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# Assessment of genetic diversity in brinjal genotypes using multivariate analysis

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## ABSTRACT

**Genetic divergence of germplasm was studied for 35 brinjal genotypes. The first principal component largely accounted for the variation among the brinjal genotypes (29.90%) followed by second principal component (20.35%) and third (20.08%). The first three principal components accounted (70.33%) of the total variation among eight characters describing 35 genotypes, while the first two accounted (50.25%). The traits which contributed more positively to PC1 were fruit weight, fruit width and yield per plant , while remaining traits in this PC1 did not contributed rather their effects were distributed among other PCs. The genotypes in the PC1 were more likely to be associated with higher fruit weight, fruit width and fruit yield whereas the genotypes with higher plant height, plant spread and number of primary branches were contributing to PC2. Based on the cluster means the important cluster was Cluster I for fruit weight, fruit length, fruit width and yield per plant. Cluster II for plant height, plant spread, and number of primary branches. Cluster III for number of fruit per plant. The maximum inter-cluster distances were recorded between the cluster I and II (278.26) followed by the distance between I and V (245.32) may be uses for hybridization. The lowest inter-cluster distance was observed between cluster II and V (35.26) followed by III and V (45.75) suggesting a close relationship among these three clusters.**

**Key words:** Brinjal, genetic diversity, multivariate analysis, principal component analysis.

## INTRODUCTION

Brinjal (*Solanum melongena* L.) is a major solanaceous vegetable crop grown throughout world. Being originated in Indo-Myanmar region a great genetic variability exists in nation. It has been an important vegetable in our diet since ancient times and very commonly used in all household. Improvement in yield and quality is normally achieved by selecting genotypes with desirable character combinations existing in the nature or by hybridization. Selection of parents identified on the basis of divergence analysis would be more promising for a hybridization programme. It was observed that more diverse the parents, greater is the chances of obtaining high heterotic $F_1$s and broad spectrum of variability in the segregating generation (Arunachalam, 1). Some related results have been reported in eggplant by Kumar *et al.* (9), Singh and Gopalakrishnan (16). Morphological characterization is the first step in the description and classification of germplasm collections (Smith *et al*., 18). The multivariate analysis is useful for characterization, evaluation and classification of plant genetic resources when a number of accessions are to be assessed for several characters of agronomic and physiological importance (Peeters and Martinelli, 12). Different types of analysis such as cluster analysis and principal component analysis (PCA) can be used to obtain idea about how identify groups of accessions that have desirable traits for breeding, and enlightening the patterns of variation in germplasm collection, to identify relationships among accessions and possible gaps (Camussi *et al.,* 3; Cowen and Frey, 4; Peeters and Martinelli, 12). PCA has been widely used in the studies of variability in germplasm collections of many species (Julier *et al*., 7; Bhargava *et al*., 2). Keeping in view these facts, the present studies were carried out to investigate the extent of genetic diversity in brinjal genotypes based on phenotypic and physical traits using multivariate analysis.

## MATERIALS AND METHODS

The present investigation was carried out at experimental farm of the Central Institute of Temperate Horticulture, Srinagar during 2009 and 2010. The material consisted of 35 variable genotypes of brinjal collected from different agro-ecological regions of India. Geographic position of the experimental site lies between latitude of 34°05 N and longitude of 74°50 E at an altitude of 1,640 m above the sea level. The average maximum 19.63°C and minimum 6.52°C temperatures, the amount of rainfall 160.72 mm and relative humidity 58.35%, evaporation 2.45 and soil characteristics, *viz*. pH = 6.81, EC = 0.36 dS $m^{-1}$ recorded during the cropping season. One-month-old healthy seedlings of each genotype were transplanted

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*Corresponding author's present address: CISH, Lucknow; E-mail: srajparmar@gmail.com in 3rd week of May at a spacing of 45 cm × 60 cm in a plot of 4.5 m × 3.6 m. The soil of experimental farm was loam with normal pH. Recommended agronomic and cultural practices were adopted to obtain good phenotypic expression of the characters. Observations were recorded on plant height, number of primary branches/plant, number of fruits/plant, fruit weight, fruit length, fruit width and average fruit weight, length and width from five randomly selected competitive plants in each genotype of a replication. The fruit yield was obtained on plot basis. The experiment was conducted under randomized block design replicated three times and pooled data of two years were analyzed as per the method suggested by Gomez and Gomez (5). Genetic diversity was studied following Mahalanobis's (10) generalized distance ($D^2$) extended by Rao (14). Clustering of genotypes was done according to Tocher's method (Rao, 18). Average intra-cluster distance was calculated by the following formula as suggested by Singh and Chaudhury (17).Trait variability analysis was performed by the PCA method, with the number of principal components being chosen based on the screen test (Kovacic, 8). Agglomerative Hierarchical cluster analysis was used to determine differences and similarities among the genotypes and as the Euclidean distance measure used was that best reflects differences existing among the genotypes (Kendall, 7). All statistical analysis was carried out based on nine pomological and chemical traits using XL STAT-2011.

## RESULTS AND DISCUSSION

Studied accessions showed high coefficient of variation for yield per plant (58.99), fruit weight (52.46) and number of fruits per plant (40.40), whereas, they showed low coefficient of variation for plant spread (16.00) and number of branches per plant (25.71) and for some other traits. Descriptive statistical analysis was also used for studying genetic variability in some other crops, such as garlic (*Allium sativum* L.) (Panthee *et al.*, 11). Genetic variability is the raw material of crop breeding on which selection acts to evolve superior genotypes. The higher amount of variation present for a character in the breeding materials, greater is the scope for its improvement through selection.

The 35 brinjal genotypes based on 8 morphological traits were classified in 6 groups using complete linkage agglomerative hierarchical algorithm as shown in Fig. 1. The maximum inter-cluster distances were recorded between the cluster I and II (278.26) followed by the distance between I and V (245.32) (Table 1).

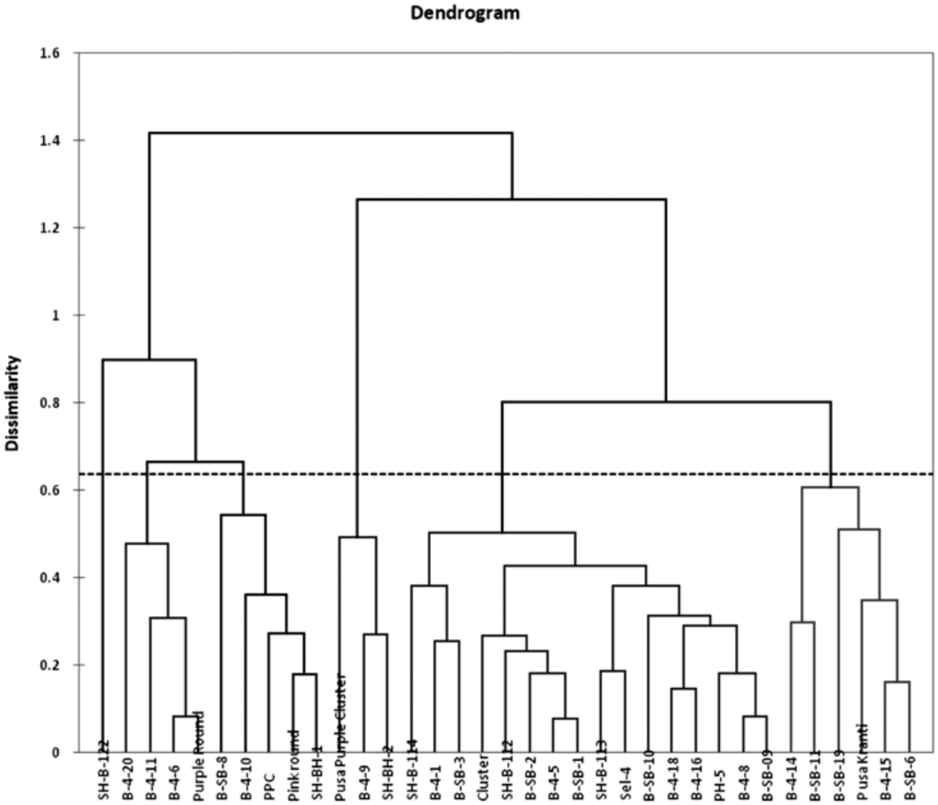

**Fig. 1.** Dendrogram depicting genetic relationships among 35 brinjal genotypes based on horticultural traits produced by complete linkage analysis (scale: Euclidean distance).

As the genetic variation is very distinct among the groups, genotypes from these four clusters if used in hybridization may produce a wide spectrum of segregating population. The lowest inter-cluster distance was observed between cluster II and V (35.26) followed by III and V (45.75) suggesting a close relationship among these three clusters. However, the intra-cluster divergence varied from 0.00 to 47.80, maximum being from cluster I that comprised of four genotypes of diverse origin, while the minimum distance was observed in cluster VI that comprised of one genotype.

Based on the cluster means (Table 2), the important cluster was Cluster I for fruit weight, fruit length, fruit width and yield per plant. Cluster II for plant height, plant spread, and number of primary branches. Cluster III for number of fruit per plant. From the results it was concluded that highest fruit weight, fruit length, fruit width and yield per plant cluster I, genotypes for plant height, plant spread, number of primary branches cluster I, brinjal genotypes for more number of fruit per plant from cluster III could be selected as parents for hybridization programme. Rahman and Munsur (13) also indicated that accessions among the cluster separated by high $D^2$ values could be used in hybridization program for obtaining wide spectrum of variations among the segregates. It is revealed that crosses should be made between accessions belonging to the distant clusters for high heterotic response.

In the present study, the maximum distances existed between cluster I and II (278.26) followed by the distance between cluster I and V. Considering group distance and other physical and yield performance, the inter-genotypic crosses between the members of cluster I with that of cluster II are expected to exhibit high heterosis and is also likely to produce new recombinants with desired traits. Similar results were also reported in tomato by Sharma and Verma (15).

Eigen value of principal component axes of total variation obtained from principal component analysis are presented in Table 3. The results revealed that the first principal component largely accounted for the variation among the brinjal genotypes (29.90%) followed by second principal component (20.35%) and third (20.08%). The first three principal components accounted (70.33%) of the total variation among eight characters describing 35 genotypes, while the first two accounted (50.25%). The traits which contributed more positively to PC1 were fruit weight, fruit width and yield per plant , while remaining traits in this PC1 did not contributed rather their effects were distributed among other PCs. The genotypes in the PC1 were more likely to be associated with higher fruit weight,

**Table 1.** Average intra- (bold face) and inter-cluster distance ($D^2$) for 35 brinjal genotypes.

| Trait | 1 | 2 | 3 | 4 | 5 | 6 |
|---|---|---|---|---|---|---|
| 1 | 47.80 | 278.265 | 204.452 | 134.921 | 245.321 | 212.371 |
| 2 | | 17.69 | 74.613 | 144.590 | 35.266 | 108.646 |
| 3 | | | 24.63 | 70.328 | 42.159 | 75.866 |
| 4 | | | | 45.46 | 110.945 | 97.355 |
| 5 | | | | | 34.23 | 85.821 |
| 6 | | | | | | 0.00 |

**Table 2.** Cluster means for nine characters in 35 brinjal genotypes.

| Character | Cluster | | | | | |
|---|---|---|---|---|---|---|
| | I | II | III | IV | V | VI |
| No. of genotypes and percentage | 4<br>(11.42%) | 3<br>(8.57%) | 16<br>(45.71%) | 5<br>(14.28%) | 6<br>(17.14%) | 1<br>(2.85%) |
| Plant height (cm) | 71.998 | 105.443 | 98.520 | 88.134 | 101.385 | 24.310 |
| Plant spread (cm) | 73.665 | 86.983 | 75.559 | 67.002 | 75.107 | 68.660 |
| No. of primary branches | 5.913 | 6.220 | 5.769 | 5.064 | 5.775 | 4.330 |
| No. of fruit per plant | 18.080 | 17.553 | 22.060 | 17.866 | 11.997 | 10.000 |
| Fruit weight (g) | 340.065 | 64.187 | 137.416 | 206.310 | 96.655 | 133.500 |
| Fruit length (cm) | 19.163 | 17.387 | 18.859 | 18.624 | 17.410 | 13.000 |
| Fruit width (cm) | 6.638 | 4.410 | 4.303 | 4.742 | 3.468 | 3.230 |
| Yield per plant (kg) | 5.315 | 1.075 | 2.916 | 3.354 | 1.068 | 1.320 |

**Table 3.** Eigen values and proportion of variance explained by 8 principal components.

| Component | Eigen value | Variability (%) | Cumulative (%) |
|---|---|---|---|
| P1 | 2.392 | 29.901 | 29.901 |
| P2 | 1.628 | 20.356 | 50.257 |
| P3 | 1.606 | 20.081 | 70.338 |
| P4 | 0.835 | 10.443 | 80.781 |
| P5 | 0.703 | 8.791 | 89.572 |
| P6 | 0.514 | 6.430 | 96.001 |
| P7 | 0.278 | 3.475 | 99.476 |
| P8 | 0.042 | 0.524 | 100.000 |

fruit width and fruit yield, whereas the genotypes with higher plant height, plant spread and number of primary branches were contributing to second PC (Table 4, Fig. 2). The selected genotypes on the basis of different groups could be identified for yield potential. The PC3 showed that number of fruit per plant and fruit length was more positively associated than any other characters. Principal component analysis has been also widely used in studying genetic variability in germplasm collections of many species (Julier *et al*., 6; Bhargava *et al*., 2). The characters contributed positively to first three principal components could be considered while selecting the best genotype without losing yield potential. When PC1 was plotted against PC2, some groups and some isolated genotypes were clearly defined, *viz.* B-SB-19, B-SB-6, B-SB-11, CITH Purple Round, B-4-20, Pusa Kranti, SH-B-122, Pusa Purple Cluster and B-SB-8 (Fig. 2). The bi-plot between PC1 against PC2 depicts the combine results of correlation among the variable and diversity among the genotypes (Fig. 2). This grouping pattern confirmed the results obtained by $D^2$ analysis and that the crosses involving parents belonging to the maximum divergent clusters were expected to manifest maximum heterosis and also wide variability in genetic architecture. The intra-cluster distance between cluster I and cluster II confirms the presence of more divergent genotypes which may directly be used for hybridization programme. Cluster I, is associated with higher fruit weight, fruit width and fruit yield where as cluster II with higher plant height, plant spread and number of primary branches and any two diverse may be used for better $F_1$s and segregates. The results of present study are thus useful as it gives information about the groups where certain traits are more important allowing breeder to conduct specific breeding programme for higher yield of brinjal under higher altitude conditions.

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**Table 4.** Latent vectors for nine traits of 35 brinjal genotypes.

| Character | P1 | P2 | P3 | P4 | P5 | P6 | P7 | P8 |
|---|---|---|---|---|---|---|---|---|
| Plant height (cm) | -0.325 | 0.416 | 0.181 | -0.481 | -0.113 | 0.616 | 0.239 | -0.094 |
| Plant spread (cm) | -0.158 | 0.541 | -0.181 | -0.365 | 0.454 | -0.538 | -0.132 | 0.051 |
| No. of primary branches | -0.107 | 0.473 | -0.163 | 0.753 | 0.272 | 0.229 | 0.210 | 0.003 |
| No. of fruit per plant | 0.229 | -0.054 | 0.638 | -0.006 | 0.515 | 0.175 | -0.109 | 0.479 |
| Fruit weight (g) | 0.526 | 0.281 | -0.148 | -0.102 | -0.355 | -0.117 | 0.464 | 0.507 |
| Fruit length (cm) | -0.065 | 0.419 | 0.486 | 0.218 | -0.541 | -0.219 | -0.443 | -0.004 |
| Fruit width (cm) | 0.442 | 0.170 | -0.410 | -0.092 | 0.029 | 0.426 | -0.646 | 0.020 |
| Yield per plant (kg) | 0.575 | 0.153 | 0.274 | -0.041 | 0.147 | -0.072 | 0.203 | -0.708 |

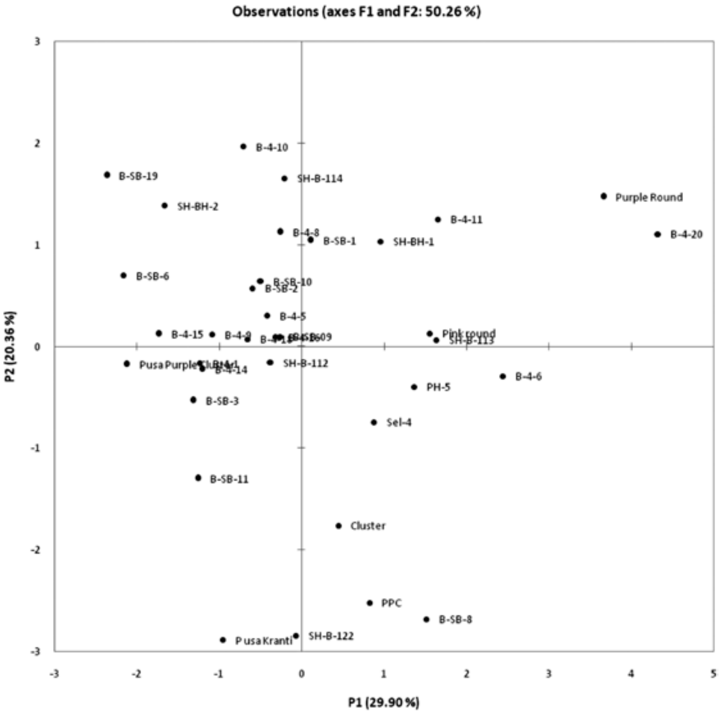

**Fig. 2.** Plot for 1st and 2nd PC for 35 brinjal genotypes of based eight horticultural traits.

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