BBSR-192-1, Jammusahi Local X BBSR-192-1, BBSR-195-3 X BBSR-192-1 and BBSR-10-26 X BBSR-192-1 were highly tolerance to bacterial wilt as well as yield and suitable for commercial exploitation as F_1 hybrid in *Solanum melongena* for eastern part of India.

Keywords *Solanum melongena*, Heritability, Combining ability, Gene action, Heterosis, Genetic improvement

Brinjal (*Solanum melongena* L.; $2n = 2x = 24$) is one of the family Solanaceae's most common warm-season and widely cultivated vegetable crops. The unripe fruit is primarily used as a cooked vegetable and raw material in pickle-making and dehydration industries. It is versatile and can be used for different culinary purposes; therefore, brinjal is often described as the king of vegetables¹. Seeds of brinjal are used as a stimulant. It has antioxidant properties and is notable for its health-promoting activities². White brinjal is said to be suitable for diabetic patients. In addition, it is also used for treating bronchitis, asthma, dysuria, dysentery, cholera^{3,4}, and colon cancer⁵. The root and leaf extract cures piles, skin diseases, throat problems, toothache, inflammation, and stomach problems⁶. Brinjal is a fair source of fatty acids and has decholesterolizing properties due to 65.1% linoleic and linolenic poly-3-unsaturated fatty acids. It has a high nutritional profile, with fruits low in calories

¹Department of Vegetable Science, Faculty of Agricultural Sciences, Siksha "O" Anusandhan Deemed to be University, Bhubaneswar, Odisha, India. ²Department of Vegetable Science, College of Agriculture, OUAT, Bhubaneswar, Odisha, India. ³Department of Horticulture, College of Agriculture – Jabalpur, Jawaharlal Nehru Krishi Vishwavidyalaya, Jabalpur, Madhya Pradesh, India. ⁴Department of Horticulture, Faculty of Agriculture, Sri Sri University, Cuttack, Odisha, India. ⁵Department of Agricultural Statistics, Faculty of Agricultural Sciences, Siksha "O" Anusandhan Deemed to be University, Bhubaneswar, Odisha, India. ⁶Department of Molecular Biology & Biotechnology, Faculty of Agricultural Sciences, Siksha "O" Anusandhan Deemed to be University, Bhubaneswar, Odisha, India. ✉email: grrout@rediffmail.com; gyanaranjanrout@soa.ac.in

and high in minerals such as potassium, phosphorus, calcium, salt, iron, zinc copper, and dietary fiber. Aside from that, brinjal fruits are said to be high in ascorbic acid and phenolics⁷.

Since the Indo-Burma region is noted as the centre of origin of brinjal, it accumulates a wide range of variability in this crop⁸. The landraces of brinjal exhibited a broad range of genetic diversity across various phenotypic traits, including fruit size, shape, color, growth habit, yield, pest and disease resistance, climate adaptability, and quality attributes. This extensive diversity presents significant opportunities for genetically improving these locally available brinjal landraces⁹. The eastern part of India, including Odisha, is considered one of the rich sources of brinjal germplasm. As these local landraces and genotypes gradually degraded, immediate attention is needed for their conservation and utilization in future breeding programs.

Characterizing collected germplasm is necessary to identify the genotype to develop a new variety¹⁰. The high degree of heritable variability within a breeding material helps to create a variety of desirable traits through selection⁸. Therefore, achieving high yield involves selecting traits characterized by high heritability and genetic advancement¹¹. Genetic diversity within and between a population has shown its utility in selecting genetically diverse parents, which can produce superior hybrids or increase the likelihood of isolating transgressive segregants¹².

In many vegetable markets of India, generally, the preference is for green-colored round fruits with uniform color distribution or green fruits with white stripes having a glossy surface and medium size, which usually suffer from low productivity and susceptibility to bacterial wilt caused by *Ralstonia solanacearum*. Bacterial wilt is regarded as a major disease to reduce the yield. The yield losses in brinjal ranged up to 95% because of its wide host range and broad geographical distribution¹³. Very scanty information is available regarding the genotype resistant to bacterial wilt¹⁴. The pathogen of this disease lives for many years in host plants and the soil, making it difficult to control¹⁵. Concerning open-pollinated cultivars, however, resistance becomes ineffective after several generations and degradations of yield and quality characteristics¹⁶. Since very little success has been achieved with chemical control, the most effective method to combat bacterial wilt is the development of disease-resistant cultivars through hybridization¹⁷. It can also lead to the exploitation of hybrid vigor.

With the increasing acceptance of F_1 hybrids among farming communities, obtaining hybrids with higher fruit yield and resistance to bacterial wilt is crucial. Hence, there is an urgent need to develop hybrids higher in fruit yield and yield-attributing parameters. The proper choice of parents is a prerequisite for an appropriate breeding program. Genetic diversity, as well as the combining ability, is considered the most important criterion for selecting parents in the production of a hybrid. Such studies also simultaneously illustrate the nature and magnitude of gene action involved in expressing desirable traits. Estimates of combining ability parameters place heterosis breeding on a further scientific footing. Diallel¹⁸ is one of the valuable tools for the preliminary evaluation of genetic stock for use in hybridization programs to identify good general and specific combiners. Therefore, the main objectives of the present study are to characterize the genetic variability of *Solanum melongena* landraces, followed by an assessment of the extent of heterosis and nature of gene action for yield and its components, and to identify good combiners, as well as development of round-fruited *Solanum melongena* F_1 hybrid (s) for higher fruit yield and tolerance to bacterial wilt.

Materials and methods

Site of experiment

The research was undertaken at the All India Co-ordinated Research Project on Vegetable Crops, Odisha University of Agriculture and Technology, located in Bhubaneswar, Odisha, India, between November 2017 and April, 2020. The experimental site is situated at approximately 20°15' N latitude and 85°52' E longitude, with an elevation of 25.5 m above mean sea level (MSL).

Experimental materials, design and procedures

In total, 52 genotypes comprising 48 local landraces were collected from various districts of Odisha, (Supplementary Figure. 1 A–C) and four released varieties, viz., Utkal Tarini, Utkal Jyoti, Utkal Keshari, and Arka Nidhi, were used as check genotypes, Supplementary Table 1). Utkal Tarini (BB 7), Utkal Jyoti (BB 13), and Utkal Keshari (BB 26) are brinjal varieties developed by Odisha University of Agriculture and Technology, Bhubaneswar and are known for their resistance/tolerance to bacterial wilt. Similarly, the Arka Nidhi, a variety developed by the Indian Institute of Horticultural Research (ICAR-IIHR), is known for its high yield (48.5 t/ha) and resistance to bacterial wilt. All 52 genotypes, including four check varieties, were allocated by adopting a randomized block design and conducted twice, resulting in a total of 104 experimental plots. Each plot measured 2 m by 2.7 m, with a 75 by 60 cm spacing between plants. Seeds were sown directly in well-prepared nursery beds. All three years, the experiments were conducted in a sick plot at Odisha University of Agriculture and Technology, Bhubaneswar, India. Thirty days old seedlings were then transplanted into pits within the experimental plots. Organic fertilizer in the form of cow dung (25 tons/hectar) and inorganic fertilizers including urea, single superphosphate (SSP), and muriate of potash (MOP) @ 125:60:100 kg per hectare were applied. Before transplanting, a basal dose containing the entire quantity of cow dung, SSP, and MOP, along with 62.50 kg of urea, was incorporated into the soil for about one week. The remaining 62.50 kg of urea was applied as top dressing one month after transplanting. A standard set of agricultural practices was uniformly applied to all genotypes to ensure optimal plant growth. Field observations were systematically recorded from randomly selected five plants according to the prescribed schedule. The collected data underwent analysis using established statistical and biometric procedures.

Based on their divergence values, nine distinct diverse brinjal landraces viz., BBSR-08-2, BBSR-10-25, Jammusahi Local, BBSR-10-26, BBSR-195-3, BBSR-192-1, Selection from BBSR-192-1, Selection from BBSR-145-1 and BBSR-09-5 were identified as parental lines for the hybridization program for the development of round fruited hybrid with higher fruit yield and tolerance to bacterial wilt.

True selfed seeds of nine brinjal landraces were sown in a well-prepared nursery bed during the first week of July 2018. In the crossing block, one-month-old seedlings of nine brinjal landraces (parents) were transplanted separately in the earthen pots containing sand, soil, and FYM to raise 36 cross combinations in a 9 × 9, half-diallel mating design in the first week of August 2018.

The crossing took place when the flowers were in full bloom. Each female line's flower buds were covered with a small butter paper bag after being emasculated between 4 and 5.30 pm. Fruit setting only happens on long or medium-styled flowers. Hence, only such flowers were used for emasculation. Hand pollination was done between 8 and 10 am. Each female line's flowers were once more covered following pollination. Every male parent and female parental lines were crossed and tagged separately. Harvested and finely diced, ripe fruit was soaked in water in a plastic container for the entire night. This process separates the seed from the pulp that adheres to it and settles in the bottom. The following morning, the seeds were carefully cleaned with fresh water. The sank seeds were collected, dried, and placed in butter paper covers after treating them with SAAF@ 2.5 g per kg of seeds for the following year's evaluation. In *rabi*, 2019–20, nine parental lines, 36 hybrids, and one standard hybrid check variety, i.e., VNR-5 of VNR Seeds, were raised by following the same method. During the last week of September 2019, thirty days old seedlings were transplanted in the main field prepared in infested soil (sick plot) at All India Co-ordinated Research Project on Vegetable Crops, Odisha University of Agriculture and Technology, Bhubaneswar. The evaluation experiment was conducted using a randomized block design (RBD) replicated thrice at 75 × 75 cm spacing for each replication in a 4.5 m × 4.5 m plot. No protection was used against bacterial wilt. To provide a sufficient bacterial load, infected plants of susceptible cultivars were planted and maintained around the vicinity.

Data recorded

The data were recorded following the minimal descriptor guidelines for vegetable crops provided by the National Bureau of Plant Genetic Resources (NBPGR), New Delhi¹⁹ (Supplementary Figures. 2–4 A–B). Frequency distribution was determined for a comprehensive set of qualitative morphological data across twenty traits and quantitative data across eighteen traits (Table 1). Plant growth habits, height, spread, and primary branches per plant were recorded at the peak fruiting stage. Observation of flower characters was noted at the peak flowering stage. The petiole color, leaf blade lobbing, and leaf blade tip angle were noted on the 5th leaf from the top at the full foliage stage. Leaf blade color and number of prickles on the upper leaf surface were recorded at the full foliage stage of the plant growth. Fruit pedicle prickles were recorded on marketable fruits. This observation was the average of the same 5 fruits at the marketable stage. Fruit curvature, fruit shape, fruit apex shape, fruit color and color distribution, and seediness of fruit were taken on marketable fruits. Samples of five randomly selected green fruits per plot were taken to measure the fruits' characteristics, i.e., fruit length (cm), pedicel length (cm), fruit breadth (cm), and test weight (100-seed weight, g) from each replication. All harvested fruits of each plant were counted and weighed to determine the average number of fruits per plant and fruit weight per plant. Total fruit yield per plant (g) was calculated by taking the total marketable and unmarketable fruit yield from tagged plants during each harvest.

Percent disease incidence (PDI) of bacterial wilt incidence

The severity of bacterial wilt disease was determined from each plant of parents, and F₁s in each replication visually at 30, 45, 60, and 90 days after transplanting (DAT) based on a 0–5 scale of Winstead and Kelman²⁰ with some modifications.

Grade	Description	Category
0	Plants did not show any wilt symptom	Highly resistant (HR)
1	1–20% plants wilted	Resistant (R)
2	21–40% plants wilted	Moderately resistant (MR)
3	41–60% plants wilted	Moderately susceptible (MS)
4	61–80% plants wilted	Susceptible (S)
5	More than 80% plants wilted	Highly susceptible (HS)

The number of plants infected in each parent and hybrid was recorded and the final PDI (%) was calculated 90 days after transplanting with the following formula:

$$\text{PDI} = \text{Number of plants showing wilt symptoms} / \text{Total number of plants} \times 100$$

Statistical analysis

Shannon-Wiener diversity index (H')

The frequency distributions were utilized to compute the Shannon-Wiener diversity index (H') for each trait²¹. The index is calculated as below.

$$H^1 = - \sum_{i=1}^s P_i \ln P_i$$

Sl. no.	The traits/ descriptor	Class or scale of descriptor	No. of genotypes	Distribution by classes of descriptor (%)	Shannon-Wiener diversity Index (H')
1	Plant growth habit	3 = Upright	3	6.25	0.896
		5 = Intermediate	33	68.75	
		7 = Prostrate	12	25.00	
2	Plant height (cm)	3 = Small(< = 50 cm)	0	0.00	0.284
		5 = Medium(50–100 cm)	44	91.67	
		7 = Tall (> 100)	4	8.33	
3	Plant spread (cm)	1 = very narrow (< = 30)	0	0.00	0.333
		3 = Narrow (>30-40)	0	0.00	
		5= intermediate (> 40-60)	0	0.00	
		7 = broad (> 60–90)	43	89.58	
		9 = very broad (>90)	5	10.42	
4	Petiole colour	1 = green	19	39.58	1.263
		2 = Greenish violet	16	33.33	
		3 = violet	8	16.67	
		4 = dark violet	5	10.42	
		5 = dark brown	0	0.00	
5	Leaf blade lobing	1 = very weak	0	0.00	0.925
		3 = weak	2	4.17	
		5 = intermediate	33	68.75	
		7 = strong	7	14.58	
		9 = very strong	6	12.50	
6	Leaf blade tip angle	1 = very acute (< = 15 degree)	4	8.33	1.103
		3 = acute(> 15-45 degree)	26	54.17	
		5 = intermediate(> 45-75 degree)	14	29.17	
		7 = obtuse(> 75–110 degree)	4	8.33	
		9 = very obtuse (> 110 degree)	0	0.00	
7	Leaf blade colour	1 = light green	15	31.25	1.457
		2 = green	7	14.58	
		3 = dark green	10	20.83	
		4 = greenish violet	14	29.17	
		5 = violet	2	4.17	
8	Number of leaf prickles (in upper surface)	0 = none	39	81.25	0.599
		3 = few (1–5)	3	6.25	
		5 = many(> 5)	6	12.50	
9	Corolla colour	1 = white	0	0.00	1.048
		2 = greenish white	0	0.00	
		3 = pale violet	10	20.83	
		4 = light violet	22	45.83	
		5 = bluish violet	16	33.33	
10	Calyx colour	1 = green	31	64.58	0.841
		2 = light purple	4	8.33	
		3 = dark purple	13	27.08	
11	Calyx spinyness	3 = smooth	26	54.17	0.998
		5 = medium thorny	9	18.75	
		7 = high thorny	13	27.08	
12	Fruit pedicel prickles	0 = none	17	35.42	1.079
		1 = few (1–5)	19	39.58	
		2 = many (> 5)	12	25.00	
13	Fruit length-breath ratio	1 = broader than long	2	4.17	1.666
		3 = as long as broad	9	18.75	
		5 = slightly longer than broad	7	14.58	
		7 = twice as long as broad	14	29.17	
		8 = three times as long as broad	6	12.50	
		9 = several times as long as broad	10	20.83	
Continued					

Sl. no.	The traits/ descriptor	Class or scale of descriptor	No. of genotypes	Distribution by classes of descriptor (%)	Shannon-Wiener diversity Index (H')
14	Fruit curvature	1 = none	45	93.75	0.268
		3 = slightly curve	2	4.17	
		5 = curved	1	2.08	
		7 = snake shaped	0	0.00	
		8 = sickle shaped	0	0.00	
		9 = U shaped	0	0.00	
15	Fruit shape	3 = long	10	20.83	1.283
		5 = round	11	22.92	
		7 = oblong	21	43.75	
		9 = oval	6	12.50	
16	Fruit apex shape	3 = prostrate	0	0.00	0.691
		5 = rounded	23	47.92	
		7 = depressed	25	52.08	
17	Fruit colour	1 = milky white	1	2.08	0.843
		2 = green	36	75.00	
		3 = deep green	0	0.00	
		4 = fire red	0	0.00	
		5 = scarlet red	0	0.00	
		6 = lilac red	0	0.00	
		7 = purple	5	10.42	
		8 = purple black	1	2.08	
		9 = black	0	0.00	
		10 = light purple	5	10.42	
18	Fruit colour distribution	1 = uniform	11	22.92	0.537
		3 = mottled	37	77.08	
		5 = irregular striped	0	0.00	
		7 = regular striped	0	0.00	
19	Fruit flesh density	1 = very loose (spongy)	0	0.00	1.170
		3 = loose(crumble)	7	14.58	
		5 = medium compact	25	52.08	
		7 = compact	12	25.00	
		9 = very compact	4	8.33	
20	Seediness	3 = low	11	22.92	1.036
		5 = medium	24	50.00	
		7 = high	13	27.08	

Table 1. Morphological descriptor, descriptor scales, frequency distribution and Shannon-wiener diversity index (H') of 48 landraces of *Solanum melongena* L.

H' = diversity index; S = Total number of descriptors in the ith descriptor; P_i = fraction of individuals belonging to the ith descriptor state (number of observations/descriptor state in ith descriptor divided by the total number of characterized plants).

Genetic parameters

The phenotypic and genotypic coefficients of variation (PCV and GCV) were computed using the formula outlined by Burton²².

$$\text{GCV} = \text{Genotypic standard deviation} / \text{Grand mean} \times 100$$

$$\text{PCV} = \text{Phenotypic standard deviation} / \text{Grand mean} \times 100$$

Categorization of the range of variation was suggested as < 10% - Low, 10–20% - Moderate, > 20% - High.

Broad sense heritability (h^2_{BS}) and genetic advance (GA) were calculated following the methods described by Allard²³ and Johnson et al.²⁴.

$$h^2_{BS} = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Traits	Mean	Std.Dev.	CV	Minimum	Maximum	Skewness	Kurtosis
Plant height (cm) at peak fruiting stage	78.92	18.05	7.21	52.60	148.00	1.65	3.77**
Plant height at final harvest (cm)	91.98	19.09	7.31	65.68	161.44	1.43*	2.57
Plant spread (cm)	81.72	10.66	5.22	61.40	126.95	1.78	6.13*
Primary branches plant ⁻¹	4.35	0.68	10.17	2.40	5.70	-0.49	0.47
Leaf petiole length (cm)	6.62	1.30	6.69	4.65	10.83	1.32**	2.01
Leaf blade length (cm)	15.93	1.64	4.70	12.00	20.70	0.18	0.60
Leaf blade width (cm)	11.07	1.42	6.62	8.80	15.90	0.88*	1.36*
Days to 1st flowering	52.00	4.78	5.72	42.50	64.30	-0.21	-0.19
Days to 50% flowering	61.44	3.62	3.78	51.10	71.90	-0.19	2.03
Flowers cluster ⁻¹	3.82	0.91	9.68	2.28	6.16	0.50	0.35
Fruit pedicel length (cm)	5.21	1.02	4.07	3.41	9.12	1.02	2.89*
Fruit length (cm)	12.82	2.74	3.06	7.41	21.10	0.78	0.76
Fruit breadth (cm)	17.28	4.86	6.61	9.67	31.40	0.96	0.48
Average fruit weight (g)	96.08	33.63	8.37	50.85	233.97	1.96*	5.21*
Fruits plant ⁻¹	19.82	7.65	9.65	5.88	40.59	0.52	0.02
100 seed weight (g)	0.39	0.06	3.11	0.28	0.56	0.57	-0.10
Bacterial wilt % at 90 DAT	6.65	7.66	22.33	0.00	37.50	1.78	4.56
Total marketable fruit yield plant ⁻¹ (g)	905.65	438.80	9.72	380.71	2720.42	1.81	4.73
Total unmarketable fruit yield plant ⁻¹ (g)	735.41	286.01	10.16	181.74	1246.20	-0.05	-0.86
Total fruit yield plant ⁻¹ (g)	1641.07	437.60	9.35	865.80	3045.70	0.78	1.34

Table 2. Descriptive statistics of measured traits of *Solanum melongena* L. ns, non-significant; *, ** indicate the significance at 5% and 1% level of probability.

h^2_{BS} = Heritability in broad sense. σ^2_g = Genotypic variance. σ^2_p = Phenotypic variance ($\sigma^2_g + \sigma^2_e$). σ^2_e = Environmental variance.

As suggested by Johnson et al.²⁴ the estimates of heritability in the broad sense were categorized as: 0–30% - Low, 30–60% - Medium, > 60% - High. The magnitude of genetic advance as percent of mean was categorized as High ($\geq 20\%$), Moderate (20% – 10%), and low ($< 10\%$).

Multivariate analysis

As per Sir P.C. Mahalanobis²⁵, D^2 statistic was used to assess the genetic divergence between populations for quantitative traits.

Estimation of heterosis

The magnitude of heterosis was calculated as percentage increase or decrease of F_1 s over the mid-parent (MP), better-parent (BP), and standard check (SC) values.

1. Heterosis percentage over the mid parent (Relative heterosis)

$$\text{Relative heterosis}(\%) = \left[\frac{\bar{F}_1 - \bar{MP}}{\bar{MP}} \right] \times 100$$

2. Heterosis percentage over the better parent (Heterobeltiosis)

$$\text{Heterobeltiosis}(\%) = \left[\frac{\bar{F}_1 - \bar{BP}}{\bar{BP}} \right] \times 100$$

3. Heterosis percentage over the standard check

$$\text{Standard heterosis}(\%) = \left[\frac{\bar{F}_1 - \bar{SC}}{\bar{SC}} \right] \times 100$$

Where \bar{F}_1 = mean of F_1 , \bar{BP} = mean of the better parent, \bar{MP} = mean of the two parents, \bar{SC} = mean of the standard check, S.E. = standard error

Test of significance of heterosis magnitude was performed by using the critical differences (CD test) at 5% and 1% error degree of freedom.

Estimation of potence ratio

The dominance estimates (D.E.) often referred to as the “potence ratio” was computed using the following formula as suggested by Smith²⁶.

$$D.E. = F_1 - MP/0.5 \times P_2 - P_1,$$

Where F_1 = mean value of the hybrid population; MP = mid-parent; P_2 = mean of the highest parent; P_1 = mean of the lowest parent.

Complete dominance was realized when $D.E. = +1$; while partial dominance is indicated when $D.E.$ is between -1 and $+1$; $D.E. = 0$ indicates absence of dominance. Over dominance was considered when $D.E.$ exceeds ± 1 . The ‘+’ and ‘-’ signs indicate the direction of dominance of either parent.

Estimation of combining ability and gene action

Analysis of variance table for combining ability with expected mean square was analysed as follows.

Source of variation	df	MSS	Expected mean square
General combining ability (GCA)	$(p-1)$	M_g	$V_e + \left[\frac{p+2}{p+1} \right] \sum g_i^2$
Specific combining ability (SCA)	$\frac{p(p-1)}{2}$	M_s	$V_e + \left[\frac{2}{n(n-1)} \right] \sum \sum S_{ij}^2$
Error	$(r-1)(g-1)$	$Me = Me/r$	V_e

Combining ability variances and effects were worked out according to Griffing’s¹⁸ Model 1 and Method 2. Method 2 applies to the present study as parents and one set of non-reciprocal F_1 s were included. Model 1 assumes that variety and block effects are constant but environmental effect is variable and the experimental material is the population about which inferences are to be made. The additive and non-additive genetic variances were estimated from the combining ability components as follows:

$$\hat{\sigma}_a^2 (\text{additive}) = 2\hat{\sigma}_g^2$$

$$\text{Where, } \hat{\sigma}_g^2 = \frac{1}{p-1} \sum \hat{\sigma}_{gi}^2 = \frac{M_g - M_e}{p+2}$$

$$\hat{\sigma}_{na}^2 (\text{non-additive}) = \hat{\sigma}_s^2$$

$$\text{Where, } \hat{\sigma}_s^2 = \frac{2}{p(p-1)} \left(\sum_i i \sum_j j \hat{s}_{ij}^2 - M_s \right) - M_e^I \text{ and } M_e^I = \hat{\sigma}_e^2$$

Basic statistical analysis such as descriptive statistics and frequency distribution was carried out by using IBM SPSS version 26. Cluster analysis and Principal Component analysis was carried out by using R Software Version 4.2.2.

Results

Morphological characterization of genotypes

Vegetative characters

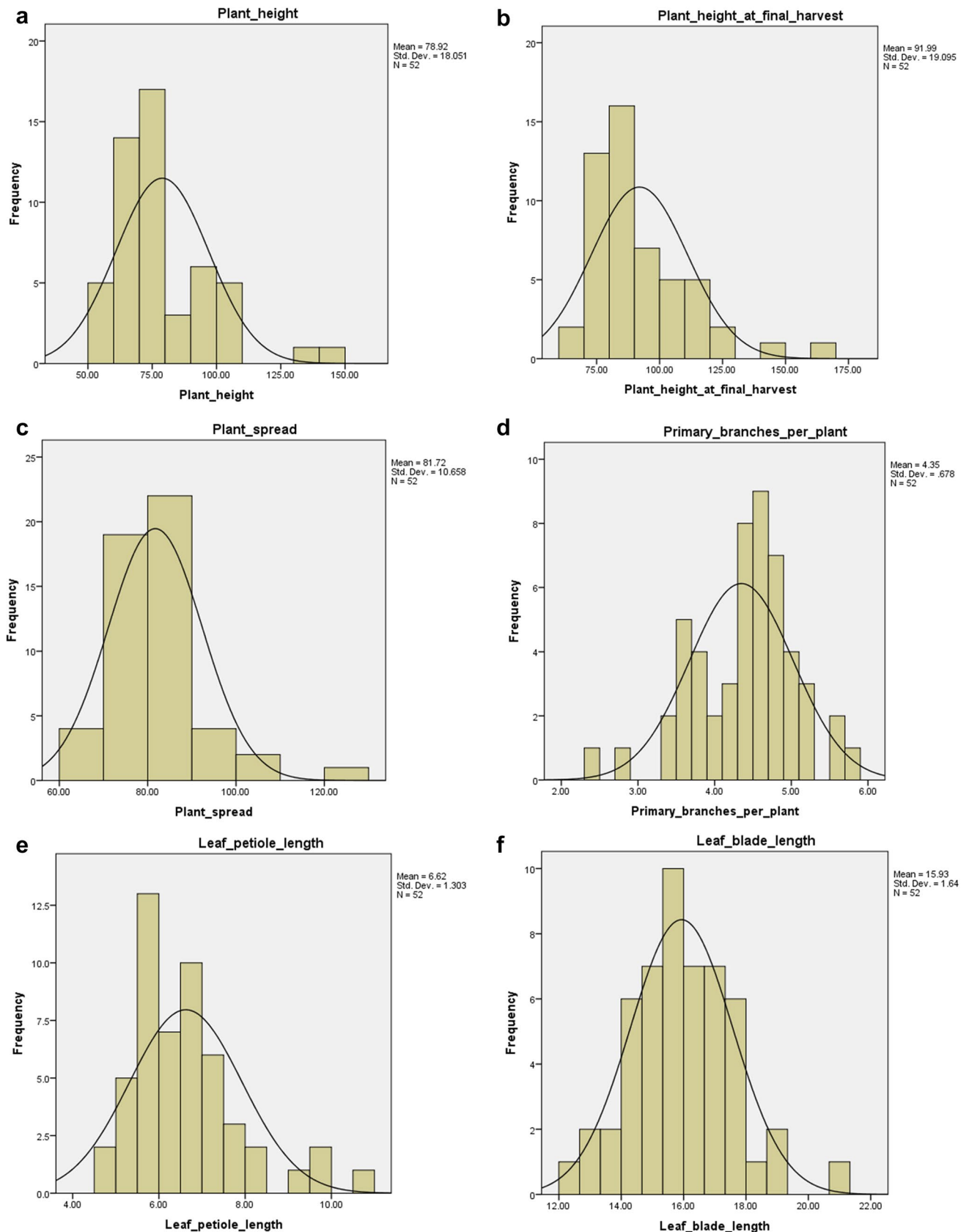
Brinjal’s three significant growth habits are upright, intermediate, and prostrate. These habits are essential for the brinjal breeding program. The predominant growth habit was intermediate (68.75%), followed by prostrate (25.00%) and upright (6.25%). The result showed that 91.67% of landraces were medium height while 8.33% as tall plants (Table 1). Plant spread was broad (89.58%) and broad (10.42%). The petiole pigmentation varied widely among the landraces, with the highest green (39.58%), greenish-violet (33.33%), violet (16.67%), and dark violet (10.42%) pigmentation. In the present study, the trait leaf blade lobbing varied from weak to very strong, i.e., weak (4.17%), intermediate (68.75%), strong (14.58%), and robust (12.50%). None of the landrace had shown very weak leaf blade lobbing. Similarly, leaf blade tip angles in 54.17% of landraces were acute. However, it was intermediate (29.17%), very acute, and obtuse (8.33%) in the rest of the landrace. Greenish violet (29.17%) color leaf blade was dominant in most of the landraces, followed by light green (31.25%), dark green (20.83%), green (14.58%), and violet (4.17%). The development of prickles on various plant parts was a prominent characteristic in brinjal. Most of the genotypes (81.25%) had non-spiny leaves, while 12.50% of landraces had many spines (>5), and the remaining 6.25% had few spines (1–5) on the leaf.

Flowering characters

The flower color showed a continuous range of colors, from pale violet to bluish violet corolla. Of 48 landraces, 45.84% showed light violet corolla, 33.33% with bluish violet, and 20.83% pale violet. Similarly, the calyx color intensity varied from green to dark purple (64.58%), light purple (8.33%), and dark purple (27.09%) colors were displayed by the collected landraces. Most of the landraces (54.17%) showed smooth calyx, while 27.08% and 18.75% showed highly thorny and medium thorny, respectively (Table 1).

Fruit characters

Fruit length and breadth are crucial parameters for marketable fruits. The fruit pedicel of 25.0% landraces had many (>5) prickles. However, nearly 39.58% of them had few (1–5) prickles; in 35.42% of genotypes, prickles were absent. The results exposed that about 29.17% (<75 g), 62.50% (75–150 g), and 8.33% (>150 g) as small, medium, and large size fruits. Among the morphological traits, the maximum variations in germplasm were seen in fruit length-breadth ratio; for this character, the landraces were classified into as broader than long (4.17%), long as broad (18.75%), slightly longer than broad (14.58%), twice as long as broad (29.17%), three times as long as broad (12.50%) and several times as long as broad (20.83%). No fruit curvature was found in



most (93.75%) of the tested landraces. The present investigation indicated that maximum landraces of oblong type fruits (43.75%) followed by round (22.95%), long (20.83%) and oval (12.50%) types. However, regarding fruit apex, the results showed 52.08% as depressed while 47.92% as round type. For the distribution of fruit color, the current study also indicated the dominance of mottled fruits (77.08%) followed by 22.92% as uniform. The

◀ **Fig. 1.** Frequency distribution of the brinjal landraces based on quantitative traits. **A.** Plant height (cm) at peak fruiting stage, **B.** Plant height at final harvest, **C.** Plant spread (cm), **D.** Primary branches per plant, **E.** Leaf petiole length (cm), **F.** Leaf blade length (cm), **G.** Leaf blade width (cm), **H.** Days to 1st flowering, **I.** Days to 50% flowering, **J.** Flowers per cluster, **K.** Fruit pedicel length (cm), **L.** Fruit length (cm), **M.** Fruit breadth (cm), **N.** Average fruit weight (g), **O.** Fruits per plant, **P.** 100 seed weight (g), **Q.** Wilt % at 90 DAT, **R.** Total marketable fruit yield per plant(g), **S.** Total unmarketable fruit yield per plant(g), **T.** Total fruit yield per plant(g).

results showed the dominance of medium seediness (50.00%) followed by 27.08% high seediness, while only 22.92% was low seediness among the tested landraces.

Shanon-Wiener diversity index (H')

Biodiversity in crops will be understood through two key components: allelic evenness and allelic richness. In morphological evaluation, descriptors correspond to loci, and descriptor states correspond to alleles. Allelic evenness in this study was assessed using the Shannon-Wiener Diversity Index, while allelic richness was determined by counting the descriptor states for each descriptor, irrespective of their frequencies. Richness indicates the number of genotypes present in a specific area, whereas evenness denotes the relative abundance of each genotype. The Shannon-Wiener diversity index (H') values for all traits ranged from 0.27 for fruit curvature to 1.67 for fruit length-to-breadth ratio. A high Shannon-Wiener diversity index, with an average value of 73%, was obtained, demonstrating significant diversity among the brinjal landraces. Traits such as fruit length-to-breadth ratio, leaf blade color, fruit shape, and petiole colour exhibited notable variations among the genotypes.

Genetic variability

The genetic variability of the morpho-physiological traits is presented in Table 2. The range of values for various traits varied significantly, from 0.28 to 0.56 g in 100-seed weight to a maximum of 865.80 to 3045.70 g in total fruit yield per plant. Similarly, the percentage difference between the minimum and maximum values of specific traits ranged from 40.70% (days to 50% flowering) to 590.31% (fruits per plant). The study also revealed wide variations in the general mean values of 18 traits, ranging from 0.39 (100-seed weight) to 1641.07 (total fruit yield per plant). Significant skewness was recorded only for plant height at final harvest, leaf petiole length, leaf blade width, and average fruit weight among the traits studied. Kurtosis value was significant in plant height at the peak fruiting stage, plant spread, leaf blade width, fruit pedicel length, and average fruit weight. Skewness values were negative for primary branches per plant, days to 1st flowering and 50% flowering, and total marketable fruit yield. The frequency distribution graph of the brinjal landraces is presented in Fig. 1A–T. Table 3 highlights the characteristics of all 18 traits, such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability (h^2_{BS}), and genetic advance as a % of the mean (GAM). It was found that for all the traits, PCV values were higher than the corresponding GCV values. Notably, the difference between PCV and GCV was minimal (less than 1) for traits such as fruit pedicel length (0.43), fruit length (0.20), fruit breadth (0.77), 100-seed weight (0.29), and bacterial wilt percentage at 90 days after transplanting (0.65). High PCV and GCV were noted for plant height at peak fruiting and final harvest, flower cluster, fruit length, fruit breadth, average fruit weight, fruits per plant, bacterial wilt % at 90 days after transplanting, and total fruit yield per plant, while medium range of PCV and GCV were recorded for traits like plant spread, primary branches per plant, leaf blade width, fruit pedicel length, and 100-seed weight. The low PCV and GCV are observed in days to 50% flowering. There is a broad sense of heritability ranging from 64.90% (primary branches per plant) to 98.17% (fruit length). The results also indicate that GA ranged from 8.78% (days to 50% flowering) to 119.32% (bacterial wilt % at 90 DAT). In the present investigation, high heritability percentages coupled with high GA percentages were noted for every character, indicating the presence of the additive gene action. In contrast, high heritability with moderate to low GA percentages was noted for days to first flowering (67.62% and 13.99%), leaf blade length (81.13% and 18.08%), and days to 50% flowering (65.87% and 8.78%).

Genetic diversity of the genotypes through multivariate analysis

Table 4 shows the genetic diversity among the clusters. Based on the distance, cluster III had the highest intra-cluster value, suggesting that genotypes belonging to this cluster are diverse. However, Cluster II had the lowest intra-cluster value. At the inter-cluster level, the most significant value was noted between Cluster III and VIII, followed by Cluster II and VIII, which indicated that the genotypes of these clusters were more diverse. Cluster V and VI had the lowest inter-cluster values, suggesting that the clusters' genotypes were closely related. Keeping the genetic diversity and the performances with particular reference to higher fruit yield (gm per plant), tolerance to bacterial wilt (%), and round-shaped fruit, nine distinct diverse local landraces namely BBSR-08-2, BBSR-10-25, Jammusahi Local, BBSR-10-26, BBSR-195-3, BBSR-192-1, Selection from BBSR-192-1, Selection from BBSR-145-1 and BBSR-09-5 (Fig. 2) were identified for hybridization program which may produce heterotic hybrids (Supplementary Table 2). The genotypes present in the cluster VIII and cluster I have not been included for hybridization programme (Supplementary Table 3).

Mode of gene action for different characters

Based on Griffing's Model 1 and Method 2, the analysis of variance displayed a highly significant mean sum of squares in the F_1 generation for all the traits, except bacterial wilt % at 90 DAT, signifying the presence of vast genetic diversity between the parents (Tables 4 and 5). The relative magnitude and significance of additive and non-additive variances in the genetic control of various quantitative characters are determined by predictability ratios. The predictability ratio was >0.80 for fruit length and bacterial wilt % 90 DAT, indicating

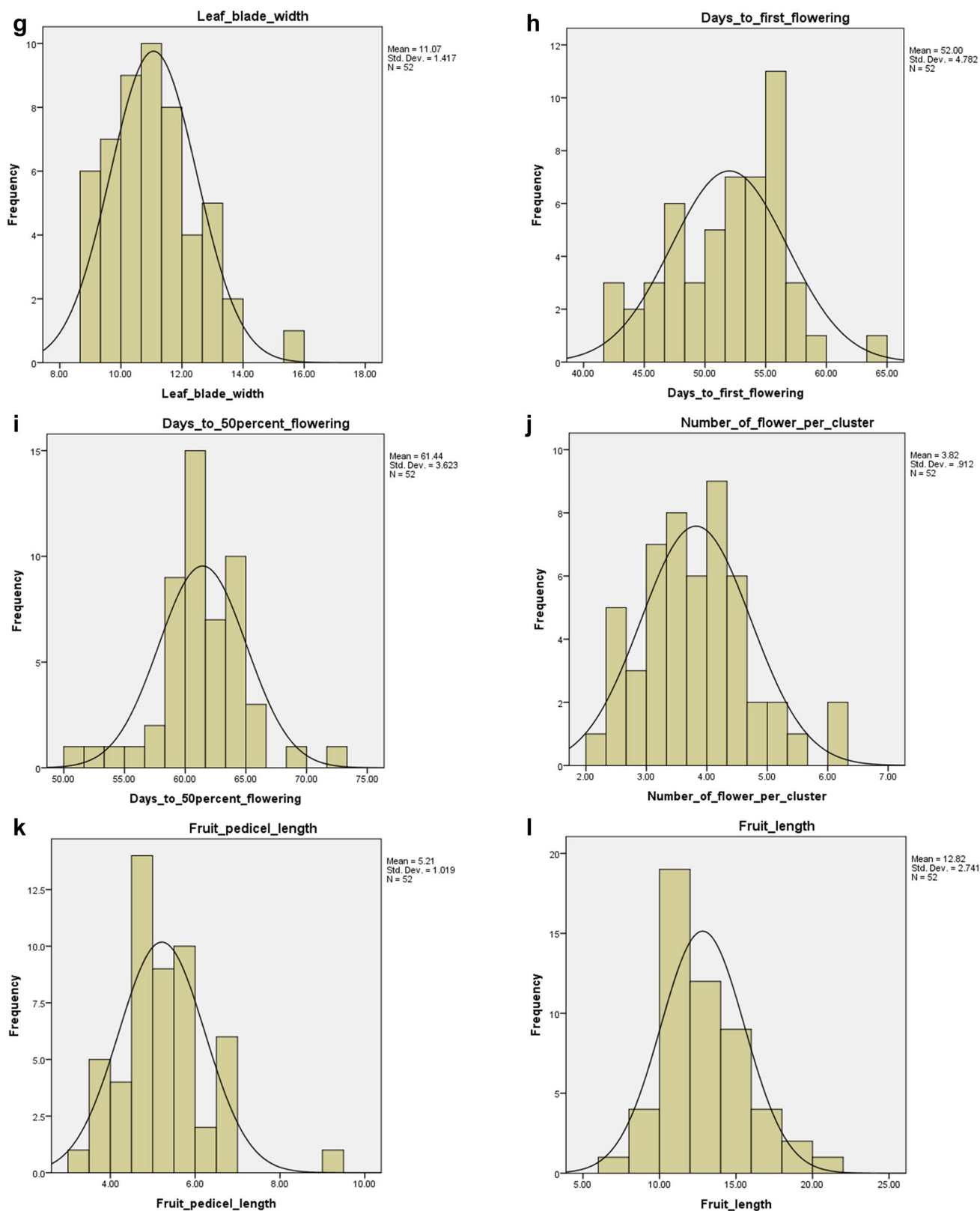


Fig. 1. (continued)

the preponderance of additive gene effects (Table 6). The trait flower cluster-1 was controlled by additive and non-additive gene action because their predictability ratios were between 0.60 and 0.80 (>0.60 and <0.80). In contrast, the remaining characters under study were controlled by non-additive gene effects, as their predictability ratios were <0.60 .

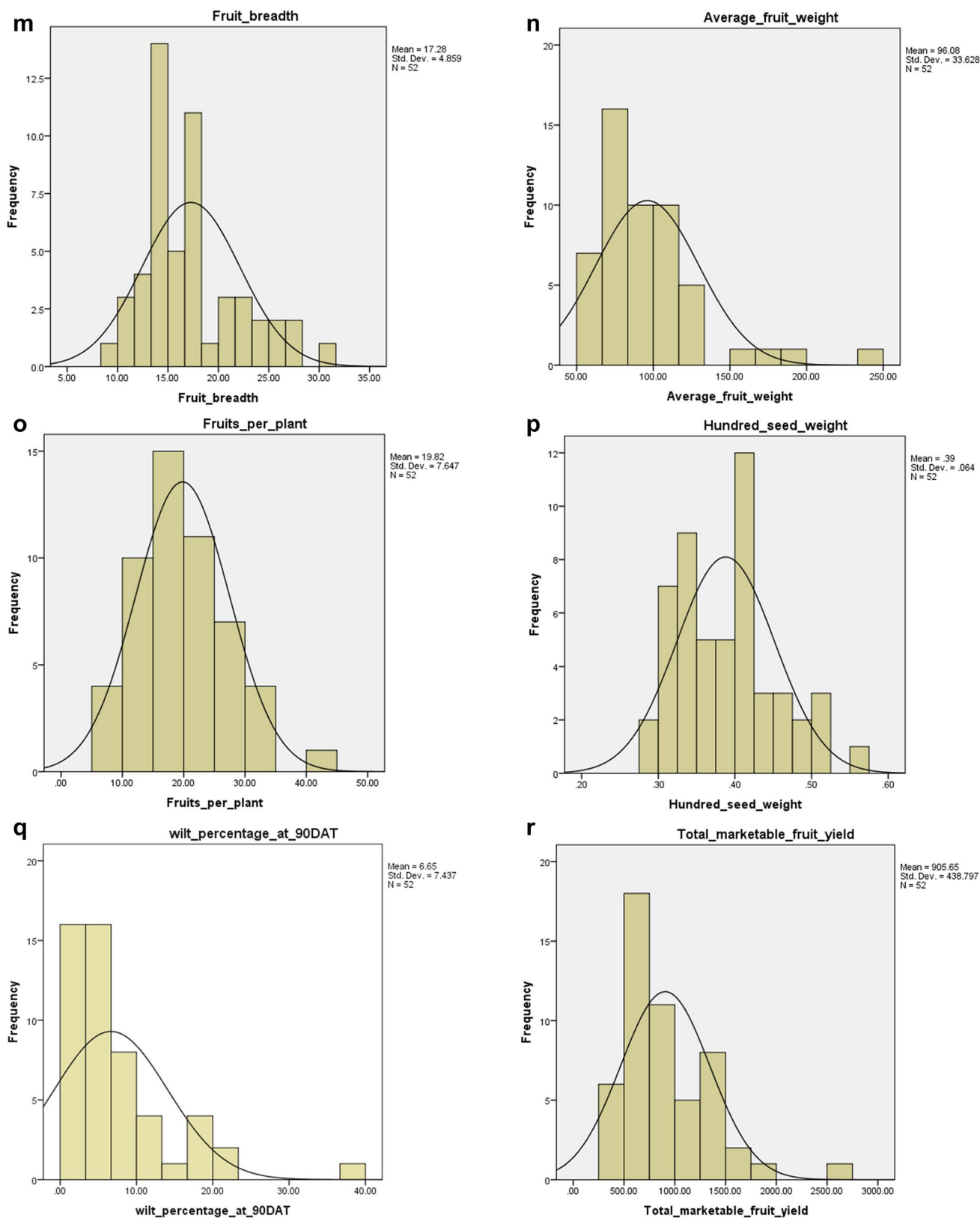


Fig. 1. (continued)

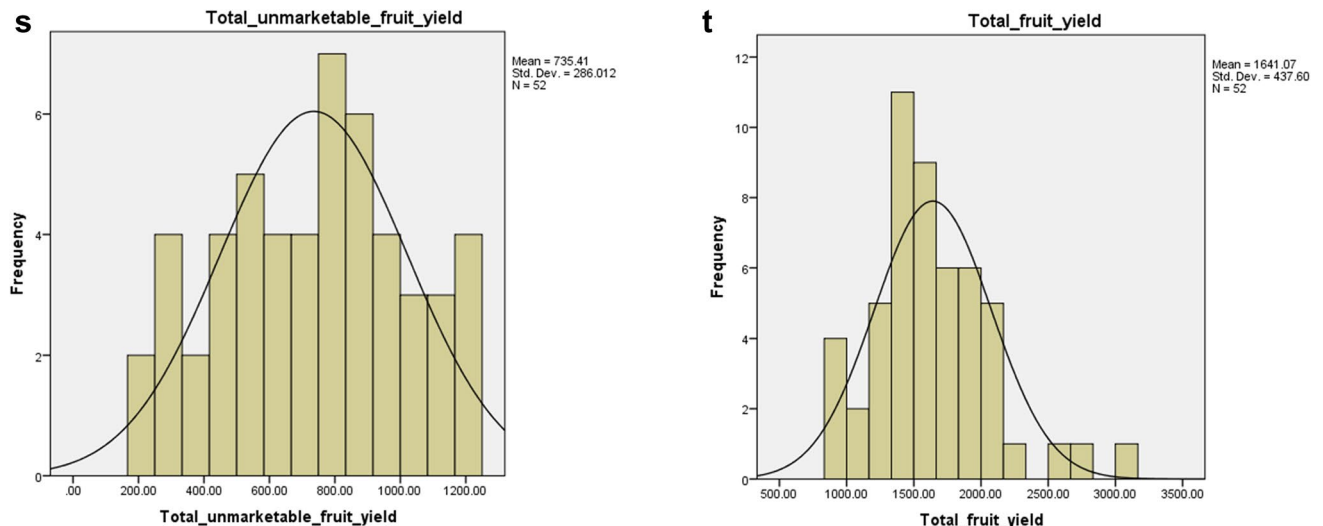


Fig. 1. (continued)

Estimation of heterosis of F_1 hybrids

The estimation of heterosis over mid-parent (relative heterosis) displayed significant effects in the desired direction on 14 hybrids for plant height at final harvest, 26 hybrids for plant spread, 28 hybrids for primary branches per plant, six hybrids for days of 1st flowering; 11 hybrids for days of 50% flowering; 12 hybrids for flowers per cluster; one hybrid for fruit length; 16 hybrids for fruit breadth; 24 for average fruit weight; 14 for fruits per plant; and 23 for total fruit yield per plant. Incidence of bacterial wilt at 90 DAT exhibited negative non-significant relative heterosis (Tables 7, 8 and 9, and 10). Similarly, in desired directions, the estimations of heterobeltiosis and standard heterosis values showed significant effects in 11 and 15 hybrids for plant height at final harvest; 15 and 20 hybrids for plant spread; 20 and 9 hybrids for primary branches per plant; 15 and 34 hybrids for days 1st flowering; 9 and 36 hybrids for days 50% flowering; 3 and 31 hybrids for flowers per cluster; 8 and 1 hybrid for fruit length; 13 and 4 hybrids for fruit breadth; 17 and 7 for average fruit weight; 6 and 30 for fruits per plant; and 16 and 7 for total fruit yield per plant, respectively. For three crosses of bacterial wilt incidence at 90 DAT (Table 11), non-significant negative heterobeltiosis was noted, and 13 crosses recorded significant negative standard heterosis.

The results showed the various magnitudes of heterobeltiosis ranged from -21.21 to 20.66% for plant height at final harvest; -19.49 to 58.07% for plant spread; -16.67 to 56.25% for primary branches per plant; -32.72 to 25.81% for days 1st flowering; -20.10 to 41.15% for days 50% flowering; -23.33 to 23.91% for flowers per cluster; -56.03 to 12.46% for fruits per plant; and -51.94 to 71.61% for total fruit yield per plant. Further, it is observed that the extent of standard heterosis varied from -19.43 to 36.53% for plant height at final harvest; -29.73 to 46.33% for plant spread; -33.94 to -3.97% for days 1st flowering; -34.41 to -6.85% for days 50% flowering; 20.59 to 88.24% for flowers per cluster; -19.03 to 64.93% for fruit length; 28.51 to 22.90% for fruit breadth; -53.38 to 34.84% for average fruit weight; -17.32 to 69.29% for fruits per plant; -59.96 to 26.97% for total fruit yield per plant and -76.20 to 82.84% for incidence of bacterial wilt at 90 DAT.

In summary, it is observed that the maximum % of average heterosis, heterobeltiosis, and standard heterosis for total fruit yield per plant was exhibited in BBSR-08-2 X BBSR-192-1 along with other economic characters (Fig. 3). However, the cross between BBSR-08-2 x BBSR-09-5, BBSR-08-2 x Jammusahi Local, and BBSR-08-2 x BBSR-192-1 exhibited significantly highest values of average heterosis, heterobeltiosis, and standard heterosis, respectively (Tables 7, 8, 9, 10 and 11). Based on *per performance*, the top hybrid for total fruit yield per plant was BBSR-08-2 x BBSR-192-1 and was statistically at par with Jammusahi Local x BBSR-192-1, BBSR-195-3 x BBSR-192-1 and BBSR-10-26 x BBSR-192-1 (Fig. 4; Table 12).

Dominance estimates of different characters

The estimation of dominance values recorded in 36 F_1 crosses are presented in Tables 7, 8 and 9, and 10. The potency ratio of plant height at final harvest depicted over dominance for 24 crosses, partial dominance for 11 crosses, and absence of dominance was observed in only a single cross. For plant spread, the potency ratios ranged from -2.3 to 30.3 , and they were more than ± 1 for 19 crosses, between ± 1 in 13 crosses, 1 in three crosses, and 0 (zero) in single cross, indicating over-dominance, partial dominance, complete dominance, and absence of dominance, respectively. Primary branches per plant showed over-dominance for 28 hybrids, partial dominance and complete dominance in three crosses, and absence of dominance in two crosses. The potency ratio of days to 1st flowering was $> \pm 1$ in 20 hybrids, indicating an over-dominance reaction. Partial dominance, complete dominance, and absence of dominance were shown by 11, three, and two hybrids, respectively. Regarding days to 50% flowering, over-dominance was exhibited in 20 crosses except for 15 hybrids where partial dominance was noticed; the absence of dominance was observed only in a single cross. The flower cluster reflected over-dominance in 21 crosses, partial dominance in 13 hybrids, and two hybrids did not show dominance (0.0). In

Sl No.	Characters	Range	General mean	PCV	GCV	Heritability (h ²)	GA	GA @ 5% mean
1	Plant height (cm) at peak fruiting stage	52.60-148.00	78.92	23.43	22.29	90.52	34.48	43.69
2	Plant height at final harvest (cm)	161.44-65.67	91.99	21.39	20.10	88.31	35.80	38.91
3	Plant spread (cm)	61.40-126.95	81.72	13.55	12.50	85.16	19.43	23.77
4	Primary branches plant ⁻¹	2.40-5.70	4.34	17.16	13.83	64.90	0.99	22.95
5	Leaf petiole length (cm)	4.65-10.83	6.62	20.22	19.08	89.07	2.45	37.11
6	Leaf blade length (cm)	12.00-20.70	15.94	10.81	9.74	81.13	2.88	18.08
7	Leaf blade width (cm)	8.80-15.90	11.06	13.63	11.91	76.39	2.37	21.45
8	Days to 1 st flowering	42.50-64.30	52.00	10.04	8.25	67.62	7.27	13.99
9	Days to 50% flowering	51.10-71.90	61.43	6.47	5.25	65.87	5.39	8.78
10	Flowers cluster ⁻¹	2.27-6.16	3.82	24.84	22.87	84.80	1.65	43.39
11	Fruit pedicel length (cm)	3.41-9.12	5.21	19.75	19.32	95.76	2.03	38.96
12	Fruit length (cm)	7.41-21.10	12.82	21.48	21.28	98.17	5.56	43.44
13	Fruit breadth (cm)	9.67-31.40	17.28	28.50	27.73	94.62	9.60	55.57
14	Average fruit weight (g)	50.85-233.97	96.08	35.49	34.49	94.43	66.35	69.05
15	Fruits plant ⁻¹	5.88-40.59	19.82	39.18	37.97	93.93	15.02	75.82
16	100 seed weight (g)	0.28-0.56	0.39	16.66	16.37	96.50	0.13	33.13
17	Wilt % at 90 DAT	0.00-22.76	9.59	59.22	58.57	97.80	11.43	119.32
18	Total fruit yield plant ⁻¹	865.80-3045.70	1641.06	27.47	25.83	88.41	821.12	50.03

Table 3. Genetic variability for fruit yield and its component in Brinjal genotypes.

Cluster	I (9)	II (6)	III (9)	IV (8)	V (6)	VI (7)	VII (5)	VIII (2)
I	465.45	1398.10	882.15	1029.29	757.29	652.61	1051.05	3482.80
II		173.00	1859.52	2631.88	1585.94	2213.14	2187.06	3705.54
III			577.78	1154.34	951.46	1004.88	1640.24	4355.99
IV				335.44	541.63	575.75	655.47	2635.02
V					348.76	513.10	802.55	2785.48
VI						261.71	998.98	3543.40
VII							421.86	1476.41
VIII								289.86

Table 4. Average intra and inter-cluster distance value of 48 landraces and four check *Solanum melongena* genotypes. *Figures in bold letters indicate maximum and minimum (intra/inter-cluster) values. **Figures in parenthesis indicate the number of genotypes retained in the clusters.

the case of fruit length, 30 crosses displayed over-dominance, four hybrids exhibited partial dominance, and one hybrid in each showed complete dominance and no dominance. Fruit breadth revealed over-dominance for 25 hybrids, partial dominance in 10 hybrids, and complete dominance and absence of dominance in a single cross each. Average fruit weight revealed over-dominance in 27 crosses, partial dominance in eight crosses, and complete dominance in the inheritance in only one hybrid. For the trait fruits per plant, over-dominance, partial dominance, and no dominance were observed for 22, 13, and 1 hybrid, respectively. The potency ratios for fruit yield per plant varied from -2.6 to 26.7 , and they were $> \pm 1$ for 23 crosses, demonstrating over-dominance and between ± 1 in 13 crosses, displaying a partial dominance inheritance pattern.

Identification of good general and specific combiner

The results indicate that only some parents have been considered good general combiners. However, the landraces Selection from BBSR-192-1 and BBSR-192-1 showed significant GCA effects in the desired direction for yield per plant, fruit per plant, fruit length, fruit breadth, and days to 50% flowering declared as a good general combiner (Table 13). Apart from these above landraces, BBSR-08-2 and BBSR-195-3 also exhibited significant GCA effects in the desired direction for plant height, primary branches per plant, fruit breadth, average fruit weight, bacterial wilt % at 90 DAT, and yield per plant. Therefore, four parents, Selection from BBSR-192-1, BBSR-192-1, BBSR-08-2, and BBSR-195-3, will be used as potential donors for fruit yield per plant and other yield-attributing traits. These four parent plants established successful resistance or tolerance against bacterial wilt. The results indicate that no cross was arbitrated as a good specific combiner for all the characters under study. The cross Selection from BBSR-145-1 x BBSR-09-5 adjusted highly significant SCA effects for total fruit yield per plant, the incidence of bacterial wilt at 90 DAT, average fruit weight, fruit length, days to 1st flowering and plant height at final harvesting the desired direction (Table 14). High and significant SCA effects for total fruit yield per plant, along with substantial SCA effects in the desired direction for incidence of bacterial wilt at 90 DAT, fruits per plant, and average fruit weight were shown by the cross Jammusahi Local x BBSR-192-1. The



Fig. 2. Nine (A: BBSR-08-2, B: BBSR-10-25, C: Jammusahi Local, D: BBSR-10-26, E: BBSR-195-3, F: BBSR-192-1, G: Selection from BBSR-192-1, H: Selection from BBSR-145-1, I: BBSR-09-5) genetically diverse parents are selected for Half Diallel Mating.

cross BBSR-10-26 x BBSR-192-1 revealed significantly higher SCA effects on total fruit yield per plant, incidence of bacterial wilt at 90 DAT, average fruit weight, fruit breadth, and flowers per cluster (Fig. 5).

Concerning fruit yield per plant, the per se performance of the cross BBSR-08-2 x BBSR-192-1 was found to be the highest and was exhibited *statistically at par* with Jammusahi Local x BBSR-192-1, BBSR-195-3 x BBSR-192-1, and BBSR-10-26 x BBSR-192-1, it will be recognized as a potential specific combiner for number fruits

Sl. No.	Characters	gca (8)	sca (36)	ERROR (44)
1	Plant height at peak fruiting stage	289.344**	90.370**	17.760
2	Plant height at final harvest stage	374.133**	99.180**	25.177
3	Plant spread	609.051**	107.278**	8.377
4	Primary branches plant ⁻¹	1.805**	0.552**	0.071
5	Days to 1st flowering	44.699**	23.147**	4.586
6	Days to 50% flowering	44.010**	38.362**	2.972
7	Flowers cluster ⁻¹	2.346**	0.413**	0.113
8	Fruit length	28.650**	2.657**	0.478
9	Fruit breadth	35.689**	8.126**	1.425
10	Average fruit weight	5757.781**	2152.518**	121.457
11	Fruits plant ⁻¹	35.461**	8.654**	0.409
12	Bacterial wilt % 90 DAT	108.633*	50.697	44.855
13	Total fruit yield plant ⁻¹	394034.490**	228308.700**	4501.838

Table 5. Analysis of variance (mean sum of squares) for combining ability in 46 (36 crosses 9 parents and one check) *Solanum melongena* L genotypes. *, ** indicate the significance at 5% and 1% level, respectively. Figure in parentheses indicate degrees of freedom for corresponding sources of variation.

Sl. No.	Characters	GCA variance (σ^2_g)	SCA variance (σ^2_s)	Potential ratio GCA/SCA (σ^2_g / σ^2_s) variance	Nature of gene action
1	Plant height at peak fruiting stage	24.69	72.61	0.34	Non-additive
2	Plant height at final harvest stage	31.72	74.00	0.43	Non-additive
3	Plant spread	54.61	98.90	0.55	Non-additive
4	Primary branches plant ⁻¹	0.16	0.48	0.33	Non-additive
5	Days to 1st flowering	3.65	18.56	0.20	Non-additive
6	Days to 50% flowering	3.73	35.39	0.11	Non-additive
7	Flowers cluster ⁻¹	0.20	0.30	0.68	Non-additive
8	Fruit length	2.56	2.18	1.18	Additive
9	Fruit breadth	3.11	6.70	0.46	Non-additive
10	Average fruit weight	512.39	2031.06	0.25	Non-additive
11	Fruits plant ⁻¹	3.19	8.25	0.39	Non-additive
12	Bacterial wilt % 90 DAT	5.80	5.84	0.99	Non-additive
13	Total fruit yield plant ⁻¹	35412.06	223806.86	0.16	Non-additive

Table 6. Nature of gene action of 46 (36 crosses, 9 parents and one check) *Solanum melongena* L genotypes. *, ** indicate the significance at 5% and 1% level, respectively.

per plant and bacterial wilt tolerance. A total of three combinations, i.e., H × L type, l × H type, and L × L type, were involved in 36 cross combinations (Table 15). H × L type (Jammusahi Local × BBSR-10-26 for days to 1st flowering; BBSR-10-26 × BBSR-192-1 for flowers per cluster; BBSR-195-3 × Selection from BBSR-145-1 for fruits breadth; BBSR-08-2 × Selection from BBSR-192-1 for average fruit weight and BBSR-08-2 × Jammusahi Local for fruit yield per plant), L × H type (BBSR-08-2 × BBSR-192-1 fruits per plant; BBSR-195-3 × BBSR-09-5, BBSR-195-3 × Selection from BBSR-192-1 and BBSR-195-3 × BBSR-192-1 for bacterial wilt % 90 DAT) and L × L type (BBSR-10-26 × Selection from BBSR-192-1 for plant height at final harvest; Jammusahi Local × BBSR-10-26 for plant spread; BBSR-192-1 × Selection from BBSR-145-1 for primary branches per plant; Selection from BBSR-192-1 × BBSR-09-5 for days to 50% flowering and BBSR-192-1 × BBSR-09-5 for fruit length (Table 15).

Sick plot field evaluation of the parents and hybrids against bacterial wilt reaction

The bacterial wilt incidence ranged from 0 to 4.17% among the parents and 0 to 29.17% in the case of hybrids (Table 16). Based on the categorization scheme, five parental lines (BBSR-08-2, BBSR-10-25, Jammusahi Local, BBSR-10-26, and Selection from BBSR-145-1) were denoted as highly bacterial wilt-resistant under field condition having the PDI values of zero. While other parents, namely, BBSR-195-3, BBSR-192-1, Selection from BBSR-192-1, and BBSR-09-5, were noted as resistant with a PDI value (4.17%). Among the hybrids, BBSR-08-2 × BBSR-10-25, BBSR-08-2 × BBSR-10-26, BBSR-08-2 × BBSR-195-3, BBSR-10-25 × BBSR-10-26, BBSR-10-25 × Selection from BBSR-192-1, Jammusahi Local × BBSR-10-26, Jammusahi Local × BBSR-195-3, Jammusahi Local × Selection from BBSR-192-1, Jammusahi Local × Selection from BBSR-145-1, BBSR-10-26 × Selection from BBSR-145-1, BBSR-195-3 × BBSR-192-1, BBSR-195-3 × Selection from BBSR-192-1 and BBSR-195-3 × BBSR-09-5 denotes as highly resistance crosses against bacterial wilt incidence.

Sl. No.	Crosses	Plant height at final harvest stage					Plant spread					Number of primary branches plant ⁻¹				
		RH (%)	HB (%)	SH (%)	DE		RH (%)	HB (%)	SH (%)	DE		RH (%)	HB (%)	SH (%)	DE	
1	BBSR-08-2 X BBSR-10-25	21.74**	16.60**	30.24**	4.9	0.81*	-1.20	31.98**	0.4	25.44**	9.28	23.26**	1.7			
2	BBSR-08-2 X Jammusahi Local	18.94**	17.07**	35.01**	11.9	39.34**	2.54	31.51**	1.1	34.86**	21.65**	37.21**	3.2			
3	BBSR-08-2 X BBSR-10-26	26.50**	12.16*	25.28**	2.1	4.27	-15.46**	8.43	0.2	8.39	-13.40*	-2.33	0.3			
4	BBSR-08-2 X BBSR-195-3	17.15*	13.22*	35.56**	4.9	12.95**	7.15*	37.43**	2.4	28.66**	13.40*	27.91**	2.1			
5	BBSR-08-2 X BBSR-192-1	18.15*	13.52*	26.81**	4.5	21.00**	0.35	28.70**	1.0	14.29	-5.16	6.98	0.7			
6	BBSR-08-2 X Selection from BBSR-192-1	33.58**	16.12**	29.71**	2.2	38.74**	14.10**	46.33**	1.8	42.28**	9.28	23.26**	1.4			
7	BBSR-08-2 X Selection from BBSR-145-1	10.59	1.87	13.79*	1.2	27.59**	1.62	30.33**	1.1	41.18**	11.34	25.58**	1.5			
8	BBSR-08-2 X BBSR-09-5	-0.75	-5.44	5.62	-0.2	24.61**	0.46	28.85**	0.8	35.17**	1.03	13.95*	1.0			
9	BBSR-10-25 X Jammusahi Local	-9.48	-14.60**	-1.52	-1.6	10.82	-19.49**	7.54	0.3	25.33**	20.51**	9.302	6.3			
10	BBSR-10-25 X BBSR-10-26	-14.57	-21.21**	-19.43**	-1.7	18.75**	-5.18	26.66**	0.7	44.62**	30.56**	9.302	4.1			
11	BBSR-10-25 X BBSR-195-3	23.03**	14.05**	36.57**	2.9	-5.06	-11.63**	18.05**	-0.7	26.03**	24.32**	6.98	19.0			
12	BBSR-10-25 X BBSR-192-1	16.59*	16.20**	19.64**	49.0	4.48	-14.73**	13.91**	0.2	47.060**	38.89**	16.28*	8.0			
13	BBSR-10-25 X Selection from BBSR-192-1	-2.98	-12.35	-10.36	-0.3	9.63	-11.25**	18.55**	0.4	45.16**	25.00**	4.65	2.8			
14	BBSR-10-25 X Selection from BBSR-145-1	1.07	-2.960	-0.77	0.3	5.01	-17.61**	10.06*	0.2	6.25	-5.56	-20.93**	0.5			
15	BBSR-10-25 X BBSR-09-5	-2.21	-2.740	-0.54	-4.0	22.73**	-2.55	30.18**	0.9	56.67**	30.56**	9.30	2.8			
16	Jammusahi Local X BBSR-10-26	15.25*	1.872	16.22*	1.1	79.75**	58.07**	26.04**	5.8	38.24**	20.51**	9.30	2.6			
17	Jammusahi Local X BBSR-195-3	2.41	0.52	20.36**	1.3	23.51**	-5.78	8.43	0.8	34.21**	30.77**	18.61**	13.0			
18	Jammusahi Local X BBSR-192-1	-13.63	-18.26**	-5.73	-2.4	17.35*	0.70	-14.94**	1.0	9.86	0.00	-9.30	1.0			
19	Jammusahi Local X Selection from BBSR-192-1	18.24*	1.42	16.96**	1.1	48.76**	28.80**	6.51	3.1	35.39**	12.82	2.33	1.8			
20	Jammusahi Local X Selection from BBSR-145-1	-0.13	-9.33	4.57	0.0	62.95**	46.30**	11.24	5.5	28.36**	10.26	0.00	1.7			
21	Jammusahi Local X BBSR-09-5	0.86	-5.35	9.16	0.1	1.06	-10.55	-29.73**	0.1	3.18	-16.67*	-24.42**	1.3			
22	BBSR-10-26 X BBSR-195-3	2.93	-11.42*	6.07	0.2	18.91**	0.64	15.83**	1.0	42.42**	27.03**	9.30	3.5			
23	BBSR-10-26 X BBSR-192-1	13.19	4.07	7.14	1.5	32.61**	28.90**	8.88*	11.3	54.10**	46.88**	9.30	11.0			
24	BBSR-10-26 X Selection from BBSR-192-1	23.22*	20.66**	4.05	10.2	30.60**	28.27**	6.07	16.8	63.64**	55.17**	4.65	11.7			
25	BBSR-10-26 X Selection from BBSR-145-1	16.44	11.65	5.06	3.8	25.55**	22.64**	-2.22	10.8	54.39**	51.72**	2.33	31.0			
26	BBSR-10-26 X BBSR-09-5	-6.69	-13.51*	-12.52*	-0.8	22.62**	21.71**	-2.96	30.3	66.04**	51.72**	2.33	7.0			
27	BBSR-195-3 X BBSR-192-1	-6.99	-13.51*	3.56	-0.9	8.08	-6.30	7.84	0.5	21.74*	13.51	-2.33	3.0			
28	BBSR-195-3 X Selection from BBSR-192-1	4.58	-11.67*	5.76	0.2	33.73**	14.91**	32.25**	2.1	52.38**	29.73**	11.63	3.0			
29	BBSR-195-3 X Selection from BBSR-145-1	-9.33	-19.04**	-3.05	-0.8	42.26**	18.12**	35.95**	2.1	29.23**	13.51	-2.33	2.1			
30	BBSR-195-3 X BBSR-09-5	20.22**	10.88*	32.77**	2.4	24.22**	4.50	20.27**	1.3	57.38**	29.73**	11.63	2.7			
31	BBSR-192-1 X Selection from BBSR-192-1	-1.69	-11.45	-8.83	-0.2	0.00	-1.05	-16.42**	0.0	0.00	-9.38	-32.56**	0.0			
32	BBSR-192-1 X Selection from BBSR-145-1	15.53*	10.56	13.83*	3.5	27.74**	21.37**	2.52	5.3	66.67**	56.25**	16.28*	10.0			
33	BBSR-192-1 X BBSR-09-5	-18.68*	-19.40**	-17.01**	-21.1	-8.17	-11.38*	-25.15**	-2.3	0.00	-12.50	-34.88**	0.0			
34	Selection from BBSR-192-1 X Selection from BBSR-145-1	7.62	0.99	-4.97	1.2	57.32**	50.98**	24.85**	13.7	33.33*	28.57**	-16.28*	9.0			
35	Selection from BBSR-192-1 X BBSR-09-5	7.49	-2.41	-1.29	0.7	29.91**	26.66**	4.73	11.6	-4.00	-7.69	-44.19**	-1.0			
36	Selection from BBSR-145-1 X BBSR-09-5	22.83**	18.55**	19.91**	6.3	27.27**	25.24**	-1.63	16.8	61.54**	50.00**	-2.33	8.0			

Table 7. Heterosis percentage (RH-relative heterosis, HB- heterobeltiosis and SH- standard heterosis) and dominance estimate (DE) of F₁ hybrids for plant height at final harvest, plant spread and primary branches per Plant of *Solanum melongena* L. *, ** indicate the significance at 5% and 1% level, respectively.

Discussion

The landraces had shown very weak leaf blade lobing in the present study. This variation in morphological characters is mainly due to the genetic structure of the plant^{27–30}. The flower and the intensity of the calyx color of the landraces showed smoothness by various researchers^{29,31}. Fruit descriptors are crucial in selecting promising genotypes for the breeding program^{32,33}. Several studies revealed that the fruit characteristics, such as shape and size, are more stable and least influenced by various stresses^{28,34}. The variations in 100 seed weight were influenced by nutrition application and prevailing environmental conditions during seed development³⁵. The present study analyzed the 20 characters to evaluate landraces and released parent types for selection for breeding programs. Based on the observation, the landraces i.e. BBSR-08-2, BBSR-192-1 and Selection from BBSR-192-1 were identified as superior landraces.

Based on the Shannon-Wiener index, the value of the tested landraces ranged from 0 to 4.6. For some landraces, the value close to zero (0) suggests uniformity, while the value near 4.6 indicates an even distribution of the brinjal landraces. A lower H' indicates uneven frequency distribution and limited diversity in traits, whereas a higher H' signifies more significant variability or diversity. Values below the overall mean suggest imbalanced frequency distribution and reduced trait diversity. Mondal et al.³⁶ used the Shannon-Wiener diversity index and noted a significant divergence in qualitative traits among brinjal genotypes based the GCV, PCV, h^2_{BS} , and GA are essential biometric tools to identify the genetic divergence among the genotypes³⁷. The more excellent value of the genetic variability in the existing population, the higher the opportunities for selection of the given trait to improve genotypes³⁸. A higher value of PCV and GCV suggested the scope of selection, as more variation results in an effective selection plan³⁹. For all the traits, the GCV values were lower than those of PCV values, indicating that the environment plays a significant role in the appearance of the characteristics. These findings align with previous studies in brinjal^{40–42}. The present study showed that high PCV and GCV were noted for plant height at peak fruiting and final harvest, flower per cluster, fruit length, fruit breadth, average fruit weight, fruits per plant, bacterial wilt percentage at 90 DAT, and total fruit yield per plant. Similar observations, exceptionally high PCV and GCV in plant height^{40,42,43}, flowers per cluster⁴⁴, fruit length^{41,45}, fruit breadth⁴⁶, average fruit weight^{47,48}, fruits per plant^{42,48}, total fruit yield per plant^{46,48} also been reported. Similarly, medium PCV and GCV for plant spread^{49,50}, primary branches per plant⁴¹, fruit pedicel length^{40,51} and 100 seed weight⁵² have also been reported. The low PCV and GCV are only in one character, i.e., days to 50% flowering. Comparable findings were also documented^{41,53}. A higher magnitude of broad sense h^2 was exhibited by all the characters under study, which reveals the highly heritable nature of these traits, suggesting that based on the phenotypic performance, the selection of these traits would be highly effective^{49,54}.

A high h^2 coupled with high GA as a % of the mean was noticed for most of the characters in the present study, suggesting that they develop superior genotypes. Whereas higher h^2 with moderate GA as a % of the mean was observed for days to initiation of flowering, leaf blade length, and days to 50% flowering, demonstrating the environmental effect on the expression of a particular character⁵⁵. These characters could be exploited through the manifestation of dominance and epistatic components of heterosis. This finding is consistent with Pujer et al.⁴⁹ and Dutta et al.⁵⁶. Therefore, effective selection relies on higher values of PCV, GCV, h^2_{BS} , and GA as % of the mean, suggesting that additive genes have a more stable influence than the environmental factors. This suggests that selecting these traits in the next generation could significantly improve the population mean.

The multivariate analysis showed that the highest inter-cluster distance was recorded between clusters VIII and III. The clusters VIII and I have not been included in the subsequent hybridization program because the objective of the investigation was the improvement of local landraces for the development of round fruited brinjal in F_1 hybrid(s) for higher fruit yield and tolerance to bacterial wilt. Since the higher inter-cluster distance between cluster II with other clusters such as IV, VI, III, V, and VII, hence it may be concluded that desirable recombinants can be produced by crossing genotypes of cluster II with other clusters (IV, VI, III, V, and VII) with maximum exploitation of heterosis for future brinjal improvement program. Because of complementary gene interaction in the divergent parents, their hybrid derivatives were usually found to be promising^{57–62}. Response of non-additive gene action for the control of plant height at final harvest, plant spread, primary branches per plant, days to 1st flowering, days to 50% flowering, fruit breadth, average fruit weight, fruits per plant, and total fruit yield per plant was expressed by the predictability ratio. Hence, there will be slow improvement in genetic level through selection. The present study showed that the nature of gene action was non-additive for most of the yield components, which specifies that these traits can be improved through heterosis breeding in brinjal.

Both additive and non-additive types of gene action were observed for the trait flower cluster. So, the improvement of this character can be made either by mass selection with concurrent random mating or by using diallel selective mating or restricted recurrent selection by intermating the most desirable segregants followed by selection⁶³. The values of heterosis over mid-parent, a better parent, and standard check revealed that for most of the characters, a greater number of crosses showed significant positive relative heterosis as compared to heterobeltiosis and standard heterosis except for days to 50% flowering in heterobeltiosis and plant height at final harvest, flower cluster, fruit length and fruit per plant in standard heterosis. Our results are in line with the findings reported by Shafeeq et al.⁶⁴ in fruit yield per plant, branches per plant⁶⁵, fruit girth, days to 50% flowering⁶⁶, fruit length⁶⁷, fruit length and fruit weight⁶⁸, plant height at final harvest, plant spread and days to 1st flowering^{9,69,70}. The cross, BBSR-08-2 X BBSR-192-1 which, exhibited the maximum standard heterosis for fruit yield per plant and also showed heterobeltiosis and relative heterosis for fruit yield per plant, fruits per plant and average fruit weight. Therefore, heterosis for fruit yield per plant could be realized through the number of fruits per plant and average fruit weight. The result also specified that higher heterosis was noticed in those crosses when BBSR-08-2 and BBSR-192-1 were involved as parents. So, to increase the fruit yield per plant, these two parents can be used in the future brinjal improvement program using standard heterosis^{7,9,45,71–73}. The potency ratio also reflects various levels of gene effects, i.e., no dominance, partial dominance, complete dominance, and over-dominance, which are involved in the inheritance of the studied characters. In particular,

Sl. No.	Crosses	Days to 1st flowering				Days to 50% flowering				Flower cluster ⁻¹			
		RH (%)	HB (%)	SH (%)	DE	RH (%)	HB (%)	SH (%)	DE	RH (%)	HB (%)	SH (%)	DE
1	BBSR-08-2 X BBSR-10-25	15.80**	2.89	-11.42**	1.3	2.89	12.84**	-12.73**	0.3	5.66	1.82	64.71**	1.5
2	BBSR-08-2 X Jamnusaahi Local	-4.40	-10.29**	-11.92**	-0.7	-20.00**	-7.05*	-28.11**	-1.4	42.47**	1.96	52.94**	1.1
3	BBSR-08-2 X BBSR-10-26	9.39	1.92	-12.25**	1.3	28.95**	38.75**	-6.85**	4.1	3.09	-1.96	47.06**	0.6
4	BBSR-08-2 X BBSR-195-3	-13.15*	-18.08**	-29.47**	-2.2	15.07**	25.37**	-17.76**	1.8	8.74	7.69	64.71**	9.0
5	BBSR-08-2 X BBSR-192-1	-3.40	-12.50**	-24.67**	-0.3	1.57	2.35	-20.84**	-0.4	13.19	0.98	51.47**	1.1
6	BBSR-08-2 X Selection from BBSR-192-1	1.91	-7.500	-20.36**	0.2	13.57**	18.81**	-8.11**	3.1	18.18	1.96	52.94**	1.1
7	BBSR-08-2 X Selection from BBSR-145-1	10.36*	6.54	-8.28*	2.9	8.89*	15.19**	-10.91**	1.6	9.91	1.67	79.41**	1.2
8	BBSR-08-2 X BBSR-09-5	-9.00	-10.58*	-23.01**	-5.1	-12.98**	-10.31**	-30.63**	-4.4	4.17	-1.96	47.06**	0.7
9	BBSR-10-25 X Jamnusaahi Local	-12.34*	-15.96**	-27.65**	-0.7	-18.53**	-14.09**	-20.70**	-3.6	29.87**	-9.09	47.06**	0.7
10	BBSR-10-25 X BBSR-10-26	8.54	3.12	-23.34**	1.6	-2.81	15.42*	-22.52**	-0.2	26.73**	16.36**	88.24**	3.0
11	BBSR-10-25 X BBSR-195-3	17.23**	9.98*	-16.06**	2.6	4.16	15.35**	-24.34**	-0.2	14.02	10.91	79.41**	5.0
12	BBSR-10-25 X BBSR-192-1	0.00	-2.13	-31.62**	0.0	-22.34**	-18.24**	-31.75**	-4.5	-3.16	-16.36**	35.29**	-0.2
13	BBSR-10-25 X Selection from BBSR-192-1	16.91**	14.15**	-19.87**	7.0	-8.54*	4.31	-19.16**	-1.9	0.00	-16.36**	35.29**	0.0
14	BBSR-10-25 X Selection from BBSR-145-1	1.69	-6.72	-25.25**	0.2	2.58	6.16*	-8.39**	0.8	6.96	2.50	80.88**	1.6
15	BBSR-10-25 X BBSR-09-5	-10.82	-19.52**	-33.11**	-1.0	-2.65	3.41	-15.11**	-0.5	20.00*	9.09	76.47**	2.0
16	Jamnusaahi Local X BBSR-10-26	-23.42**	-32.72**	-33.94**	-1.7	-0.33	25.83**	-15.52**	0.0	38.24**	2.17	38.24**	1.1
17	Jamnusaahi Local X BBSR-195-3	-9.49	-19.56**	-21.03**	-0.8	-12.57**	11.94**	-26.57**	-0.6	8.11	-23.08**	17.65	0.2
18	Jamnusaahi Local X BBSR-192-1	-10.15	-23.10**	-24.50**	-0.6	-6.10	4.52	-12.73**	-0.6	32.26*	2.50	20.59*	1.1
19	Jamnusaahi Local X Selection from BBSR-192-1	2.46	-12.14**	-13.74**	0.1	-16.47**	-7.62**	-21.96**	-1.7	52.54**	21.62*	32.35**	2.1
20	Jamnusaahi Local X Selection from BBSR-145-1	-17.55**	-25.13**	-26.49**	-1.7	-3.04	6.00*	-8.53**	-0.4	26.83**	-13.33*	52.94**	0.6
21	Jamnusaahi Local X BBSR-09-5	1.74	-6.07	-7.78*	0.2	0.83	13.29**	-6.99**	0.1	2.99	-23.33**	1.47	0.1
22	BBSR-10-26 X BBSR-195-3	0.00	-1.30	-24.67**	0.0	35.30**	36.89**	-10.21**	30.4	-4.08	-9.62	38.24**	-0.7
23	BBSR-10-26 X BBSR-192-1	-3.33	-6.24	-30.30**	-1.1	4.92	17.71**	-20.98**	0.5	32.56**	23.91**	67.65**	4.7
24	BBSR-10-26 X Selection from BBSR-192-1	15.24*	12.03*	-16.72**	5.3	6.27	20.00**	-19.44**	0.5	25.30*	13.04	52.94**	2.3
25	BBSR-10-26 X Selection from BBSR-145-1	-9.33	-12.60**	-29.97**	-2.5	-7.38	5.83	-28.95**	-0.6	0.00	-11.67*	55.88**	0.0
26	BBSR-10-26 X BBSR-09-5	-12.72*	-17.33**	-31.29**	-2.3	-6.28	4.17	-30.07**	-0.6	-12.09	-13.04	17.65	-11.0
27	BBSR-195-3 X BBSR-192-1	31.37**	25.81**	-3.97	7.1	16.70**	32.62**	-13.01**	1.4	-8.70	-19.23**	23.53*	-0.7
28	BBSR-195-3 X Selection from BBSR-192-1	4.18	0.00	-23.68**	1.0	-4.94	8.74*	-28.67**	-0.4	-1.12	-15.39*	29.41**	-0.1
29	BBSR-195-3 X Selection from BBSR-145-1	19.37**	16.53**	-6.63	8.0	21.92**	41.15**	-7.41**	1.6	-17.86*	-23.33**	35.29**	-2.5
30	BBSR-195-3 X BBSR-09-5	7.17	2.79	-14.57**	1.7	12.69**	26.87**	-16.78**	1.1	10.59	4.44	38.24**	-0.4
31	BBSR-192-1 X Selection from BBSR-192-1	1.89	1.65	-28.64**	8.0	-8.41*	-7.87**	-23.08**	-14.4	-2.60	-6.25	10.29	-0.7
32	BBSR-192-1 X Selection from BBSR-145-1	13.91*	6.61	-14.57**	2.0	-6.59	-5.03	-20.70**	-4.0	22.00**	1.67	79.41**	1.1
33	BBSR-192-1 X BBSR-09-5	1.73	-6.38	-22.19**	0.2	-16.89**	-16.18**	-31.19**	-20.0	-10.59	-15.56*	11.77	-1.8
34	Selection from BBSR-192-1 X Selection from BBSR-145-1	-6.61	-12.40**	-29.80**	-1.0	-12.37**	-11.42**	-25.18**	-11.6	25.77**	1.67	79.41**	1.1
35	Selection from BBSR-192-1 X BBSR-09-5	1.30	-6.57	-22.35**	0.2	-21.24**	-20.10**	-34.41**	-14.8	14.63	4.44	38.24**	1.5
36	Selection from BBSR-145-1 X BBSR-09-5	-17.65**	-19.12**	-32.78**	-9.7	-4.65	-2.22	-19.72**	-1.9	12.38	-1.67	73.53**	0.9

Table 8. Heterosis percentage (RH-relative heterosis, HB- heterobeltiosis and SH- standard heterosis) and dominance estimate (DE) of F₁ hybrids for days to 1st flowering, days to 50% flowering and flower per cluster of *Solanum melongena* L. *, ** indicate the significance at 5% and 1% level, respectively.

Sl. No.	Crosses	Fruit length			Fruit breadth			Average fruit weight					
		RH (%)	HB (%)	SH (%)	DE	RH (%)	HB (%)	SH (%)	DE	RH (%)	HB (%)	SH (%)	DE
1	BBSR-08-2 X BBSR-10-25	27.00**	21.85**	17.76**	6.4	23.53**	22.31**	2.94	23.4	47.99**	43.12**	-9.34	14.1
2	BBSR-08-2 X Jamnusaahi Local	10.76*	-13.24**	35.97**	0.4	5.20	-6.25	0.86	0.4	22.14**	-11.31**	16.07**	0.6
3	BBSR-08-2 X BBSR-10-26	10.97	5.45	3.96	2.1	12.67	5.79	-10.97*	1.9	56.96**	46.48**	-13.31*	8.0
4	BBSR-08-2 X BBSR-195-3	15.99*	2.52	18.58**	1.2	22.71**	20.36**	1.30	11.7	29.76**	17.05*	-13.85**	2.7
5	BBSR-08-2 X BBSR-192-1	12.02	9.46	1.87	5.1	18.10**	9.33*	8.07	2.3	74.53**	72.19**	4.71	54.8
6	BBSR-08-2 X Selection from BBSR-192-1	18.08*	14.65*	8.06	6.1	17.92**	17.00**	0.04	22.7	79.87**	79.46**	6.20	347.6
7	BBSR-08-2 X Selection from BBSR-145-1	19.26**	12.04*	13.21*	3.0	23.69**	21.47**	2.23	12.1	53.01**	38.27**	1.36	5.0
8	BBSR-08-2 X BBSR-09-5	17.26*	7.25	14.85**	1.8	18.10**	14.80**	2.34	6.3	68.63**	66.14**	1.31	45.9
9	BBSR-10-25 X Jamnusaahi Local	14.88**	-7.14*	45.52**	0.6	8.35	-4.29	2.97	0.6	-21.35**	-41.64**	-23.62**	-0.6
10	BBSR-10-25 X BBSR-10-26	20.28**	19.08**	17.39**	20.4	-2.63	-7.71	-23.87**	-0.5	-9.49	-18.11*	-48.13**	-0.9
11	BBSR-10-25 X BBSR-195-3	14.59*	5.16	21.64**	1.6	20.55**	19.42**	-1.49	22.0	26.13**	17.34*	-13.64**	3.5
12	BBSR-10-25 X BBSR-192-1	9.44	7.41	3.81	5.0	1.60	-6.81	-7.88	0.2	36.67**	33.94**	-15.15**	18.0
13	BBSR-10-25 X Selection from BBSR-192-1	6.43	5.10	1.57	5.1	8.03	6.13	-9.26*	4.5	10.97	7.08	-32.17**	3.0
14	BBSR-10-25 X Selection from BBSR-145-1	17.63**	15.07**	16.27**	7.9	2.24	1.40	-16.36**	2.7	-7.82	-14.08*	-37.02**	-1.1
15	BBSR-10-25 X BBSR-09-5	9.89	4.53	11.94*	1.9	-16.70*	-19.81**	-28.51**	-4.3	41.00**	38.37**	-12.35*	21.5
16	Jamnusaahi Local X BBSR-10-26	6.36	-13.38**	35.75**	0.3	-6.20	-20.89**	-14.89**	-0.3	-6.39	-34.86**	-14.74**	-0.1
17	Jamnusaahi Local X BBSR-195-3	0.66	-12.52**	37.09**	0.0	28.84**	12.89**	21.45**	2.0	28.55**	0.42	31.43**	1.0
18	Jamnusaahi Local X BBSR-192-1	5.11	-16.24**	31.27**	0.2	5.53	1.24	8.92	1.3	40.68**	3.02	34.84**	1.1
19	Jamnusaahi Local X Selection from BBSR-192-1	31.45**	5.24	64.93**	1.0	27.30**	14.24**	22.90**	2.4	33.43**	-3.25	26.62**	0.9
20	Jamnusaahi Local X Selection from BBSR-145-1	26.17**	3.76	62.61**	1.2	21.97**	6.98	15.09**	1.6	-44.65**	-56.82**	-43.49**	-1.6
21	Jamnusaahi Local X BBSR-09-5	21.64**	2.38	60.45**	1.2	2.61	-6.19	0.93	0.3	5.61	-22.59**	1.31	0.2
22	BBSR-10-26 X BBSR-195-3	14.61*	6.13	22.76**	1.8	-1.85	-6.15	-24.02**	-0.4	28.96**	9.40	-19.48**	1.6
23	BBSR-10-26 X BBSR-192-1	36.24**	32.40**	30.52**	12.6	33.86**	16.96**	15.61**	2.3	79.29**	65.23**	0.48	9.3
24	BBSR-10-26 X Selection from BBSR-192-1	6.08	3.71	2.24	2.7	14.29*	6.52	-8.92	2.0	42.03**	32.83**	-21.75**	6.1
25	BBSR-10-26 X Selection from BBSR-145-1	5.89	4.58	5.67	4.8	-3.05	-7.40	-24.85**	-0.7	4.80	-10.95	-34.72**	0.3
26	BBSR-10-26 X BBSR-09-5	6.62	2.37	9.63	1.6	-11.34	-18.93**	-27.73**	-1.2	23.72*	13.88	-30.56**	2.7
27	BBSR-195-3 X BBSR-192-1	17.63**	6.13	22.76**	1.6	14.30*	3.95	2.75	1.4	60.35**	46.42**	7.77	6.3
28	BBSR-195-3 X Selection from BBSR-192-1	24.09**	12.58**	30.22**	2.3	22.61**	19.35**	2.05	8.3	24.80*	12.34	-17.31**	2.2
29	BBSR-195-3 X Selection from BBSR-145-1	11.02	4.00	20.30**	1.6	24.08**	23.91**	0.56	209.8	60.87**	60.54**	18.17**	299.2
30	BBSR-195-3 X BBSR-09-5	8.74	4.71	21.12**	2.3	21.74**	16.14**	3.53	4.5	66.81**	53.55**	13.01*	7.2
31	BBSR-192-1 X Selection from BBSR-192-1	-3.97	-4.59	-10.08	-6.3	0.02	-6.73	-7.81	0.0	-2.82	-4.34	-41.83**	-1.8
32	BBSR-192-1 X Selection from BBSR-145-1	11.34	6.94	8.06	2.8	-9.64	-17.73**	-18.68**	-1.0	-7.74	-15.60*	-38.13**	-0.8
33	BBSR-192-1 X BBSR-09-5	-19.09**	-24.39**	-19.03**	-2.7	-19.72**	-23.66**	-24.54**	-3.8	-23.44*	-23.54**	-53.38**	-172.4
34	Selection from BBSR-192-1 X Selection from BBSR-145-1	-7.51	-10.63*	-9.70	-2.2	1.28	-1.30	-15.61**	0.5	18.47	6.84	-21.68**	1.7
35	Selection from BBSR-192-1 X BBSR-09-5	14.03*	7.18	14.78**	2.2	-5.07	-7.01	-17.10**	-2.4	28.81**	26.62**	-22.79**	16.7
36	Selection from BBSR-145-1 X BBSR-09-5	-9.93	-12.47*	-6.27	-3.4	-6.89	-11.07*	-20.73**	-1.5	87.81**	72.02**	26.10**	9.6

Table 9. Heterosis percentage (RH-relative heterosis, HB- heterobeltiosis and SH- standard heterosis) and dominance estimate (DE) of F₁ hybrids for fruit length, fruit breadth and average fruit weight of *Solanum melongena* L. *, ** indicate the significance at 5% and 1% level, respectively.

Sl. No.	Crosses	Fruit per plant				Total fruit yield per plant			
		RH (%)	HB (%)	SH (%)	DE	RH (%)	HB (%)	SH (%)	DE
1	BBSR-08-2 X BBSR-10-25	21.02**	2.70	49.61**	1.2	74.87**	63.51**	-2.14	10.8
2	BBSR-08-2 X Jammusahi Local	51.83**	12.40*	14.17**	1.5	84.60**	71.61**	2.71	11.2
3	BBSR-08-2 X BBSR-10-26	-20.45**	-37.47**	11.02*	-0.8	38.67**	27.10**	-8.70**	4.2
4	BBSR-08-2 X BBSR-195-3	-32.82**	-43.90**	-14.96**	-1.7	-7.75	-22.70**	-31.54**	-0.4
5	BBSR-08-2 X BBSR-192-1	28.99**	12.46**	53.54**	2.0	77.37**	52.40**	26.97**	4.7
6	BBSR-08-2 X Selection from BBSR-192-1	-8.03*	-32.98**	48.82**	-0.2	36.52**	5.00	16.77**	1.2
7	BBSR-08-2 X Selection from BBSR-145-1	7.81	3.57	14.17**	1.9	69.74**	63.54**	5.60	18.4
8	BBSR-08-2 X BBSR-09-5	17.50*	9.30	11.02*	2.3	89.18**	67.86**	0.47	7.0
9	BBSR-10-25 X Jammusahi Local	13.36*	-24.32**	10.24*	0.3	16.53*	15.82*	-39.70**	26.7
10	BBSR-10-25 X BBSR-10-26	-27.41**	-33.93**	17.32**	-2.8	-15.05*	-26.73**	-47.37**	-0.9
11	BBSR-10-25 X BBSR-195-3	6.49	4.42	58.27**	3.3	27.34**	1.10	-10.46**	1.1
12	BBSR-10-25 X BBSR-192-1	-4.00	-7.03*	35.43**	-1.2	59.69**	29.75**	8.10*	2.6
13	BBSR-10-25 X Selection from BBSR-192-1	-19.06**	-32.98**	48.82**	-0.9	17.87**	-13.47**	-3.77	0.5
14	BBSR-10-25 X Selection from BBSR-145-1	-20.37**	-30.05**	1.89	-1.5	-9.65	-18.40**	-47.30**	-0.9
15	BBSR-10-25 X BBSR-09-5	28.38**	2.70	49.61**	1.1	38.43**	30.84**	-31.87**	6.6
16	Jammusahi Local X BBSR-10-26	-4.35	-39.02**	8.27	-0.1	22.71**	5.28	-24.37**	1.4
17	Jammusahi Local X BBSR-195-3	22.59**	-18.96**	22.84**	0.4	44.71**	14.37**	1.29	1.7
18	Jammusahi Local X BBSR-192-1	59.76**	8.42*	48.03**	1.3	78.20**	44.10**	20.06**	3.3
19	Jammusahi Local X Selection from BBSR-192-1	-27.91**	-56.03**	-2.36	-0.4	25.81**	-8.01**	2.30	0.7
20	Jammusahi Local X Selection from BBSR-145-1	51.49**	9.29*	20.47**	1.3	-12.29	-21.22**	-49.13**	-1.1
21	Jammusahi Local X BBSR-09-5	21.39*	-5.41	-17.32**	0.8	-5.07	-9.75	-53.59**	-1.0
22	BBSR-10-26 X BBSR-195-3	-27.75**	-33.04**	18.90**	-3.5	-1.34	-10.66**	-20.88**	-0.1
23	BBSR-10-26 X BBSR-192-1	-7.74	-18.40**	44.88**	-0.6	52.18**	41.70**	18.05**	7.1
24	BBSR-10-26 X Selection from BBSR-192-1	-31.43**	-38.30**	37.01**	-2.8	-6.45	-23.01**	-14.38**	-0.3
25	BBSR-10-26 X Selection from BBSR-145-1	-2.60	-21.06**	40.16**	-0.1	27.13**	20.71**	-13.29**	5.1
26	BBSR-10-26 X BBSR-09-5	-0.15	-25.50**	32.28**	0.0	33.23**	9.60*	-21.27**	1.5
27	BBSR-195-3 X BBSR-192-1	17.54**	11.69**	69.29**	3.4	39.52**	35.38**	19.90**	12.9
28	BBSR-195-3 X Selection from BBSR-192-1	-28.77**	-40.07**	33.07**	-1.5	5.16	-5.55	5.04	0.5
29	BBSR-195-3 X Selection from BBSR-145-1	-29.02**	-38.70**	-7.09	-1.8	-8.12	-20.56**	-29.65**	-0.5
30	BBSR-195-3 X BBSR-09-5	2.14	-19.48**	22.05**	0.1	52.20**	15.94**	2.68	1.7
31	BBSR-192-1 X Selection from BBSR-192-1	-31.92**	-45.04**	22.05**	-1.3	-36.80**	-44.73**	-38.53**	-2.6
32	BBSR-192-1 X Selection from BBSR-145-1	19.99**	8.42*	48.03**	1.9	17.05**	3.89	-13.45**	1.3
33	BBSR-192-1 X BBSR-09-5	28.01**	4.96	43.31**	1.3	-38.24**	-51.94**	-59.96**	-1.3
34	Selection from BBSR-192-1 X Selection from BBSR-145-1	-22.28**	-41.84**	29.13**	-0.7	-18.44**	-35.54**	-28.32**	-0.7
35	Selection from BBSR-192-1 X BBSR-09-5	-8.40*	-36.17**	41.73**	-0.2	35.55**	-3.98	6.79*	0.9
36	Selection from BBSR-145-1 X BBSR-09-5	21.12**	8.57	19.69**	1.8	1.20	-13.07**	-43.87**	0.1

Table 10. Heterosis percentage (RH-relative heterosis, HB- heterobeltiosis and SH- standard heterosis) and dominance estimate (DE) of F_1 hybrids for fruit perplant and total fruit yield per Plant of *Solanum melongena* L. *, ** indicate the significance at 5% and 1% level, respectively.

the role of dominance and partial-dominance actions for most crosses has been documented in the inheritance of these traits. The results on the dominance effect of various characteristics in round-fruited brinjal are in harmony with the findings of Shende et al.⁷⁴. The results also revealed that additive and non-additive gene effects play a crucial role in the inheritance of the present study's traits. The results comply with the findings of Joshi et al.⁷⁵, Mishra et al.^{9,76,77}. The high additive gene effects are responsible for good general combiners and poor general combiners generally possess more non-additive gene effects. The genetic control of studied traits revealed three combinations for 36 crosses.

At least one parent had a significant negative or positive GCA effect in crosses of H x L type or L x H type. It was revealed that the additive effect of a good combiner and the complementary epistatic impact of a poor combiner acted balanced to maximize the expression of the trait of interest⁷⁸. However, SCA effects play a crucial role in the cross-involving L x L category, and better performance was due to non-additive gene action. Hence, both additive and non-additive gene effects can be used through heterosis breeding and recurrent selection⁷⁹. Parents with H x H SCA effects do not always produce the best cross-combinations, but they may occur in other types of parental cross-combinations. For a trait, the presence of unfavorable gene combinations in the parents leads to the appearance of adverse SCA effects in crosses⁸⁰. Top general combiners may not always produce the best cross combinations. So, exploring promising transgressive segregants for inclusion into breeding programs in subsequent generations is necessary. Therefore, while selecting the cross combinations, it is crucial to give

Sl. No.	Crosses	RH (%)	HB (%)	SH (%)
1	BBSR-08-2 X BBSR-10-25	0.00	0.00	-76.20*
2	BBSR-08-2 X Jammusahi Local	160.12	160.12	-38.10
3	BBSR-08-2 X BBSR-10-26	0.00	0.00	-76.20*
4	BBSR-08-2 X BBSR-195-3	-44.46	0.00	-76.20*
5	BBSR-08-2 X BBSR-192-1	44.46	160.12	-38.10
6	BBSR-08-2 X Selection from BBSR-192-1	215.00	467.19**	34.97
7	BBSR-08-2 X Selection from BBSR-145-1	160.12	160.12	-38.10
8	BBSR-08-2 X BBSR-09-5	90.45	242.92	-18.40
9	BBSR-10-25 X Jammusahi Local	307.07	307.07*	-3.13
10	BBSR-10-25 X BBSR-10-26	0.00	0.00	-76.20*
11	BBSR-10-25 X BBSR-195-3	44.46	160.12	-38.10
12	BBSR-10-25 X BBSR-192-1	44.46	160.12	-38.10
13	BBSR-10-25 X Selection from BBSR-192-1	-44.46	0.00	-76.20*
14	BBSR-10-25 X Selection from BBSR-145-1	320.24	320.24*	0.00
15	BBSR-10-25 X BBSR-09-5	90.45	242.92	-18.40
16	Jammusahi Local X BBSR-10-26	0.00	0.00	-76.20*
17	Jammusahi Local X BBSR-195-3	-44.46	0.00	-76.20*
18	Jammusahi Local X BBSR-192-1	44.46	160.12	-38.10
19	Jammusahi Local X Selection from BBSR-192-1	-44.46	0.00	-76.20*
20	Jammusahi Local X Selection from BBSR-145-1	0.00	0.00	-76.20*
21	Jammusahi Local X BBSR-09-5	133.39	320.24*	0.00
22	BBSR-10-26 X BBSR-195-3	44.46	160.12	-38.10
23	BBSR-10-26 X BBSR-192-1	90.45	242.92	-18.40
24	BBSR-10-26 X Selection from BBSR-192-1	126.08	307.07*	-3.13
25	BBSR-10-26 X Selection from BBSR-145-1	0.00	0.00	-76.20*
26	BBSR-10-26 X BBSR-09-5	44.46	160.12	-38.10
27	BBSR-195-3 X BBSR-192-1	-61.56	-61.56	-76.20*
28	BBSR-195-3 X Selection from BBSR-192-1	-61.56	-61.56	-76.20*
29	BBSR-195-3 X Selection from BBSR-145-1	44.46	160.12	-38.10
30	BBSR-195-3 X BBSR-09-5	-61.56	-61.56	-76.20*
31	BBSR-192-1 X Selection from BBSR-192-1	61.56	61.56	0.00
32	BBSR-192-1 X Selection from BBSR-145-1	90.45	242.92	-18.40
33	BBSR-192-1 X BBSR-09-5	61.56	61.56	0.00
34	Selection from BBSR-192-1 X Selection from BBSR-145-1	179.37	403.04**	19.70
35	Selection from BBSR-192-1 X BBSR-09-5	195.38**	195.38**	82.84*
36	Selection from BBSR-145-1 X BBSR-09-5	133.39	320.24*	0.00

Table 11. Heterosis percentage (RH-relative heterosis, HB- heterobeltiosis and SH- standard heterosis) of F_1 hybrids for bacterial wilt % at 90 DAT. *, ** indicate the significance at 5% and 1% level, respectively.

priority to their per se performances^{80–82}. Based on bacterial wilt incidence at 90 DAT, the promising hybrids, BBSR-08-2 x BBSR-192-1, Jammusahi Local x BBSR-192-1, and BBSR-195-3 x BBSR-192-1, were categorized as bacterial wilt resistant.

Conclusion

The present study concluded that the qualitative traits exhibited notable variations across the germplasm collected from Odisha except in corolla color, fruit color distribution, and fruit curvature. In quantitative terms, the broadest range of variability was observed for total fruit yield per plant, followed by average fruit weight. It also noted that selecting the genetic parameters such as PCV, GCV, h^2 , and GA can enhance brinjal fruit yield and related traits. Based on the cluster analysis, except for clusters I and VIII, parents from other clusters will be identified for the crossing program and included in breeding efforts toward bacterial wilt resistance and high fruit yield. The nature of gene action was non-additive for yield, and most of the yield components specified that these traits could be improved through heterosis breeding in brinjal. Four good combiners, i.e., Selections from BBSR-192-1, BBSR-192-1, BBSR-08-2, and BBSR-195-3, were identified as promising general combiners for fruit yield and yield-attributing traits for utilization in breeding programs with bacterial wilt tolerance when crossed with other parents. Overall, based on the performance, heterotic response as well as estimates of combining

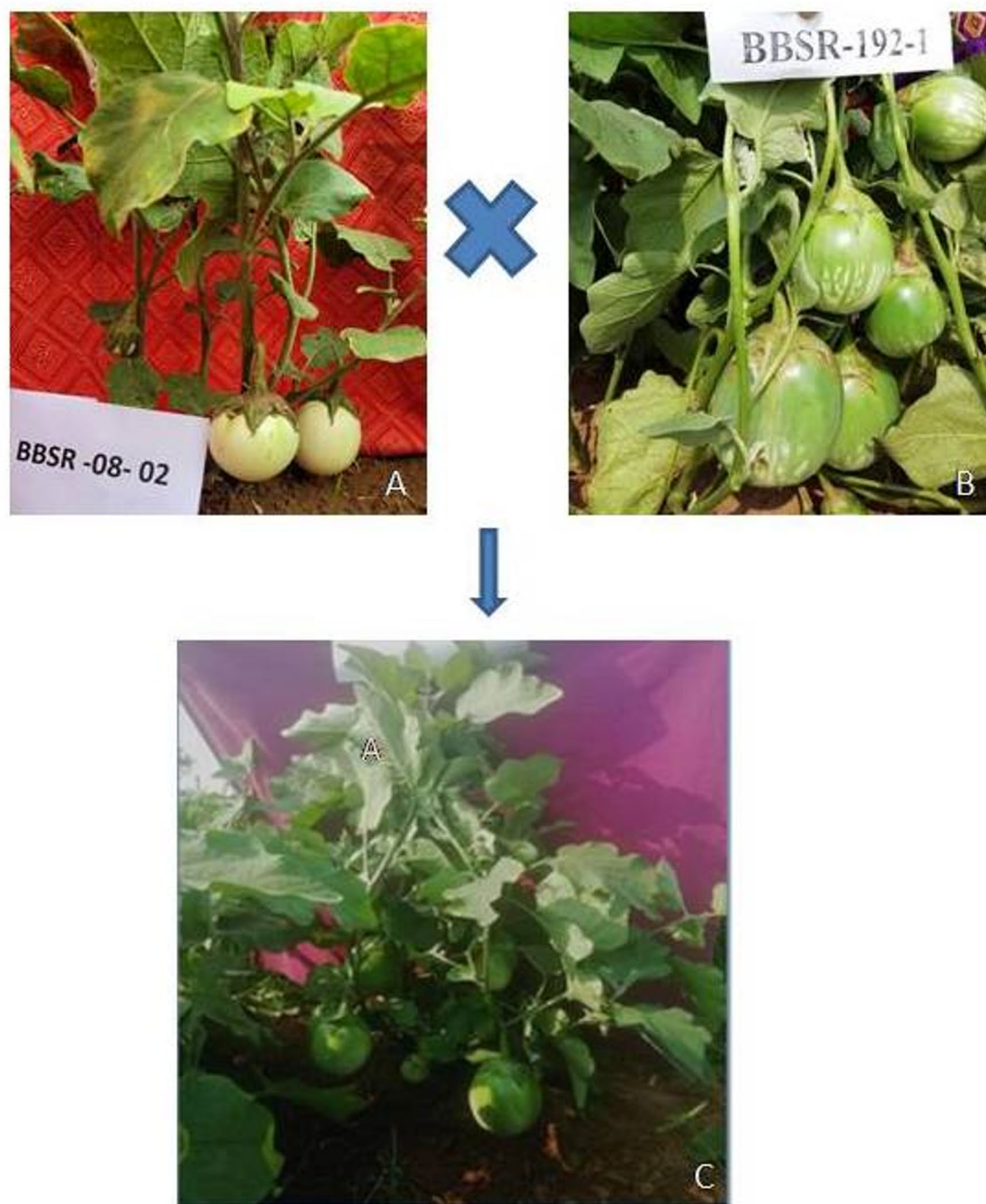


Fig. 3. Better heterotic cross combinations based on relative heterosis, heterobeltiosis, and standard heterosis for fruit yield and attributing traits(A:BBSR-08-2, B: BBSR -192-1, C: F₁ hybrid).



Fig. 4. Based on performance, the top hybrid for total fruit yield per plant was BBSR-08-2 x BBSR-192-1 (A), and was statistically *at par* with BBSR-195-3 x BBSR-192-1 (B), Jammusahi Local x BBSR-192-1 (C) and BBSR-10-26 x BBSR-192-1 (D).

ability, the four essential crosses namely, BBSR-08-2 x BBSR-192-1, Jammusahi Local x BBSR-192-1, BBSR-195-3 x BBSR-192-1 and BBSR-10-26 x BBSR-192-1 were highly suitable for commercial exploitation as F_1 hybrid in brinjal with high fruit yield and tolerance to bacterial wilt. These cross-combinations can be exploited in subsequent segregating generations to develop high-yielding varieties in brinjal.

Sl. No.	Crosses	Plant height at peak fruiting stage (cm)	Plant height at final harvest stage (cm)	Plant spread (cm)	Number of primary branches plant ⁻¹	Days to First Flowering	Days to 50% Flowering	Flowers per cluster ⁻¹	Fruit length (cm)	Fruit breadth (cm)	Average fruit weight (g)	Fruits per plant ⁻¹	Bacterial wilt % at 90 DAT (Square root transformation value)	Total fruit yield plant ⁻¹ (g)
1	BBSR-08-2	72.50	90.05	86.70	4.85	52.00	55.30	5.10	11.90	22.64	128.69	12.90	0.00 (0.71)	1275.50
2	BBSR-10-25	73.10	82.44	90.30	3.60	40.40	66.00	5.50	12.95	22.19	137.75	18.50	0.00 (0.71)	1109.67
3	Jannusahi Local	76.00	92.97	40.90	3.90	59.30	73.20	2.20	21.00	28.94	284.60	6.20	0.00 (0.71)	1096.00
4	BBSR-10-26	59.60	69.62	53.90	2.90	44.90	48.00	4.60	13.21	19.88	111.50	22.55	0.00 (0.71)	1530.90
5	BBSR-195-3	83.70	96.53	77.80	3.70	46.10	46.90	5.20	15.50	21.78	160.05	19.25	4.17 (1.87)	1887.30
6	BBSR-192-1	67.80	83.00	57.10	3.20	42.20	59.70	4.00	12.47	26.59	132.24	17.34	4.17 (1.87)	1775.50
7	Selection from BBSR-192-1	52.90	66.52	55.90	2.60	42.40	60.40	3.70	12.63	23.00	128.10	28.20	4.17 (1.87)	2370.00
8	Selection from BBSR-145-1	64.80	75.86	51.40	2.80	48.40	61.70	6.00	13.54	21.83	159.40	14.00	0.00 (0.71)	1376.15
9	BBSR-09-5	68.60	81.54	53.10	2.40	50.20	58.70	4.50	14.35	23.98	132.60	11.10	4.17 (1.87)	988.00
10	BBSR-08-2 X BBSR-10-25	89.85	105.00	89.22	5.30	53.50	62.40	5.60	15.78	27.69	197.15	19.00	0.00 (0.71)	2085.50
11	BBSR-08-2 X Jannusahi Local	91.10	108.84	88.90	5.90	53.20	51.40	5.20	18.22	27.13	252.40	14.50	4.17 (1.87)	2188.90
12	BBSR-08-2 X BBSR-10-26	87.10	101.00	73.30	4.20	53.00	66.60	5.00	13.93	23.95	188.50	14.10	0.00 (0.71)	1945.80
13	BBSR-08-2 X BBSR-195-3	96.40	109.29	92.90	5.50	42.60	58.80	5.60	15.89	27.25	187.34	10.80	0.00 (0.71)	1458.90
14	BBSR-08-2 X BBSR-192-1	84.40	102.23	87.00	4.60	45.50	56.60	5.15	13.65	29.07	227.70	19.50	4.17 (1.84)	2705.80
15	BBSR-08-2 X Selection from BBSR-192-1	92.10	104.57	98.92	5.30	48.10	65.70	5.20	14.48	26.91	230.94	18.90	16.67 (4.01)	2488.50
16	BBSR-08-2 X Selection from BBSR-145-1	79.80	91.74	88.10	5.40	55.40	63.70	6.10	15.17	27.13	220.40	14.50	4.17 (1.84)	2250.50
17	BBSR-08-2 X BBSR-09-5	71.40	85.15	83.70	4.90	46.50	49.60	5.00	15.39	27.53	220.30	14.10	8.33 (2.97)	2141.00
18	BBSR-10-25 X Jannusahi Local	69.32	79.39	72.70	4.70	43.70	56.70	5.00	19.50	27.70	166.10	14.00	12.50 (3.61)	1285.10
19	BBSR-10-25 X BBSR-10-26	51.88	64.95	85.62	4.70	46.30	55.40	6.40	15.73	20.48	112.80	14.90	0.00 (0.71)	1121.65
20	BBSR-10-25 X BBSR-195-3	91.80	110.10	79.80	4.60	50.70	54.10	6.10	16.30	26.50	187.80	20.10	4.17 (1.84)	1908.10
21	BBSR-10-25 X BBSR-192-1	81.20	96.45	77.00	5.00	41.30	48.80	4.60	13.91	24.78	184.50	17.20	4.17 (1.84)	2303.70
22	BBSR-10-25 X Selection from BBSR-192-1	59.90	72.26	80.14	4.50	48.40	57.80	4.60	13.61	24.41	147.50	18.90	0.00 (0.71)	2050.80
23	BBSR-10-25 X Selection from BBSR-145-1	69.45	80.00	74.40	3.40	45.15	65.50	6.15	15.58	22.50	136.95	12.94	8.33 (2.97)	1123.00
24	BBSR-10-25 X BBSR-09-5	68.30	80.18	88.00	4.70	40.40	60.70	6.00	15.00	19.23	190.60	19.00	8.33 (2.97)	1451.90
25	Jannusahi Local X BBSR-10-26	82.60	93.69	85.20	4.70	39.90	60.40	4.70	18.19	22.90	185.40	13.75	0.00 (0.71)	1611.70
26	Jannusahi Local X BBSR-195-3	85.88	97.03	73.30	5.10	47.70	52.50	4.00	18.37	32.67	285.80	15.60	0.00 (0.71)	2158.50
27	Jannusahi Local X BBSR-192-1	60.10	76.00	57.50	3.90	45.60	62.40	4.10	17.59	29.30	293.20	18.80	4.17 (1.84)	2558.50
28	Jannusahi Local X Selection from BBSR-192-1	80.80	94.29	72.00	4.40	52.10	55.80	4.50	21.10	33.06	275.34	12.40	0.00 (0.71)	2180.20
29	Jannusahi Local X Selection from BBSR-145-1	75.10	84.30	75.20	4.30	44.40	65.40	5.20	21.79	30.96	122.88	15.30	0.00 (0.71)	1084.20
30	Jannusahi Local X BBSR-09-5	72.50	88.00	47.50	3.25	55.70	66.50	3.45	21.50	27.15	220.30	10.50	8.33 (2.97)	989.15
31	BBSR-10-26 X BBSR-195-3	74.60	85.51	78.30	4.70	45.50	64.20	4.70	16.45	20.44	175.10	15.10	4.17 (1.84)	1686.18
32	BBSR-10-26 X BBSR-192-1	74.10	86.37	73.60	4.70	42.10	56.50	5.70	17.49	31.10	218.50	18.40	8.33 (2.97)	2515.80
33	BBSR-10-26 X Selection from BBSR-192-1	72.90	83.88	71.70	4.50	50.30	57.60	5.20	13.70	24.50	170.15	17.40	12.50 (3.61)	1824.60
34	BBSR-10-26 X Selection from BBSR-145-1	74.50	84.70	66.10	4.40	42.30	50.80	5.30	14.16	20.22	141.95	17.80	0.00 (0.71)	1847.90
35	BBSR-10-26 X BBSR-09-5	58.10	70.53	65.60	4.40	41.50	50.00	4.00	14.69	19.44	151.00	16.80	4.17 (1.84)	1677.90
36	BBSR-195-3 X BBSR-192-1	67.70	83.49	72.90	4.20	58.00	62.20	4.20	16.45	27.64	234.35	21.50	0.00 (0.71)	2555.10
37	BBSR-195-3 X Selection from BBSR-192-1	75.90	85.26	89.40	4.80	46.10	51.00	4.40	17.35	27.45	179.80	16.90	0.00 (0.71)	2238.50

Continued

Sl. No.	Crosses	Plant height at peak fruiting stage (cm)	Plant height at final harvest stage (cm)	Plant spread (cm)	Number of primary branches plant ⁻¹	Days to First Flowering	Days to 50% Flowering	Flowers per cluster ⁻¹	Fruit length (cm)	Fruit breadth (cm)	Average fruit weight (g)	Fruits per plant ⁻¹	Bacterial wilt % at 90 DAT (Square root transformation value)	Total fruit yield plant ⁻¹ (g)
38	BBSR-195-3 X Selection from BBSR-145-1	67.10	78.16	91.90	4.20	56.40	66.20	4.60	16.12	27.05	256.95	11.80	4.17 (1.84)	1499.20
39	BBSR-195-3 X BBSR-09-5	90.40	107.03	81.30	4.80	51.60	59.50	4.70	16.23	27.85	245.75	15.50	0.00 (0.71)	2188.10
40	BBSR-192-1 X Selection from BBSR-192-1	60.40	73.50	56.50	2.90	43.10	55.00	3.75	12.05	24.80	126.50	15.50	8.33 (2.97)	1310.00
41	BBSR-192-1 X Selection from BBSR-145-1	78.80	91.77	69.30	5.00	51.60	56.70	6.10	14.48	21.88	134.54	18.80	8.33 (2.97)	1844.50
42	BBSR-192-1 X BBSR-09-5	55.60	66.90	50.60	2.80	47.00	49.20	3.80	10.85	20.30	101.38	18.20	8.33 (2.97)	853.35
43	Selection from BBSR-192-1 X Selection from BBSR-145-1	66.30	76.61	84.40	3.60	42.40	53.50	6.10	12.10	22.70	170.30	16.40	12.50 (3.61)	1527.60
44	Selection from BBSR-192-1 X BBSR-09-5	65.70	79.57	70.80	2.40	46.90	46.90	4.70	15.38	22.30	167.90	18.00	29.17 (5.45)	2275.80
45	Selection from BBSR-145-1 X BBSR-09-5	83.50	96.66	66.50	4.20	40.60	57.40	5.90	12.56	21.33	274.20	15.20	8.33 (2.97)	1196.30
46	VNR-5 (Check)	69.40	80.62	67.60	4.30	60.40	71.50	3.40	13.40	26.90	217.45	12.70	8.33 (2.97)	2131.10
	Grand Mean	73.80	86.82	73.78	4.22	47.63	58.15	4.89	15.47	25.11	186.41	16.19	4.80 (1.82)	1775.49
	Grand Mean of Parents	68.78	82.06	63.01	3.33	47.32	58.88	4.53	14.17	23.42	152.77	16.67	1.85 (1.23)	1489.89
	SE (m)±	4.17	4.96	2.91	0.27	2.10	1.71	0.33	0.69	1.19	10.90	0.64	0.93	66.71
	C.D.	11.91	14.18	8.31	0.78	6.01	4.87	0.95	1.97	3.41	31.14	1.84	NS	190.64
	C.V.	7.99	8.08	5.57	9.18	6.25	4.145	9.61	6.30	6.71	8.27	5.61	19.72	5.31

Table 12. Per se performance of 46 *Solanum melongena* L. Genotypes (36 F₁ crosses, nine parents and one check). *Figures in parentheses indicate square root transformed values for corresponding values.

Sl. No.	Parents	Plant height at peak fruiting stage(cm)	Plant height at final harvest stage (cm)	Plant spread (cm)	Number of primary branches plant ⁻¹	Days to First Flowering	Days to 50% Flowering	Flowers cluster ⁻¹	Fruit length (cm)	Fruit breadth (cm)	Average fruit weight (g)	Fruits plant ⁻¹	Bacterial wilt % at 90 DAT	Total fruit yield plant ⁻¹ (g)
1	BBSR-08-2	8.92**	10.76**	12.39**	0.78**	2.74**	0.62	0.27**	-0.75**	0.98**	11.36**	-1.05**	-1.51	172.74**
2	BBSR-10-25	-1.01	-1.48	8.03**	0.17*	-1.94**	1.35**	0.49**	-0.29	-1.05**	-23.48**	0.94**	-1.51	-215.15**
3	Jannusahi Local	2.76*	3.45*	-7.74**	0.17*	2.66**	3.54**	-0.87**	3.98**	3.42**	46.68**	-3.22**	-2.61	-151.59**
4	BBSR-10-26	-4.00**	-5.42**	-2.91**	-0.01	-2.65**	-1.91**	0.13	-0.39	-2.58**	-26.43**	0.97**	-3.04	-56.58**
5	BBSR-195-3	7.11**	7.22**	6.93**	0.28**	1.74**	-1.48**	-0.03	0.88**	0.84*	19.62**	0.28	-3.21	141.04**
6	BBSR-192-1	-3.74**	-2.44	-7.33**	-0.25**	-1.18	-1.07*	-0.33**	-1.41**	0.99**	-6.55*	1.81**	2.03	207.46**
7	Selection from BBSR-192-1	-5.38**	-6.05**	-0.32	-0.42**	-1.60*	-1.31*	-0.26**	-0.86**	0.09	-12.05**	2.56**	4.34*	247.30**
8	Selection from BBSR-145-1	-1.35	-3.08*	-1.86*	-0.19*	0.31	2.19**	0.67**	-0.76**	-1.07**	-7.29*	-1.09**	0.50	-155.52**
9	BBSR-09-5	-3.30**	-2.95*	-7.18**	-0.54**	-0.09	-1.94**	-0.08	-0.38	-1.64**	-1.87	-1.20**	4.99*	-189.70**
	SE (gi)±	1.20	1.41	0.82	0.08	0.61	0.49	0.10	0.20	0.34	3.13	0.18	1.90	19.04
	CD(P=0.05)	3.63	4.28	2.48	0.23	1.84	1.48	0.29	0.59	1.03	9.47	0.54	8.16	57.57

Table 13. Estimates of general combining ability (GCA) effects of parents for fruit yield and its component in *Solanum melongena*L. Genotypes, *, ** indicate the significance at 5% and 1% level, respectively.

Sl. No.	Crosses	Plant height at peak fruiting stage (cm)	Plant height at final harvest stage (cm)	Plant spread (cm)	Number of primary branches plant ⁻¹	Days to First Flowering	Days to 50% Flowering	Flowers cluster ⁻¹	Fruit length (cm)	Fruit breadth (cm)	Average fruit weight (g)	Fruits plant ⁻¹	Bacterial wilt % at 90 DAI	Total fruit yield plant ⁻¹ (g)
1	BBSR-08-2 X BBSR-10-25	8.04*	8.77	-5.11	0.13	5.54**	2.57	-0.17	1.37*	2.64*	23.55*	2.84**	-4.700	336.33**
2	BBSR-08-2 X Jamnusaahi Local	5.52	7.68	10.33**	0.73**	0.63	-10.62**	0.79*	-0.46	-2.39*	8.65	2.50**	4.780	376.17**
3	BBSR-08-2 X BBSR-10-26	8.28*	8.71	-10.10**	-0.79**	5.74**	10.04**	-0.41	-0.39	0.43	17.86	-2.09**	-3.170	38.07**
4	BBSR-08-2 X BBSR-195-3	6.47	4.36	-0.33	0.22	-9.05**	1.80	0.35	0.31	0.31	-29.36**	-4.71**	-3.000	-646.46**
5	BBSR-08-2 X BBSR-192-1	5.32	6.96	8.02**	-0.16	-3.22	-0.81	0.20	0.36	1.98	37.17**	2.47**	0.140	534.03**
6	BBSR-08-2 X Selection from BBSR-192-1	14.66**	12.91**	12.94**	0.72**	-0.21	8.54**	0.18	0.64	0.72	45.91**	1.12	12.830*	276.89**
7	BBSR-08-2 X Selection from BBSR-145-1	-1.67	-2.90	3.66	0.59*	5.18*	3.04	0.15	1.23	2.11	30.62**	0.36	1.670	441.71**
8	BBSR-08-2 X BBSR-09-5	-8.12*	-9.62*	4.58	0.44	-3.31	-6.94**	-0.20	1.07	3.07**	25.09*	0.08	0.840	366.39**
9	BBSR-10-25 X Jamnusaahi Local	-6.33	-9.52*	-1.51	0.14	-4.18*	-6.05**	0.37	0.37	0.22	-42.82**	0.01	11.400*	-139.74*
10	BBSR-10-25 X BBSR-10-26	-17.01**	-15.09**	6.58*	0.32	3.73	-1.90	0.78*	0.96	-1.01	-23.01*	-3.28**	-3.170	-398.19**
11	BBSR-10-25 X BBSR-195-3	11.80**	17.41**	-9.07**	-0.08	3.74	-3.63*	0.63*	0.27	1.59	5.94	2.61**	5.380	190.64**
12	BBSR-10-25 X BBSR-192-1	12.05**	13.42**	2.38	0.85**	-2.74	-9.34**	-0.57	0.16	-0.28	28.81**	-1.82**	0.140	519.82**
13	BBSR-10-25 X Selection from BBSR-192-1	-7.61	-7.16	-1.48	0.53*	4.78*	-0.09	-0.64*	-0.69	0.26	-2.69	-0.87	-10.550	227.08**
14	BBSR-10-25 X Selection from BBSR-145-1	-2.09	-2.39	-5.68*	-0.80**	-0.38	4.11**	-0.02	1.18	1.42	-17.10	-3.18**	10.060	-297.90**
15	BBSR-10-25 X BBSR-09-5	-1.29	-2.34	13.24**	0.85**	-4.73*	3.44*	0.58	0.23	-3.19**	30.23**	2.99**	0.840	65.18
16	Jamnusaahi Local X BBSR-10-26	9.94*	8.71	21.92**	0.32	-7.28**	0.92	0.43	-0.86	-3.06**	-20.56*	-0.27	-2.080	28.30
17	Jamnusaahi Local X BBSR-195-3	2.11	-0.59	0.19	0.43	-3.87	-7.42**	-0.12	-1.93**	3.29**	33.78**	2.27**	-1.910	377.48**
18	Jamnusaahi Local X BBSR-192-1	-12.83**	-11.97*	-1.36	-0.24	-3.04	2.07	0.29	-0.43	-0.23	67.35**	3.95**	1.240	711.06**
19	Jamnusaahi Local X Selection from BBSR-192-1	9.52*	9.94*	6.14*	0.43	3.88	-4.28**	0.62	2.54**	4.44**	54.99**	-3.20**	-9.460	292.92**
20	Jamnusaahi Local X Selection from BBSR-145-1	-0.21	-3.03	10.88**	0.10	-5.74**	1.82	0.39	3.12**	3.50**	-102.22**	3.34**	-5.620	-400.26**
21	Jamnusaahi Local X BBSR-09-5	-0.86	0.55	-11.50**	-0.60*	5.97**	7.04**	-0.62	2.46**	0.26	-10.23	-1.35*	6.660	-461.13**
22	BBSR-10-26 X BBSR-195-3	-2.40	-3.24	0.36	0.21	-0.76	9.74**	-0.41	0.51	-2.94*	-3.81	-2.42**	6.910	-189.85**
23	BBSR-10-26 X BBSR-192-1	7.94*	7.28	9.92**	0.74**	-1.23	1.63	0.89**	3.84**	7.57**	65.76**	-0.65	5.330	573.35**
24	BBSR-10-26 X Selection from BBSR-192-1	8.39*	8.40	1.01	0.71**	-0.81	2.97	0.32	-0.50	1.87	22.92*	-2.39**	5.970	-157.69*
25	BBSR-10-26 X Selection from BBSR-145-1	5.95	6.25	-3.05	0.38	-2.53	-7.33**	-0.51	-0.61	-1.25	-10.04	1.65**	-5.190	268.43**
26	BBSR-10-26 X BBSR-09-5	-8.50*	-8.05	1.77	0.73**	-2.92	-4.00*	0.24	0.01	-1.46	-6.42	0.76	-1.290	132.61*
27	BBSR-195-3 X BBSR-192-1	-9.57*	-8.24	-0.62	-0.06	10.28**	6.89**	0.64*	1.54*	0.69	35.56**	3.14**	-6.550	415.03**
28	BBSR-195-3 X Selection from BBSR-192-1	0.28	-2.86	8.88**	0.72**	-1.21	-4.07*	-0.33	1.89**	1.40	-13.49	-2.21**	-8.850	58.59
29	BBSR-195-3 X Selection from BBSR-145-1	-12.56**	-12.93**	12.92**	-0.11	7.18**	7.64**	-1.05**	0.55	2.17	58.90**	-3.67**	3.370	-277.89**
30	BBSR-195-3 X BBSR-09-5	12.69**	15.81**	7.64**	0.84**	2.79	5.06**	-0.21	0.29	3.53**	42.28**	0.15	-9.510	445.19**
31	BBSR-192-1 X Selection from BBSR-192-1	-4.38	-4.97	-9.77**	-0.66**	-1.28	-0.48	-0.68*	-1.13	-1.40	-40.62**	-5.13**	2.680	-936.33**
32	BBSR-192-1 X Selection from BBSR-145-1	9.99*	10.33*	4.57	1.22**	5.31**	-2.28	0.75*	-1.23	-3.16**	-37.34**	1.81**	1.790	0.99
33	BBSR-192-1 X BBSR-09-5	-11.26**	-14.67**	-8.81**	-0.63*	1.11	-5.65**	-0.81*	-2.81**	-4.17**	-75.92**	1.32*	2.030	-955.98**
34	Selection from BBSR-192-1 X Selection from BBSR-145-1	-0.87	-1.21	12.67**	-0.01	-3.47	-5.23**	0.68*	-1.73**	-1.43	3.92	-1.34*	7.860	-355.75**
35	Selection from BBSR-192-1 X BBSR-09-5	0.48	1.61	4.38	-0.86**	1.43	-7.70**	1.43**	1.18	-1.27	-3.90	0.38	15.550**	426.63**
36	Selection from BBSR-145-1 X BBSR-09-5	14.25**	15.74**	1.63	0.71**	-6.78**	-0.70	0.30	-1.75**	-1.08	97.64**	1.22*	3.520	829.45**

Continued

Sl. No.	Crosses	Plant height at peak fruiting stage (cm)	Plant height at final harvest stage (cm)	Plant spread (cm)	Number of primary branches plant ⁻¹	Days to First Flowering	Days to 50% Flowering	Flowers cluster ⁻¹	Fruit length (cm)	Fruit breadth (cm)	Average fruit weight (g)	Fruits plant ⁻¹	Bacterial wilt % at 90 DAT	Total fruit yield plant ⁻¹ (g)
	SE(i) ±	3.87	4.55	2.64	0.24	1.96	1.57	0.31	0.63	1.09	10.08	0.58	5.418	61.26
	CD(P=0.05)	11.49	13.52	7.84	0.72	5.82	4.67	0.91	1.88	3.24	29.95	1.72	81.555	182.04

Table 14. Estimates of specific combining ability (SCA) effects of crosses for fruit yield and its components in *Solanum melongena*L. , * ** indicate the significance at 5% and 1% level, respectively.



Fig. 5. Best performance Specific Combiners for high yield, round fruits & tolerance to bacterial wilt.(A: Selection from BBSR-145-1 x BBSR-09-5,B:Jammusahi Local x BBSR-192-1, C: BBSR-10-26 xBBSR-192-1.

Characters	Crossed with high heterobeltiosis (%) in the desired direction	Parents with gca effects	Crosses having sca effects with per se performance	Type of combination
Plant height at final harvest (cm)	BBSR-10-26 X Selection from BBSR-192-1 (20.66)	BBSR-10-26 (-5.42**), Selection from BBSR-192-1 (-6.05**)	8.40 (83.88)	L x L
Plant spread (cm)	Jammusahi Local X BBSR-10-26(58.07)	Jammusahi Local (-7.74**), BBSR-10-26 (-2.91**)	21.92** (85.20)	L x L
Primary branches plant ⁻¹	BBSR-192-1 X Selection from BBSR-145-1(56.25)	BBSR-192-1 (-0.25**), Selection from BBSR-145-1 (-0.19*)	1.22** (5.00)	L x L
Days to 1st flowering	Jammusahi Local X BBSR-10-26 (-32.72)	Jammusahi Local (2.66**), BBSR-10-26 (-2.65**)	-7.28** (39.90)	H x L
Days to 50% flowering	Selection from BBSR-192-1 X BBSR-09-5(-20.10)	Selection from BBSR-192-1 (-1.31*), BBSR-09-5 (-1.94**)	-7.70** (46.90)	L x L
Flowers cluster ⁻¹	BBSR-10-26 X BBSR-192-1(23.91)	BBSR-10-26 (0.13), BBSR-192-1 (-0.33**)	0.89** (5.70)	H x L
Fruit length (cm)	BBSR-192-1 X BBSR-09-5 (-24.39)	BBSR-192-1 (-1.41**), BBSR-09-5 (-0.38)	-2.81** (10.85)	L x L
Fruit breadth (cm)	BBSR-195-3 X Selection from BBSR-145-1(23.91)	BBSR-195-3 (0.84*), Selection from BBSR-145-1 (-1.07**)	2.17 (27.05)	H x L
Average fruit weight (g)	BBSR-08-2 X Selection from BBSR-192-1 (79.46)	BBSR-08-2 (11.36**), Selection from BBSR-192-1 (-12.05**)	45.91** (230.94)	H x L
Fruits plant ⁻¹	BBSR-08-2 X BBSR-192-1(12.46)	BBSR-08-2 (-1.05**), BBSR-192-1 (1.81**)	2.47** (19.50)	L x H
Bacterial wilt % 90 DAT	BBSR-195-3 X BBSR-09-5(-61.56)	BBSR-195-3 (-3.21), BBSR-09-5 (4.99*)	-9.51 (0.00)	L x H
	BBSR-195-3 X Selection from BBSR-192-1 (-61.56)	BBSR-195-3 (-3.21), Selection from BBSR-192-1 (4.34*)	-8.85 (0.00)	L x H
	BBSR-195-3 X BBSR-192-1 (-61.56)	BBSR-195-3 (-3.21), BBSR-192-1 (2.03)	-6.55 (0.00)	L x H
Fruit yield plant ⁻¹ (g)	BBSR-08-2 X Jammusahi Local (71.61)	BBSR-08-2 (172.74**) X Jammusahi Local (-151.59**)	376.17** (2188.90)	H x L

Table 15. Selected crosses with high heterobeltiosis, their corresponding GCA and SCA effects, and type of combinations. GCA – general combining ability in parents, SCA – specific combining ability of crosses, per se performance in parentheses. *, ** indicate the significance at 5% and 1% level, respectively. H = Positive GCA effect, L = Negative SCA effect.

Sl. No.	Parents/Crosses	Bacterial wilt % at 90 DAT (Square root transformation value)	Reaction
1	BBSR-08-2	0.00 (0.71)	Highly resistant
2	BBSR-10-25	0.00 (0.71)	Highly resistant
3	Jammusahi Local	0.00 (0.71)	Highly resistant
4	BBSR-10-26	0.00 (0.71)	Highly resistant
5	BBSR-195-3	4.17 (1.87)	Resistant
6	BBSR-192-1	4.17 (1.87)	Resistant
7	Selection from BBSR-192-1	4.17 (1.87)	Resistant
8	Selection from BBSR-145-1	0.00 (0.71)	Highly resistant
9	BBSR-09-5	4.17 (1.87)	Resistant
10	BBSR-08-2 X BBSR-10-25	0.00 (0.71)	Highly resistant
11	BBSR-08-2 X Jammusahi Local	4.17 (1.87)	Resistant
12	BBSR-08-2 X BBSR-10-26	0.00 (0.71)	Highly resistant
13	BBSR-08-2 X BBSR-195-3	0.00 (0.71)	Highly resistant
14	BBSR-08-2 X BBSR-192-1	4.17 (1.84)	Resistant
15	BBSR-08-2 X Selection from BBSR-192-1	16.67 (4.01)	Resistant
16	BBSR-08-2 X Selection from BBSR-145-1	4.17 (1.84)	Resistant
17	BBSR-08-2 X BBSR-09-5	8.33 (2.97)	Resistant
18	BBSR-10-25 X Jammusahi Local	12.50 (3.61)	Resistant
19	BBSR-10-25 X BBSR-10-26	0.00 (0.71)	Highly resistant
20	BBSR-10-25 X BBSR-195-3	4.17 (1.84)	Resistant
21	BBSR-10-25 X BBSR-192-1	4.17 (1.84)	Resistant
22	BBSR-10-25 X Selection from BBSR-192-1	0.00 (0.71)	Highly resistant
23	BBSR-10-25 X Selection from BBSR-145-1	8.33 (2.97)	Resistant
24	BBSR-10-25 X BBSR-09-5	8.33 (2.97)	Resistant
25	Jammusahi Local X BBSR-10-26	0.00 (0.71)	Highly resistant
26	Jammusahi Local X BBSR-195-3	0.00 (0.71)	Highly resistant
27	Jammusahi Local X BBSR-192-1	4.17 (1.84)	
28	Jammusahi Local X Selection from BBSR-192-1	0.00 (0.71)	Highly resistant
29	Jammusahi Local X Selection from BBSR-145-1	0.00 (0.71)	Highly resistant
30	Jammusahi Local X BBSR-09-5	8.33 (2.97)	Resistant
31	BBSR-10-26 X BBSR-195-3	4.17 (1.84)	Resistant
32	BBSR-10-26 X BBSR-192-1	8.33 (2.97)	Resistant
33	BBSR-10-26 X Selection from BBSR-192-1	12.50 (3.61)	Resistant
34	BBSR-10-26 X Selection from BBSR-145-1	0.00 (0.71)	Highly resistant
35	BBSR-10-26 X BBSR-09-5	4.17 (1.84)	Resistant
36	BBSR-195-3 X BBSR-192-1	0.00 (0.71)	Resistant
37	BBSR-195-3 X Selection from BBSR-192-1	0.00 (0.71)	Highly resistant
38	BBSR-195-3 X Selection from BBSR-145-1	4.17 (1.84)	Resistant
39	BBSR-195-3 X BBSR-09-5	0.00 (0.71)	Resistant
40	BBSR-192-1 X Selection from BBSR-192-1	8.33 (2.97)	Resistant
41	BBSR-192-1 X Selection from BBSR-145-1	8.33 (2.97)	Resistant
42	BBSR-192-1 X BBSR-09-5	8.33 (2.97)	Resistant
43	Selection from BBSR-192-1 X Selection from BBSR-145-1	12.50 (3.61)	Resistant
44	Selection from BBSR-192-1 X BBSR-09-5	29.17 (5.45)	Moderately resistant
45	Selection from BBSR-145-1 X BBSR-09-5	8.33 (2.97)	Resistant
46	VNR-5 (Check)	8.33 (2.97)	Resistant

Table 16. Incidence of bacterial wilt among *Solanum melongena* parents, hybrids, and standard check at 90 DAT.

Data availability

Data is available with first author (Barsha Tripathy).

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References

- Choudhary, B. & Gaur, K. ISAAA Brief No., 38 1–102 (2009).
- Nandi, L. L. et al. Bioactive compounds, antioxidant activity And elements content variation in Indigenous And exotic *Solanum* sp. And their suitability in recommended daily diet. *Sci. Hortic.* **287**, 110232 (2021).
- Chauhan, A., Chandel, K. S. & Singh, S. P. Studies on correlation and path analysis for yield and yield contributing traits in eggplant (*Solanum melongena* L.) involving bacterial wilt resistant genotypes. *Vegetos* **30** (4), 1–4 (2017).
- Bharathi, K. I., Shanthi, A. & Manikandan, M. Assessment of genetic diversity of brinjal (*Solanum melongena* L.) in the coastal region of Karaikal, India. *J. Sci. Res. Rep.* **30** (6), 407–411 (2024).
- Fraikue, F. B. *Unveiling the Potential Utility of Eggplant: A Review, Conference Proceedings of INCEDI* 883–895 (2016).
- Zabbar, M. A. et al. Morphological characterization and genetic diversity analysis of yield and yield contributing parameters in Brinjal (*Solanum melongena* L.) genotypes. *SAARC J. Agric.* **22** (1), 59–71 (2024).
- Singh, A. K., Pan, R. S. & Bhavana, P. Combining ability and gene action studies in Brinjal (*Solanum melongena* L.). *Veg. Sci.* **45** (1), 27–30 (2021).
- Kousalya, R., Praneetha, S., Vethamani, P. I., Ravichandran, V. & Iyanar, K. N. S. Unveiling the genetic variability, character association and principal component analysis for yield and yield contributing traits in Brinjal (*Solanum melongena* L.) genotypes. *Indian J. Agric. Sci.* **94** (10), 1039–1044 (2024).
- Mishra, S. L. et al. Study of heterosis, combining ability and gene action in Brinjal (*Solanum melongena* L.) landraces of Odisha. *Electron. J. Plant Breed.* **14** (2), 572–583 (2023).
- Parida, H. R., Mandal, J. & Mohanta, S. A note on morphological characterization of Brinjal (*Solanum melongena* L.) genotypes. *Jour Crop Weed.* **16** (1), 250–255 (2020).
- Shaktawat, C., Pandey, S. K. & Kumawat, S. L. Studies on genetic variability and character association in Brinjal (*Solanum melongena* L.). *Int. J. Agric. Sci.* **20** (2), 344–349 (2024).
- Alekhyia, C. & Nambodiri, R. V. Exploring genetic diversity in Brinjal (*Solanum melongena* L.) - Insights from D2 analysis and principal component analysis. *J. Trop. Agric.* **62** (1), 65–71 (2024).
- Mary, D. S., Biswal, G., Sahu, G. S., Senapati, A. K. & Samal, K. C. Screening of brinjal genotypes against bacterial wilt caused by *Ralstonia solanacearum*. *Biological Forum – Int. J.* **15** (1), 201–205 (2023).
- Bhanwar, R. R., Tiwari, P. K. & Thakur, A. K. Screening of Brinjal cultivars against bacterial wilt disease under artificially inoculated conditions at Bastar plateau zone of Chhattisgarh. *Int. J. Curr. Microbiol. App Sci.* **8** (2), 3113–3119 (2019).
- Mugisa, I. O. et al. Incidence and severity of bacterial wilt disease on three eggplant (*Solanum melongena* L.) varieties in central Uganda. *Uganda J. Agric. Sci.* **22**, 45–54 (2024).
- Chattopadhyay, A. et al. Breeding eggplant for higher productivity and bacterial wilt tolerance. *Int. J. Veg. Sci.* **18**, 376–392 (2012).
- Sivasankarreddy, K. et al. An insight into bacterial wilt of eggplant—A review. *Trop. Plant. Pathol.* <https://doi.org/10.1007/s40858-024-00683-z> (2024).
- Griffing, B. Concept of general and specific combining ability in relation to diallel system. *Aust J. Biol. Sci.* **9**, 463–493 (1956).
- Srivastava, U., Mahajan, R. K., Gangopadhyay, K. K., Singh, M. & Dhillon, B. S. In *Minimal Descriptors of Agri Horticultural Crops. Part II: Vegetable Crops. National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi* ix + 31–38 (2001).
- Winstead, N. N. & Kelman, A. Inoculation techniques for evaluating resistance to *Pseudomonas solanacearum*. *Phytopathol* **42** (11), 628–634 (1952).
- Zeven, A. C. & Hennink, S. The interpretation of Nei and Shannon-Weaver within population variation indices. *Euphytica* **51**, 235–240 (1991).
- Burton, G. W. Quantitative inheritance in grass. In *Proceedings of the 6th International Grassland Congress* 277–283 (1952).
- Allard, R. W. *Principles of Plant Breeding* (Wiley, 1960).
- Johnson, H. W., Robinson, H. & Fand-Comstock, R. E. Genotypic and phenotypic correlations in soybeans and their implication in selection. *Agron. J.* **47**, 477–483 (1955).
- Mahalanobis, P. C. On the generalized distance in statistics. *Proc. Natl. Inst. Sci. India* **12**, 49–55 (1936).
- Smith, H. H. In *Fixing Transgressive Vigour in Nicotiana rustica* (eds. Heterosis) (Iowa State College, 1952).
- Rajatha, K. D. Varietal characterization and abiotic stress studies on seed quality of brinjal (*Solanum melongena* L.) varieties. M.Sc. Thesis, University of Agricultural Sciences, Bengaluru, Karnataka (2015).
- Tiwari, S. K., Bisht, I. S., Kumar, G. & Karihaloo, J. L. Diversity in Brinjal (*Solanum melongena* L.) landraces for morphological traits of evolutionary significance. *Veg. Sci.* **43** (1), 106–111 (2016).
- Dash, S. P. Divergence, combining ability and heterosis for fruit yield and its components in brinjal (*Solanum melongena* L.). Ph. D. (Hort.) Thesis, IGKV, Raipur (C.G.), India. (2017).
- Dhatt, A. S., Kaur, G., Sidhu, M. K. & Kaur, S. Morphological and molecular characterization of *Solanum melongena* and related species. *Veg. Sci.* **44** (1), 1–11 (2017).
- Panchadi, V. R. Studies on genetic variability, correlation, path analysis and divergence in brinjal genotypes (*Solanum melongena* L.). M.Sc. (Hort.) Thesis, Dr. YSRHU, Venkataramannagudem, West Godavari, Andhra Pradesh. (2012).
- Bhatt, R. P., Adhikari, R. S., Biswas, V. R. & Kumar, N. Genetic analysis for quantitative and qualitative traits in tomato (*Lycopersicon esculentum*) under open and protected environment. *Indian J. Genet.* **64** (2), 125–129 (2004).
- Singh, O. & Kumar, J. Variability heritability and genetic advance in Brinjal. *Ind. J. Hort.* **62** (3), 265–267 (2005).
- Damodhar, K. S. Studies on growth and yield parameters of various local brinjal (*Solanum melongena* L.) genotypes. M.Sc. (Hort.) Thesis, Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth, Dapoli, Ratnagiri, Maharashtra, India. (2018).
- Boyaci, T. V., Tepe, A., Yildirim, I. K., Oten, M. & Aktas, A. Morphological & molecular characterization and relationship of Turkish local eggplant heirlooms. *Bot. Hort. Agrobot. Cluj.* **43** (1), 100–107 (2015).
- Mondal, R. et al. Morphological and genetic variations among advance breeding lines and varieties of Brinjal grown in Eastern gangetic plains of India. *Int. J. Curr. Microbiol. App Sci.* **9** (04), 2008–2028 (2020).
- Rasheed, A. et al. Study of genetic variability, heritability, and genetic advance for yield-related traits in tomato (*Solanum lycopersicon* MILL). *Front. Genet.* **13** (1030309), 1–13 (2023).
- Hussain, K. et al. Genetic variability studies in Cherry tomato for growth, yield, and quality traits in open field conditions. *Int. J. Agricul App Sci.* **2**, 60–64 (2021).
- Islam, S., Hassan, L. & Hossain, M. A. Breeding potential of some exotic tomato lines: a combined study of morphological variability, genetic divergence, and association of traits. *Phyton* **91**, 97–114 (2022).
- Shilpa, B. M., Dheware, R. M. & Kolekar, R. B. Variability studies in Brinjal (*Solanum melongena* L.). *Int. J. Bio-res Stress Manag.* **9** (5), 576–579 (2018).

41. Tirkey, M., Saravana, S. & Lata, P. Studies on variability, heritability and genetic advance for yield and yield attributes in Brinjal (*Solanum melongena* L.). *Jour Pharmacogn Phytochem.* **SP1**, 1181–1183 (2018).
42. Arti, D. & Sharma, A. K. Genetic variability studies for yield and quality parameters in Brinjal (*Solanum melongena* L.). *J. Pharmacogn Phytochem.* **7** (5), 2494–2496 (2018).
43. Magar, P. G., Shinde, K. G., Bhalekar, M. N. & Magar, V. G. Genetic variability studies in Brinjal (*Solanum melongena* L.). *J. Contemp. Res.* **7** (4), 200–203 (2017).
44. Madhavi, N., Mishra, A. C., Prasad, J. M. & Bahuguna, S. Studies on variability, heritability and genetic advance in Brinjal (*Solanum melongena* L.). *Pl Arch.* **15** (1), 277–281 (2015).
45. Chaudhari, B. N., Patel, A. I. & Vashi, J. M. Study on heterosis over environments in Brinjal (*Solanum melongena* L.). *Int. J. Curr. Microbiol. App Sci.* **9** (7), 3358–3367 (2020).
46. Banerjee, S. et al. Genetic variability, correlation coefficient and path coefficient analysis in Brinjal germplasm. *Int. J. Chem. Stud.* **6** (4), 3069–3073 (2018).
47. Reshmika, P. K., Gasti, V. D., Evoor, S., Jayappa, J. & Mulge, R. Genetic variability studies for growth, earliness, yield and quality parameters in Brinjal (*Solanum melongena* L.). *J. Env Ecol.* **33** (2), 761–766 (2015).
48. Koundinya, A. V. V., Das, A., Layek, S., Chowdhury, R. & Pandit, M. K. Genetic variability, character association and path analysis for yield and fruit quality components in Brinjal. *J. Appl. Nat. Sci.* **9** (3), 1343–1349 (2017).
49. Pujar, P., Jagadeesha, R. C. & Cholin, S. Genetic variability, heritability and genetic advance for fruit yield, yield related components of Brinjal (*Solanum melongena* L.) genotypes. *Int. J. Pure Appl. Biosci.* **5** (5), 872–878 (2017).
50. Dasmohapatra, A. & Sharma, D. Mean performance and variability analysis in long fruited Brinjal (*Solanum melongena* L.) for Chhattisgarh. *Bull. Env Pharmacol. Life Sci.* **8** (2), 28–31 (2019).
51. Yadav, N., Dhankar, S. K., Chandanshive, A. V. & Kumar, V. Studies on variability, heritability and genetic advance in Brinjal (*Solanum melongena* L.). *Bioscan* **11** (4), 3001–3005 (2016).
52. Mili, C., Bora, G. C., Das, B. J. & Paul, S. K. Studies on variability, heritability and genetic advance in *Solanum melongena* L. (brinjal) genotypes. *Direct Res. J. Agri Food Sci.* **2** (11), 192–194 (2014).
53. Patel, V. K., Singh, U., Goswami, A., Tiwari, S. K. & Singh, M. Genetic variability, interrelationships and path analysis for yield attributes in eggplant. *Jour Env Ecol.* **35** (2A), 877–880 (2017).
54. Vidhya, C. & Kumar, N. Genetic variability studies in Brinjal (*Solanum melongena*) for fruit yield and quality. *Electron. J. Plant. Breed.* **6** (3), 668–671 (2015).
55. Shankar, A., Reddy, R., Sujatha, M. & Pratap, M. Genetic variability studies in F_1 generation of tomato (*Solanum lycopersicon* L.). *IOSR J. Agric. Vet. Sci.* **4**, 31–34 (2013).
56. Dutta, T., Bhattacharjee, T., Maurya, P. K., Dutta, S. & Chattopadhyay, A. Studies on genetic variability and identification of selection indices in Brinjal (*Solanum melongena* L.). *J. Pharmacogn Phytochem.* **7** (5), 1259–1264 (2018).
57. Dutta, R., Mandal, A. K., Maity, T. K. & Hazra, P. Multivariate genetic divergence in Brinjal (*Solanum melongena* L.). *J. Crop Weed.* **5** (1), 67–70 (2009).
58. Shekhar, K. C., Ashok, P. & Sasikala, K. Studies on heritability and multivariate analysis in Brinjal (*Solanum melongena* L.). *Veg. Crops Res. Bull.* **76**, 79–88 (2012).
59. Arunkumar, B., Sunil, K. S. V. & Chandra, P. J. Genetic variability and divergence studies for morpho economic characters in Brinjal (*Solanum melongena* L.). *Int. J. Agri Sci.* **10**, 529–533 (2014).
60. Begum, M. N. S., Shirazy, B. J., Mahub, M. M. & Siddique, M. A. Performance of brinjal (*Solanum melongena*) genotypes through genetic variability analysis. *Am. Jour Pl Biol.* **3** (1), 2–9 (2017).
61. Bhatt, P. K., Zapadiya, V. J., Sapovadiya, M. H. & Chetariya, C. P. Estimation of heterobeltiosis and standard heterosis for fruit yield and its attributes in brinjal (*Solanum melongena* L.). *J. Pharmacogn Phytochem.* **8** (4), 1384–1388 (2019).
62. Pandey, S., Mishra, S., Kumar, N., Yadav, G. C. & Pandey, V. P. Studies on genetic divergence for yield and its component traits in Brinjal or eggplant (*Solanum melongena* L.). *J. Pharmacogn Phytochem.* **8** (1), 1167–1169 (2019).
63. Shende, K. G., Bhalekar, M. N. & Patil, B. T. Characterization of Brinjal (*Solanum melongena* L.) germplasm. *Veg. Sci.* **39** (2), 186–188 (2012).
64. Shafeeq, A., Hanchinal, R. R. & Kolakar, S. S. Heterosis breeding in Brinjal. *Int. J. Plant Sci.* **8** (2), 377–380 (2013).
65. Mistry, C. R., Kathiria, K. B., Sabolu, S. & Kumar, S. Heterosis and inbreeding depression for fruit yield attributing traits in eggplant. *Curr. Plant. Biol.* **16**, 27–31 (2018).
66. Singh, S., Sharma, H. D., Dogra, R. K., Verma, V. & Aditika, S. Study of heterosis for vegetative and quantitative traits in Brinjal (*Solanum melongena* L.). *J. Pharm. Innov.* **10** (12), 335–338 (2021).
67. Susmitha, J. R., Eswaran, R. & Kumar, N. S. Heterosis breeding for yield and its attributes in Brinjal (*Solanum melongena* L.). *Electron. J. Plant. Breed.* **14** (1), 114–120 (2023).
68. Pramila, Kushwaha, M. L. & Singh, Y. P. Studies on heterosis in Brinjal (*Solanum melongena* L.). *Int. J. Curr. Microbiol. App Sci.* **6** (11), 641–651 (2017).
69. Reddy, C. V. K., Deshmukh, J. D. & Kalpande, H. V. Heterosis for fruit and its yield attributing traits in Brinjal (*Solanum melongena* L.). *J. Pharmacogn Phytochem.* **9** (6), 480–486 (2020).
70. Makasare, P. V., Bagade, A. B. & Kalyankar, S. V. Identification of heterotic hybrids for yield and yield traits in Brinjal. *J. Pharmacogn Phytochem.* **9** (6), 333–336 (2020).
71. Rani, M., Kumar, S. & Kumar, M. Estimation of heterosis for yield and its contributing traits in Brinjal. *Jour Environ. Bio.* **39**, 710–718 (2018).
72. Deshmukh, J. D., Kalpande, H. V. & Kalyankar, S. V. Heterosis and combining ability analysis for productivity traits in Brinjal (*Solanum melongena* L.). *J. Pharm. Innov.* **9** (11), 177–180 (2020).
73. Bagade, A. B., Deshmukh, J. D. & Kalyankar, S. V. Heterosis studies for yield and yield traits in Brinjal. *J. Pharm. Innov.* **9** (11), 205–208 (2020).
74. Shende, V. D., Chattopadhyay, A., Yadav, Y., Seth, T. & Mukherjee, S. Breeding round fruited Brinjal for export from Eastern India. *Agric. Res.* **5** (3), 219–229 (2016).
75. Joshi, D. P., Patel, N. B., Patel, A. M. & Chaudhary, G. K. Exploitation of gene action and combining ability for high yielding and good fruit quality characters of Brinjal in different environments of Gujarat. *J. Pharm. Innov.* **12** (8), 1370–1374 (2023).
76. Gami, R. A., Kugashiya, K. G., Solanki, R. S. & Patel, R. N. Diallel analysis in sorghum for forage yield and attributes by Griffing and Hayman's approaches. *Electron. J. Plant. Breed.* **14** (3), 794–802 (2023).
77. Thota, H. & Delvadiya, I. R. Unveiling the genetic potential of eggplant (*Solanum melongena* L.) genotypes, hybrids for yield and fruit borer resistance. *Electron. J. Plant. Breed.* **15** (1), 53–62 (2024).
78. Bhutia, N. D., Seth, T., Shende, V. D., Dutta, S. & Chattopadhyay, A. Estimation of heterosis, dominance effect and genetic control of fresh fruit yield, quality and leaf curl disease severity traits of Chilli pepper (*Capsicum annum* L.). *Sci. Hortic.* **18**, 47–55 (2015).
79. Chaurasia, N. K., Sarmah, P., Sarma, N. & Sarma, B. D. Combining ability and heterosis studies in Brinjal (*Solanum melongena* L.). *Veg. Sci.* **45** (1), 68–72 (2018).
80. Mishra, S. K., Tiwari, A., Vishen, G. S. & Verma, S. R. Combining ability analysis for yield and contributing traits in Brinjal (*Solanum melongena* L.) genotypes and hybrids. *Int. J. Adv. Biochem.* **8** (8), 1220–1224 (2024).
81. Nikhila, J. P. J., Gowda, T. H. & Dushyanthkumar, B. Combining ability studies for yield and yield attributing traits in Brinjal (*Solanum melongena* L.). *Jour Pharm. Innov.* **12** (3), 4572–4578 (2023).

82. Anvesh, S., Delvadiya, I. R., Farooq, F. & Abhilash, P. V. Elucidation of nature of geneaction and Estimation of combining ability effects for fruit yield and its componenttraits and resistance to fruit and shoot borer in Brinjal (*Solanum melongena* L.). *J. Appl. Nat. Sci.* **16** (2), 584–591 (2024).

Author contributions

Authors' contributions: Barsha Tripathy & P. Tripathy- Preparation of the draft manuscript, G.S. Sahu & S.K. Dash – provided germplasm and field facility to conduct the experiment, Jyothsna J & Meenakshi Badu – preparation and arrangement of figures, Subrat Kumar Mahapatra – preparation of graphs and statistical analysis. GRRout – edited the final manuscript. All authors read and approved the final manuscript.

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Correspondence and requests for materials should be addressed to G.R.R.

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