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Morpho-molecular diversity in Indian brinjal genotypes

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Abstract

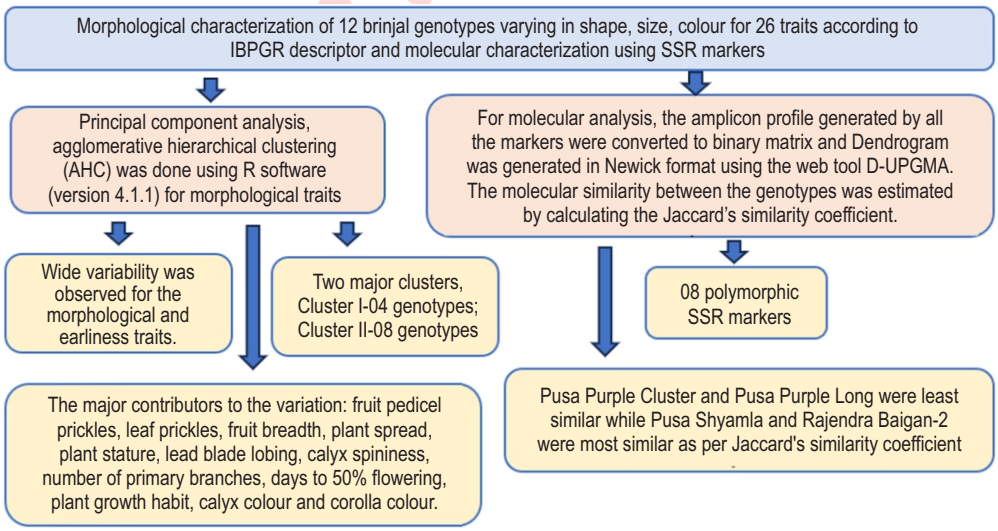
Aim: To identify morphological and molecular diversity of eggplant genotypes for utilization in breeding programmes for widening the narrow genetic base of brinjal.

Methodology: Twelve brinjal genotypes varying in shape, size and colour were studied for twenty-six morphological traits, based on which principal component analysis and agglomerative hierarchical clustering were performed. Molecular characterization was done using SSR markers.

Results: Wide variability was observed for the morphological and earliness traits. The first three principal components accounted for 74.88% of the total variation. The major contributors to the variation were fruit pedicel prickles, leaf prickles, fruit breadth, plant spread, plant stature, calyx spininess, number of primary branches, days to 50% flowering, and plant growth habit. Clustering of genotypes formed two major clusters, with big sized round or oblong genotypes in one cluster and long or oval smaller-sized genotypes in the other cluster and crossing between the genotypes of different clusters would be an effective breeding strategy. Eight polymorphic SSR markers could distinguish between these twelve genotypes. Jaccard's similarity coefficient showed that Pusa Purple Cluster and Pusa Purple Long were least similar, while Pusa Shyamla and Rajendra Baigan-2 were most similar, and lesser similar genotypes would be potential parental lines for brinjal.

Interpretation: Genotypes in different clusters, with dissimilarity based on both morphological and molecular characterization may be used as parental lines for breeding programmes. The major contributor traits identified for the variation may be used as selection criteria.

Key words: Brinjal genotypes, Morpho-molecular diversity, PCA biplot, SSR markers



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Introduction

Brinjal is one of the most popular solanaceous fruit vegetables grown widely throughout the globe. It is typically cultivated by marginal farmers in Asia, and its sale is an important source of cash income (Rashid *et al.,* 2003). It is native to India, and the country holds the second rank in its production share in the world after China, with the production of 12.998 million tons cultivated in 0.683 million hectare area (Department of Agriculture & Farmers Welfare, 2025). Brinjal is an indigenous vegetable of India, however, the crop has a narrow genetic base, which is a bottleneck in its improvement. In India, a great variation of cultivars is observed distributed throughout the country. Brinjal fruits of diverse cultivars chiefly differ in fruit shape, size, colour and taste (Frary *et al.,* 2007). The consumer preference for the crop varies from region to region, even within a state, but globally it has been observed that purple coloured brinjal fruits are more preferred (Kumari *et al.,* 2022). Huge diversity exists among indigenous brinjal in plant type, stem colour, leaf size and tip, midrib colour, fruit size, shape and colour, fruit yield, and tolerance to biotic and abiotic stresses (Ullah *et al.,* 2014). Improvement in the crop may be achieved by exploiting the available sources of variability (Sangam *et al*., 2020).

For improvement of the crop, it is necessary to select genetically diverse parental lines, which is possible through genetic divergence study (Uddin *et al.,* 2014). The extent of genetic diversity between the available germplasm and the relative contribution of different traits towards diversity can be estimated through multivariate analysis (Quamruzzaman *et al.,* 2009; Amin *et al.,* 2014; Nalla *et al.,* 2014). Molecular markers are being used for diversity studies in various crops at DNA level. In brinjal, molecular diversity studies have been done by seed protein (Karihaloo *et al.,* 2002; Lester and Hasan, 1991), isozymes (Lester and Hasan, 1991), allozymes (Isshiki *et al.,* 1994), mitochondrial DNA (Isshiki *et al.,* 2003), chloroplast DNA (Isshiki *et al.,* 1998), RAPD markers (Nunome *et al.,* 2001), AFLP markers (Furini and Wunder, 2004) and microsatellites (Nunome *et al.,* 2001; 2003). However, most of these studies aimed at determining the relation between the cultivated brinjal and the wild species. Simple sequence repeat (SSR) markers have high reproducibility, abundance and wide genome coverage, with multi-allelic nature, co-dominant inheritance.

SSRs are ideal markers for mapping and diversity studies, fingerprinting and population genetics due to high level of polymorphism (Nunome *et al.,* 2003). SSR markers are more effective than RAPD markers for assessing brinjal genetic diversity and variations (Akhther *et al.,* 2021; Musa *et al.,* 2024). However, limited studies have been conducted on the use of SSR markers to differentiate Indian brinjal cultivars, the studies often involve wild genotypes, lesser number of markers with reproducible results (Quaiyum *et al.,* 2025). The simultaneous morphological and molecular diversity studies in cultivated brinjal genotypes would be of great interest to brinjal breeders and reveal valuable information on variation and genetic base of the crop, which would determine the parental lines for future breeding programmes. Principal components analysis can reveal information regarding the contribution of diverse traits in variation among the genotypes and the SSR marker assisted characterization of the set of genotypes would be confirmatory discrimination of the genotypes.

The limitation of SSR-marker assisted differentiation in brinjal genotypes determine the suitability of its use as parental line in a breeding programme. Integration of SSR-marker aided diversity with PCA studies offers a novel and detailed aspect on the trait contribution and diversity of the genotypes. In view ot the above, this study was planned with the objectives of morphological and molecular characterization of diverse brinjal genotypes, diversity analysis of the genotypes through principal components analysis and UPGMA clustering of the genotypes to define the morphological variation in cultivated brinjal coupled with molecular diversity among the same.

Materials and Methods

Plant materials: Twelve brinjal genotypes were collected from different regions of India and maintained at the Vegetable Research Section of the Bihar Agricultural University, Sabour, Bhagalpur were used for the study (Table 1).

Experimental details: The experiment was laid in a Randomised Block Design with three replications during spring summer season of 2019-20 and summer-rainy season of 2020. The plants were spaced at 75 cm x 60 cm and the size of each plot was 3.75m x 3.0 m. The pooled data of two seasons were used for analyses. These genotypes were grown in the spring-summer season (transplanted in December, 2019), summer-rainy season (transplanted in February, 2020).

Morphological characterization: The morphological characterization was done according to the IBPGR eggplant descriptor (IBPGR, 1990). Plant growth habit, plant height, plant spread, number of primary branches, petiole colour, leaf blade length, leaf blade width, leaf blade lobing, leaf blade colour, leaf tip angle, leaf prickles, days to 50% flowering, corolla colour, calyx colour, calyx spininess, fruit pedicel prickles, fruit length, fruit breadth, fruit length: breadth ratio, fruit curvature, fruit shape, fruit apex shape, fruit colour and fruit colour distribution were studied.

The yield attributing characters like fruit length, fruit breadth, fruit length: breadth ratio play an important role in determining the economic yield of the crop. Important plant growth traits such as plant height, plant spread and primary branch number were recorded at 120 days after transplanting. Earliness indicator days to 50 percent flowering was noted when 50% of the plants per replication attained flowering. Fruit morphological traits like fruit length and fruit diameter were measured from fruits harvested at edible maturity stage from the second, fourth and sixth harvest and their average values were used for analyses.

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Table 1: Source of genotypes used in study

Genotypes	Sources
BRBL-01(IC 633633)	Developed and maintained at Bihar Agricultural University, Sabour
BRBL-02	Developed and maintained at Bihar Agricultural University, Sabour
BRBL-07(IC 639101)	Developed and maintained at Bihar Agricultural University, Sabour
Rajendra Baigan-2	Developed and maintained at Bihar Agricultural University, Sabour
Swarna Mani	Collected from ICAR-RCER, Ranchi and maintained at Bihar Agricultural University, Sabour
VR-2	Collected from IIVR, Varanasi and maintained at Bihar Agricultural University, Sabour
Pant Samrat	Collected from GBPAUT, Pantnagar and maintained at Bihar Agricultural University, Sabour
Pusa Purple Cluster	Collected from IARI, New Delhi and maintained at Bihar Agricultural University, Sabour
Pusa Purple Long	Collected from IARI, New Delhi and maintained at Bihar Agricultural University, Sabour
Nawada Local	Local genotype collected from Nawada, Bihar
Muktakeshi	Maintained at Bihar Agricultural University, Sabour
Pusa Shyamla	Collected from IARI, New Delhi and maintained at Bihar Agricultural University, Sabour

Table 2: Polymorphic SSR markers used

Marker name	Primer sequences (5′-3′)	Amplified bands (bp*)
emb01M15	Forward: GCAAGGCTCAAAGTCACAAGTCAA Reverse: GGCTCTGCCCCTAACATCTACAAA	~240 / ~260
eme05B09	Forward: ATGAAAACTCCACTCTACTCTACTCCAC Reverse: GTTTGCTAACGTACGCCTCAATTGCTCT	~200 / ~250
emf01O01	Forward: AGGAATTGGATTTCCACTCATACG Reverse: GTTTGGAAGATGAGATTCCTTTCTTGA	~290 / ~320
emb01D10	Forward: AAGAATCGGTCCTCTTTGCATTGT Reverse: TGCTTTTCACCTCTCCGCTATCTC	~200 / ~220 / ~240
emf21K08	Forward: ATCAATGACACCCAAAACCCATTT Reverse: GTTTGAAAACCCAATACAAATCCGA	200 / 230
emb01J19	Forward: GACAGGGATAGGGGTACGGATAGG Reverse: ATCCATGTGATGCCTCGATTTTCT	270 / 300
emf01J09	Forward: ATAGCACCCACACTAAACCTTGGG Reverse: GTTTCACTTCTTGGTCCATTGTTCAGA	300 / 320
emk03O04	Forward: ATGATTTGGGCAGCCACTTTTGTA Reverse: GTTTGGAACCAACTAAACTTAGGGCA	160 / 185

*bp = base-pairs

Genomic DNA extraction and polymerase chain reaction (PCR): The genomic DNA of 12 brinjal genotypes was isolated from young leaves following a rapid DNA isolation protocol (Kumar *et al.,* 2017). From the isolated genomic DNA, 2 µl was used for a 12 µl PCR volume containing 1X reaction buffer [10 mM Tris-Cl (pH 8.3), 50 mM KCl, 1.5 mM $MgCl_2$ and 0.1 % (v/v) Triton X-100], 0.1 mM dNTPs, 5 pmole of each forward and reverse primers (Table 2) and 1U of Taq DNA polymerase (Xcelris). PCR was programmed as initial denaturation for 4 min at 94 °C, 40 cycles of denaturation at 94 °C for 30 sec, annealing at appropriate temperature for 30 sec and extension at 72 °C for 30 sec followed by a final extension at 72 °C for 7 min and hold at 4 °C for 2 min. The amplicons generated were visualized and imaged in gel documentation system (Genei, Bangalore) after electrophoresis in 1.5 % (w/v) agarose gel containing ethidium bromide. 27 SSR markers were used out of which 8 exhibited polymorphism (Table 2).

Statistical analyses: The morphological data were subject to Principal Components Analysis (PCA). PCA-Biplot analysis was used to describe multivariate relationships among different genotypes. Euclidean distance was applied to estimate genetic dissimilarity component and Ward's method was used for agglomerative hierarchical clustering (AHC), thereafter, a dendogram was created. Core Team, 2021 Software R (version 4.1.1) was used for all statistical analyses.

The utilized packages were: Agricolae, Factoextra, FactoMineR, Cluster, dplyr, corrplot, ggplot2 and RColorBrewer. For molecular analysis, the amplicon profile generated by all the markers were converted to 1/0 matrix on the basis of presence/absence of a specific band. This matrix was used to generate Dendrogram in Newick format using the web tool D-UPGMA (https: // usuaris.tinet.cat/ debb/UPGMA/). A phylogenetic tree was visualized using the web tool TreeDyn

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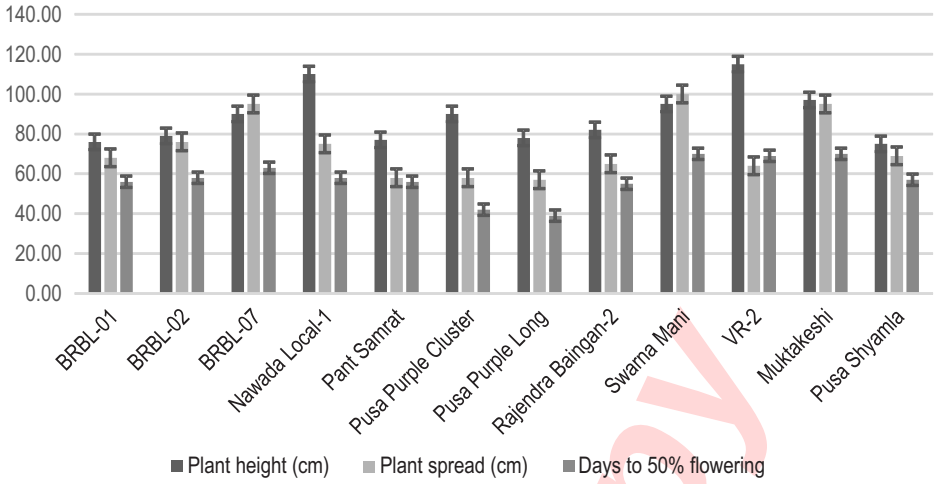


Fig. 1: Plant height, plant spread and days to 50% flowering in brinjal genotypes.

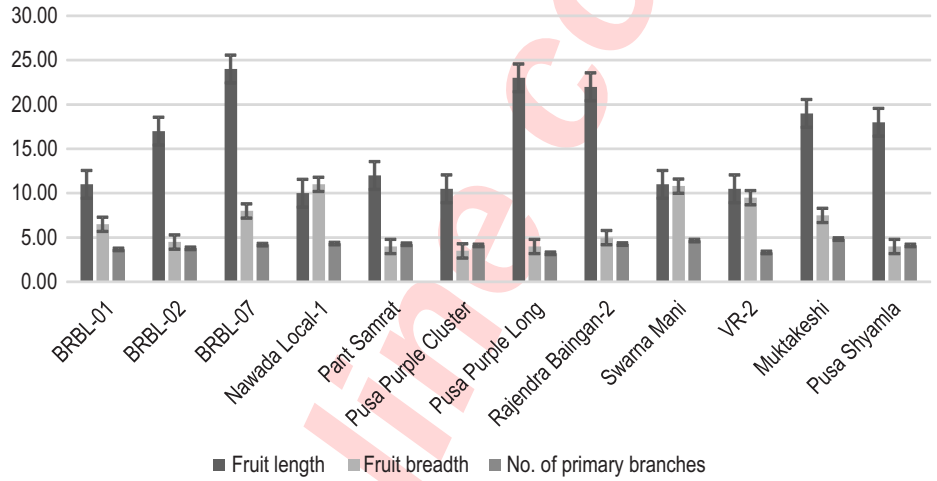


Fig. 2: Fruit length, fruit breadth and number of primary branches in brinjal genotypes.

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(http://www.phylogeny.fr/one_task.cgi?task_type=treedyn). Molecular similarity between the genotypes was estimated by calculating the Jaccard's similarity coefficient.

Results and Discussion

The qualitative morphological traits of egg plant genotypes have been depicted in Table 3 and 4. The growth traits of 25 percent of egg plant genotypes was upright, 25 percent was prostrate while 50 percent genotypes had intermediate growth. It was observed that 33.33 percent genotypes showed fever leaf prickles, while 66.67 percent genotypes did not exhibit any leaf prickles. The fruits of 8.33 percent genotypes were oval, 16.67 percent genotypes oblong, 25 percent round and 50 percent long. Twenty five percent of these genotypes had green fruits, 33.33 percent purple fruits and 41.67 percent purple black fruits. There were regular stripes on the fruits of 8.33 percent genotypes, mottling in other 8.33 percent, while 83.33 percent genotypes showed uniform colour distribution in fruits. These results show that ample diversity existed among the genotypes that was expressed at the morphological level, and this diversity will be useful while selecting the lines as parents in breeding programme. Islam *et al.* (2018) studied 40 diverse brinjal genotypes of Bangladesh and could observe similar types of morphological traits for plant growth habit, leaf blade lobing, leaf prickles, leaf tip angle, fruit apex shape, fruit colour, fruit colour distribution. These results are also in line with the findings of Solaimana *et al.* (2015). The quantitative traits of brinjal genotypes under study are depicted in Fig. 1 and 2.

The plant height of the genotypes varied from 75 cm in Pusa Shyamla to 115 cm in VR-2. The plant spread ranged from

Table 3: Morphological traits of twelve brinjal genotypes characterized as per DUS descriptor for eggplant

Genotype → / Trait ↓	BRB L-01	BRB L-02	BRB L-07	Nawada Local-1	Pant Samrat	Pusa Purple Cluster	Pusa Purple Long	Rajendra Baingan-2	Swarna Mani	VR-2	Muktakeshi	Pusa Shyamla
Plant growth habit	Upright	Intermediate	Prostrate	Intermediate	Intermediate	Intermediate	Upright	Intermediate	Prostrate	Upright	Prostrate	Intermediate
Plant spread	Broad	Broad	Very broad	Broad	Intermediate	Intermediate	Intermediate	Broad	Very broad	Broad	Very broad	Broad
Petiole colour	Green	Violet	Dark violet	Greenish violet	Greenish violet	Dark violet	Greenish violet	Green	Dark violet	Green	Dark violet	Violet
Leaf blade length	Short	Short	Intermediate	Intermediate	Short	Short	Short	Intermediate	Intermediate	Intermediate	Intermediate	Short
Leaf blade width	Intermediate	Intermediate	Intermediate	Intermediate	Intermediate	Intermediate	Intermediate	Intermediate	Intermediate	Intermediate	Intermediate	Intermediate
Leaf blade lobing	Intermediate	Intermediate	Intermediate	Strong	Intermediate	Intermediate	Weak	Intermediate	Strong	Intermediate	Intermediate	Weak
Leaf blade colour	Green	Greenish violet	Greenish violet	Greenish violet	Greenish violet	Violet	Dark green	Green	Greenish violet	Green	Greenish violet	Dark green
Leaf tip angle	Intermediate	Intermediate	Intermediate	Intermediate	Intermediate	Intermediate	Acute	Acute	Acute	Intermediate	Intermediate	Acute
Leaf prickles	None	None	Very few	Very few	None	None	None	None	Very few	None	Very few	None
Corolla colour	Light violet	Light violet	Bluish violet	Bluish violet	Light violet	Bluish violet	Light violet	White	Bluish violet	Pale violet	Bluish violet	Bluish violet
Calyx colour	Green	Light purple	Dark purple	Light purple	Light purple	Dark purple	Light purple	Green	Dark purple	Green	Dark purple	Light purple
Calyx spininess	Very few	Very few	Very few	Very few	None	None	None	None	Very few	None	Very few	None
Fruit pedicel prickles	None	None	Few	Few	None	None	None	None	Few	None	Few	None
Fruit length-breadth ratio	Twice as long as broad	Several timesas long as broad	Thrice as long as broad	Broader than long	Several times as long as broad	Several times as long as broad	Several times as long as broad	Several times as long as broad	As long as broad	Slightly longer than broad	Thrice as long as broad	Several times as long as broad
Fruit curvature	None	Slightly curved	None	None	Curved	None	Curved	Curved	None	None	None	Curved
Fruit shape	Oval	Long	Oblong	Round	Long	Long	Long	Long	Round	Round	Oblong	Long
Fruit apex shape	Rounded	Rounded	Rounded	Depressed	Protruded	Rounded	Rounded	Protruded	Depressed	Rounded	Rounded	Protruded
Fruit colour	Green	Purple	Purple black	Purple	Purple black	Purple	Purple	Green	Purple black	Green	Purple black	Purple black
Fruit colour distribution	Regular striped	Uniform	Uniform	Mottled	Uniform	Uniform	Uniform	Uniform	Uniform	Uniform	Uniform	Uniform

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Table 4: Eigen values, and variation proportion across the axes 26 traits of 12 brinjal genotypes

Principal Components	Eigen value	Variance percent	Cumulative variance percent
PC1	10.26	41.03	41.03
PC2	5.98	23.91	64.94
PC3	2.49	9.95	74.88
PC4	1.99	7.98	82.86
PC5	1.21	4.85	87.71
PC6	1.12	4.49	92.21
PC7	0.71	2.86	95.07
PC8	0.52	2.08	97.15
PC9	0.38	1.54	98.69
PC10	0.20	0.82	99.51
PC11	0.12	0.49	100.00

Table 5: Principal components of 26 traits of 12 brinjal genotypes – non-rotated loadings

Traits	PC1	PC2	PC3	PC4	PC5
Plant growth habit (PGH)	0.676	0.661	0.217	-0.011	0.161
Plant height (PH)	0.291	-0.719	-0.093	-0.508	0.011
Plant stature (PS)	0.768	0.066	0.514	0.319	0.060
Petiole colour (PeC)	0.503	0.782	-0.197	0.030	0.043
Leaf blade length (LBLe)	0.705	-0.211	0.550	-0.295	0.090
Leaf blade width (LBW)	0	0	0	0	0
Leaf blade lobing (LBLo)	0.777	-0.269	-0.139	-0.148	0.121
Leaf blade colour (LBC)	0.316	0.712	-0.305	-0.329	0.195
Leaf tip angle (LTA)	0.250	-0.221	-0.481	0.108	0.728
Leaf prickles (LP)	0.844	0.028	-0.013	-0.130	-0.281
Corolla colour (CoC)	0.536	0.471	-0.526	0.165	-0.204
Calyx colour (CaC)	0.536	0.756	-0.274	-0.063	-0.021
Calyx spininess (CaS)	0.755	-0.015	-0.066	0.538	0.021
Fruit pedicel prickles (FrPP)	0.929	0.187	0.104	0.008	-0.114
Fruit length-breadth ratio (FrL.FrB)	-0.722	0.531	0.122	0.221	0.314
Fruit curvature (FrCu)	-0.755	0.297	0.303	-0.162	-0.263
Fruit shape (FrS)	0.563	-0.707	-0.073	0.359	-0.087
Fruit apex shape (FrAS)	0.755	-0.246	-0.352	-0.015	-0.320
Fruit colour (FrCo)	0.318	0.789	-0.300	-0.117	-0.202
Fruit colour distribution (FrCD)	0.017	-0.580	-0.291	0.677	-0.073
Plant height measured (PHcm)	0.648	-0.454	-0.007	-0.520	0.131
Plant spread (PScm)	0.852	0.279	0.308	0.281	-0.012
Number of primary branches (NPB)	0.636	0.488	0.144	-0.043	0.134
Days to 50% flowering (D50F)	0.691	-0.181	0.461	0.083	0.262
Fruit length (FrLcm)	-0.248	0.499	0.597	0.150	-0.099
Fruit breadth (FrBcm)	0.849	-0.460	0.140	-0.101	-0.134

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57 cm (Pusa Purple Long) to 100 cm (Swarna Mani) genotype. Pusa Purple Long showed early 50% flowering (39 days after transplanting), while Muktakeshi showed late 50% flowering (70 days after transplanting). Fruit length ranged from 10 cm (Nawada Local) to 24 cm (BRBL-07), while fruit width ranged from 3.5 cm (Pusa Purple Cluster) to 11 cm (Nawada Local). The number of primary branches ranged between 3.23 (Pusa Purple Long) to 4.83 (Muktakeshi). The range of different quantitative characters is in accordance with Kaur *et al*. (2018) who reported plant height of 74.67-145.67 cm, fruit length of 6.83-13.70 cm, fruit breadth of 4.83-9.97 cm, and primary branch number ranging between 2.33 to 6.33 and Kumari *et al*. (2018) who reported days taken to 50% flowering in brinjal genotypes ranging between 46 to 69, and fruit length of 8.83-22.91 cm. The results show that there was wide variation among the genotypes for growth traits like plant height, plant spread, number of primary branches, earliness trait like days to 50% flowering, and fruit morphological traits like fruit length and fruit breadth. Collection of genotypes from various parts of the country may have attributed to wide variation among the genotypes for different quantitative traits since diverse local materials including landraces from different geographic regions introduces a broad gene pool (Rajappa *et al*., 2023), that serves as a source of wide variation.

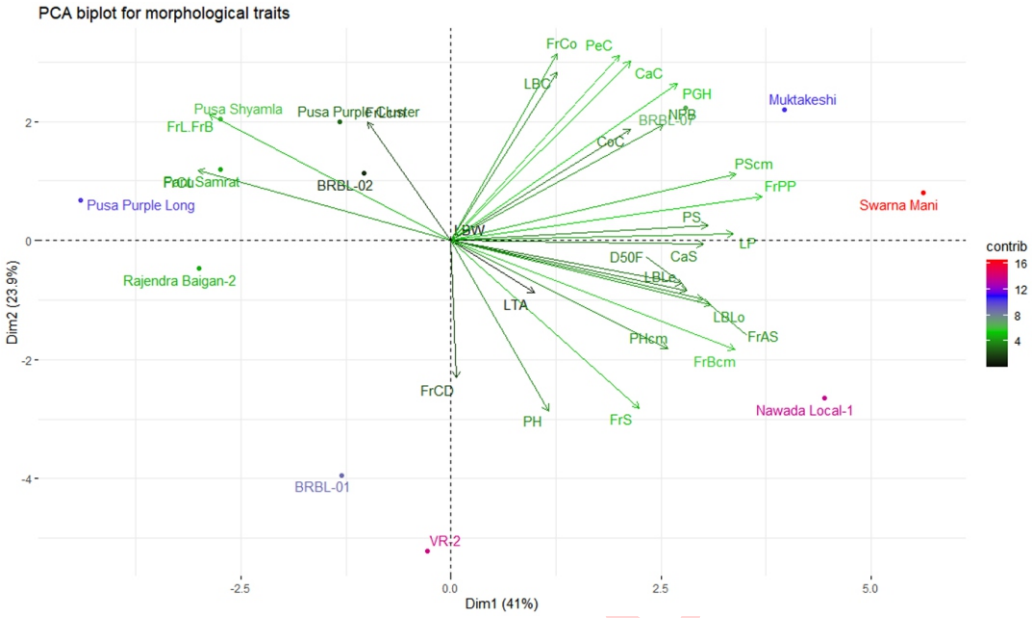


Fig. 3: PCA biplot for morphological traits in 12 brinjal genotypes. Note: Plant growth habit: PGH; Plant height: PH; Plant stature: PS; Petiole colour: PeC; Leaf blade length: LBLe; Leaf blade width: LBW; Leaf blade lobing: LBLo; Leaf blade colour: LBC; Leaf tip angle: LTA; Leaf prickles: LP; Corolla colour: CoC; Calyx colour: CaC; Calyx spininess: CaS; Fruit pedicel prickles: FrPP; Fruit length-breadth ratio: FrL.FrB; Fruit curvature: FrCu; Fruit shape: FrS; Fruit apex shape: FrAS; Fruit colour: FrCo; Fruit colour distribution: FrCD; Plant height measured: PHcm; Plant spread: PScm; Number of primary branches: NPB; Days to 50% flowering: D50F; Fruit length: FrLcm; Fruit breadth: FrBcm.

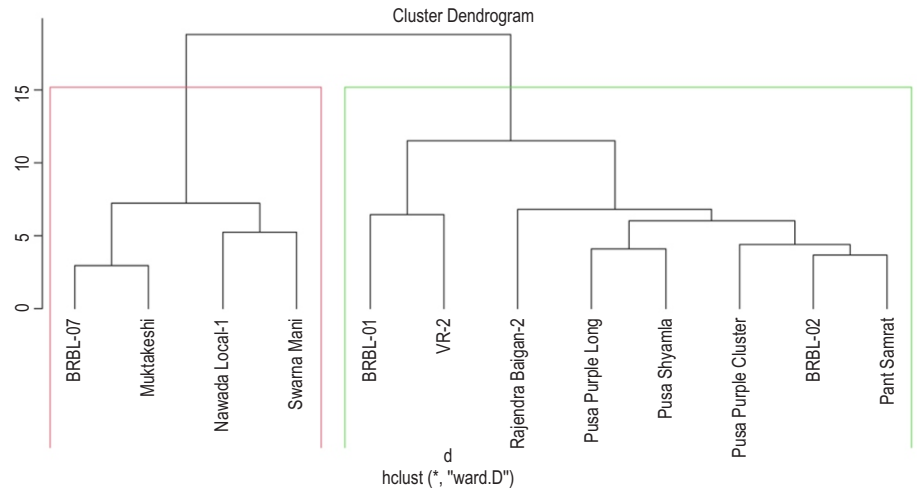


Fig. 4: Clustering of twelve brinjal genotypes based on morphological traits.

The morphological data were subjected to principal component analysis to depict the relationship between the genotypes and the morphological traits under study. It is a descriptive method exhibiting variation of traits in the genotypes and depicts a multi-dimensional relationship among the traits and genotypes (Nwangburuka *et al.,* 2011). Variations accounted in each principal component is depicted through Eigen values. The first three principal components showed Eigen values greater than 2 and also accounted for 74.88% of the total variation, while the first five principal components accounted for a cumulative of 87.71% variation in the twelve genotypes for twenty-six traits that were studied. Nandini *et al.* (2025) reported that the first five PCs accounted for 79.84% of the total variation, while Rameshkumar *et al.* (2016) reported 75.82% of the total variation. The first

Table 6: Jaccard's similarity co-efficient values of 12 brinjal genotypes on the basis of polymorphism at 8 SSR loci

	BRBL-01	BRBL-02	BRBL-07	Rajendra Baigan-2	Swarna Mani	VR-2	Pant Samrat	Pusa Purple Cluster	Pusa Purple Long	Nawada Local	Muktakeshi	Pusa Shyamla
BRBL-01	1	0.455	0.455	0.545	0.333	0.231	0.500	0.333	0.333	0.364	0.333	0.600
BRBL-02		1	0.600	0.417	0.455	0.333	0.364	0.778	0.231	0.364	0.778	0.455
BRBL-07			1	0.417	0.455	0.600	0.364	0.455	0.231	0.154	0.455	0.455
Rajendra Baigan-2				1	0.308	0.417	0.778	0.308	0.308	0.455	0.545	0.889
Swarna Mani					1	0.455	0.250	0.333	0.333	0.364	0.600	0.333
VR-2						1	0.364	0.455	0.231	0.154	0.455	0.455
Pant Samrat							1	0.250	0.364	0.556	0.500	0.875
PusaPurple Cluster								1	0.143	0.250	0.600	0.333
PusaPurple Long									1	0.364	0.333	0.333
Nawada Local										1	0.500	0.500
Muktakeshi											1	0.600
PusaShyamla												1

principal component accounted for 41.03% variation and the major contributors to the variation were fruit pedicel prickles, leaf prickles, fruit breadth, plant spread, plant stature, lead blade lobing, calyx spininess, number of primary branches, days to 50% flowering, plant growth habit, calyx colour and corolla colour. Karim *et al.* (2016) reported that the first PC was responsible for 48.22% of the total variation in brinjal, while Kumari *et al.* (2022) reported 43.7% contribution of PC1 towards variation in brinjal grown in summer season.

The first principal component was found responsible for the maximum number of traits accountable for the variations and similar trend has been observed in previous studies of Verma *et al.* (2025). PC2 contributed 23.91% to the variation and in this component the highest loadings were contributed by fruit colour, petiole colour, calyx colour, leaf blade colour, plant growth habit, fruit length-breadth ratio (Table 5). Rahaman *et al.* (2025) reported that PC2 accounted for 29.45% variation in brinjal, while PC3 contributed towards 9.95% of the total variation. The major traits contributor to the variation were fruit length, leaf blade length and plant stature. PC4 accounted for 7.98% of the total variation and calyx spininess was the dominant trait affecting variation in this component. PC5 was responsible for 4.85% of the total variation, and leaf tip angle showed the highest loading in this component. Fig. 3 shows the PCA biplot for 26 morphological traits in 12 brinjal genotypes under study.

It shows that the major contributors to PC1 and PC2 were fruit breadth, fruit pedicel prickles, plant growth habit, pedicel colour, calyx colour, fruit shape, plant spread, fruit colour and leaf prickles. Previous studies of Rahaman *et al.* (2014) also reported fruit breadth as an important contributor towards brinjal diversity. Selection among groups with high mean and high variability as well as high mean and low variability could be worthwhile and result in transgressive segregants (Rameshkumar *et al.,* 2016). Swarna Mani, Muktakeshi, Pusa Purple Long, Nawada Local, Rajendra Baigan-2 and Pant Samrat showed high scores for PC1, while VR-2, BRBL-01, Pusa Plurple Cluster, BRBL-02 showed high

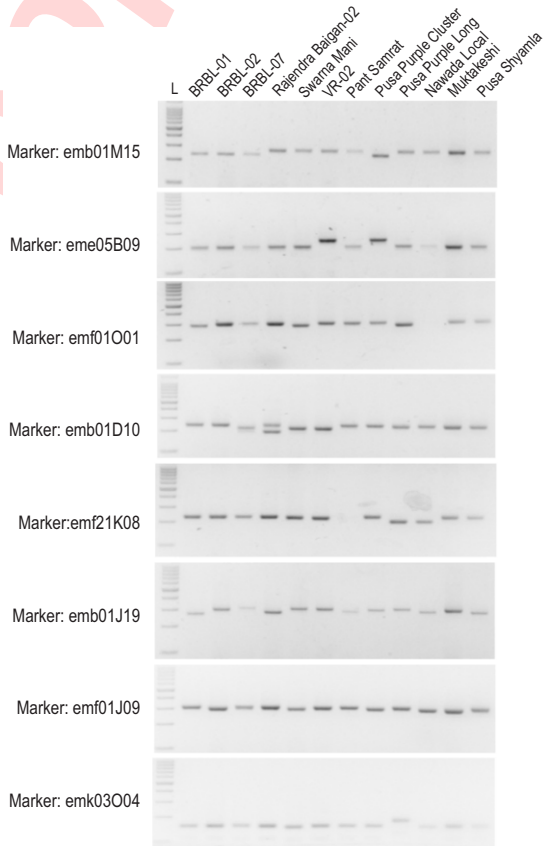


Fig. 5: Inverse image of 2% agarose gel showing amplicons generated by 8 polymorphic SSR markers in 12 brinjal genotypes.

scores for PC2. Hierarchical cluster analysis (HCA) was performed and the genotypes were grouped based on enhanced dissimilarity. It was analyzed by Euclidean distance as a measure of distinctness of the genotypes and Ward's method for clustering. The dendrogram depicted in Fig. 4 shows that there were two major clusters, the

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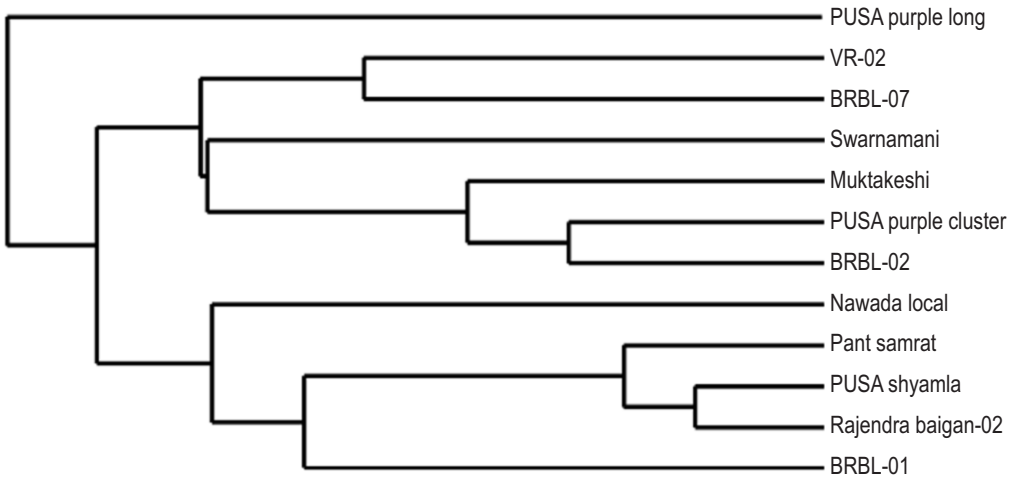


Fig. 6: Dendrogram of 12 brinjal genotypes on the basis of polymorphism at 8 SSR loci.

first cluster having four genotypes (BRBL-07, Muktakeshi, Nawada Local and Swarna Mani). The second major cluster possessed eight genotypes (BRBL-01, VR-2, Rajendra Baigan-2, Pusa Purple Long, Pusa Purple Cluster, BRBL-02, Pant Samrat). Cluster-I is comprised of genotypes with more fruit weight, fruit breadth and uniform dark purple in colour with few leaf and pedicel prickles. Cluster-II consisted of genotypes devoid of leaf and pedicel prickles and lesser fruit width. It was clearly observed that the round and oblong genotypes with higher fruit length and fruit width were placed in Cluster I and all of them were purple in colour having uniform colour distribution, and also having calyx and fruit pedicel prickles. On the other hand, the genotypes in Cluster II were long or oval, with less fruit length, fruit breadth, having colour green or purple, with uniform distribution or presence of stripes or patches and absence of calyx spines, fruit pedicel prickles or leaf prickles. Selection of parental genotypes from different clusters are expected to create high diversity, and therefore may be used in future breeding programmes. Previous work on cluster analysis of brinjal by Verma *et al.* (2025) has also been in accordance of these findings who showed that accessions belonging to distinct clusters were ideal for breeding.

Molecular tools have been used on a low scale in brinjal compared to other solanaceous vegetables, despite being efficient for selective breeding. Use of RAPD and SSR markers have been done previously by Verma *et al.* (2012), Parvin *et al.* (2020), Dash *et al.* (2023), while there are reports of use of sequence-related amplified polymorphism (SRAP) markers by Li *et al.* (2010). While all these markers have been able to differentiate genotypes at molecular level, markers like RAPD are not reproducible and SSR markers are the most reproducible, and hence widely accepted for molecular level differentiation between genotypes. Combining morphological and molecular diversity analyses is expected to provide deeper insights into genetic diversity among eggplant accessions (Kaur *et al.,* 2020; Verma *et al.,* 2025). Polymorphic bands are necessary for showing distinctness of genotypes and in this study eight SSR markers showed polymorphism for various traits, and the amplification profile of these eight polymorphic markers is presented in Fig. 5. In this study, 1-2 bands were observed, which is in accordance with the study of Dash *et al.* (2023). The presence and absence of these bands were put in binary form and Jaccard's similarity coefficient was estimated. Jaccard's similarity co-efficient values between these 12 brinjal genotypes is summarised in Table 6. Least similarity was recorded between Pusa Purple Long and Pusa Purple Cluster, whereas the highest similarity was observed between Pusa Shyamla and Rajendra Baigan-2 genotypes.

The overall genotyping of these 12 brinjal genotypes at 8 polymorphic loci was used to generate dendrogram (Fig. 6), which could identify all the genotypes individually. Three major clusters were observed, viz., Cluster I with Pusa Purple Long; Cluster II with VR-2 and BRBL-07, Swarna Mani, Muktakeshi, Pusa Purple Cluster and BRBL-02; Cluster III with Nawada Local, Pant Samrat, Pusa Shyamla, Rajendra Baingan-2 and BRBL-01. Kumar *et al.* (2025) grouped 19 brinjal genotypes into two major clusters and four subclusters through SSR-marker mediated study.

There was wide variation in the various morphological traits under study and fruit pedicel prickles, leaf prickles, fruit breadth, plant spread, plant stature, lead blade lobing, calyx spininess, number of primary branches, days to 50% flowering, plant growth habit, calyx colour and corolla colour could be identified as the major contributors to variation. The diversity studies on morphological and molecular basis could identify round fruited genotypes Swarna Mani, Nawada Local, oblong fruited genotypes Muktakeshi, BRBL-07 and long fruited genotypes Pusa Purple Long, Pusa Purple Cluster as promising parental lines for future breeding programmes. Crossing between these genotypes is expected to create transgressive segregants and improved varieties.

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