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Research Note

Genetic divergence in brinjal (*Solanummelongena* L.)

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Abstract
Genetic divergence among 50 genotypes of brinjal for 16 characters was estimated using Mahalanobis D^2 statistic. The genotypes were grouped into eight clusters on the basis of relative magnitude of D^2 values. Among the eight clusters, cluster IV was the largest, comprising of 17 genotypes. The maximum and minimum intracluster distances were found in cluster VI and cluster I, respectively. The inter cluster D^2 values was maximum between the cluster VI and VII while the minimum inter cluster distance was observed between cluster I and II. The mean value for most of the traits was highest in cluster VII. The characters like average fruit weight, days to last harvest and bacterial wilt incidence contributed maximum to genetic divergence and hence played a major role in improvement of brinjal.

Keywords
Brinjal, diversity, clusters, intra and inter cluster distance, genetic divergence.

Brinjal (*Solanummelongena* L.)is a common, popular and principal vegetable crop which is widely grown in tropics and sub tropics and also in the temperate regions during the warm season. The region across India and Indochina is considered as the centre of diversity of brinjal(Vavilov 1951; Zeven and Zhukovsky, 1975). India being the centre of origin of brinjal a wide range of variability exists, and a large number of landraces have evolved in different agro-ecological zones. The fundamental pre-requisite in using genetic variability in plants involves assessment of genetic diversity that exists in the available germplasm (Kahler*et al.,* 1986). The knowledge of morphological variability, its nature and magnitude are essential for selecting genotypes from the germplasm for successful utilization in breeding programme. Among the several techniques used to express divergence, the Mahalanobis' generalized distance (D^2) stands out as one of the most robust (Rao, 1952). The cluster analysis based on D^2 is used for grouping samples in such a way that a high level of homogeneity within each group and high heterogeneity between groups is obtained (Johnson and Wichern, 1982).

This experiment was carried out at Horticultural College and Research Institute, Anantharajupet. The field experiment comprised of 50 diverse genotypes of brinjal, obtained from different sources and the trial was laid out in a randomized block design with three replications during *kharif*2011.Planting of each genotype was done in a single row plot of 5m length accommodating 10 plants in a row with inter and intra row spacing of 60 and 50 cm respectively, with three replications. The recommended package of practices and plant protection measures were followed to raise a successful crop. Observations were recorded on five randomly selected plants in each plot on sixteen different traits *viz.*,plant height (cm), number of branches per plant, number of flower clusters per plant, number of flowers per cluster, days to first flowering, days to 50% flowering, days to first fruit harvest, days to last fruit harvest, no. of fruits per cluster, no. of fruits per plant, average fruit weight (g), fruit length (cm), fruit width (cm), yield per plant (g), ascorbic acid (mg/100g) and percent bacterial wilt incidence. Genetic diversity was estimated as per Mahalanobis (1936) D^2 statistics between different pairs of genotypes. While method of cluster composition was done as per Tocher's method as described by Rao (1952).

The analysis of variance for 16 characters studied, including bacterial wilt incidence for 50 accessions of brinjalrevealed highly significant differences among the genotypes for all the characters under study depicting greater diversity in the existing material. Based on D^2 values, the 50 genotypes were grouped into eight clusters. This genetic diversity among the genotypes could be due to factors like heterogeneity, genetic architecture of the populations and developmental traits as described by Murty and Arunachalam(1966). Among the eight clusters, cluster IV was the largest, comprising of 17 genotypes followed by cluster V with 10

genotypes, cluster VI with eight genotypes, cluster II with six genotypes and III with five genotypes, cluster I with two genotypes, cluster VII and VIII were solitary with only one genotype in each cluster. The genotypes sharing the same origin were grouped into different clusters and the genotypes from different origin were grouped in same clusters. The clustering pattern of the genotypes suggested no parallelism between genetic diversity and the geographical distribution of the genotypes. Mehta *et al.* (2004) also reported that genetic diversity was independent of geographical origin.

Average intra and inter cluster D^2 values are given in Table 2.The intra cluster distance ranged from zero (Cluster VII and VIII) to 216.56 (cluster VI). Among the eightclusters, the intra cluster distance was maximum in cluster VI followed by cluster V (157.41) and cluster IV (150.10), while it was minimum in cluster I (23.06) followed by cluster II (64.88). The intra cluster distance of solitary clusters VII and VIII was zero.The intra cluster values are lesser than the intercluster values which indicates the homogenous and heterogenous nature of the genotypes within and between the clusters.

The inter cluster D^2 values was maximum between the cluster VI and VII (939.69) indicating wide genetic distance between these clusters.The genotypes belonging to the clusters with maximum inter cluster distanceshow high genetic diversity and hybridization between genotypes of divergent clusters is likely to produce wide variability with desirable segregants (Arunachalam, 1981). The minimum inter cluster distance was observed between cluster I and II (91.69) suggesting the lowest degree of divergence and close genetic makeup of the genotypes included in these clusters.

The diversity in the genotypes was also substantiated by the considerable amount of variation among cluster means for different characters (Table 3) which might be the reason for large inter cluster distances. Cluster VII recorded the highest mean for characters like plant height, number of fruits per cluster, fruit width, average fruit weight and fruit yield per plant. The genotypes of cluster VIII recorded maximum number of branches per plant, fruit length and minimum number of days to first flowering, days to 50 percent flowering anddays to first harvest. The maximum mean values for characters, number of flower clusters per plant and ascorbic acid content were recorded in cluster I. The genotypes of cluster III recorded maximum mean values for number of flowers per cluster andfruits per plant. The genotypes of cluster VI recorded maximum days to last harvest and minimum incidence of bacterial wilt.

An assessment of relative contribution of 16 characters towards total genetic divergence (Table 4) revealed that the three characters *viz.*,average fruit weight, days to last harvest and bacterial wilt incidence are the major traits contributing towards genetic divergence and hence selection for divergent parents based on these traits will be useful for exploitation of hybrid vigour in brinjal.

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Table.1 List of genotypes of brinjal *(Solanum melongena* L.) selected for genetic diversity studies

Acc.No.	Genotype	Source	Acc.No.	Accession	Source	Acc.No.	Accession	Source
A_1	IC 285125	NBPGR, Hyderabad	A_{21}	IC 305048	NBPGR, Hyderabad	A_{41}	IC 345740	NBPGR, Hyderabad
A_2	IC 545853	NBPGR, Hyderabad	A_{22}	IC 136056	NBPGR, Hyderabad	A_{42}	IC 354597	NBPGR, Hyderabad
A_3	IC 111072	NBPGR, Hyderabad	A_{23}	IC 112741	NBPGR, Hyderabad	A_{43}	IC 137683	NBPGR, Hyderabad
A_4	IC 345333	NBPGR, Hyderabad	A_{24}	IC 383102	NBPGR, Hyderabad	A_{44}	Arka Shirish	IIHR, Bangalore
A_5	IC 135929	NBPGR, Hyderabad	A_{25}	IC 545948	NBPGR, Hyderabad	A_{45}	Arka Keshav	IIHR, Bangalore
A_6	NIC 23771	NBPGR, Hyderabad	A_{26}	IC 439263	NBPGR, Hyderabad	A_{46}	Bhagyamati	VRI, Hyderabad
A_7	IC281072	NBPGR, Hyderabad	A_{27}	IC 090084	NBPGR, Hyderabad	A_{47}	Gulabi	VRI, Hyderabad
A_8	IC90785	NBPGR, Hyderabad	A_{28}	IC 446756	NBPGR, Hyderabad	A_{48}	Surya	KAU, Thrissur
A_9	IC021621	NBPGR, Hyderabad	A_{29}	IC 090783	NBPGR, Hyderabad	A_{49}	Arka Neelkanth	IIHR, Bangalore
A_{10}	IC 104086	NBPGR, Hyderabad	A_{30}	IC 090915	NBPGR, Hyderabad	A_{50}	Arka Nidhi	IIHR, Bangalore
A_{11}	IC 090942	NBPGR, Hyderabad	A_{31}	IC 112322	NBPGR, Hyderabad			
A_{12}	IC 272927	NBPGR, Hyderabad	A_{32}	IC112991	NBPGR, Hyderabad			
A_{13}	IC 281112	NBPGR, Hyderabad	A_{33}	IC111439	NBPGR, Hyderabad			
A_{14}	IC 281104	NBPGR, Hyderabad	A_{34}	IC110667	NBPGR, Hyderabad			
A_{15}	IC 99701	NBPGR, Hyderabad	A_{35}	IC281092	NBPGR, Hyderabad			
A_{16}	IC 345747	NBPGR, Hyderabad	A_{36}	IC545890	NBPGR, Hyderabad			
A_{17}	IC 90925	NBPGR, Hyderabad	A_{37}	IC104101	NBPGR, Hyderabad			
A_{18}	IC 136280	NBPGR, Hyderabad	A_{38}	IC090084	NBPGR, Hyderabad			
A_{19}	IC 345309	NBPGR, Hyderabad	A_{39}	IC136056	NBPGR, Hyderabad			
A_{20}	IC 127024	NBPGR, Hyderabad	A_{40}	IC 345333	NBPGR, Hyderabad			

Table 2. Clustering pattern of 50 genotypes of brinjal (Tocher's method)

Cluster	No.of genotypes	Genotypes
I	**2**	A_1, A_{30}
II	**6**	A_{21}, A_{22}, A_{24}, A_{27}, A_{28}, A_{31}
III	**5**	A_{20}, A_{33}, A_{38}, A_{39}, A_{46}
IV	**17**	A_2, A_5, A_6, A_8, A_9, $A_{10,}$ A_{11}, A_{12}, A_{15}, A_{17}, A_{18}, A_{26}, A_{29}, A_{32}, A_{34}, A_{43}, A_{44}
V	**10**	A_4, A_{13}, A_{14}, $A_{19,}$ A_{35}, A_{36}, A_{37}, A_{40}, A_{41}, A_{42}
VI	**8**	$A_{7,}$ A_{23}, A_{25}, A_{45}, A_{47}, A_{48}, A_{49}, A_{50}
VII	**1**	A_3
VIII	**1**	A_{16}

Table 3. Average intra (bold) and inter-cluster D^2 values for eight clusters in 50 genotypes of brinjal. (Tocher's method)

Clusters	I	II	III	IV	V	VI	VII	VIII
I	**23.06**	91.69	95.89	297.24	161.39	226.54	746.58	610.99
II		**64.88**	116.88	210.18	235.49	264.50	529.08	511.33
III			**88.35**	374.35	252.52	240.12	801.37	776.59
IV				**150.10**	467.91	447.51	292.09	242.98
V					**157.41**	439.54	867.18	743.68
VI						**216.56**	939.69	773.72
VII							**0.00**	292.07
VIII								**0.00**

*Bold diagonal values indicate intra cluster distance, rest of the values show the inter cluster distances.

Table 4. Mean values of clusters for 16 characters in 50 genotypes of brinjal (Tocher's method)

Clusters	Plant height (cm)	No. of branches / Plant	Days to first flowering	Days to 50% flowering	No. of flower clusters/ Plant	No. of flowers/ cluster	No. of fruits/ cluster	No. of fruits/ plant	Days to first harvest	Days to last harvest	Fruit length (cm)	Fruit width (cm)	Average fruit weight (g)	Ascorbic acid mg/100g	Fruit yield/ Plant (g)	Cumulative wilt Per cent incidence (arc sine)
I	107.77	16.37	37.13	44.83	21.83	2.68	1.63	29.93	59.57	157.90	10.51	4.32	49.83	7.33	1489.60	88.00 (70.31)
II	106.67	16.29	46.02	51.00	20.98	2.56	1.86	25.85	64.56	151.68	10.02	5.63	56.01	5.56	1443.82	84.40 (67.11)
III	104.75	15.01	48.58	54.13	20.67	3.47	2.10	32.99	68.73	157.71	10.55	5.08	46.45	6.36	1535.30	83.71 (66.66)
IV	104.31	15.58	41.88	47.71	19.02	2.76	1.60	20.55	63.00	146.14	15.43	6.38	73.96	6.37	1516.04	80.33 (64.12)
V	106.37	16.09	38.37	43.33	20.34	2.88	1.77	29.64	56.91	143.52	10.37	5.69	42.42	6.02	1222.41	86.40 (68.85)
VI	99.43	13.85	44.99	50.75	21.09	3.20	2.15	28.00	66.33	161.52	14.28	3.92	51.39	5.89	1362.10	43.00 (37.58)
VII	112.27	17.00	41.80	47.33	13.07	3.40	2.25	18.13	66.93	140.13	13.71	12.97	91.85	6.00	1665.62	89.33 (71.19)
VIII	110.53	17.67	33.80	40.00	15.60	3.27	1.22	13.93	56.80	131.93	15.84	3.64	87.81	5.33	1223.48	78.67 (62.51)

Table 5. Percent contribution of different traits towards divergence of 50 germplasm lines of brinjal

Character	No. of times ranked first	Contribution %
1 Plant height (cm)	0	0.00
2 No. of branches per plant	0	0.00
3 No. of flower clusters per plant	11	0.90
4 No. of flowers per cluster	1	0.08
5 Days to first flowering	1	0.08
6 Days to 50% flowering	20	1.63
7 Days to first harvest	31	2.53
8 Days to Last harvest	162	13.22
9 No. of fruits per cluster	9	0.73
10 No. of fruits per plant	87	7.10
11 Fruit length (cm)	69	5.63
12 Fruit width (cm)	75	6.12
13 Average fruit weight (g)	633	51.67
14 Ascorbic acid mg/100g	0	0.00
15 Fruit yield per plant (g)	28	2.29
16 Cumulative wilt (%)	98	8.00