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Research Article

Insight into the genetic diversity of eggplant (*Solanum melongena* L.) genotypes through D^2 analysis

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Abstract

The present investigation was carried out during *Rabi* 2014-15 at College of Horticulture, Hiriyur, Karnataka with 62 eggplant genotypes. Mahalanobis' D^2 analysis was done to study the genetic diversity among the genotypes using 12 quantitative traits. Among the different traits studied, number of primary branches/plant contributed maximum towards total genetic divergence. D^2 statistic grouped the genotypes into 11 diverse clusters. The inter cluster D^2 value was maximum (3128.62) between cluster IX and XI which indicates that these clusters are diverse from each other. Crossing between the superior genotypes of above diverse cluster pairs may provide desirable transgressive segregants for developing high yielding varieties. Five genotypes namely R-2585, IIHR-355, Arka Kusumaker, IC420590 and R-2582 formed solitary clusters which hints at their uniqueness for most of the traits. Based on cluster mean scoring, cluster II ranked first indicating the presence of elite genotypes, which includes Punjab Barsati, IC104083, IVBL-9, Lal Gulab, IC90785, IC333527, Arka Abilash, IIHR-7 and Arka Kranti. So these genotypes can be extensively used for further breeding programme to generate new material.

Key words
Brinjal, D^2 analysis, Eggplant, Genetic Diversity

Introduction

Brinjal or Eggplant (*Solanum melongena* L.) is an important warm season vegetable crop belonging to Solanaceae family, mainly grown in tropical and subtropical regions of the world. India being the center of diversity of eggplant, has large genetic diversity accumulated as land races and cultivars in various parts of the country. The quantification of genetic divergence through biometrical procedures has made it possible to choose genetically diverse parents for a successful hybridization program (Uddin *et al.*, 2014). In crop improvement programme, to increase the productivity breeder needs to maintain a pool of diverse desirable donor parents (Joshi *et al.*, 2013). Moreover, evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm (Tomooka, 1991). Systematic improvement of any crop depends mainly on the information on genetic variability and diversity which forms the basis for any crop breeding programme (Gobu *et al.*, 2017). Genetic diversity in crop plants is essential to sustain the level of high productivity (Tripathi *et al.*, 2013). A new variety can be developed from an assembled diverse genetic stock of any crop. Hence, the present study was aimed to examine the genetic diversity in eggplant genotypes.

Materials and Methods

The experiment was conducted during *Rabi* 2014-15 at College of Horticulture, Hiriyur which is located in the Central Dry Zone (Zone-4) of Karnataka at 13º 57' North latitude, 76º 40' East longitudes with an altitude of 630 meters above the mean sea level. The experimental material consists of 62 genotypes collected from Vegetable Research Station, Kalyanpur (U.P.), IIHR, Bangalore, Karnataka, Zonal Research Station, Chianky, Palamu, Jharkhand, IIVR, Varanasi, (U.P.), NBPGR, New Delhi, TNAU, Coimbatore, Tamil Nadu and Local Collections. The experiment was laid out in randomized block design with three replications. Standard package of practices was followed to raise a good crop. Observations were recorded on five randomly selected plants in each replication excluding the border plants for 12 quantitative characters. Plant height at 30, 60 and 90 days (cm), Number of Primary Branches/Plant, Days to 50 percent Flowering, Percent Flower Drop (%), Fruit Length (cm), Fruit Circumference (cm), Number of Fruits/Plant, Fruit yield/Plant (g), Average fruit weight (g) and Total Soluble Solids (brix) were the twelve characters recorded. In order to identify the genetically diverse genotypes for their uses in recombination breeding programme, Mahalanobis' generalized distance (D^2) analysis was carried out using the mean values of 12 characters. D^2 analysis was done by using the WINDOSTAT software. Further, Clustering was done using Tocher's method as described by Rao (1952). The intra and inter cluster distances were calculated by the formula given by Singh and Chaudhary (1977).

Results and Discussion

Analysis based on the diversity analysis, contribution of different characters towards divergence was computed and presented in fig. 1. Out of twelve characters studied, number of primary branches per plant contributed maximum towards total genetic divergence (45.32 %) followed by total soluble solids (22.21 %), days to 50 per cent flowering (12.22 %), average fruit weight (8.41 %), fruit yield per plant (5.87 %), fruit circumference (2.27 %), fruit length (1.37 %), per cent flower drop (1.22 %), number of fruits per plant (0.85 %), plant height at 30 days after transplanting (0.26 %). However, two traits *viz*., plant height at 60 and 90 days after transplanting did not significantly contributed towards divergence. So, it is suggested that these traits should be given due importance during hybridization and selection in segregating populations.

Based on the D^2 values, the genotypes were grouped into eleven clusters using Tocher's method given by Rao (1952) in such a way that genotypes within each cluster had smaller D^2 statistic than in other cluster. The distribution pattern of these genotypes are presented in Table 1. Clustering pattern revealed that, 20 genotypes were congregated in cluster I constituting the largest cluster, followed by cluster IV with 13 genotypes, cluster III with 11 genotypes, cluster II with 9 genotypes, cluster VIII and IX each with 2 genotypes and cluster V, VI, VII, X and XI formed solitary clusters with one genotype in each cluster. Genotypes in solitary cluster indicate uniqueness of that genotype for most of the traits. It is obvious to use these genotypes in hybridization programme to generate breeding material with high diversity.

The intra cluster D^2 values depict the differences among the genotypes within the same cluster. The intra cluster D^2 values are given in Table 3. The intra cluster distance was observed only in clusters I (157.49), II (153.63), III (230.36), IV (326.36), VIII (163.75) and IX (191.43) as remaining five clusters *viz*., V, VI, VII, X and XI contained only one genotype each. Intra cluster distance was highest in cluster IV (326.36) followed by cluster III (230.36). Higher intra cluster distance indicates existence of some diversity within the genotypes of the same cluster. Similar intra cluster variation was also reported in the studies of Saurabh *et al.* (2011), Babu and Patil (2004) and Mehta *et al.* (2004). But it is ingenious to avoid using genotypes of same cluster as parents during hybridization in order to maintain the broad genetic base.

The inter cluster D^2 values are given in the Table 3 and the nearest and farthest clusters from each cluster based on D^2 values are presented in the Table 2. The inter cluster D^2 value was maximum (3128.62) between cluster IX and XI followed by between cluster VI and IX with D^2 value of 2469.94. This indicates that those clusters are diverse from each other and can be utilized for producing superior heterotic combinations as suggested by Vidya and Kumar (2014). The crossing between superior genotypes of above diverse cluster pairs (i.e. between cluster IX and XI and between VI and IX) may provide desirable transgressive segregants for developing high yielding varieties. The minimum distance observed was 220.21 between cluster V and XI followed by between clusters VI and V with D^2 value of 236.40 which indicate close relationship among the genotypes involved.

Cluster IX was the most diverse as many clusters showed maximum inter cluster distances with it followed by cluster XI. According to Falconer (1981), larger the divergence between the accessions, higher will be the heterosis. So, it is desirable to select genotypes from these cluster showing high inter cluster distance and also with high fruit yield as parents in recombination breeding programmes for obtaining wide variability and desirable segregants. Similar conclusions were given by Mehta *et al.* (2004) and Saurabh *et al.* (2011). Kalloo *et al.* (1980) also suggested that the crosses between selected genotypes from widely separated clusters were more likely to give desirable recombinants.

The cluster means for all the twelve characters are presented in Table 4 along with overall cluster score and cluster rank. The maximum plant height at 30 days after planting was exhibited by genotype in cluster X (22.04 cm) followed by cluster III (10.30 cm). For plant height at 60 days after transplanting, cluster VIII exhibited maximum value of 46.35 cm followed by cluster V (42.07 cm). Plant height at 90 days after transplanting was found maximum in cluster III (67.28 cm) followed by cluster IX (66.11 cm).

Genotype in cluster IX had highest number of primary branches (11.85) followed by cluster II (10.52). Cluster XI recorded lowest number of primary branches (3.10). Minimum days to 50 per cent flowering was recorded in cluster X (25.67 days) followed by cluster VIII (37.17 days) while the maximum days was recorded in cluster XI (50.67 days). Minimum flower drop per cent was exhibited by genotype present in cluster V (24.79 per cent) followed by cluster XI (27.79 per cent) while the maximum flower drop per cent was noticed in cluster IX (91.56 per cent).

Cluster VI recorded maximum fruit length (17.59 cm) followed by cluster VII (16.13 cm), while cluster X recorded minimum fruit length of 5.74 cm. Fruit circumference in cluster VIII was the highest (6.06 cm) among the other clusters followed by cluster IX (5.34 cm) but the lowest fruit circumference of 2.23 cm was recorded in cluster V. The maximum number of fruits per plant was produced by genotype present in cluster X (31.89) followed by genotype of cluster V (31.11) while the minimum number of fruits per plant was recorded in cluster IX (8.45).

The maximum fruit yield per plant was recorded in cluster VIII (1876.95 g) followed by cluster III (1317.45 g), while cluster VII had the lowest fruit yield per plant (340.00 g). Maximum average fruit weight was recorded in cluster VIII (135.28 g) followed by cluster III (89.52 g), while minimum average fruit weight was recorded in cluster X (17.90 g). Total soluble solids in cluster IX was the highest (8.25 brix) among all clusters followed by cluster VII (6.00 brix) and the least value was in cluster X (4.00 brix).

A critical appraisal of the above findings indicates that, none of the clusters had all the desirable features but many desirable traits are accumulated in different clusters which can be favorably assembled by crossing the desirable genotypes based on the breeding objectives.

Character wise scoring (1 to 11) of the cluster means was done by assigning score 1 to the most desirable magnitude of the trait. Hence, the cluster with least overall score across 12 characters assigned with rank 1.0 and that cluster with the highest score gets the 11th rank (Table 4). Based on this overall cluster mean score, cluster II ranked first with the least score of 48 and the last ranked cluster was cluster XI with highest overall cluster mean score of 101. This indicates the presence of elite genotypes in cluster II. The genotypes of this cluster were Punjab Barsati, IC104083, IVBL-9, Lal Gulab, IC90785, IC333527, Arka Abilash, IIHR-7, Arka Kranti. So these genotypes can be extensively used for further breeding programme to generate new material.

It is concluded that, crosses can be planned based on the above findings to breed new cultivars with all the desirable traits coupled with broad genetic base to avoid the genetic vulnerability in the emerging era of climate change.

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Table 1. Clustering pattern among eggplant genotypes based on 12 different characters

Clusters	No. of Entries	Genotypes
I	20	IIHR-322, IC112341, R-2581, Very Green Long, IC112950, Long Green, IC90151, IC354597, Round Green, R-2591, R-2590, Swarna Pratibha, IC89912, CO-2, IC354140, L-3268, Annamalai, Arka Keshav, L-2230, IC397557
II	9	Punjab Barsati, IC104083, IVBL-9, Lal Gulab, IC90785, IC333527, Arka Abhilash, IIHR-7, Arka Kranti
III	11	Pusa Ankur, Swarna Manjari, Jawahar Brinjal -69, Bhagyamati, Malapur Local, IC545884, R-2594, Aruna, Mattigulla, Early Round, Rampur Local
IV	13	R-2580, Arka Shirish, R-2584, IC49358, IIHR-3, Pusa Bindu, Arka Nidhi, Pusa Purple Long, L-3272, Raidurga Green Round, Jawahar Brinjal -8, L-2232, CH-215
V	1	R-2585
VI	1	IIHR-355
VII	1	Arka Kusumaker
VIII	2	Swarna Shyamali, Swarna Shree
IX	2	Jawahar Brinjal – 18, Pusa Upkar
X	1	IC420590
XI	1	R-2582

Table 2. Nearest and farthest clusters from each cluster based on D^2 values in eggplant genotypes

Sl. No.	Clusters	Nearest cluster	Farthest cluster
1	I	II (331.27)	IX (1151.14)
2	II	I (331.27)	XI (1992.40)
3	III	II (421.16)	XI (2043.46)
4	IV	I (342.13)	IX (1778.41)
5	V	XI (220.21)	IX (2041.95)
6	VI	V (236.40)	IX (2469.94)
7	VII	I (350.48)	VIII (1225.09)
8	VIII	IV (655.51)	IX (2012.15)
9	IX	II (676.79)	XI (3128.62)
10	X	I (430.04)	IX (1913.95)
11	XI	V (220.21)	IX (3128.62)

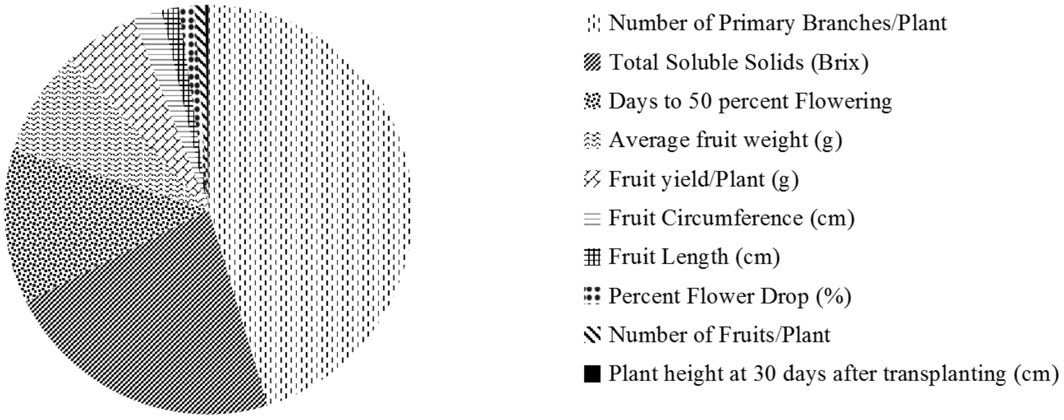

Fig.1. Contribution of yield and yield attributing traits towards genetic divergence in eggplant genotypes

Table 3. Average inter and intra cluster distances in eggplant genotypes based on 12 different characters

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	**157.49**	331.27	422.07	342.13	692.12	955.85	350.48	676.30	1151.14	430.04	1092.89
II		**153.63**	421.16	792.47	1235.88	1592.68	526.79	1061.14	676.79	705.05	1992.40
III			**230.36**	776.79	1571.38	1959.32	1059.37	723.91	1318.51	721.06	2043.46
IV				**326.36**	467.36	701.27	500.68	655.51	1778.41	557.76	637.60
V					**0.00**	236.40	386.36	1040.19	2041.95	930.61	220.21
VI						**0.00**	574.10	1070.89	2469.94	1056.27	268.84
VII							**0.00**	1225.09	1024.95	837.73	903.40
VIII								**163.75**	2012.15	802.08	1121.97
IX									**191.43**	1913.95	3128.62
X										**0.00**	1255.47
XI											**0.00**

Table 4. Cluster means for 12 different characters in eggplant genotypes

Clusters	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	Overall Cluster score	Cluster rank
I	8.47 (5)	37.02 (6)	64.19 (4)	8.44 (4)	42.45 (6)	80.89 (8)	9.79 (6)	3.50 (7)	15.66 (6)	781.25 (6)	54.29 (5)	4.74 (7)	70	5.5
II	9.13 (3)	39.81 (3)	65.42 (3)	10.52 (2)	37.74 (3)	77.39 (6)	11.86 (4)	3.27 (8)	18.82 (4)	1049.14 (4)	58.62 (4)	5.62 (4)	48	1
III	10.30 (2)	39.77 (4)	67.28 (1)	9.89 (3)	39.48 (5)	70.51 (5)	8.30 (8)	5.01 (3)	16.36 (5)	1317.45 (2)	89.52 (2)	4.20 (10)	50	2
IV	7.47 (6)	38.23 (5)	57.71 (7)	6.66 (7)	46.31 (7)	63.20 (3)	9.57 (7)	3.87 (4)	19.09 (3)	877.03 (5)	52.13 (6)	4.35 (9)	69	4
V	5.25 (9)	42.07 (2)	58.10 (6)	5.00 (9)	49.33 (10)	24.79 (1)	13.42 (3)	2.23 (11)	31.11 (2)	1159.00 (3)	37.22 (9)	5.50 (5)	70	5.5
VI	3.82 (10)	33.17 (9)	38.58 (11)	3.71 (10)	39.00 (4)	79.32 (7)	17.59 (1)	3.55 (5)	10.73 (10)	451.00 (10)	42.18 (8)	5.73 (3)	88	10
VII	6.20 (7)	34.41 (7)	61.18 (5)	8.05 (5)	48.00 (8)	87.87 (10)	16.13 (2)	2.45 (10)	11.88 (9)	340.00 (11)	28.59 (10)	6.00 (2)	86	9
VIII	8.75 (4)	46.35 (1)	49.32 (8)	5.66 (8)	37.17 (2)	67.94 (4)	7.52 (9)	6.06 (1)	14.28 (7)	1876.95 (1)	135.28 (1)	4.75 (6)	52	3
IX	5.38 (8)	33.54 (8)	66.11 (2)	11.85 (1)	48.17 (9)	91.56 (11)	6.95 (10)	5.34 (2)	8.45 (11)	579.75 (7)	76.36 (3)	8.25 (1)	73	7
X	22.04 (1)	22.86 (11)	42.50 (9)	7.29 (6)	25.67 (1)	86.52 (9)	5.74 (11)	3.55 (5)	31.89 (1)	569.61 (8)	17.90 (11)	4.00 (11)	84	8
XI	3.60 (11)	30.30 (10)	41.27 (10)	3.10 (11)	50.67 (11)	27.79 (2)	10.59 (5)	2.76 (9)	12.17 (8)	564.33 (9)	47.23 (7)	4.50 (8)	101	11

Figures in parenthesis indicate the ranks based on cluster mean, highest (1) to lowest (11), except for days to 50 per cent flowering and per cent flower drop where least value is given highest rank. Overall cluster score is the summation of rank number for all the 12 characters.

Where, X_1 – Plant height at 30 days (cm), X_2 – Plant height at 60 days (cm), X_3 - Plant height at 90 days (cm), X_4 – Number of Primary Branches/Plant, X_5 – Days to 50 percent Flowering, X_6 – Percent Flower Drop (%),X_7 – Fruit Length (cm), X_8 – Fruit Circumference (cm), X_9 – Number of Fruits/Plant, X_{10} – Fruit yield/Plant (g), X_{11} – Average fruit weight (g) and X_{12} – Total Soluble Solids (brix)