Received: 05 Jan 2021 | Revised: 21 Oct 2021 | Accepted: 01 Nov 2021

Electronic Journal of Plant Breeding

Research Article

# Genetic divergence in brinjal genotypes for growth and yield parameters

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**Abstract**
Field investigations were carried out during 2019 and 2020 to study the genetic diversity among 112 brinjal genotypes. Mahalanobis's $D^2$ analysis was done for ten growth and nine yield attributing characters. All 112 genotypes were grouped into seven clusters. Cluster IV (23.975) registered the highest intra cluster distance, whereas cluster II (5.683) recorded the lowest cluster distance. The maximum inter cluster distance was observed for clusters I and IV (24.912). Minimum inter cluster distance was registered between clusters II and III (10.431). Fruit yield per plant, fruit girth and the number of seeds per fruit retained the highest contribution in order towards total divergence. Cluster IV registered the maximum mean for average fruit yield per plant (1647.37). Therefore, the selection of parents from the diverse clusters would yield good segregants for the improvement of yield in brinjal.

**Key words:** Brinjal, Genetic diversity, $D^2$ analysis, intra cluster distance, inter cluster distance.

## INTRODUCTION

Brinjal (*Solanum melongena* L.) is a widely consumed vegetable of South East Asia grown throughout the year. In India, it occupies an area of 0.73 m. ha with the production of 128.0 m. tons and productivity of 17.5 tons per hectare (NHB, 2018). India is recognized as the primary center of origin of this crop. It exhibits large variations collectively as cultivars and land races in various parts of the country. Brinjal is normally developed by selecting the accessions with a suitable combination of characters from the germplasm or by the crossing of selected lines. There are different methods to study the genetic divergence in the genotypes and most often Mahalanobis $D^2$ estimates (Mahalanobis, 1936) is used. This is a substantial tool for assuming the degree of divergence between populations to the total divergence. It is a highly effective technique of measure of genetic divergence as recorded by various workers (Reddy *et al.,* 2013; Meena and Bahadur, 2015). The present study was therefore undertaken to evaluate the extent of genetic diversity in the available gene pool based on ten growth and nine yield traits.

## MATERIALS AND METHODS

Field investigations were carried out during July-December 2019 and March- July 2020 at a village, Venanallur located in Ariyalur District. The site is located at $10^{0}$.53′-$11^{0}$.26′ North latitude, 78˚.56′ -$79^{0}$.31′ East longitudes. The experimental material consisted of 112 genotypes out of which seventy five genotypes were obtained from NBPGR, New Delhi, thirty landraces from Cuddalore, Villupuram, Erode, Ariyalur, Puducherry, Pudukkottai, Namakkal, Karaikal and Vellore, four varieties from Agricultural Institutes, (Tamil Nadu Agricultural University & Annamalai Univerisity), two varieties from a private seed company, (Saadhana Agro Seeds and Indo- American Hybrid Seeds Pvt. Ltd) and one variety from National Institute, (IIHR, Bangalore). Individual genotype was grown in plots of size 4 x 3 m accommodating 25 plants and at a spacing of 75 x 60 cm. Three replications were maintained in Randomized Block Design. All the other standard cultivation practices were followed to maintain the crop healthy. Observations were documented for 19 quantitative characters. The data recorded in both the seasons were pooled (Kachouli *et al.,* 2019) and the statistical analyses work was done through “GENSTAT” software.

## RESULTS AND DISCUSSION

The analysis of variance showed significant differences among the 112 genotypes for 19 characters implying the existence of a sufficient amount of diversity. Assessment of genetic diversity is the predominant aspect of various breeding programs and possesses enormous significance. It is an inevitable study for achievements in crop improvement, thus resulting in the production of superior plants (Ravali *et al.,* 2017). To distinguish the genotypes, characteristic differences were observed based on their morphology. Based on $D^2$ analysis, all the genotypes were categorized into seven clusters (**Table 1**), which indicated a wide range of variation among the genotypes studied. Similar studies were done earlier and reported in brinjal (Sindhuja *et al.,* 2019). In clustering pattern, cluster V accommodated the maximum of 46 genotypes; cluster I housed 30 genotypes; cluster VII had 26 genotypes, cluster IV had 4 genotypes, while each of the clusters namely II, III and VI consisted of two genotypes each and none of the clusters is mono-genotypic. The clustering pattern obtained in the present investigation recorded that geographic diversity did not seem to have a direct association with genetic diversity. Bansal and Mehta (2007) and Mehta and Sahu (2009) revealed that genetic and geographical diversity was unrelated. Similar finding was reported earlier by Vidhya and Kumar (2014) in brinjal.

In the present study, it was observed that $D^2$ values between all possible 6,216 pairs of 112 genotypes ranged from 10.431 to 24.912. This indicated the presence of an adequate amount of genetic diversity in the materials studied. The mean value of inter and intra cluster distance was assessed for seven clusters and are presented in **Table 2**. Cluster II showed the lowest intra cluster distance (5.683), thus indicated that the genotypes in this cluster resembled one another genetically and appeared to have evolved from a common gene pool (Gurve *et al.,* 2019). The highest intra cluster distance was indicated by cluster IV (23.975) followed by cluster VI (23.370), thus suggesting that these genotypes might have different genetic architecture (Muniappan *et al.,* 2010). This kind of clustering of different genotypes from different eco- geographic locations into the same cluster was attributed to the free exchange of genotypes from one region to another. The range of values was from 5.683 to 23.975.

Maximum inter cluster distance values existed between clusters I and IV (24.912). This was followed by clusters IV and V (24.752); clusters I and V (23.997); clusters IV and VII (23.055) and clusters I and VII (22.280). Genotypes from the above four clusters if involved in hybridization may give rise to a broad range of variation for growth and yield traits. A similar result was revealed earlier by Babu and Patil (2004) in Brinjal. The inter- cluster distance was minimum between cluster II and III (10.431) and thus suggested that the genetic constitution of the genotypes in these clusters was in close proximity.

**Table 1. Distribution of brinjal genotypes based on $D^2$ analysis**

| Cluster | Number of genotypes | Genotypes |
|---|---|---|
| Cluster I | 30 | IC- 136366, IC-386589, IC-136452, IC-136268, IC-136061, IC-112315, IC-089905, IC-144515, IC-136303, IC-136231, IC-136546, IC-89910, IC-136188, IC-144527-C, IC-089888, IC-136182, IC-136299, IC-089875, IC-144525, IC-136184. IC-136017, IC-136308, IC-136461, IC-089876-C, IC-136181, IC-136300, IC-136349, IC-136148, IC-345590, IC-427029 |
| Cluster II | 2 | IC-136189, IC-545862 |
| Cluster III | 2 | Naanamedu -2, Sevathapatti |
| Cluster IV | 4 | IC-136249, IC-136196, IC-422585, Ujala Brinjal |
| Cluster V | 46 | IC-089900, IC-136177, IC-136222, IC-136290, IC-136006, IC-137751, IC-136309, IC-90795, IC-136455, IC-136266, IC-136093, IC-446655, IC-203589, IC-136307, IC-136258, IC-446654, IC-136292, IC-136296, IC-136251, IC-144575, IC-112991, IC-345335, IC-136311, IC-112341, IC-154517, IC-111074. IC-136018, IC-212426, IC-136297, IC- 322352, IC-382587, IC-361838, IC-383119, IC-216794, IC-394902, IC- 344674, IC-334660, IC-427008, IC-355370, IC-411485, CO$_{2,}$ PLR-1, PLR-2, Annamalai, Arka Harshitha, Bhavani. |
| Cluster VI | 2 | Gandarvakottai, Athur Local |
| Cluster VII | 26 | Elavambadi, Namakkal Local, Kalanchipatti, Utha Nilam, Udha Brinjal, Urundai, Adarvaripachai, Udumalai Samba, Purple Round, Karnataka, Paramathi Local, Varipachai, Thengaithittu, Kallipattu-1, Kallipattu-2, Vikravandi-1, Vikravandi-2, Villupuram, Mathavidupatti, Panruti, Naanamedu -1, Paravai Local, Green Round, Parur-1, Round, Indam RB 63. |
| Total | 112 | |

https://doi.org/10.37992/2021.1204.192

**Table 2. Intra and inter cluster distance D $^{2}$ and D values in brinjal genotypes based on ten growth and nine yield characters**

| Cluster | I | II | III | IV | V | VI | VII |
|---|---|---|---|---|---|---|---|
| I | **500.058**<br>**(22.362)** | 397.152<br>(19.929) | 421.457<br>(20.529) | 620.597<br>(24.912) | 575.859<br>(23.997) | 452.058<br>(21.262) | 496.389<br>(22.280) |
| II | | **32.302**<br>**(5.683)** | 108.802<br>(10.431) | 408.441<br>(20.210) | 370.867<br>(19.258) | 133.198<br>(11.541) | 269.657<br>(16.421) |
| III | | | **48.853**<br>**(6.990)** | 485.198<br>(22.027) | 411.237<br>(20.279) | 116.620<br>(10.799) | 271.523<br>(16.478) |
| IV | | | | **574.793**<br>**(23.975)** | 612.637<br>(24.752) | 461.607<br>(21.485) | 531.536<br>(23.055) |
| V | | | | | **546.158**<br>**(23.370)** | 392.517<br>(19.812) | 473.600<br>(21.762) |
| VI | | | | | | **60.203**<br>**(7.759)** | 267.794<br>(16.812) |
| VII | | | | | | | **386.052**<br>**(19.648)** |

The cluster mean values for ten growth and nine yield characters are interpreted in **Table 3**. The maximum mean value for plant height was possessed by cluster II (83.08) and the lowest mean value by cluster IV (70.32). The cluster means performance for plant spread was the highest in cluster IV (53.90) followed by cluster I (46.38) and the lowest in cluster III (39.95). Branching was profuse in cluster IV (10.14) and it was lesser in genotypes of cluster VI (7.46). The maximum leaf area index was observed in cluster IV (3.05) and the minimum mean value was registered in cluster VI (2.54).

The genotypes under cluster I took a minimum number of days to first flowering (52.12) followed by cluster VI (52.34), while the genotypes of cluster II took a longer duration for first flowering (52.69). The genotypes of cluster I (63.11) registered the minimum values for days to 50% flowering and the maximum (65.01) was registered in cluster II. Cluster I recorded the highest number of long styled flowers (29.08) followed by cluster IV (26.38). The number of medium styled flowers per plant was maximum in cluster II (22.07). The minimum number of pseudo and true short styled flowers per plant was recorded in cluster I (11.38). The number of flowers per plant was maximum in cluster II (69.88), followed by cluster VI (68.92). The minimum number of flowers per plant was observed in cluster I (54.48). Therefore if the breeding program is aimed for earliness, then accessions in these clusters can be chosen and the results were also stated by Meena and Bahadur (2013) in Tomato.

**Table 3. Cluster mean values for ten growth and nine yield characters in genotypes of brinjal**

| Cluster/ Character | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| I | 77.93 | 46.38 | 8.84 | 2.80 | 52.12 | 63.11 | 29.08 | 13.74 | 11.38 | 54.48 | 19.81 | 37.02 | 9.09 | 12.35 | 41.66 | 6.86 | 312.73 | 0.32 | 1502.43 |
| II | 83.08 | 43.67 | 9.45 | 2.62 | 52.69 | 63.64 | 22.32 | 22.07 | 25.48 | 69.88 | 17.65 | 25.32 | 8.80 | 9.70 | 38.21 | 6.26 | 248.29 | 0.39 | 829.92 |
| III | 71.15 | 39.95 | 8.47 | 2.56 | 52.36 | 63.19 | 22.99 | 19.57 | 25.89 | 68.46 | 15.50 | 22.74 | 7.87 | 10.20 | 41.63 | 5.88 | 242.08 | 0.28 | 991.73 |
| IV | 70.32 | 53.90 | 10.14 | 3.05 | 52.66 | 63.29 | 26.38 | 16.08 | 16.31 | 58.78 | 20.75 | 36.77 | 11.60 | 8.90 | 38.66 | 7.42 | 242.18 | 0.30 | 1647.37 |
| V | 79.59 | 43.87 | 9.45 | 2.79 | 52.65 | 63.91 | 25.18 | 19.25 | 22.94 | 67.38 | 18.27 | 29.38 | 10.20 | 10.54 | 42.46 | 7.00 | 351.12 | 0.34 | 1394.47 |
| VI | 71.69 | 40.60 | 7.46 | 2.54 | 52.34 | 62.18 | 24.37 | 19.30 | 25.24 | 68.92 | 16.31 | 23.79 | 8.92 | 7.67 | 36.00 | 6.46 | 341.88 | 0.32 | 842.82 |
| VII | 73.33 | 42.73 | 9.10 | 2.56 | 52.63 | 63.29 | 24.25 | 19.53 | 20.77 | 64.69 | 17.14 | 28.46 | 10.08 | 10.56 | 40.38 | 6.82 | 314.11 | 0.33 | 1206.95 |

1. Plant height (cm), 2. Plant spread (cm), 3. Number of branches / plant, 4. Leaf area index, 5. Days to 1st flowering, 6. Days to 50 per cent flowering, 7. Number of long styled flowers, 8. Number of medium styled flowers, 9. Number of pseudo and true short styled flowers, 10. Number of flowers per plant,11. Number of fruits per plant,12. Fruit set percentage, 13. Fruit length, 14. Fruit girth, 15. Average fruit weight, 16. Number of pickings 17. Number of seeds per fruit, 18. 100 Seed weight, 19. Fruit yield per plant.

The highest mean for the number of fruits per plant was noted in cluster IV (20.75). This was followed by cluster I (19.81) and te minimum in cluster III (15.50). Fruit set percentage was maximum in cluster I (37.02). This was followed by cluster IV (36.77) and the minimum percentage of fruit set was registered in cluster III (22.74). Cluster IV registered the maximum fruit length (11.60). The maximum fruit diameter was observed in cluster I (12.35) followed by cluster VII (10.56) and the minimum fruit girth was recorded in cluster VI (7.67).

The genotypes of cluster V (42.65) registered the maximum mean value for average fruit weight followed by cluster I (41.66). The minimum mean value of average fruit weight was registered in cluster VI (36.00). Cluster IV recorded the maximum number of pickings per plant (7.42) and the minimum number of pickings per plant was registered in cluster III (5.88). The cluster V (351.12) had the more number of seeds per fruit. This was lesser in cluster III (242.08). The 100 seed weight was the maximum in cluster II (0.39) and the minimum was registered by cluster III (0.28). Fruit yield per plant showed the highest mean value in cluster IV (1647.37) followed by cluster I (1502.43) and the lowest mean value was recorded in the genotypes of cluster II (829.92). The above comparison implies that clusters I, II, IV and V had the maximum mean value for most of the characters. Therefore, these clusters are considered as the more preferable for selecting genotypes for further breeding. A similar finding was registered by Rekha and Celine (2015) in Brinjal.

The selection of parents mainly depends upon the relative contribution of ten growth and nine yield attributing characters towards genetic divergence. The relative contribution per cent of different characters to divergence is given in **Table 4.** Fruit yield per plant (24.79%) contributed the maximum to the total genetic diversity among the genotypes followed by fruit girth (20.56%), seed number per fruit (17.97%), fruit length (7.16%), leaf area index (6.66%), fruit number per plant (6.16%), average fruit weight (2.70%), plant spread (2.51%), the number of branches per plant (2.36%), the number of pickings per plant (2.11%), the number of pseudo and short styled flowers (2.08%), 100 seed weight (1.80%), fruit set % (1.49%), plant height (1.19 %), days to first flowering (0.21%), the number of long styled flowers (0.16 %), the number of flowers per plant (0.05%), the number of medium styled flowers and days to 50% flowering (0.02 %). The characters contributed the maximum percentage towards genetic diversity could be given due importance for the selection of genotypes for further improvement. These observations are conforming to the findings of Kumar *et al.* (2012) in brinjal.

**Table 4. Relative contribution of ten growth and nine yield attributing characters in brinjal**

| S.No. | Characters | Contribution (%) |
|---|---|---|
| 1 | Plant height | 1.19 |
| 2 | Plant spread | 2.51 |
| 3 | Number of branches per plant | 2.36 |
| 4 | Leaf area index | 6.66 |
| 5 | Days to 1 $^{st}$ flowering | 0.21 |
| 6 | Days to 50 per cent flowering | 0.02 |
| 7 | Number of long styled flowers | 0.16 |
| 8 | Number of medium styled flowers | 0.02 |
| 9 | Number of pseudo and true short styled flowers | 2.08 |
| 10 | Number of flowers per plant | 0.05 |
| 11 | Number of fruits per plant | 6.16 |
| 12 | Fruit set per cent | 1.49 |
| 13 | Fruit length | 7.16 |
| 14 | Fruit girth | 20.56 |
| 15 | Fruit weight | 2.70 |
| 16 | Number of pickings | 2.11 |
| 17 | Number of seeds per fruit | 17.97 |
| 18 | 100 seed weight | 1.80 |
| 19 | Fruit yield per plant | 24.79 |
|  | **Total** | 100 |

Studies on genetic divergence will be helpful in the identification of superior parents. Genetic divergence studies grouped 112 brinjal genotypes into seven clusters. The inter cluster divergence was found to be maximum between clusters I and IV, clusters IV and V, clusters I and V, clusters IV and VII. Cluster IV registered the maximum intra cluster distance, while cluster II recorded the minimum intra cluster distance. The specific genotypes selected for various characters from clusters I, II, III, IV, V, and VII could be used as parents in the crossing programmes. The genotypes with high mean values of yield characters from the selected clusters could be utilized in the hybridization programme to generate more heterotic $F_1$s and better segregants in the $F_2$ generation.

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