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Genetic divergence study in brinjal (*Solanum melongena* L.)

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Abstract

Genetic divergence in brinjal was studied through non-hierarchical Euclidean cluster analysis. The results showed the presence of sufficient amount of genetic diversity among 110 genotypes of brinjal. The cluster analysis grouped all 110 brinjal genotypes into 8 major clusters based on D^2 value. Maximum numbers of genotypes were grouped into cluster VI including twenty eight genotypes. The maximum intra cluster distance was observed in cluster IV (3.784) closely followed by cluster VII (3.148) indicating maximum diversity within these clusters, while minimum intra cluster distance was observed in cluster II. The maximum inter cluster value (9.061) was obtained between cluster II and IV and minimum diversity was observed between cluster V and VI (2.426) which suggested that members of these two clusters are genetically very close. The genotypes of heterogeneous origin are grouped together in some of the major clusters suggesting no parallelism between geographical and genetic diversity suggesting thereby that parents should be selected on the basis of total divergence for the characters used for an overall improvement in the yield.

Keywords: Cluster analysis, brinjal (*Solanum melongena* L.), genetic divergence

Introduction

Brinjal (*Solanum melongena* L. $2n = 24$), one of the important vegetable crops, belongs to the family Solanaceae, a major vegetable crop throughout the tropics and subtropics. Brinjal is native of India. It is a major vegetable crop grown throughout India for its tender fruits. 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 program. A previous knowledge of the structure of the genetic diversity within a large collection of germplasm may be of great help to make decisions on management procedures, as well as on breeding strategies to use in current and future breeding programs. Assessment of genetic variation in a species is a prerequisite for initiating an efficient breeding programme, as it provides a basis for tailoring desirable genotypes. Genetically diverse parents are likely to segregates/ to produce high heterotic crosses. More diverse the parents, greater are the chances of obtaining high heterotic F₁s and broad spectrum of variability in segregating generations (Arunachalam, 1981). Genetic diversity study also permits to select the genetically divergent parents to obtain the desirable recombinant in the segregating generations of eggplants. The aim of the present study was to characterize eggplant genotypes collected from different regions of India and exotic sources to assess the genetic diversity within the germplasm.

Materials and Methods

The present investigation was carried out in the Department of Vegetable Science, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh during *kharif* 2015. The experimental material of present study comprised of a set of one hundred ten genotypes out of which one hundred six genotypes were collected from various part of Chhattisgarh and Odisha, two from GBPUAT, Panthnagar (Pant Rituraj and Pant Samrat), one genotype from IIVR, Varanasi (Kashi Taru) and one genotype from IGKV, Raipur (IBWL) were grown to estimate genetic divergence during *kharif* 2015. The genotypes were grown in Randomized Block Design and replicated with three replications during *kharif* season 2015. In each replication each genotype was grown in a four rows and five columns plot with a spacing of 75 cm x 60 cm, row-to-row spacing and plant-to-plant spacing respectively. The recommended package of practices was

followed to raise a successful crop and necessary prophylactic plant protection measures were carried out to safeguard the crop from pests and diseases.

The Mahalanobis (1936) D^2 statistic was used to measure the genetic divergence between the populations. The D^2 value was estimated on the basis of 'P' character by the formula:

Formula:

$$D^2 P = \sum_{i=1}^p \sum_{j=1}^p (\lambda_{ij}) \lambda_i \lambda_j$$

Where,

(λ_{ij}) is the reciprocal or (λ_{ji}) , the pooled common dispersion

matrix (*i.e.* error matrix)

i = the difference in the mean value for the i^{th} character

j = the difference in the mean value for the j^{th} character

For calculating the D^2 values, the variance and covariance were calculated. The genotypes were grouped into different clusters by Tocher's method. The population was arranged in order of their relative distances from each other. For including a particular population in the clusters, a level of D^2 was fixed by taking the maximum D^2 values between any two populations in the first row of the table where D^2 values were arranged in increasing order of magnitude. In all the combinations each character was ranked on the basis of their contribution towards divergence between two entries ($d_{ij} = y_{ji} - y_{ij}$). Rank I was given to the highest mean difference and

rank 'P' to the lowest difference; p is the total number of characters considered.

Results and Discussion

The choice of genetically diverse parents for hybridization is an important feature of any crop improvement programmed for getting desirable segregate. The multivariate analysis based on Mahalanobis D^2 or non-hierarchical Euclidean cluster analysis is used for divergence analysis. The D^2 analysis classifies the genotype into relatively homogeneous groups in such a way that within cluster diversity is minimized and between clusters diversity is maximized. The respective genotypes from diverse cluster can be utilized in breeding programmed depending upon breeding objectives. The results of quantitative assessment of genetic divergence among 110 genotypes of brinjal for yield and yield contributing characters following Mahalanobis's D^2 statistic are presented below. Since all the sixteen variables were correlated, they were transformed into uncorrelated linear combination through pivotal condensation method. This indicated that substantial diversity existed in all the genotypes evaluated in the present study. This present study also suggests that, there is no relationship between geographical and genetic diversity as genotype chosen from different eco-geographical regions are grouped in different clusters.

The procedure suggested by Tocher (Rao, 1952) was used to group 110 brinjal genotypes into eight clusters by treating estimated D^2 values as the square of the generalized distance. The pattern of distribution of 110 genotypes in to various clusters is indicated in Table 1.

Table 1: Composition of clusters into various clusters of brinjal genotype during *kharif*, 2015

Cluster number	Number of genotypes included	Names of genotypes
I	12	IGB-19, IGB-21, IGB-26, IGB-3, IGB-34, IGB-42, IGB-47, IGB-52, IGB-53, IGB-58, IGB-78 and IGB-79
II	2	IGB-92 and IGB-93
III	11	IGB-1, IGB-3, IGB-5, IGB-13, IGB-28, IGB-31, IGB-41, IGB-55, IGB-57, IGB-59 and IGB-89
IV	10	IGB-2, IGB-8, IGB-15, IGB-18, IGB-20, IGB-24, IGB-30, IGB-44, IGB-45 and IBWL
V	21	IGB-43, IGB-65, IGB-66, IGB-68, IGB-72, IGB-73, IGB-76, IGB-81, IGB-82, IGB-83, IGB-84, IGB-85, IGB-86, IGB-90, IGB-91, IGB-94, IGB-95, IGB-98, IGB-99, IGB-100 and IGB-103
VI	28	IGB-4, IGB-37, IGB-38, IGB-39, IGB-40, IGB-46, IGB-50, IGB-51, IGB-56, IGB-61, IGB-63, IGB-64, IGB-67, IGB-69, IGB-70, IGB-71, IGB-74, IGB-75, IGB-77, IGB-80, IGB-87, IGB-88, IGB-96, IGB-97, IGB-101, IGB-102, IGB-104 and IGB-105
VII	19	IGB-6, IGB-7, IGB-9, IGB-10, IGB-11, IGB-12, IGB-14, IGB-16, IGB-22, IGB-23, IGB-25, IGB-27, IGB-29, IGB-32, IGB-35, IGB-36, IGB-48, IGB-49 and IGB-106
VIII	7	IGB-17, IGB-54, IGB-60, IGB-62, Pant Rituraj, Pant Samrat and Kashi Taru

The mean intra and inter cluster D^2 values among the eight clusters are given in the Table 2 (Fig.1). The intra cluster distance ranged from 2.095 to 3.784. Cluster IV had the maximum D^2 value (3.784) followed by cluster VII (3.148), cluster VIII (3.099), cluster V (2.873), cluster III (2.865), cluster VI (2.749) and cluster I (2.710), while, cluster II found minimum D^2 value (2.095). The inter cluster D^2 values of the eight clusters revealed that highest inter cluster generalized distance (9.061) was between cluster II and cluster IV followed by cluster I and cluster II (7.502), cluster II and cluster VII (7.151), cluster II and cluster III (6.763), cluster II and cluster VI (6.590), cluster II and cluster V (6.429), cluster VIII and cluster I (5.924), cluster VIII and cluster V (5.827), cluster V and cluster IV (5.708), cluster VIII and cluster II (5.670), cluster VIII and cluster IV (5.419), cluster I and cluster IV (5.261), cluster III and cluster IV (5.218), cluster VI and cluster IV (5.039), cluster III and cluster VIII (4.959),

cluster VI and cluster VIII (4.899), cluster VII and cluster VIII (4.306), cluster VI and cluster VII (3.928), cluster IV and cluster VII (3.718), while, the lowest (2.426) was between cluster V and cluster VI followed by cluster I and cluster VI (2.907), cluster III and cluster VI (2.978), cluster III and cluster VII (3.130), cluster I and cluster V (3.208), cluster VI and cluster VII (3.259). The inter cluster distance was minimum between cluster V and VI indicating narrow genetic diversity and maximum between clusters II and IV followed by I and II indicating wider genetic diversity among the genotypes included in these groups. Selection of parents from these diverse clusters for hybridization programme would help in achieving novel recombinants. Similar observations were reported Babu and Patil (2004) [2], Senapati *et al.* (2009) [13], Muniappan *et al.* (2010) [9], Islam *et al.* (2011) [4], Lokesh *et al.* (2013) [6] and Khan and Singh (2015) [5].

Table 2: Intra (bold) and Inter cluster distance values in brinjal

Cluster	I	II	III	IV	V	VI	VII	VIII
I	2.710	7.502	2.892	5.261	3.208	2.907	3.506	5.924
II		2.095	6.763	9.061	6.429	6.590	7.151	5.670
III			2.865	5.218	3.692	2.978	3.130	4.959
IV				3.784	5.708	5.039	3.718	5.419
V					2.873	2.426	3.928	5.827
VI						2.749	3.259	4.899
VII							3.148	4.306
VIII								3.099

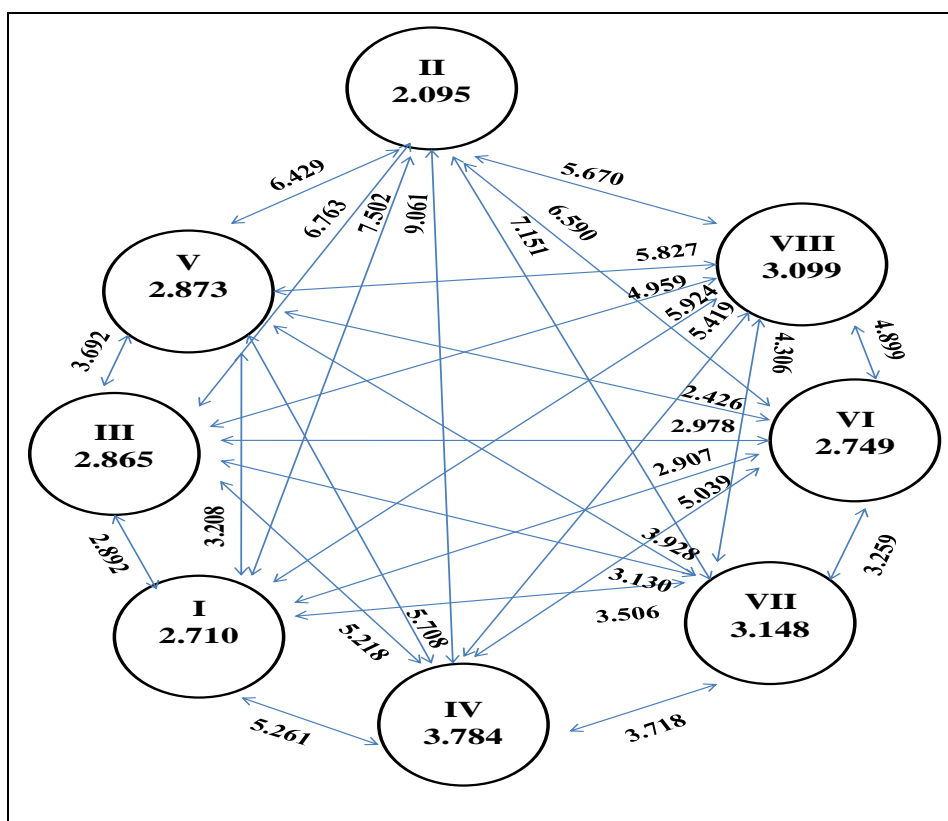


Fig 1: Statistical distance among 110 brinjal genotypes (not to scale)

Mean value of clusters for different characters presented in Table 3. Maximum mean value of plant height (cm) recorded cluster II recorded highest (85.53) followed by cluster VII (75.41), while lower plant height was observed in cluster I (50.31). The cluster mean performance for plant spread was the highest in cluster III (86.86) followed by cluster VII (84.74), cluster IV (78.52), cluster VIII (76.93), cluster VI (60.39) and lowest in cluster II (47.80). More number of branches per plant was recorded in cluster VI (9.48) followed by cluster V (9.00), cluster VIII (8.52), cluster II (8.17), cluster IV (7.17), cluster I (6.92) and cluster VII (6.32), while less number of branches per plant for genotypes of cluster III (5.85). The character days to 50 per cent flowering recorded its minimum mean value for the genotypes of cluster IV (39.16) followed by cluster VII (41.31), cluster III (41.58), cluster I (42.00) cluster VIII (42.52) and cluster V (49.59), while the genotypes of cluster II (56.23) registered maximum mean value for days to 50 per cent flowering. The genotypes of cluster IV (59.67) took less number of days to first fruit harvest followed by cluster I (60.19), cluster III (62.39), cluster VI (62.65), cluster VII (62.84), cluster V (68.84) and cluster VIII (66.71) and maximum number of days to first harvest was recorded in cluster II (91.00). Maximum number of clusters per plant was recorded in the genotypes of cluster IV (17.39) followed by cluster VII (16.87), cluster VI (13.39),

cluster VIII (13.10), whereas, minimum value was recorded in the genotypes of cluster V (10.29) followed by cluster I (10.78) and cluster II (11.13). Number of flowers per inflorescence exhibited the highest mean performance for cluster IV (5.54) followed by cluster VII (4.37), cluster VIII (4.33), cluster I (3.95), cluster VI (3.22) and lowest for cluster V (2.10). The maximum mean for number of fruits per cluster was noted in cluster IV (4.60) followed by cluster VIII (3.33), cluster VII (2.23), cluster V (1.84) and minimum for cluster II (1.33). The genotypes of cluster IV recorded highest mean value for number of fruits per plant (20.78) followed by cluster VIII (12.81), cluster VII (11.16), cluster VI (9.91), while the genotypes of cluster II (9.03) recorded lowest mean value for number of fruits per plant followed by cluster I (9.25).

The maximum fruit length (cm) was recorded in the genotypes of cluster II (14.50) followed by cluster VIII (14.00), cluster VII (13.94), cluster V (11.77), cluster I (11.65) and cluster VI (11.65), whereas, minimum value was recorded in the genotypes of cluster III (8.92) followed by cluster IV (11.11). The genotypes of cluster II registered more fruit girth (cm) (22.47) followed by cluster VIII (17.76), cluster III (16.98), cluster I (15.18), cluster VII (13.61) while the genotypes of cluster V (10.79) observed less fruit width followed by cluster VI (12.20), cluster IV (13.22).

Average fruit weight (g) recorded its maximum mean value in the genotypes of cluster II (101.13) followed by cluster VIII (90.85), cluster I (71.91), cluster III (63.89), cluster VI (56.27), cluster VII (53.66) and cluster V (46.09). The minimum mean value was recorded in the genotypes of cluster IV (33.26). The genotypes of cluster II (5.75) had maximum pericarp thickness (mm) followed by cluster VIII (5.53), cluster III (4.86), cluster VI (4.72), cluster IV (4.02), cluster VII (3.36) cluster V (3.27), while minimum pericarp thickness found cluster I (2.89).

The character, number of fruits per plant per picking registered its maximum mean value in the genotypes of cluster IV (10.30) followed by cluster VII (7.14), cluster VIII (6.55), cluster V (3.67), cluster III (3.40) and cluster I (3.14) and cluster VI (3.14). The minimum mean value was recorded

in the genotypes of cluster II (2.97). The character fruit yield per plant (kg) recorded its highest mean value in the genotypes of cluster VIII (2.07) followed by cluster II (1.60), cluster IV (1.20), cluster VII (1.20), cluster VI (0.95), cluster III (0.95) and cluster V (0.93), whereas, the lowest mean value was recorded in the genotypes of cluster I (0.7). The highest mean value for fruit yield per hectare (q) was recorded in the genotypes of cluster VIII (372.3) followed by cluster II (349.97), cluster VII (264.71), cluster IV (250.93), cluster VI (208.70), cluster III (205.80) and cluster V (202.12). The lowest mean value was recorded in cluster I (153.45). Cluster mean values showed a wide range of mean values among the characters studied indicating presence of wide variation among the genotypes studied.

Table 3: Mean performance of genotypes in individual cluster for fruit yield and its components in brinjal during *kharif* 2015

Characters Clusters	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	
I	12	50.31	64.78	6.92	42.00	60.19	10.78	3.95	1.83	9.25	11.65	15.18	71.91	2.89	3.14	0.7	153.45
II	2	85.53	47.80	8.17	56.23	91.00	11.13	2.60	1.33	9.03	14.50	22.47	101.13	5.75	2.97	1.60	349.97
III	11	63.72	86.86	5.85	41.58	62.39	11.61	2.45	1.82	9.59	8.92	16.98	63.89	4.86	3.40	0.95	205.80
IV	10	59.63	78.52	7.17	39.16	59.67	17.39	5.54	4.60	20.78	11.11	13.22	33.26	4.02	10.30	1.20	250.93
V	21	60.02	62.73	9.00	49.59	68.84	10.29	2.10	1.84	9.52	11.77	10.79	46.09	3.27	3.67	0.93	202.12
VI	28	67.65	60.39	9.48	42.39	62.65	13.39	3.22	1.65	9.91	11.65	12.20	56.27	4.72	3.14	0.95	208.70
VII	19	75.41	84.74	6.32	41.31	62.84	16.87	4.37	2.23	11.16	13.94	13.61	53.66	3.36	7.14	1.2	264.71
VIII	7	75.04	76.93	8.52	42.52	66.71	13.10	4.33	3.33	12.81	14.00	17.76	90.85	5.53	6.55	2.07	439.32

1. Plant height (cm)	2. Plant spread (cm)	3. Number of primary branches per plant	4. Days to 50 per cent flowering
5. Days to first fruit harvest	6. Number of clusters per plant	7. Numbers of flower per inflorescence	8. Number of fruits per cluster
9. Number of fruits per plant	10. Fruit length (cm)	11. Fruit girth (cm)	12. Average fruit weight (g)
13. Pericarp thickness (mm)	14. Number of fruits per plant per picking	15. Fruit yield per plant (kg)	16. Fruit yield per hectare (q)

Number of times each of sixteen traits appeared in first rank and its respective per cent contribution towards genetic divergence are presented in Table 4. The results showed that the character pericarp thickness contributed maximum (52.26 %) towards diversity by taking first ranking 3084 times, followed by number of fruits per plant per picking (12.33 %) by 728 times, fruit yield per plant (7.35 %) by 434 times, fruit length (4.91%) by 290 times, number of fruits per plant (4.66 %) by 275 times, days to 50 per cent flowering (3.79 %) by 226 times, average fruit weight (3.5 %) by 207 times, plant spread (3.42 %) by 202 times, fruit girth (2.4 %) by 145 times, number of fruits per cluster (1.77 %) each by 105 times, plant height (1.3 %) by 79 times, number of flowers per inflorescence (0.9 %) by 57 times, number of clusters per plant (0.7 %) by 44 times, days to first fruit harvest (0.61%) by 37 times and number of primary branches per plant and fruit yield per hectare (q) (0.1%) each by 6 times.

Patel *et al.* (2014) number of branches per plant, fruit girth found maximum per cent contribution towards divergence in brinjal, Whereas, Sadarunnisa *et al.* (2015) [12] found maximum genetic divergence by average fruit weight, fruit

length (cm), fruit girth (cm), days to 50% flowering, days to first harvest, days to last harvest, number of fruits per cluster, number of fruits per plant, fruit yield per plant (kg) and cumulative wilt(%). For number of fruits per plant, Singh *et al.* (2006) [14] and Senapati *et al.* (2009) [13] record maximum contribution towards divergence and for fruit yield per plant (kg) Babu and Patil (2004) [2] and Das *et al.* (2010) [3] observed such maximum contribution of to total divergence. Apart from the high divergence, the performance of the genotypes and the characters with maximum contribution towards divergence should also be given due consideration as they appears as desirable for inclusion in brinjal improvement.

Hence, apart from selecting genotypes from the clusters which have high inter- cluster distance for hybridization, one can also think of selecting parents based on extent of genetic divergence with respect to a particular character of interest. This means that, if breeders' intention is to improve fruit yield, he can select parents which are highly divergent with respect to these characters.

Table 4: Contribution of each character to divergence in brinjal

Sr. No.	Characters	Number of times appearing first time	Per cent contribution
01.	Plant height (cm)	79	1.3
02.	Plant spread (cm)	202	3.42
03.	No. of primary branches per plant	6	0.1
04.	Days to 50 per cent flowering	226	3.79
05.	Days to first fruit harvest	37	0.61
06.	No. of clusters per plant	44	0.74
07.	No. of flowers per inflorescence	57	0.9
08.	No. of fruits per cluster	105	1.77
09.	No. of fruits per plant	275	4.66

10.	Fruit length (cm)	290	4.91
11.	Fruit girth (cm)	145	2.4
12.	Average fruit weight (g)	207	3.5
13.	Pericarp thickness (mm)	3084	52.26
14.	No. of fruits per plant per picking	728	12.33
15.	Fruit yield per plant (kg)	434	7.35
16.	Fruit yield per hectare (q)	6	0.1

Conclusion

It can be concluded from present investigation that D^2 value recorded for fruit yield and its components indicated the presence of appreciable amount of genetic diversity among the genotypes and it revealed that geographic distribution had no relation to genetic diversity as genotypes belonged to different places of origin.

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