



Assessment of Genetic Diversity in Morphological and Yield Traits of Brinjal (*Solanum melongena* L.) by Mahalanobis' D² Statistics

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ABSTRACT

The study was conducted during *rabi* season (September, 2022–February, 2023) at District Seed Farm, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, Nadia, West Bengal, India to investigate the diverse brinjal genotypes for fruit yield and its component traits. Thirty genotypes of brinjal were evaluated systematically for polymorphism on the basis of nine morphological traits in Randomized Block Design with three replications. Analysis of D² values revealed significant genetic variation, grouping the genotypes into eleven highly divergent clusters. Cluster-6 housed the highest number of genotypes (8), while cluster-11 had only one genotype. A low intra-cluster distance indicated homogeneity in the genotypes in a particular cluster. The superior cluster means for fruit yield plant⁻¹, fruits plant⁻¹, plant height, primary branches plant⁻¹, harvesting index and days to 50% flowering were recorded in cluster-5. The mean intra and inter cluster D² values, revealed that the least intra cluster distance was in cluster-11 followed by cluster-2, while the maximum intra cluster distance was recorded in cluster-10. The highest inter cluster distance was recorded between cluster-9 and cluster-5 followed by cluster-7 and cluster-5 suggesting the use of genotypes from these clusters would give high heterotic hybrids or superior segregants, while least inter cluster distance was recorded between cluster-2 and cluster-4. The traits harvesting index (40.23%) and fruit yield plant⁻¹ (19.77%) contributed maximum towards divergence, which accounted for 60% of total divergence. From the study it was evident that the genetic heterogeneity in the genotypes made them suitable candidates for hybridization programs aimed at exploiting heterosis and producing superior segregants.

KEYWORDS: Brinjal, diversity, cluster analysis, heterotic hybrids, divergence

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1. INTRODUCTION

Brinjal is named as “poor man’s vegetable” because of its low cost of production, ease of culture and availability throughout the year. Brinjal is mainly cultivated for their immature fruits as vegetable. Fruits are widely used in various culinary preparations viz., sliced bhaji, stuffed curry, bertha, chutni, pickles etc. If we go to its nutritive value it is rich in vitamins like thiamine, niacin, pantothenic acid and folacin as well as essential minerals like calcium (Ca), iron (Fe), potassium (K), and zinc (Zn), copper (Cu) and manganese (Mn). According to USDA National Nutrient data base, it is having 5.7 g Carbohydrates, 1 g Protein, 3.40 g Dietary Fibre (100 g)⁻¹ of edible portion. Due to its low calorific value (24 kcal 100 g⁻¹) and high potassium content (200 mg 100 g⁻¹), it is suitable for diabetes, hypertensive and obese patients (Prabhuet al., 2009; Yarmohammadet al., 2021). Presence of phenolic like compounds Caffeic, p-coumaric, ferulic, gallic, protocatechuic and p-hydroxy benzoic acids and Kowalski and Kowalski, 2005, Cayan et al., 2020) supply good amount of antioxidants to the human body, which helps in binding of free ion radicals there by protects the body tissues from damage and diseases like cancer, rheumatism which are associated with ageing. Anthocyanin pigments present in brinjal fruits are protective against a variety of diseases, particularly cardiovascular disease and some types of cancer (Horbowicz et al., 2008, Deis et al., 2021). Moreover, it fetches good prices in the market and supports the grower economically rather than any other vegetable. Brinjal (*Solanum melongena* L.) is widely regarded as having originated in the Indian subcontinent. Across India, the crop demonstrates extensive phenotypic variation, expressed through differences in growth habit, foliage characteristics, flower attributes, and fruit features including form, dimensions, pigmentation, and surface textures. This wide-ranging variability has emerged over long periods as a result of domestication processes, continuous farmer-led selection, natural introgression from wild relatives and adaptation to diverse environmental and agro-climatic conditions (Sivasankarreddy et al., 2024; Upadhyay et al., 2024). For an effective breeding program, information concerning the extent and nature of genetic diversity within the crop species is essential. It is useful for characterizing individual accessions and cultivars and as a genetic guide in the selection of the parents for hybridization. The rich morphological variability in Indian brinjal, beyond its taxonomic relevance, represents a valuable asset for genetic improvement aiming at enhanced productivity, resistance to biotic stresses, and improved fruit quality and conservation. Preserving this diversity is particularly important under changing climatic scenario and shifting consumer preferences, as it provides a broad spectrum of adaptive and agronomically important traits (Joseph et al.,

2021). Effective conservation approaches must therefore safeguard diverse landraces to maintain a resilient genetic base for future selection. Distinct morphological descriptors, such as calyx prickliness plant growth habits with upright and intermediate to prostrate forms and fruit length–breadth index that facilitate differentiation between cultivated forms and naturally introgressed genotypes from wild progenitors, e.g. *S. insanum* (Sivasankarreddy et al., 2024, Saikia et al., 2021). Among all the traits, fruit characters exhibit the greatest variability in brinjal with varied patterns of pigmentation ranging from deep purple, green to white and striped types (Chetan et al., 2023). It is known that genetically diverse parents are likely to contribute desirable segregants and the more diverse the parents, greater are the chances of obtaining high heterotic F_1 s and broad spectrum of variability in the segregating generations (Kumar et al., 2013, Kumar et al., 2020). Keeping these points in view, the present investigation was carried out to assess the diverse brinjal genotypes for fruit yield and its component traits.

2. MATERIALS AND METHODS

The present investigation was carried out in *rabi* season (September, 2022–February, 2023) at District Seed Farm (2.97°N and 88.43°E) in randomized block design with three replications. The genetic material evaluated consisted of local cultivars and genotypes numbering 30 obtained from various sources and regions. The experimental soil was sandy loam. The spacing followed in both the seasons was 75×75 cm² and 20 plants were maintained for each genotype in each replication. Observations on various traits were recorded from five randomly selected competitive plants from each genotype and from each replication excluding border plants on the following traits: Fruit yield plant⁻¹, Fruits plant⁻¹, Fruit weight (g), Plant height (cm), Primary branches plant⁻¹, Days to flowering^{1st}, Days to 50% flowering, fresh green plant weight and harvest index. Standard crop husbandry recommendations were followed to raise the crop. Genetic diversity was worked out following Mahalanobis generalized distance, i.e. D² statistic (Mahalanobis, 1936) extended by Rao (1952) to clustering in Tocher’s method. Intra and inter- cluster distances and contribution of characters towards divergence calculated as per Singhand Chowdhury (1986).

3. RESULTS AND DISCUSSION

The genetic divergence among the brinjal genotypes was estimated using the Mahalanobis D² statistic based on the mean values of all the fifteen characters studied. The D² values between any two genotypes were computed as the sum of squares of the differences between their mean trait values, which served as the basis for grouping the genotypes into clusters. Based on the calculated D² values, the genotypes

were grouped in to eleven highly divergent clusters (Table 1), indicating the presence of considerable genetic variability within the experimental material and the biplot (Figure 1) effectively visualizes the genetic relationships and divergence pattern among brinjal genotypes. From the biplot it was clear that F_1 and F_2 together explained 63.44% (39.491% and 24.727%, respectively) of the total variation, indicating a substantial proportion of the genetic variability present among the genotypes and represented the major source of genetic difference among the genotypes. Genotypes from cluster III and V as the parents in future breeding programme.. Among the eleven clusters, Cluster VI was the largest, comprising eight genotypes, followed by Cluster

I with four genotypes. Cluster XI was the smallest cluster containing only one genotype, suggesting that this genotype was genetically distinct from the rest of the population. The remaining clusters contained two genotypes each, except Cluster V, which consisted of three genotypes. Similar grouping of brinjal germplasm into multiple clusters based on genetic divergence had also been reported by Mohanty and Prusti (2001); Mehta et al. (2004); Dharwad et al. (2011); Kumar et al. (2013); Islam et al. (2018) and Kaur et al. (2021), indicating the usefulness of multivariate analysis for assessing diversity in brinjal.

The cluster mean values for the nine characters studied (Table 2) revealed considerable variation among clusters, reflecting the differential performance of genotypes for important agronomic and yield traits. From the present results, Cluster V, followed by Cluster VI, recorded the highest mean values for fruit yield per plant and plant height, suggesting that genotypes belonging to these clusters possess superior yield potential and vegetative vigor. In contrast, Cluster VI, followed by Cluster V, exhibited fewer days to 50% flowering, indicating early flowering tendency in these groups. The number of fruits per plant was highest in Cluster V, whereas fruit weight was found to be maximum in Cluster IX, indicating that different clusters possessed superiority for different yield components. The highest number of primary branches plant⁻¹ was observed in Cluster XI, followed by Cluster V, suggesting the presence of highly branched plant types in these clusters. Early flowering was particularly evident in Cluster IV, followed by Cluster VIII, which recorded the lowest number of days to flowering. Green plant weight, an indicator of biomass production, was highest in Cluster VII, followed by Cluster II. Similarly, the harvest index was found to be maximum in Cluster XI, followed by Cluster V, suggesting that these clusters

Table 1: Distribution of genotypes in clusters

Cluster No.	No. of genotypes	Name of the genotypes
1	4	LambaKuli, Muktamala, Muktakeshi, Kerala collection-1
2	2	Nandini, KS-5144
3	2	KS-8407, KS-8317
4	2	MuktakeshiLal, KS-7812
5	3	Samrat, LalKuli, Mala
6	8	GolMakra, Makra, MakraMidlong, KaloMakra, Panna, LalLamba, BCB-320, BCB-123
7	2	BR-112, KS-63.08
8	2	KS-8102, KS-7848
9	2	KS-2011-1, H-8
10	2	Muktazhuri, Heera
11	1	SadaMakra

Table 2: Inter and intra cluster distances

Cluster No.	1	2	3	4	5	6	7	8	9	10	11
1	8.11	10.75	9.40	8.63	9.35	9.88	12.71	10.61	11.95	9.11	7.82
2		2.41	6.75	4.91	15.33	11.70	6.96	6.61	9.16	13.36	12.32
3			2.86	5.25	13.63	10.81	9.65	5.50	9.16	12.07	8.46
4				2.95	13.80	9.64	8.99	6.28	7.20	12.27	8.59
5					4.88	12.56	15.82	14.83	16.87	6.30	11.86
6						8.62	11.40	13.14	10.57	12.99	9.75
7							5.84	10.91	11.05	14.61	14.72
8								7.30	11.16	12.68	10.94
9									8.81	16.05	10.42
10										8.87	11.89
11											0.00

Table 3: Cluster mean values for economically important characters of brinjal and contribution of characters towards divergence

Cluster No.	Fruit yield plant ⁻¹ (g)	Fruits plant ⁻¹	Fruit weight (g)	Plant height (cm)	Primary branches plant ⁻¹	Days to 1 st flowering (DAP)	Days to 50% flowering	Green plant weight (g)	Harvest index
1	833.50	9.67	98.60	58.10	5.58	37.80	60.80	462.50	62.50
2	345.60	3.75	127.4	54.90	4.40	39.60	58.00	725.70	32.20
3	256.40	2.75	93.20	71.80	6.28	39.00	58.20	515.00	33.40
4	413.00	4.05	139.90	64.10	4.24	34.10	61.20	514.00	44.60
5	1207.9	19.43	57.50	77.10	6.33	38.20	59.00	536.30	67.10
6	985.22	7.12	140.20	74.10	5.57	40.80	52.60	759.60	53.70
7	572.30	4.50	136.00	67.70	5.09	36.40	64.00	1179.3	29.70
8	204.75	2.70	79.70	63.80	4.95	34.40	62.70	420.50	35.10
9	488.40	2.75	218.0	67.50	4.79	36.10	60.70	539.70	37.70
10	871.00	16.90	56.00	65.80	5.75	35.70	61.70	505.20	63.10
11	620.20	4.90	126.50	61.50	6.79	42.10	64.00	261.00	70.30
% contribution to divergence	19.77	13.56	7.35	1.38	3.22	2.30	3.45	8.73	40.23

had a greater efficiency in partitioning assimilates towards economic yield.

The intra- and inter-cluster distances were estimated to assess the magnitude of genetic divergence among clusters (Table 3). The analysis revealed that the lowest intra-cluster distance was observed in Cluster XI (0.00), followed by Cluster II (2.41), indicating high genetic similarity among the genotypes within these clusters. In contrast, the highest intra-cluster distance was recorded in Cluster X (8.87), suggesting comparatively greater heterogeneity among the genotypes present within this cluster. Generally, lower intra-cluster distance indicates greater homogeneity among genotypes belonging to that cluster, while higher values indicate more variability.

The inter-cluster distance provides an estimate of genetic divergence between clusters and helps to identify suitable parents for hybridization programmes and the contribution of individual characters towards genetic divergence (in terms of number of times it ranked first) has been given in Figure 4. In the present study, the maximum inter-cluster distance was observed between Cluster IX and Cluster V (16.87), followed by Cluster VII and Cluster V (15.82). The large genetic distance between these clusters indicates that the genotypes present in these groups are highly divergent genetically. Therefore, crossing genotypes from these clusters is likely to produce high heterotic combinations and superior segregants in subsequent generations. The minimum inter-cluster distance was recorded between Cluster II and Cluster IV (4.91), suggesting a close genetic relationship between the genotypes of these clusters. Similar observations regarding the usefulness of divergent clusters

in parent selection had been reported earlier by Mohanty and Prusti (2001); Mehta et al. (2004); Patel et al. (2004); Dharwad et al. (2011); Kumar et al. (2013) and Younas et al. (2022).

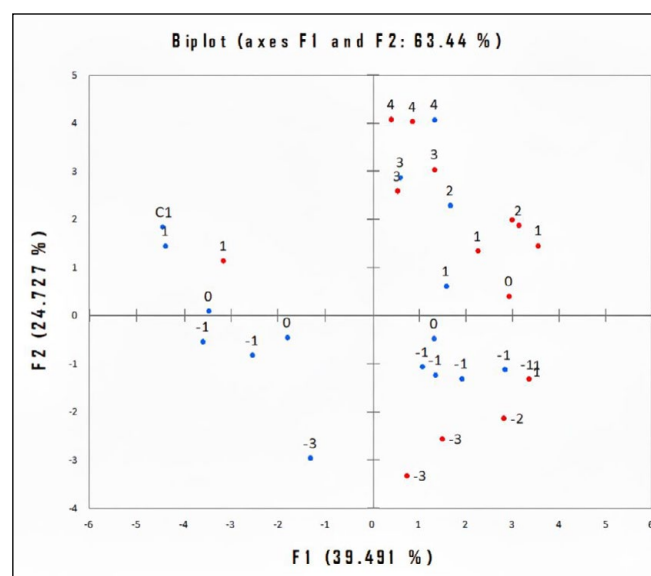


Figure 1: Bi-plot graph for different variances; Variances (Var):Fruit yield plant⁻¹ (Var 1), Fruits plant⁻¹ (Var 2), Fruit weight (Var 3), Plant height (Var 4), Primary branches plant⁻¹ (Var 5), Days to flowering 1st (Var 6), Days to 50% flowering (Var 7), Green plant weight (Var 8), Harvest index (Var 9)

On an overall basis, Cluster V emerged as the most promising cluster as it exhibited superior mean performance for several important characters such as fruit yield plant⁻¹, number of fruits plant⁻¹, plant height, primary branches

plant⁻¹, harvest index, and days to 50% flowering. Therefore, genotypes belonging to this cluster may be effectively utilized in hybridization programmes with genotypes from highly divergent clusters to exploit maximum heterosis and to generate superior recombinants in segregating generations.

The contribution of individual characters to genetic divergence was also estimated (Table 2). Among the characters studied, harvest index (40.23%) contributed the highest towards total divergence, followed by fruit yield plant⁻¹ (19.77%). Together, these two characters accounted for nearly 60% of the total genetic divergence, indicating that yield-related traits played a dominant role in differentiating the genotypes. Therefore, greater emphasis should be placed on these characters during selection and parent choice in breeding programmes. A similar high contribution of yield traits towards genetic divergence in brinjal had also been reported by Kumar et al. (2013) and Tabasum et al. (2023).

The Principal Component Analysis (PCA) biplot further provided a graphical representation of the genetic relationships among genotypes. The spatial distribution of genotypes across the four quadrants of the biplot revealed a wide range of variability within the experimental material. The first two principal components (PC1 and PC2) together explained 63.44% of the total variation, with PC1 accounting for 39.49% and PC2 accounting for 24.73% of the total variation. This indicates that a substantial proportion of the variability among genotypes was captured by these two components, making the biplot a reliable representation of the genetic structure of the population. Genotypes located far apart from each other on the biplot were genetically more divergent, whereas those grouped closely together were genetically similar. The wide scattering of genotypes across all four quadrants further confirmed the presence of substantial genetic diversity among the studied genotypes.

The distribution pattern of genotypes in the biplot also supported the cluster analysis results, which grouped the genotypes into eleven distinct clusters based on Mahalanobis D² values. Such concordance between cluster analysis and PCA indicates the robustness of the diversity analysis. Genotypes belonging to Cluster III and Cluster V appeared particularly promising and could be utilized as potential parents in future breeding programmes aimed at improving yield and related traits.

The dendrogram analysis further illustrated the genetic relationships among the genotypes. The dendrogram showed the formation of two major clusters at a relatively low squared Euclidean distance, indicating strong similarity among genotypes within each group. However, a large increase in distance before the final merging of the clusters

suggested the presence of substantial genetic divergence between the two major groups (Figure 2). The non-hierarchical clustering approach effectively minimized intra-cluster variation while maximizing inter-cluster differences, which was evident from the clear separation among clusters (Figure 3).

Interestingly, the results also indicated that geographical origin was not necessarily related to genetic diversity. Genotypes collected from the same geographical region were often placed in different clusters, while genotypes

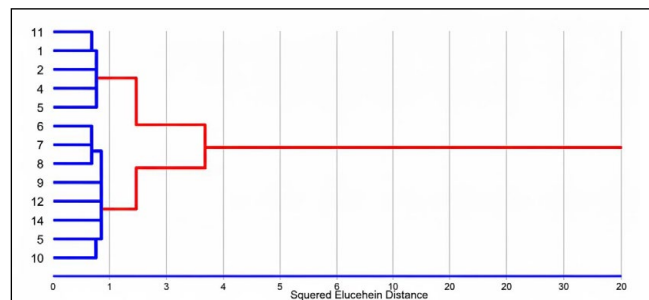


Figure 2 : Dendrogram plotted following Ward's method by using squared Euclidean distance

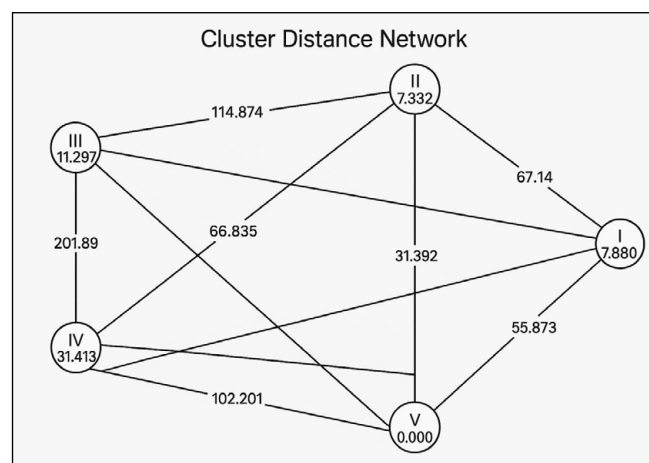


Figure 3: Mahalanobis Euclidean distance through Tocher's method (not to scale)

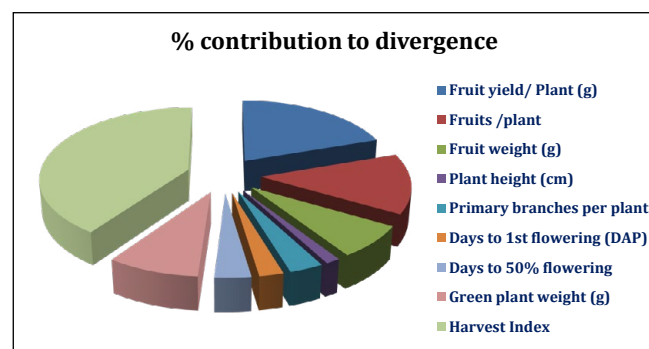


Figure 4: Pie chart of per cent contribution of different characters to divergence

from different regions sometimes grouped together in the same cluster. This phenomenon may be attributed to the exchange of germplasm, natural hybridization, and human selection practices, which often lead to the redistribution of genetic variability across different regions.

Overall, the high cumulative variance explained by the first two principal components, together with the wide dispersion of genotypes in the biplot and the formation of distinct clusters in cluster analysis, clearly demonstrated the presence of substantial genetic variability among the studied brinjal genotypes. Such diversity provides ample scope for selecting genetically divergent parents for hybridization programmes aimed at exploiting heterosis and developing high yielding and improved brinjal varieties, as also reported by Begum et al. (2024) and Basavaraj et al. (2024).

4. CONCLUSION

Out of 11 clusters, Cluster 5 exhibited superior mean performance, while large inter-cluster distances among Clusters 5, 7, and 9 indicated strong potential for heterotic hybrid development. Harvest index (40.23%) and fruit yield plant⁻¹ (19.77%) together contributed nearly 60% of total genetic divergence, highlighting substantial variability. Crossing genetically distant clusters with desirable traits, particularly harvest index and yield could be rewarding and help conserving diverse landraces against genetic erosion for brinjal improvement under subtropical conditions.

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