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# Elucidation of genetic diversity in distinct brinjal genotypes: Multivariate analysis using $D^2$

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## Abstract

Genetic divergence study among 45 brinjal genotypes was performed using Mahalanobsis $D^2$ statistics to find prospective genotypes for use in a breeding programme. The genotypes were assessed for 11 traits and divided into twelve clusters based on Tocher's method. Cluster I had the most genotypes (18), followed by cluster III (5), cluster V (4), cluster IV, VI and IX (3 each), cluster II, VII and X (2 each) and cluster VIII, XI and XII (1 each). The intra-cluster distances ranged between 0 and 1064.87. Cluster X has the largest intra-cluster distance (1064.87), followed by Cluster IV (831.08). Cluster VIII, XI, and XII had the smallest intra-cluster distance (0). The inter-cluster distances varied from 804.88 to 4758.26. The largest inter-cluster distance was between IX and XI (4758.26), followed by III and XII (3923.90), and the shortest distance was between cluster II and III (804.88). Genotypes from the cluster with a large inter-cluster distance could be selected as parents to produce superior $F_1$ hybrids and segregants. The three characters, fruit length (29.70%), number of primary branches (18.89%), and plant height (14.55%), altogether account for 63.14% of overall divergence. As a result, the combination of those traits could be exploited to develop superior varieties with higher yields.

## Keywords

clusters; distances; divergence; mahalanobsis method; per cent contribution

## Introduction

Brinjal, an herbaceous plant belonging to the Solanaceae family, is considered to have originated in India. The family Solanaceae contains about 90 genera and over 2000 species. China is considered the secondary centre of the origin of brinjal (1). India cultivates 0.72 million hectares and produces 12.66 million tons of brinjal (NHB Database, 2018-2019). Brinjal serves as a source of various minerals like phosphorus, potassium, calcium, magnesium, manganese, potassium and copper. Fruits of brinjal can be eaten boiled, grilled, roasted, stewed, baked, dried, pickled, pureed or breaded, microwaved, mashed and fried (2). Brinjal plant has analgesic, antioxidant, premenstrual syndrome, hypolipidemic and anaphylactic reaction inhibitory activities (3).

A wide range of diversity is seen in this crop including plant stature, stem colour, size, shape and angle of leaf, fruit size and shape, fruit colour and texture and tolerance to biotic and abiotic stress (4). In any crop development program, understanding genetic diversity among breeding materials is critical. It helps to choose suitable parents for the hybridization program, resulting in superior hybrids and desired recombinants. Mahalanobis $D^2$ analysis appears to be a powerful tool for measuring genotypic divergence between biological populations and determining the proportional contributions of various components to overall divergence at inter and intra-cluster levels (5, 6). Its ability to consider multiple traits and their correlations makes it a valuable tool for developing new plant varieties with desirable characteristics. In light of this, efforts were made to obtain information regarding the genetic diversity found in the 45 different genotypes of brinjal, as this aids in the breeding process by enabling the selection of promising parents for future advancements.

## Materials and Methods

The study was conducted in the Department of Vegetable Science at Tami Nadu Agricultural University in Coimbatore in both Kharif and Rabi seasons of 2023–2024. Forty-five brinjal genotypes gathered from various locations in Tamil Nadu were used as base material for this experiment (Table 1). The investigation was carried out in Randomized Block Design (RBD) with three replications. The standard package of practices was adopted uniformly. The following observations *viz.,* Plant height (cm), Number of primary branches , Days to 1st flowering, Days to 50% flowering, Days to 1st harvesting, Fruit length (cm), Fruit girth (cm), Fruit weight (g), Fruit borer incidence (%), Number of fruits per plant and Fruit yield (kg/plant) were recorded.

The genetic divergence of brinjal genotypes was evaluated using the $D^2$ approach proposed by Mahalanobis. Tocher's approach was used for grouping genotypes (7). Inter and intra-cluster distances, as well as the percentage of each trait contributing to diversity were calculated (8). The statistical analyses were performed using TNAUSTAT software package.In another studyeight clusters were recorded among 30 brinjal genotypes, in which

## Results and Discussion

The results of the ANOVA indicated that majority of the traits had significant differences, suggesting that there is an enormous amount of variability present among the genotypes. Using Mahalanobis's $D^2$ approach, 45 genotypes were categorized into twelve unique groups. Table 2 displays the clustering pattern for 45 genotypes. Among the clusters, cluster I recorded 18 genotypes which was followed by cluster III with 5 genotypes, cluster V with 4 genotypes, cluster IV, VI and IX with 3 genotypes each and cluster II, VII and X, with 2 genotypes each. Clusters VIII, XI and XII had the least number of genotypes (1 genotype each). A previous study noticed five clusters among 20 genotypes, in which cluster IV was the largest consisting of 6 genotypes (9). In another research, eight clusters among 30 brinjal genotypes were recorded, in which cluster I had 22 genotypes (10).

Table 3 illustrates the average intra- and inter-cluster values. The intra-cluster values were lower than the inter-cluster values, indicating that genotypes are

**Table 1.** List of 45 brinjal genotypes used in the study.

| S.No | Genotypes | Source |
|---|---|---|
| 1 | Periyakottai Kathiri | Sivagangai |
| 2 | Varikathiri | Coimbatore |
| 3 | Puliampoo kathiri | Erode |
| 4 | Sevanthampatti local | Trichy |
| 5 | Dindigul green long | Dindigul |
| 6 | Poonaithalai kathiri | Salem |
| 7 | Pachai kathiri | Madurai |
| 8 | Puliampatti kathiri | Krishnagiri |
| 9 | Ariyanayagipuram local | Tirunelveli |
| 10 | Kannadi kathirikathiri | Erode |
| 11 | Kinathukadavu local | Coimbatore |
| 12 | Negamam kathiri | Coimbatore |
| 13 | Andarkulam | Kanyakumari |
| 14 | Aladipatti local | Virudhunagar |
| 15 | Pandiyur local | Ramanathapuram |
| 16 | Kottampatti kathiri | Coimbatore |
| 17 | Sankarankoil kathiri | Tenkasi |
| 18 | Vasudevanallur kathiri | Tenkasi |
| 19 | Alavayal kathiri | Pudukkottai District |
| 20 | Salur Kathiri | Sivagangai |
| 21 | Vazhuthanai kathiri | Kanyakumari |
| 22 | Udha neela kathiri | Salem |
| 23 | Udha kathiri | Coimbatore |
| 24 | Virudhunagar local | Virudhunagar |
| 25 | Annur local | Coimbatore |
| 26 | Ujala cluster | Tiruvallur |
| 27 | Ujala long | Perambalur |
| 28 | Ujala oblong | Tiruvallur |
| 29 | Neela kathiri | Salem |
| 30 | Vilakethi kathiri | Erode |
| 31 | Rayakotai kathiri | Krishnagiri |
| 32 | Kumbakonam kathiri | Kumbakonam |
| 33 | Namakkal kathiri | Nammakal |
| 34 | Bhavani long | Erode |
| 35 | Bhavani oblong | Erode |
| 36 | Dharapuram kathiri | Tirupur |
| 37 | Kallimandhayam kathiri | Dindigul |
| 38 | Vellore kathiri | Vellore |
| 39 | Bhavani cluster | Erode |
| 40 | Vellakoil kathiri | Tirupur |
| 41 | Yenthal purple type | Tiruvannmalai |
| 42 | Sillukkudi oblong | Tiruvannmalai |
| 43 | Sillukkudi round | Tiruvannmalai |
| 44 | Pungavadi kathiri | Salem |
| 45 | Hosur local | Krishnagiri |

**Table 2.** Clustering pattern of 45 genotypes of brinjal.

| Clusters | Number of genotypes | Genotypes |
|---|---|---|
| I | 18 | Pungavadi kathiri, Hosur local, Ariyanayagipuram local, Sillukkudi oblong, Puliampoo kathiri, Sillukkudi round, Alavayal kathiri, Kinathukadavu local, Aladipatti local, Puliampatti kathiri, Pachai kathiri, Annur local, Salur Kathiri, Vellakoil kathiri, Poonaithalai kathiri, Sankarankoil kathiri, Ujala long, Ujala oblong |
| II | 2 | Neela kathiri, Dharapuram kathiri |
| III | 5 | Vilakethi kathiri, Vellore kathiri, Kallimandhayam kathiri, Namakkal kathiri, Kannadi kathiri-kathiri |
| IV | 3 | Varikathiri, Kottampatti kathiri, Bhavani cluster |
| V | 4 | Dindigul green long, Vasudevanallur kathiri, Udha kathiri, Negamam kathiri |
| VI | 3 | Sevanthampatti local, Bhavani long, Bhavani oblong |
| VII | 2 | Periyakottai Kathiri, Rayakotai kathiri |
| VIII | 1 | Ujala cluster |
| IX | 3 | Vazhuthanai kathiri, Udha neela kathiri, Kumbakonam kathiri |
| X | 2 | Pandiyur local, Andarkulam |
| XI | 1 | Yenthal purple type |
| XII | 1 | Virudhunagar local |

**Table 3.** Intra and inter-cluster $D^2$ values of 12 clusters of brinjal.

| Clusters | I | II | III | IV | V | VI | VII | VIII | IX | X | XI | XII |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **I** | **707.45** | 1163.83 | 1291.59 | 956.73 | 1445.26 | 1324.21 | 1266.02 | 1294.81 | 3033.35 | 2412.55 | 1295.37 | 2641.92 |
| **II** | | **702.83** | 804.88 | 1557.45 | 2235.67 | 2504.94 | 1337.57 | 1268.00 | 2679.73 | 2514.60 | 1689.96 | 3784.57 |
| **III** | | | **692.30** | 1229.78 | 2239.58 | 2079.66 | 1385.87 | 1529.42 | 2119.97 | 2102.38 | 1794.30 | 3923.90 |
| **IV** | | | | **831.08** | 1204.13 | 939.58 | 1939.22 | 909.16 | 2735.07 | 2391.10 | 1650.95 | 2929.32 |
| **V** | | | | | **437.37** | 1357.57 | 2858.49 | 1457.54 | 2454.70 | 2406.44 | 3236.46 | 1316.09 |
| **VI** | | | | | | **292.33** | 2569.47 | 1321.91 | 3039.85 | 2635.00 | 1554.02 | 1947.88 |
| **VII** | | | | | | | **766.23** | 2794.25 | 2734.62 | 3768.22 | 1380.83 | 3823.26 |
| **VIII** | | | | | | | | **0** | 3823.03 | 2814.76 | 1507.35 | 3037.58 |
| **IX** | | | | | | | | | **739.54** | 3666.79 | 4758.26 | 3608.41 |
| **X** | | | | | | | | | | **1064.87** | 3846.18 | 3159.85 |
| **XI** | | | | | | | | | | | **0** | 3778.55 |
| **XII** | | | | | | | | | | | | **0** |

homogeneous within each cluster but heterogeneous between them. These results are consistent with previous studies (11, 12, 13). The average intra-cluster distance ranged from 0 to 1064.87, as shown in Table 3. Cluster X (1064.87) had the greatest intra-cluster distance, followed by clusters IV (831.08), VII (766.23), IX (739.54), clusters I (707.45),II (702.83), III (692.30), V (437.37) and VI (292.33). Cluster VIII, XI, and XII had the shortest intra-cluster distance (0). Cluster X, followed by Cluster IV, showed the highest intra-cluster distance, indicating that the genotypes in these clusters were more divergent than in any other cluster. The maximum and minimum intra-cluster values in clusters V and IV were 171.37 and 84.27, respectively (14). Cluster III had the largest intra-cluster distance (103.53), whereas clusters II, VI and VII had the smallest (15). The average inter-cluster distance ranged from 804.88 to 4758.26. The inter-cluster distance was largest between IX and XI (4758.26), followed by III and XII (3923.90), X and XI (3846.18) and VII and XII (3823.26), with clusters II and III having the least distance (804.88). The greatest inter-cluster distance was recorded between IX and XI, followed by III and XII. As a result, the genotypes in these clusters were highly divergent, and the parent could be chosen from these clusters for the crossing programme to produce superior $F_1$ hybrids and segregants. Maximum and minimum inter-cluster distance values of 8362.80 (cluster III and cluster V) and 1387.00 (cluster II and cluster) respectively were noticed by (16). In contrast, the range from 35.96 (I and II) to 1584.40 (VIII and X) was found in another study among 110 genotypes of brinjal (17).

Cluster means for 45 genotypes are shown in Table 4. For plant height, Cluster XI exhibited maximum values whereas, minimum value was noticed in the cluster II (59.91). For number of primary branches, cluster XII possessed higher value (13.25), while cluster III showed less value (4.21). For earliness traits like days to 1st flowering, days to 50% flowering and days to 1st harvest, minimum values of 34.31, 46.58 and 56.50 were found in the cluster V respectively. For fruit length maximum value was found in cluster IX (19.36) and a minimum value was found in cluster XI (5.84). For girth and weight of fruit maximum values were exhibited in cluster X of 19.34 and 99.90 respectively. Minimum value for fruit girth and fruit weight was recorded in the cluster II (11.25) and cluster VII (36.82). Cluster V showed minimum fruit borer infestation of 13.76 whereas, maximum infestation was noticed in cluster VII (18.26). Cluster VIII had the greatest mean value for number of fruits (42.94) and yield per plant (2.88). While lowest values for these traits were recorded in cluster X (22.69) and cluster VII (1.16). For earliness and maximum yield, genotypes in cluster V and VIII could be used as parents to produce superior hybrids or transgressive segregants in future generations. From this result, it is evident that different traits indicated superiority with corresponding clusters so breeders should select genotypes from specific clusters based on the needs of the crop improvement programme. These results are consistent with the findings of (13, 18, 19).

**Table 4.** Cluster means of 11 traits in brinjal.

| S.No | Traits | Cluster means of brinjal | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | I | II | III | IV | V | VI | VII | VIII | IX | X | XI | XII |
| 1 | PH | 79.79 | 59.91 | 81.06 | 91.17 | 59.99 | 116.04 | 86.85 | 78.07 | 73.82 | 68.41 | 119.09 | 72.02 |
| 2 | PB | 6.40 | 4.94 | 4.21 | 5.68 | 8.29 | 8.84 | 6.08 | 6.51 | 6.91 | 5.34 | 7.38 | 13.25 |
| 3 | DTFF | 38.70 | 50.18 | 46.60 | 37.42 | 34.31 | 37.81 | 42.92 | 49.22 | 39.36 | 42.84 | 50.36 | 41.24 |
| 4 | DFPF | 50.51 | 61.84 | 57.20 | 47.96 | 46.58 | 47.50 | 53.39 | 60.17 | 48.32 | 53.87 | 61.34 | 53.27 |
| 5 | DTFH | 59.72 | 72.28 | 67.61 | 58.58 | 56.50 | 57.44 | 61.88 | 70.17 | 60.33 | 63.85 | 71.43 | 64.30 |
| 6 | FL | 8.00 | 10.98 | 12.73 | 9.67 | 10.57 | 8.44 | 10.68 | 8.28 | 19.36 | 10.40 | 5.84 | 9.42 |
| 7 | FG | 13.05 | 11.25 | 14.60 | 14.25 | 15.25 | 12.68 | 14.26 | 12.34 | 12.30 | 19.34 | 13.78 | 18.80 |
| 8 | FW | 57.51 | 57.54 | 62.38 | 63.89 | 67.45 | 72.44 | 36.82 | 67.01 | 62.17 | 99.90 | 48.60 | 69.14 |
| 9 | FB | 17.16 | 17.24 | 17.90 | 15.30 | 13.76 | 15.81 | 18.26 | 14.31 | 18.06 | 15.91 | 17.23 | 16.34 |
| 10 | NFPP | 34.62 | 33.04 | 33.69 | 40.55 | 40.68 | 34.73 | 31.69 | 42.94 | 34.62 | 22.69 | 32.14 | 30.62 |
| 11 | YPP | 1.98 | 1.89 | 2.08 | 2.58 | 2.73 | 2.50 | 1.16 | 2.88 | 2.17 | 2.23 | 1.56 | 2.11 |

**PH**-Plant height (cm),-**PB**-Number of primary branches, **DTFF**-Days to 1st flowering,-**DFPF**-Days to 50 % flowering, **DTFH**- Days to 1st harvesting,-**FL**-Fruit length (cm), -**FG**-Fruit girth (cm),-**FW**-Fruit weight (g), **FB**-Fruit borer incidence (%), **NFPP**-Number of fruit/ plant, **YPP**-Yield/plant (kg).

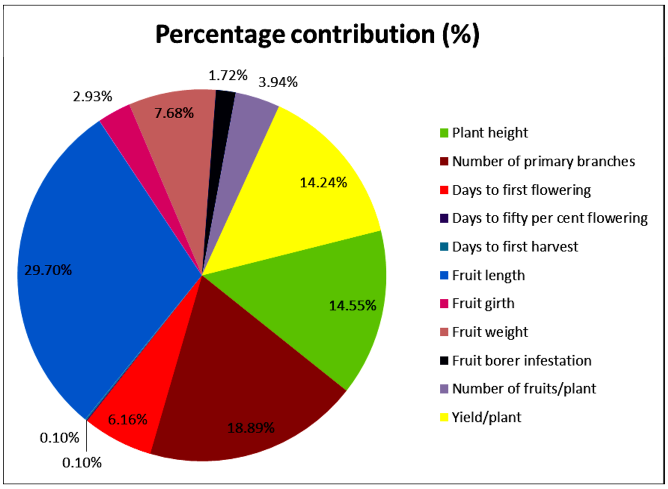

**Fig. 1.** Percentage contribution of traits to genetic diversity.

The percentage contribution of each attribute to genetic diversity is depicted in Fig. 1. Fruit length made the most significant contribution to genetic diversity, accounting for around 29.70%. This was followed by the trait number of primary branches (18.89 %), Plant height (14.55 %), yield per plant (14.24 %), fruit weight (7.68 %), days to 1st flowering (6.16 %), number of fruits per plant (3.94 %), fruit girth (2.93 %), fruit borer infestation (1.72 %), days to 50 % flowering (0.10 %) and days to 1st harvest (0.10 %). Thus, fruit length, number of primary branches, plant height and yield per plant are the major factors leading to genetic divergence. Thus, selecting divergent parents based on these characteristics will be beneficial for harnessing hybrid vigour in brinjal. The factors that contributed most to genetic diversity were fruit yield per hectare (15.71%), followed by fruit length (15.67%) and plant height (13.76%) (18). Similar studies were also carried out by (11) and (15).

## Conclusion

The present investigation revealed significant genetic divergence among the 45 brinjal genotypes. From cluster means, it is evident that different traits indicated superiority with corresponding clusters, so breeders should select genotypes from specific clusters based on the needs of the crop improvement programme. Traits such as fruit length, number of primary branches, plant height and yield per plant were the main contributors to genetic diversity. So, higher production recombinants could be produced by selecting parents with different fruit lengths followed by the number of primary branches, and plant height. Cluster X has the largest intra-cluster distance, followed by cluster IV. Clusters IX and XI had the greatest inter-cluster distance, followed by III and XII, and clusters II and III had the shortest distance (804.88). Thus, genotypes from the cluster with a large inter and intra-cluster distance could be chosen as parents to produce superior $F_1$ hybrids and segregants in future generations.

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## Authors' contributions

RK conducted the research experiments and wrote the manuscript. PI, RV and SV helped in conducting the experiments. SP designed the study and supervised it. KI helped to perform statistical analysis. SP helped in genotype collection and corrected and revised the manuscript.

## Compliance with ethical standards

**Conflict of interest**: Authors do not have any conflict of interests to declare.

**Ethical issues**: None

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