



Assessment of Genetic Variability in Brinjal [*Solanum melongena* L.] Genotypes Using Morphological, Biochemical and Molecular Approaches

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ABSTRACT: Brinjal (*Solanum melongena* L.) is an economically important vegetable crop widely cultivated in tropical and subtropical regions. The present study was conducted to assess genetic variability, heritability, genetic advance, correlation, path coefficient, genetic divergence and molecular diversity using SSR markers among 35 brinjal genotypes during *kharif-rabi* 2024-25 at the Main Vegetable Research Station, Anand Agricultural University, Anand in a randomized complete block design with three replications. Analysis of variance revealed highly significant differences among the genotypes for all 13 quantitative characters studied. The genotypic coefficient of variation (GCV) ranged from 6.28 per cent (days to 50% flowering) to 46.20 per cent (total number of fruits per plant), while phenotypic coefficient of variation (PCV) ranged from 7.17 to 48.15 per cent. High heritability (>60%) coupled with high genetic advance as per cent over mean (>20%) was recorded for total number of fruits per plant, total soluble sugar, fruit length and petiole length, indicating prevalence of additive gene action. Fruit yield per plant showed significant positive correlation with leaf width and total soluble solids. Path coefficient analysis revealed that total soluble solids, total number of fruits per plant and fruit girth had the highest positive direct effects on fruit yield. The D² analysis grouped the 35 genotypes into four clusters; the highest inter-cluster distance was observed between Cluster II (GP-BRJ-268, GGB 9) and Cluster IV (AB 22-11). Molecular characterization using SSR markers showed that out of 60 primers screened, 7 were polymorphic producing 14 alleles with 100 per cent polymorphism and an average PIC value of 0.418.

Keywords: Brinjal, Genetic variability, Heritability, Genotypic coefficient of variation, Phenotypic coefficient of variation, SSR markers.

INTRODUCTION

Brinjal (*Solanum melongena* L.), commonly known as eggplant, is one of the most widely cultivated vegetable crops in tropical and subtropical regions. It belongs to the family Solanaceae and has a somatic chromosome number of $2n = 2x = 24$ (Kashyap *et al.*, 2003). The Indo-Burma region is considered the centre of origin of brinjal (Isshiki *et al.*, 1994). Globally, brinjal production is estimated at around 64 million tonnes, with India contributing approximately 13.5 million tonnes cultivated over about 1.95 million hectares worldwide (Kumar *et al.*, 2022). The major brinjal producing states in India include West Bengal, Maharashtra, Bihar, Odisha, Gujarat and Andhra Pradesh.

Brinjal fruits are nutritionally rich, containing essential amino acids and significant medicinal value. In Ayurveda, brinjal is valued for its therapeutic properties, particularly for managing Type 2 diabetes due to its high dietary fiber and low carbohydrate content. Scientific

investigations have also demonstrated anticancer potential from methanolic extracts of brinjal peel.

Understanding the nature and extent of genetic variability is crucial for implementing effective selection programs in brinjal breeding. Combining heritability estimates with genetic variability provides accurate predictions for potential improvements through selection (Burton *et al.*, 1952). High estimates of GCV, PCV, heritability and genetic advance indicate the influence of additive gene action, which is vital for designing efficient breeding programs. Correlation and path coefficient analysis help identify yield-contributing traits (Dewey and Lu 1959). Mahalanobis's D² technique and molecular markers such as SSRs enable precise assessment of genetic divergence and diversity among genotypes. Keeping these facts in view, the present study on brinjal was undertaken with the following objectives: (1) to study the extent of genetic variability, (2) to estimate the correlation and path coefficient between yield and yield contributing characters, (3) to assess

genetic divergence using D² analysis, and (4) to assess brinjal variability using molecular markers.

MATERIALS AND METHODS

The experiment was conducted during the *kharif-rabi* season of 2024-25 at the Main Vegetable Research Station, Anand Agricultural University, Anand (23°35'N, 72°55'E; elevation 45.1 m). The experimental soil belongs to the Alfisol group with sandy loam texture. The region receives an average annual rainfall of around 870 mm.

A total of 35 brinjal genotypes (Table 1) were evaluated in a randomized complete block design (RCBD) with three replications at a spacing of 90 cm × 45 cm. Data were recorded from five randomly selected plants per plot. Thirteen quantitative traits were studied: days to 50% flowering, plant height (cm), leaf length (cm), leaf width (cm), petiole length (cm), fruit girth (cm), fruit length (cm), total number of fruits per plant, total soluble solid (°Brix), total soluble sugar (%), total moisture content (%), total phenol content (mg/100 g) and fruit yield per plant (kg/plant). Twenty qualitative

morphological descriptors were assessed as per DUS guidelines.

Statistical Analysis. Analysis of variance was carried out as per Panse and Sukhatme (1978). Genotypic and phenotypic coefficients of variation were computed following Burton (1952). Heritability in broad sense was estimated as per Allard (1960). Genetic advance was estimated at 5 per cent selection intensity ($K = 2.06$) using the formula of Allard (1960). Correlation coefficients and path coefficient analysis were performed as per Singh and Choudhary (1985) and Dewey and Lu (1959), respectively. Genetic divergence was assessed using Mahalanobis D² statistics (Rao, 1952) with Tocher's method for cluster grouping. For molecular diversity, genomic DNA was extracted from 35-day-old leaves using the CTAB method (Doyle and Doyle, 1990). Sixty SSR primers were screened, and polymorphic markers were used for PCR amplification. Data were scored as presence (1) or absence (0) of bands. PIC was estimated by the formula of Botstein *et al.* (1980). Cluster analysis was performed using UPGMA via NTSYS-pc (Rohlf, 1998).

Table 1: List of 35 brinjal genotypes evaluated.

Sr. No.	Genotype	Sr. No.	Genotype	Sr. No.	Genotype
1.	AB 22-03	13.	AB 22-15	25.	GP-BRJ-263
2.	AB 22-04	14.	AB 22-16	26.	GP-BRJ-264
3.	AB 22-05	15.	AB 22-17	27.	GP-BRJ-265
4.	AB 22-06	16.	AB 22-18	28.	GP-BRJ-266
5.	AB 22-07	17.	GP-BRJ-255	29.	GP-BRJ-267
6.	AB 22-08	18.	GP-BRJ-256	30.	GP-BRJ-268
7.	AB 22-09	19.	GP-BRJ-257	31.	GP-BRJ-269
8.	AB 22-10	20.	GP-BRJ-258	32.	GAOB 2 (C)
9.	AB 22-11	21.	GP-BRJ-259	33.	GRB 8 (C)
10.	AB 22-12	22.	GP-BRJ-260	34.	GGB 9 (C)
11.	AB 22-13	23.	GP-BRJ-261	35.	SWARNAMANI BLACK (C)
12.	AB 22-14	24.	GP-BRJ-262		

(C) = Check genotype

RESULTS AND DISCUSSION

Morphological Variability. The qualitative characterization of 35 brinjal genotypes for 20 morphological traits revealed considerable variability indicating rich genetic diversity. Dentate leaf margin was predominant (25 genotypes), while sinuate and entire types were less common. Leaf spineness was absent in all genotypes except GAOB 2, which exhibited strong spines. Leaf blade colour was mainly green (31 genotypes) with a few purple types; most genotypes exhibited medium colour intensity. Leaf vein colour was largely purple (27 genotypes) with variation in intensity. Stem anthocyanin pigmentation was present in 24 genotypes with varying intensities, and stem pubescence also showed variation. Most genotypes produced 1-3 flowers per inflorescence while some had more than three.

Fruit colour varied widely with purple being dominant, followed by green, white and black. Fruit shape showed high diversity ranging from globular to cylindrical and other forms. Most genotypes had rounded apex and straight fruits. Fruit stripes were mostly absent and solitary fruiting was more common than cluster type. Calyx colour was predominantly green with some purple types, and calyx spineness was observed in only a few genotypes.

Analysis of Variance. The analysis of variance (Table 2) indicated highly significant differences among the 35 genotypes for all 13 characters studied, indicating the presence of substantial genetic variability, providing ample scope for selection in brinjal improvement programmes. These findings are in agreement with earlier reports of Ravali *et al.* (2017); Jyoti *et al.* (2019).

Table 2: Analysis of variance (mean sum of squares) for different characters in brinjal.

Characters	Replications (df=2)	Genotypes (df=34)	Error (df=68)
Days to 50% flowering	6.87	24.17**	2.23
Plant height (cm)	12.27	1084.80**	46.07
Leaf length (cm)	1.73	24.64**	1.75
Leaf width (cm)	0.47	21.99**	0.67
Petiole length (cm)	0.17	8.53**	0.15
Fruit girth (cm)	1.00	47.57**	2.18
Fruit length (cm)	0.04	53.99**	1.24
Total number of fruits per plant	8.95	589.03**	16.46
Total soluble solid (°Brix)	0.60	1.75**	0.21
Total soluble sugar (%)	0.03	4.32**	0.04
Total moisture content (%)	7.21	142.63**	44.26
Total phenol content (mg/100 g)	14.72	202.90**	24.06
Fruit yield per plant (kg/plant)	0.02	0.82**	0.12

** Significant at 1% level of probability

Variability Parameters. The genotypic and phenotypic coefficients of variation, heritability and genetic advance expressed as per cent over mean for all 13 characters are presented in Table 3.

Genotypic coefficient of variation (GCV) ranged from 6.28 per cent for days to 50% flowering to 46.20 per cent for total number of fruits per plant. High GCV (>20%) was observed for total number of fruits per plant (46.20%), total soluble sugar (43.96%), fruit length (39.66%) and petiole length (36.70%). Moderate GCV (10-20%) was recorded for plant height (22.76%), fruit girth (22.23%), fruit yield per plant (19.11%), leaf length (17.54%), total phenol content (12.95%) and total soluble solid (11.49%). Low GCV (<10%) was observed for total moisture content (6.86%) and days to 50% flowering (6.28%). Similar results were reported by Balasubramaniyam *et al.* (2021); Lodhi *et al.* (2023).

Phenotypic coefficient of variation (PCV) ranged from 7.17 per cent for days to 50% flowering to 48.15 per cent for total number of fruits per plant. PCV values were slightly higher than corresponding GCV values for all characters, indicating the influence of environmental factors on trait expression, though the close magnitude between them indicates a predominance of genetic control. These findings are in agreement with Kuswaha *et al.* (2023); Choudhary *et al.* (2023).

Heritability estimates ranged from 42.56 per cent for total moisture content to 97.26 per cent for total soluble

sugar. High heritability (>60%) was recorded for total soluble sugar (97.26%), petiole length (94.81%), fruit length (93.41%), total number of fruits per plant (92.06%), leaf width (91.32%), plant height (88.26%), fruit girth (87.36%), leaf length (81.27%), days to 50% flowering (76.64%), total phenol content (71.24%) and total soluble solid (70.82%). Moderate heritability was recorded for fruit yield per plant (64.30%) and total moisture content (42.56%). Similar results were reported by Sakriya *et al.* (2020); Lodhi *et al.* (2023).

Genetic advance expressed as percentage of mean ranged from 9.22 per cent for total moisture content to 91.32 per cent for total number of fruits per plant. High genetic advance (>20%) was observed for total number of fruits per plant (91.32%), total soluble sugar (89.30%), fruit length (78.96%), petiole length (73.60%), leaf width (47.79%), plant height (44.06%), fruit girth (42.81%), leaf length (32.57%), fruit yield per plant (31.56%) and total phenol content (22.51%). High heritability coupled with high genetic advance for traits such as total number of fruits per plant, total soluble sugar, fruit length and petiole length indicates the prevalence of additive gene action, suggesting these traits can be effectively improved through direct selection. Similar observations were reported by Mishra *et al.* (2024a).

Table 3: Estimates of variability parameters for yield and quality traits in brinjal.

Sr. No.	Character	GV (σ^2_g)	PV (σ^2_p)	GCV (%)	PCV (%)	h ² b (%)	GAM (%)
1.	Days to 50% flowering	7.29	9.55	6.28	7.17	76.64	11.32
2.	Plant height (cm)	346.33	392.44	22.76	24.23	88.26	44.06
3.	Leaf length (cm)	7.62	9.36	17.54	19.46	81.27	32.57
4.	Leaf width (cm)	7.13	7.78	24.28	25.41	91.32	47.79
5.	Petiole length (cm)	2.79	2.96	36.70	37.69	94.81	73.60
6.	Fruit girth (cm)	15.13	17.31	22.23	23.79	87.36	42.81
7.	Fruit length (cm)	17.56	18.84	39.66	41.04	93.41	78.96
8.	Total number of fruits per plant	190.72	207.07	46.20	48.15	92.06	91.32
9.	Total phenol content (mg/100 g)	59.60	83.72	12.95	15.34	71.24	22.51
10.	Total soluble solid (°Brix)	0.52	0.72	11.49	13.65	70.82	19.92
11.	Total soluble sugar (%)	1.42	1.46	43.96	44.57	97.26	89.30
12.	Total moisture content (%)	32.83	77.09	6.86	10.52	42.56	9.22
13.	Fruit yield per plant (kg/plant)	0.23	0.36	19.11	23.83	64.30	31.56

GV: Genotypic variance; PV: Phenotypic variance; GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; h²b: Heritability (broad sense); GAM: Genetic advance as per cent over mean

Correlation Coefficient Analysis. Genotypic correlations were generally higher than phenotypic correlations, indicating strong genetic associations among traits. Days to 50% flowering showed a significant positive correlation with total soluble solid at both genotypic ($r_g = 0.510^{**}$) and phenotypic ($r_p = 0.301^*$) levels. Plant height exhibited a highly significant positive correlation with leaf width ($r_g = 0.562^{**}$, $r_p = 0.519^{**}$). Leaf length was positively correlated with leaf width ($r_g = 0.366^*$, $r_p = 0.319^{**}$) and fruit girth ($r_g = 0.400^*$, $r_p = 0.353^{**}$) but negatively with total number of fruits per plant ($r_p = -0.254^*$).

Leaf width showed a highly significant positive correlation with fruit yield per plant ($r_g = 0.455^{**}$, $r_p = 0.381^{**}$), indicating that genotypes with wider leaves tended to produce higher yield. Fruit girth showed a highly significant negative correlation with total number of fruits per plant ($r_g = -0.764^{**}$, $r_p = -0.676^{**}$), indicating a trade-off between fruit size and fruit number. Fruit length exhibited a highly significant positive correlation with total soluble sugar ($r_g = 0.549^{**}$, $r_p = 0.537^{**}$). Total soluble solid showed a significant positive association with fruit yield per plant ($r_g = 0.363^*$, $r_p = 0.306^*$). Fruit yield per plant showed significant positive correlation with leaf width and total soluble solid, which agrees with Vashi *et al.* (2022); Rathod *et al.* (2024); Lakshmi *et al.* (2014).

Path Coefficient Analysis. Path coefficient analysis revealed the direct and indirect effects of different characters on fruit yield per plant. Total soluble solid exhibited the highest positive direct effect (0.920) on fruit yield per plant followed by total number of fruits per plant (0.814), fruit girth (0.712), petiole length (0.171), fruit length (0.122) and leaf width (0.101). Negative direct effects were recorded for days to 50% flowering (-0.329), total moisture content (-0.354), total phenol content (-0.200), leaf length (-0.134) and total soluble sugar (-0.117). The residual effect of 0.441

indicated that the characters included in the study explained a considerable proportion of variability in yield. Similar results for positive direct effects of total soluble solid and total number of fruits per plant on fruit yield were reported by Chetan *et al.* (2023); Rathod *et al.* (2024).

Genetic Divergence (D^2 Statistics). The 35 brinjal genotypes were grouped into four clusters using Tocher's method (Table 4). Cluster I was the largest, containing 31 genotypes. Cluster II contained two genotypes (GP-BRJ-268, GGB 9), while Clusters III and IV each comprised a single genotype (AB 22-10 and AB 22-11 respectively), indicating high divergence of these genotypes.

The intra-cluster distance was highest in Cluster I (231.38). The maximum inter-cluster distance was observed between Cluster II and Cluster IV (1000.69), followed by Cluster II and Cluster III (767.52) and Cluster I and Cluster III (704.96), indicating greater genetic divergence among these clusters. The minimum inter-cluster distance was recorded between Cluster I and Cluster II (429.53), suggesting a relatively closer genetic relationship.

Cluster mean analysis showed that Cluster II had higher values for plant height (87.67 cm), leaf length (19.73 cm), leaf width (13.33 cm) and fruit girth (19.50 cm), indicating vigorous vegetative growth. Cluster IV showed the highest mean value for total number of fruits per plant (78.90) indicating better yield potential. Cluster III exhibited higher values for total moisture content (93.00%) and total phenol content (72.72 mg/100 g). Character contribution analysis revealed that total soluble sugar contributed the highest proportion (26.94%) to genetic divergence, followed by petiole length (14.79%), total number of fruits per plant (13.91%) and fruit length (10.02%). Similar results were reported by Tabasum *et al.* (2023).

Table 4: Grouping of 35 brinjal genotypes in various clusters based on D^2 statistics.

Cluster	No. of Genotypes	Name of Genotypes
I	31	AB 22-03, AB 22-04, AB 22-05, AB 22-06, AB 22-07, AB 22-08, AB 22-09, AB 22-12, AB 22-13, AB 22-14, AB 22-15, AB 22-16, AB 22-17, AB 22-18, GP-BRJ-255, GP-BRJ-256, GP-BRJ-257, GP-BRJ-258, GP-BRJ-259, GP-BRJ-260, GP-BRJ-261, GP-BRJ-262, GP-BRJ-263, GP-BRJ-264, GP-BRJ-265, GP-BRJ-266, GP-BRJ-267, GP-BRJ-269, GAOB 2, GRB 8, SWARNAMANI BLACK
II	2	GP-BRJ-268, GGB 9
III	1	AB 22-10
IV	1	AB 22-11

Table 5: Average intra and inter-cluster distance (D^2) among 35 brinjal genotypes.

Clusters	I	II	III
I	231.38		
II	429.53	202.52	
III	704.96	767.52	0.00
IV	591.22	1000.69	640.77

Molecular Diversity Using SSR Markers. Out of 60 SSR primers screened, 26 showed successful PCR amplification. Among these, 7 were polymorphic

producing 14 alleles with 100 per cent polymorphism. Heterozygosity ranged from 5.71 per cent (EES021) to 54.29 per cent (emd18B04), indicating significant

outcrossing. PIC values ranged from 0.184 (emf11L21) to 0.500 (emg01B17) with an average of 0.418, indicating moderately informative markers (Table 6). Based on Botstein *et al.* (1980) classification, most markers fell in the moderately informative category (PIC = 0.25-0.50). UPGMA cluster analysis grouped the 35 genotypes into five main clusters (A to E). Cluster B1

had the maximum number of genotypes (11), while A1, C2 and E each contained a single genotype. Genotype GP-BRJ-266 was the most diverse at the molecular level, followed by GGB 9 and SWARNAMANI BLACK. Similar results were reported by Akhther *et al.* (2021); Faizan *et al.* (2022); Musa *et al.* (2024).

Table 6: Summary of SSR marker analysis in brinjal.

Sr. No.	Primer Name	Heterozygosity (%)	Band Size (bp)	PIC Value
1.	emg01B17	11.43	200-300	0.500
2.	emf11L21	11.43	200-300	0.184
3.	emd18B04	54.29	150-250	0.483
4.	EES021	5.71	200-300	0.497
5.	emf21K08	14.29	200-300	0.349
6.	emf01O01	40.00	150-250	0.498
7.	EES026	34.29	200-300	0.418
	Average	24.49	—	0.418

CONCLUSIONS

The overall study revealed significant variability among 35 brinjal genotypes in growth, yield and quality traits, as well as in morphological traits. Analysis of variance confirmed highly significant differences among genotypes for all characters studied. High GCV, PCV, heritability and genetic advance for total number of fruits per plant, total soluble sugar, fruit length and petiole length indicated the predominance of additive gene action and good scope for improvement through direct selection. Fruit yield per plant showed significant positive correlation with leaf width and total soluble solid. Path coefficient analysis showed that total soluble solid, total number of fruits per plant and fruit girth had strong positive direct effects on fruit yield. Genetic divergence analysis grouped the genotypes into four clusters, indicating substantial diversity; crosses between genotypes from Cluster II and Cluster IV are expected to produce superior hybrids. At molecular level, seven polymorphic SSR markers produced 14 alleles with 100 per cent polymorphism and an average PIC value of 0.418, indicating their suitability for genetic diversity assessment in brinjal.

FUTURE SCOPE

Wide range of variability was observed for all the characters studied. Hence, attention needs to be given to traits such as total number of fruits per plant, total soluble sugar and fruit length during selection for improvement of fruit yield. The genotypes AB 22-10, AB 22-11, GP-BRJ-268 and GGB 9, which showed high divergence, should be evaluated further and used in crossing programs to develop superior brinjal hybrids. The identified polymorphic SSR markers can be used for marker-assisted selection in brinjal improvement programmes.

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