



RESEARCH ARTICLE

Diversity analysis of long- and round-fruited brinjal genotypes using multivariate analysis

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Abstract

For sustainable production and climate change adaptation, farmers need better brinjal varieties. This study aimed to identify suitable long and round brinjal genotypes for utilization in future breeding programmes. About 69 brinjal genotypes, including long- and round-fruited types collected from different sources, were evaluated following a randomized complete block design. Characters such as plant height, plant spread (N-S), petiole length, leaf blade length and width, days to 50% flowering, fruit weight, length, number of fruits/plant, and marketable fruit yield/plant emerged as the most reliable characters irrespective of fruit shape in brinjal for selection. Fruit weight and number of fruits/plants, irrespective of fruit shape, emerged as the most important selection indices. Six clusters formed in this study do not correspond to geographic locations, suggesting that genotypes inside a cluster were genetically distinct from genotypes collected in the same location. Multivariate analysis and average values of economic characters suggest that 8 genotypes' Bidhan Supreme, 2020/BRL VAR-10, 2021/BRL VAR-5, 2022/BRL VAR-12, 2022/BRL VAR-13, 2022/BRL VAR-8, 2022/BRL VAR-6 and 2022/BRL VAR-1' in long-fruited brinjal, and 4 genotypes, 2021/BRR VAR-2, 2021/BRR VAR-8, 2021/BRR VAR-12 and 2021/BRR VAR-11 in round-fruited brinjal could be potential donors for future brinjal breeding. Breeders might be able to introduce potential alleles into commercial genotypes to obtain prospective recombinants that possess desired economic characteristics.

Keywords: Brinjal, Genetic variability, Correlation, Path analysis, Multivariate analysis.

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Citation: Rahaman, M.A., Sengupta S., Sarkar, M., Sarkar, J., Baul D., Mallick R.G., Mandal A.K., & Chattopadhyay A. (2025). Diversity analysis of long- and round-fruited brinjal genotypes using multivariate analysis. *Vegetable Science* 52(1): 30-38.

Source of support: Nil

Conflict of interest: None.

Received: 25/04/2024 **Revised:** 20/03/2025 **Accepted:** 25/04/2025

Introduction

Brinjal (*Solanum melongena* L.) is one of the most widely produced vegetable crops in India, with the exception of higher altitudes (Hazra et al., 2011). The previous name, aubergine, implies that the initial arrivals were little egg-shaped fruits and that different sizes and shapes gradually developed as a result of strong selection pressure and other breeding techniques. In our country, a variety of landraces/cultivars with different fruit shapes and colors—from oval to long club-shaped—and from white, yellow, and green to varying degrees of purple pigmentation to nearly black were available. Fruits contain a variety of antioxidants and phytochemicals, including delphinidin in the peel (Wu et al., 2009) and chlorogenic acid in the flesh (Whitaker and Stommel, 2003), which have been shown to have health benefits (Akanitapichat et al., 2010). Additionally, it has some medical benefits for treating diabetes, asthma, cholera, bronchitis, diarrhea, high blood cholesterol, and liver problems (Tomar and Kalda, 1998). Brinjal is frequently referred to as the "King of Vegetables" because of its adaptability and ability to be employed in a variety of culinary applications (Choudhary and Gaur, 2009).

Although the crop is grown all across the nation, West Bengal, Orissa, Gujarat, Bihar, and Madhya Pradesh are the main states that produce brinjal (Akanksha *et al.*, 2023). West Bengal covers the largest area (162.99 lakh ha) under brinjal cultivation with a productivity of 18.58 t/ha (NHB, 2021-22). Due to its reliance on cultivars of local preference, West Bengal is still trailing behind in achieving the highest levels of output. Evaluation of the most recent breeding lines is crucial because genetic diversity holds the possibility of continued crop improvement. Yield is a complicated variable that is strongly influenced by a variety of polygenically inherited traits. The division of variability into heritable and non-heritable components and the development of suitable genotypes through phenotypic and genotypic correlations substantially facilitate the formulation of selection strategies. Understanding the relationship between yield and the traits that contribute to it is fundamental, and guidelines for plant selection should be sought out first. Partitioning of total correlation into direct and indirect effects by path coefficient analysis helps in making the selection more effective. Precise information on the nature and degree of genetic divergence would help the plant breeder in choosing promising parents for a purposeful hybridization program. The Mahalanobis (1936) D^2 statistic, used in multivariate analysis, is an effective tool for measuring genotype divergence. Therefore, this investigation precisely aimed to study the nature of genetic variability existing among eggplant genotypes irrespective of fruit shape along with the economic traits and to analyze genetic divergence of materials to identify diverse parents for hybridization.

Materials and Methods

Plant Materials and Field Growing

A field experiment was carried out during *autumn-winter* season of 2022- 23 at the research plot of the All India Coordinated Research Project on Vegetable Crops, Bidhan Chandra Krishi Viswavidyalaya, Kalyani, Nadia, West Bengal. About 67 advanced breeding lines comprising both long- and round-fruited types were collected from the Project Coordinator cell, ICAR-Indian Institute of Vegetable Research, Varanasi, along with two released varieties Bidhan Supreme and Bidhan Super collected from AICRP on Vegetable Science, BCKV center constituted the plant materials for this study. Genotypes (34 long and 35 round types) were grown in Randomized Complete Block Design with three replications. The seeds, treated with Thiram (3 g/ kg of seed), were sown in the 4th week of June 2022, spaced 5 cm apart at a shallow depth. Finally, when the seedlings reached thirty days old, they were transplanted to the main field at a spacing of 75 cm in both ways in a plot measuring 3.75 m × 3.75 m during the last week of July 2022. A fertilizer dose of 150 kg N, 75 kg P_2O_5 and 75 kg K_2O /ha, along with 10 t FYM/ha was given. Management practices as scheduled for cultivation were followed as per Chattopadhyay *et al.* (2007).

Observations recorded

Data were collected from 15 plants chosen at random from each plot within each replication. The observations such as plant height (cm), number of branches per plant, plant spread (cm), petiole length (cm), leaf blade length and width (cm), days to 50% flowering, fruit pedicel length (cm), fruit length (cm), fruit diameter (cm), number of fruits per plant, fruit weight (g) and marketable fruit yield per plant (kg) were recorded.

Statistical analysis

The mean value of the characters from each genotype in each replication was used for statistical analysis. The traits studied were analyzed using the Analysis of Variance (ANOVA) method, following the approach described by Panse and Sukhatme (1967). The genotypic (GCV) and phenotypic (PCV) coefficients of variations were calculated as per Burton (1952). Heritability in a broad sense (h^2) was estimated by the formula suggested by Hanson *et al.* (1956). The estimated genetic advance was calculated as per Johnson *et al.* (1955). Phenotypic and genotypic correlation coefficients for all possible combinations were worked out utilizing the pooled data as per Al-Jibouri *et al.* (1958). Data on phenotypic correlation coefficients were utilized to estimate the direct and indirect effects of different characters on marketable yield/plant, as per Dewey and Lu (1959). D^2 statistic (Mahalanobis, 1936) was used for assessing the genetic divergence of 69 genotypes for 14 quantitative traits. The grouping of the populations was done by using Tocher's method as described by Rao (1952). Hierarchical cluster analysis was performed to observe the degree of association according to characteristics expressed in a dendrogram (Ward, 1963). Principal component analysis (PCA) was used to identify the factor dimension of the data and to summarize varietal information in a reduced number of factors for the selection of the best-performing genotype(s). Statistical analyses were done using statistics analytical software SPSS Professional Version 13.0 and SAS 9.3 Professional Version.

Results and Discussion

Genetic variability and heritability of quantitative traits

The analysis of variance for 14 quantitative characters for 69 genotypes of brinjal is presented in Table 1. The results from the analysis of variance revealed highly significant differences among genotypes for most characters under study, which clearly endorsed the justification of studying the genetic variability of different characters employing these genotypes. Very high variance (mean sum of squares for genotype) recorded in the top three characters were fruit yield/plant, fruit weight and plant height, which indicated a very wide range of diversity for these characters concerned.

Table 2: Mean, range and estimates of genetic variability of 14 characters of 69 brinjal genotypes

Character	Mean	Range	PCV (%)	GCV (%)	Heritability (bs) (%)	Genetic advance as % of mean
						5%
Plant height (cm)	68.82	45.66-91.66	16.54	15.50	87.90	29.94
Plant spread E-W (cm)	77.49	56.33-94.33	12.09	11.53	91.00	22.67
Plant spread N-S (cm)	76.85	57.33-92.66	11.58	11.12	92.30	22.01
Number of branches/plant	6.06	2.66-8.33	25.58	25.40	4.50	2.34
Petiole length (cm)	4.98	3.03-7.76	21.57	19.76	83.90	37.27
Leaf blade length (cm)	17.42	11.63-21.76	13.08	12.03	84.60	22.80
Leaf blade width (cm)	11.59	7.11-14.93	15.91	13.46	71.50	23.46
Days to 50% Flowering	55.08	41.33-66.67	10.88	10.48	92.70	20.78
Fruit pedicel length (cm)	5.74	3.17-9.17	24.25	23.73	95.80	47.86
Fruit length (cm)	12.01	5.10-23.50	37.01	36.59	97.70	74.51
Fruit diameter (cm)	6.23	3.43-10.23	31.17	30.81	97.70	62.75
Number of fruit/plant	10.82	6.33-15.67	21.82	20.62	89.30	40.16
Fruit weight (g)	161.48	60.67-315.00	34.36	34.14	98.70	69.88
Marketable fruit yield/plant (g)	1704.41	407.33-2835.00	30.04	28.20	88.10	54.55

GCV = Genotypic coefficient of variation; PCV = Phenotypic coefficient of variation ; bs = broad sense.

that heritability estimates, along with genetic gain, are usually more helpful than heritability alone for selecting the best individuals. Therefore, all traits except the number of branches per plant can be regarded as most important for selection and this was supported by the findings of Chattopadhyay et al. (2011), and Banerjee et al. (2018). From the study of genetic variability and heritability, plant height, plant spread (N-S), petiole length, leaf blade length and width, days to 50% flowering, fruit weight, length, number of fruits per plant, and marketable fruit yield per plant emerged as most reliable characters irrespective of fruit shapes in brinjal for selection because of their probable conditioning by the additive gene action (Panse, 1957).

Study on correlation and path analysis

The genotypic and phenotypic correlations between marketable fruit yield/plant and other component traits are presented in Table 3. Significance has been tested with a view to their linearity in association. In general, the genotypic correlations were higher than the phenotypic ones, which indicated that the phenotypic expression of the correlation is reduced under the influence of the environment, although there is a strong inherent association between the various characters. Marketable fruit yield per plant was significantly and positively correlated at the phenotypic level with plant spread (N-S) ($r = 0.328^*$), plant spread (E-W) ($r = 0.319^*$), fruit diameter ($r = 0.394^*$), fruit weight ($r = 0.711^{**}$), and number of fruits per plant ($r = 0.279^*$) (Table 3). These results were in conformity with the findings of Shinde et al. (2012), Dutta

Table 3: Phenotypic and genotypic correlations and direct effects of 13 characters at phenotypic level on marketable fruit yield/plant

Character	r_p	r_g	Direct effect on marketable fruit yield/plant
Plant height (cm)	0.284	0.312**	-0.044
Plant spread E-W (cm)	0.319**	0.330**	0.118
Plant spread N-S (cm)	0.328**	0.349**	-0.056
Number of branches/plant	0.062	0.288*	0.020
Petiole length (cm)	0.056	0.083	0.045
Leaf blade length (cm)	0.094	0.073	-0.033
Leaf blade width (cm)	0.129	0.169	0.046
Days to 50% Flowering	-0.032	-0.034	-0.036
Fruit pedicel length (cm)	-0.095	-0.081	0.023
Fruit length (cm)	0.034	0.040	-0.074
Fruit diameter (cm)	0.394**	0.426**	-0.033
Number of fruit/plant	0.279*	0.230	0.708
Fruit weight (g)	0.711**	0.741**	1.025

r_p = Phenotypic correlation coefficient; r_g = Genotypic correlation coefficient

*, ** Significant at 0.05 and 0.01 level of probability, respectively.

Residual effect = 0.019

et al. (2018), and Bhattacharjee et al. (2021). However, a negative correlation between marketable fruit yield per plant and days to 50% flowering was recorded. From the above discussion, it became evident that marketable fruit yield per plant can be increased through an increase in important component traits like plant spread, fruit diameter, fruit weight and number of fruits per plant irrespective of fruit shapes in brinjal.

The direct and indirect effect of different characters on marketable fruit yield per plant at the phenotypic level is presented in Table 3. Two characteristics, namely, fruit weight and number of fruits per plant, exerted the maximum direct effects on marketable yield per plant (Table 3). The residual effect of the path analysis was low, suggesting the inclusion of maximum fruit yield influencing characters in the present study. From the study of character association ship, combining correlation and path co-efficient analysis, the characters, namely, number of fruits per plant and fruit weight, were the most important selection indices irrespective of fruit shapes in brinjal as they exerted high positive direct effects on marketable fruit yield per plant. The significance of these characters influencing fruit yield in brinjal was also supported by many workers (Chattopadhyay et al., 2011; Banerjee et al., 2018).

Divergence study

Based on the degree of divergence, all genotypes were grouped into 6 clusters (Table 4). The numbers of genotypes in clusters were in the order: Cluster I (20) > Cluster II and Cluster IV (12 each) > Cluster III and Cluster V (9 each) > Cluster VI (7). Several earlier studies reported different sets of genotypes were grouped under 6–10 clusters (Lalramhlimi et al., 2019; Bhattacharjee et al., 2022), with which this work agreed. The pattern of distribution of genotypes from diverse geographical regions into different clusters was random. This might be due to the free and frequent exchange of

genetic material among the breeders of different regions. The absence of a relationship between genetic diversity and geographical distance indicates exchange of genetic stock, genetic drift, spontaneous mutation, and natural and artificial selections are responsible for genetic diversity. Selection of genotypes for hybridization should be based on genetic divergence rather than geographic diversity. Environmental influence on the composition of cluster occurs in brinjal (Shende et al., 2016; Dutta et al., 2018; Lalramhlimi et al., 2019; Sulaiman et al., 2020; Yadav et al., 2024).

The intra- and inter-cluster distance represents the index of genetic diversity among clusters. The intra-cluster distance among 69 brinjal genotypes revealed that Cluster V exhibited the maximum intra-cluster value (450), indicating that genotypes included in this cluster are diverse (Table 5). At the inter-cluster level, the maximum value was observed between Cluster III and VI (648), indicating a distant relationship among the genotypes included in these clusters. Hence, intermating between brinjal genotypes irrespective of fruit shapes included in Clusters III, V and VI will be expected to give transgressive segregates in the early segregating generation (Kalloo et al., 1980).

The cluster means of 69 genotypes (Table 6) showed that Cluster VI had the maximum marketable fruit yield per plant, followed by Cluster II. Cluster VI had the maximum fruit diameter and fruit weight. The highest number of fruits per plant was produced by Cluster II, followed by Cluster I. Genotypes belonging to Clusters VI and II could serve as useful sources of genes for improving productivity irrespective of fruit shapes in brinjal. For yield improvement in brinjal, inter-crossing among genotypes with outstanding mean performance was advocated by previous workers (Bhattacharjee et al., 2022; Khan et al., 2023). However, there should be an optimal level of diversity, beyond which relative heterosis does not increase due to unfavorable interaction of

Table 4: Cluster classification of 69 brinjal genotypes

Cluster	Genotype
Cluster I [20]*	2020/BRL VAR-2, 2020/BRL VAR-3, 2021/BRL VAR-5, 2021/BRL VAR-7, 2021/BRL VAR-8, 2021/BRL VAR-10, 2022/BRL VAR-2, 2022/BRL VAR-3, 2022/BRL VAR-4, 2022/BRL VAR-5, 2020/BRR VAR-4, 2021/BRR VAR-8, 2021/BRR VAR-10, 2022/BRR VAR-1, 2022/BRR VAR-2, 2022/BRR VAR-4, 2022/BRR VAR-6, 2022/BRR VAR-8, 2022/BRR VAR-9, 2022/BRR VAR-10
Cluster II [12]	2020/BRL VAR-5, 2020/BRL VAR-6, 2020/BRL VAR-7, 2020/BRL VAR-9, 2021/BRL VAR-2, 2021/BRL VAR-3, 2021/BRL VAR-4, 2021/BRL VAR-9, 2020/BRR VAR-8, 2021/BRR VAR-2, 2021/BRR VAR-5, 2022/BRR VAR-5
Cluster III [9]	2020/BRL VAR-8, 2020/BRL VAR-11, 2021/BRL VAR-1, 2022/BRL VAR-13, 2022/BRL VAR-14, 2020/BRR VAR-5, 2021/BRR VAR-3, 2021/BRR VAR-11, 2022/BRR VAR-7
Cluster IV [7]	2020/BRL VAR-10, 2020/BRR VAR-3, 2021/BRR VAR-12, 2021/BRR VAR-13, 2021/BRR VAR-15, 2022/BRR VAR-11, 2022/BRR VAR-13
Cluster V [9]	2020/BRL VAR-12, 2022/BRL VAR-1, 2022/BRL VAR-6, 2022/BRL VAR-7, 2022/BRL VAR-8, 2022/BRL VAR-9, 2022/BRL VAR-11, 2022/BRL VAR-12, 2022/BRR VAR-14
Cluster VI [12]	2022/BRL VAR-10, Bidhan Supreme, 2020/BRR VAR-1, 2020/BRR VAR-2, 2020/BRR VAR-6, 2020/BRR VAR-9, 2021/BRR VAR-1, 2021/BRR VAR-9, 2021/BRR VAR-14, 2022/BRR VAR-3, 2022/BRR VAR-12, Bidhan Super

*Figures in parentheses indicate number of genotypes

Table 5: Intra-and inter-cluster distances of 69 brinjal genotypes

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	433.00*	482.00	544.00	489.00	563.00	477.00
Cluster II		414.00	526.00	538.00	613.00	559.00
Cluster III			396.00	498.00	525.00	648.00
Cluster IV				378.00	555.00	469.00
Cluster V					450.00	636.00
Cluster VI						419.00

*Bold values indicate intra-cluster distance between genotypes.

Table 6: Cluster means of 69 brinjal genotypes.

Character	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Per cent contribution towards divergence
Plant height (cm)	76.38	69.96	59.99	66.1	53	75.13	1.45%
Plant spread E-W (cm)	82.43	82.5	69.69	70.95	66.48	82.19	1.75%
Plant spread N-S (cm)	81.69	81.42	68.28	71.19	66.26	81.89	0.17%
Number of branches/plant	5.98	5.81	5.3	5.19	6.11	6.22	0%
Petiole length (cm)	5.07	4.56	4.67	5.22	5.33	5.08	0.68%
Leaf blade length (cm)	17.91	14.62	17.14	17.47	19.25	18.21	1.15%
Leaf blade width (cm)	12.26	9.38	10.59	12.15	12.4	12.51	0.04%
Days to 50% Flowering	54.8	54.69	56.26	60.95	49.74	55.61	5.07%
Fruit pedicel length (cm)	5.88	5.2	5.3	5.91	7.02	5.34	12.49%
Fruit length (cm)	11.92	12.36	9.95	9.18	17.28	11.03	16.67%
Fruit diameter (cm)	6.02	5.21	4.52	7.97	5.13	8.68	14.32%
Number of fruit/plant	11.38	12.39	10.11	9.1	11.37	9.44	0.64%
Fruit weight (g)	155	146.81	92.48	198.52	136.63	235.72	44.46%
Marketable fruit yield/plant (g)	1742.25	1824.31	925.22	1716.33	1562.7	2205.14	1.11%

co-adopted gene complexes (Dhillon et al., 2003). Therefore, the choice of diverse parents, along with good combining ability, is a prerequisite for an efficient hybridization program. The top four characters that contributed most toward genetic divergence were fruit weight followed by fruit length, fruit diameter and fruit pedicel length (Table 8). These characters may be used in selecting genetically diverse parents for hybridization to exploit either maximum heterosis or to execute efficient selection in the segregating generation.

Principal component analysis

PCA was performed to obtain a simplified view of the relationship between the characters' fruit weight and fruit pedicel length. These traits explained a 60.62% contribution towards divergence, and variable loadings for components PC₁ (fruit weight) and PC₂ (fruit pedicel length) were determined (Table 7). These components were chosen because their eigenvalues exceeded 1.0. The first component (PC₁, fruit weight) explained 31.17% of the total

accounted for variance in which an increase in fruit weight resulted in an increase in fruit pedicel length (Table 8). The second component (PC₂, fruit pedicel length) explained an additional 29.45% of the variance in which a decrease in fruit pedicel length resulted in an increase in fruit weight.

The PCA was determined to establish connections between various Indian brinjal genotypes and locate a range of diverse parents for a hybridization program (Shende et al., 2017; Bhattacharjee et al., 2022). There are no clear guidelines to determine the importance of a trait coefficient for each principal component. Johnson and Wichern (1988) regard a coefficient greater than half of the coefficient, divided by the square root of the standard deviation of the eigenvalue of the respective principal component, as significant. The dendrogram produced following Ward (1963) using squared Euclidean distance indicated there was high diversity among brinjal genotypes along with strong relationships among genotypes (Figure 1).

The scatter diagram was formed based on the fruit shape of brinjal genotypes separately. Genotypes in close

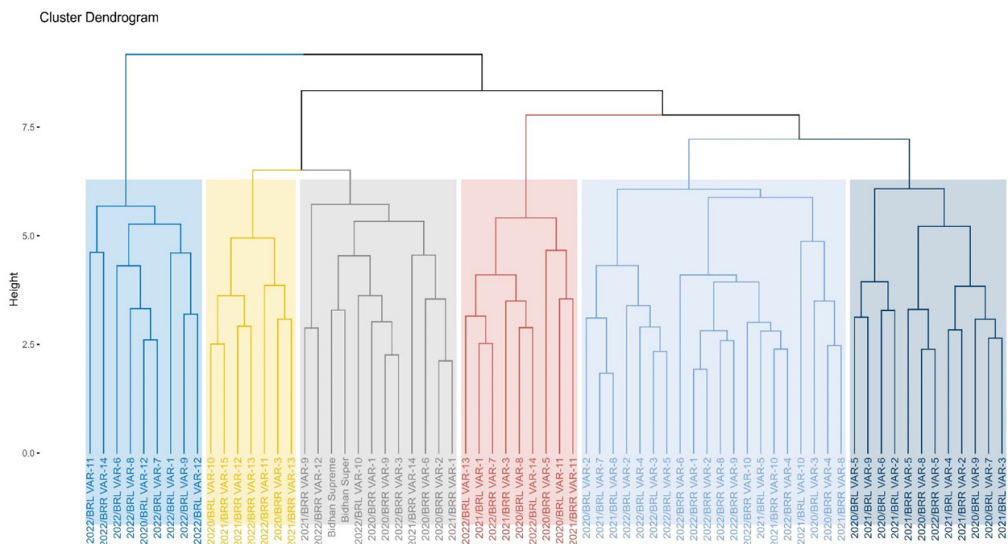


Figure 1: Dendrogram of 69 brinjal genotypes following Ward's method

Table 7: Results of principal component analysis (PCA) for characters contributing to divergence in brinjal

Principal components	Eigenvalue %	% Variance	% Cumulative variance
Eigenvalues and variance accounted for (%) by PCA based on correlation matrix			
PC ₁	1.8701	31.17	31.17
PC ₂	1.7672	29.45	60.62

Table 8: Contribution of diverse traits in the principal components of brinjal

Variables	PC ₁	PC ₂
Factor loadings due to PCs with eigenvalues greater than 1		
Fruit weight (g)	0.442387	0.519871
Fruit pedicel length (cm)	0.406341	-0.258166

proximity were perceived as being similar in PCA; genotypes further apart were more diverse (Figure 2, 3). The genotypes Bidhan Supreme, 2020/BRL VAR-10, 2021/BRL VAR-5, 2022/BRL VAR-12, 2022/BRL VAR-13, 2022/BRL VAR-8, 2022/BRL VAR-6 and 2022/BRL VAR-1 were substantially different from others. Based on multivariate analysis and *per se* performance for fruit yield per plant and other horticultural traits, the genotypes Bidhan Supreme, 2020/BRL VAR-10, 2021/BRL VAR-5, 2022/BRL VAR-12, 2022/BRL VAR-13, 2022/BRL VAR-8, 2022/BRL VAR-6 and 2022/BRL VAR-1 were identified as potential donors for utilization in long brinjal breeding (Figure 2). Round-type genotypes close together were seen as similar in PCA, whereas genotypes further apart were interpreted as more varied (Figure 3). The genotypes 2021/BRR VAR-2, 2021/BRR VAR-8, 2021/BRR VAR-12 and 2021/BRR VAR-11 were substantially different from others. Based

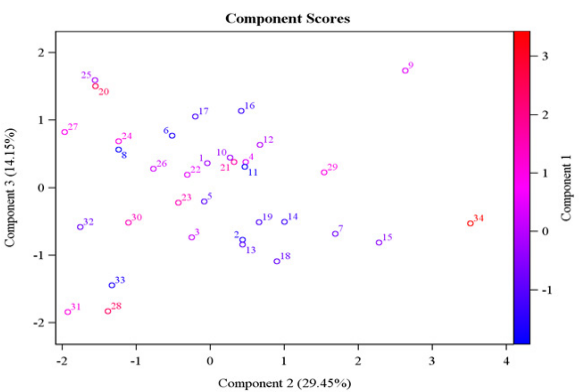


Figure 2: Scatter diagram of regression factor scores for the 1st, 2nd and 3rd components as determined by PCA in long brinjal genotypes. Outliers on the X-axis, that is, 34 = Bidhan Supreme, 9 = 2020/BRL VAR-10, 15 = 2021/BRL VAR-5, 31 = 2022/BRL VAR-12, 32 = 2022/BRL VAR-13, 27 = 2022/BRL VAR-8, 25 = 2022/BRL VAR-6, 20 = 2022/BRL VAR-1, indicate genotype diversity

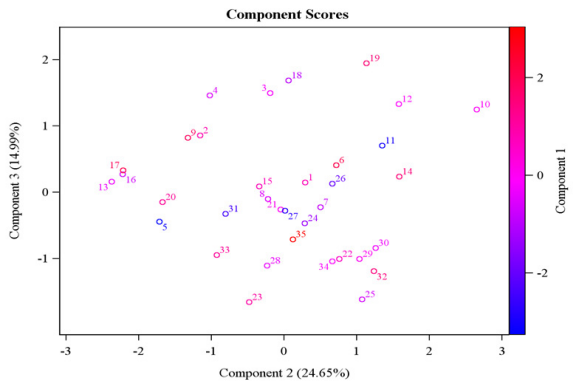


Figure 3: Scatter diagram of regression factor scores for the 1st, 2nd and 3rd components as determined by PCA in round brinjal genotypes. Outliers on the X-axis, that is, 10=2021/BRR VAR-2, 13 = 2021/BRR VAR-8, 17 = 2021/BRR VAR-12, 16 = 2021/BRR VAR-11, indicate genotype diversity

on multivariate analysis and *per se* performance for fruit yield per plant and other horticultural traits, the genotypes 2021/BRR VAR-2, 2021/BRR VAR-8, 2021/BRR VAR-12 and 2021/BRR VAR-11, were identified as potential donors for utilization in round brinjal breeding.

Conclusion

Wide variations in quantitative traits were recorded in brinjal genotypes irrespective of fruit shape. Two characters, fruit weight and number of fruits per plant, were identified as important selection indices for yield improvement in brinjal irrespective of fruit shape. The results of the present study are thus useful as they give information regarding the traits of fruit weight, fruit length, fruit diameter and fruit pedicel length that influence genetic diversity, which could be well utilized for a selection of breeding methods for the improvement of brinjal. Geographic diversity and genetic divergence were unrelated in brinjal with respect to fruit shape and other economic traits. Eight potential donor parents, Bidhan Supreme, 2020/BRL VAR-10, 2021/BRL VAR-5, 2022/BRL VAR-12, 2022/BRL VAR-13, 2022/BRL VAR-8, 2022/BRL VAR-6 and 2022/BRL VAR-1 in long-fruited brinjal and four potential genitors, 2021/BRR VAR-2, 2021/BRR VAR-8, 2021/BRR VAR-12 and 2021/BRR VAR-11 in round-fruited brinjal could be identified for future utilization in brinjal breeding.

Acknowledgments

We acknowledge the Project Coordinator, AICRP on Vegetable Crops, ICAR-IIVR, Varanasi, for providing genetic materials for the present study.

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सारांश

टिकाऊ उत्पादन और जलवायु परिवर्तन अनुकूलन के लिए, किसानों को बेहतर बैंगन किस्मों की आवश्यकता है। इस अध्ययन का उद्देश्य भविष्य के प्रजनन कार्यक्रम में उपयोग के लिए उपयुक्त लंबे और गोल बैंगन जीनोटाइप की पहचान करना था। विभिन्न स्रोतों से एकत्र किए गए लंबे और गोल फल वाले प्रकारों सहित उनहत्तर बैंगन जीनोटाइप का मूल्यांकन यादृच्छिक पूर्ण ब्लॉक डिजाइन के बाद किया गया था। पौधे की ऊंचाई, पौधे का फैलाव (एन-एस), डंठल की लंबाई, पत्ती के ब्लेड की लंबाई और चौड़ाई, 50% फूल आने के दिन, फल का वजन, लंबाई, फलों/पौधे की संख्या और विपणन योग्य फल उपज/पौधे जैसे लक्षण चयन के लिए बैंगन में फल के आकार के बावजूद सबसे विश्वसनीय लक्षण के रूप में उभरे। फल के आकार के बावजूद फल का वजन और फलों/पौधे की संख्या सबसे महत्वपूर्ण चयन सूचकांक के रूप में उभरी। बहुभिन्नरूपी विश्लेषण और आर्थिक विशेषताओं के औसत मूल्यों से पता चलता है कि लंबे फल वाले बैंगन में 8 जीनोटाइप 'बिधान सुप्रीम, 2020/BRL VAR-10, 2021/BRL VAR-5, 2022/BRL VAR-12, 2022/BRL VAR-13, 2022/BRL VAR-8, 2022/BRL VAR-6 और 2022/BRL VAR-1' और गोल फल वाले बैंगन में 4 जीनोटाइप, 2021/BRR VAR-2, 2021/BRR VAR-8, 2021/BRR VAR-12 और 2021/BRR VAR-11 भविष्य में बैंगन के प्रजनन के लिए संभावित दाता हो सकते हैं। प्रजनक संभावित एलील को व्यावसायिक जीनोटाइप में शामिल करने में सक्षम हो सकते हैं ताकि संभावित पुनः संयोजक प्राप्त किए जा सकें जिनमें वांछित आर्थिक विशेषताएँ हों।