

Multivariate genetic divergence in brinjal (*Solanum melongena* L.)

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ABSTRACT

The investigations were carried out in Department of Vegetable crops, Bidhan Chandra Krishi Viswavidyalaya, West Bengal to examine the magnitude of genetic divergence among 70 entries of brinjal. The lot of 70 entries (10 elite varieties, 16 stable breeding lines and 44 indigenous cultivars of India and Bangladesh) based on multivariate analysis using Mahalanobis' D^2 -statistic employing 18 growth, yield components, fruit yield and fruit quality could be grouped into 6 clusters. Relatively lesser number of clusters, moderate and consistent intra-cluster divergence and low contribution of all the characters towards divergence indicated that either common character constellation was manifested simultaneously in the genotypes or mutual balancing in character expression was operative the genotypes of brinjal.

Key words : Cluster, divergence, genotype and genetic distance.

There are several criteria by which a breeder can choose suitable parents for successful hybridization, of which the two important are: combining ability of the parents and genetic diversity between the parents. The great interest in genetic diversity arises from the possibility of demonstrating that phenotypic mean values express, in a larger or smaller degree, the genotypic value of an individual. Thus, while evaluating the divergence among populations, based on average phenotypic values, the divergence among genotypic values associated with gene frequency in different sample units (populations, varieties, clones, etc.) is also evaluated. Among the several techniques used to express divergence between samples genetic base, the Mahalanobis' generalized distance (D^2) stands out as one of the most robust (Rao, 1952). The cluster analysis based on D^2 data 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). The present investigation was designed to elucidate the kind of relationship that exists between parental diversity and heterosis over both mid-parent and better parent in brinjal.

MATERIALS AND METHODS

Materials for the investigation comprised of 70 entries of eggplant entries consisting of 10 elite varieties of India, 16 stable breeding lines developed at different Agricultural Universities and Research institutes of India and 44 indigenous cultivars collected from the farmers of eastern and north-eastern part of India and Bangladesh conserved at the Department of Vegetable crops, Bidhan Chandra Krishi Viswavidyalaya, West Bengal, India. These entries were evaluated following randomized block design with 3 replications at Central Research Station, Bidhan Chandra Krishi Viswavidyalaya during

autumn-winter season (September to March) for 18 growth, yield components, fruit yield and fruit quality traits viz., plant height (cm), primary branches/plant, terminal shoots/plant, thickness of terminal shoot (cm), leaves/plant, mean leaf area (cm^2), leaf area/plant (m^2), calyx length, calyx diameter (cm), fruit length (cm), fruit girth (cm), fruits/plant, fruit weight (g), fruit yield/plant(kg), moisture (%), crude protein (g/100g fresh), total phenol (mg/100g fresh) and total sugar (%) contents of fruits of marketable maturity. Each entry was grown in 2 rows of 6.0 m long with a spacing of 70 × 70 cm following all recommended agronomic practices for raising a healthy crop and observations on 18 characters were recorded on 5 randomly selected plants of each entry in a replication. Different biochemical compositions of fresh fruits of marketable maturity (15-25 days after anthesis depending on the genotype) were estimated from the sampled fruits of all the entries following standard methods: 1) total sugars by anthrone method (Dubois *et al.* 1951), 2) crude protein through estimation of nitrogen by micro-kjeldahl method (Sadasivam and Manickam, 1996) and 3) total phenols by folin-ciocalteu reagent method (Bray and Thrope, 1954) and expressed on fresh weight basis. Genetic divergence among the entries was estimated by the Mahalanobis' generalized distance ((Mahalanobis, 1936) as per Rao (1952) which is defined as: $D^2 = d'W^{-1}d$, where d' is transpose of the vector of difference among means of accesses for all p characters, W is the $p \times p$ matrix of residual variances and covariances and d is the vector of differences among means of accesses for all p characters. The Tocher method (Rao, 1952) was used to define similarity groups. Estimation of inter and intra-cluster distance averages was performed according to Singh and Chaudary (1979).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the 70 entries in respect of all the 18 characters. The D^2 values were computed for all possible 2415 pairs of comparisons. Based on the divergence between the entries, as measured by the D^2 statistic, the 70 entries were grouped into 6 distinct clusters (Table 1). Cluster 1, the largest one contained 39 genotypes followed by cluster 2 with 22 genotypes and cluster 5 and 6, the smallest with one genotype each in them. Despite considering as many as 18 wide arrays of characters, grouping of the entries in relatively lesser number of clusters, as also reported in earlier studies (Doshi *et al.* 1998, Kumar *et al.* 1998, Da Silva *et al.* 2001), indicated that either common character constellation was manifested simultaneously in the genotypes or mutual balancing in character expression was operative the genotypes of brinjal. For this reason, despite the existence of extreme variability of brinjal germplasm in India, they had the tendency of grouping together in little number of clusters. In most of the cases, flowering and fruiting habit and fruit shape and colour did not interfere clustering pattern in multivariate analysis. For example, Nawabganj Local and Malapur Local having solitary flowering and fruiting pattern grouped in different clusters (Cluster 1 and 4); the green fruited genotypes viz., Kanta Makra, Makra, Makra Long, Makra Round, Orissa Green, Green Rocket and Nawabganj Local fell in 3 different clusters (Table 1). It revealed lack of correspondence between geographical origin and genetic divergence of the entries (Table 1) which was also recorded earlier (Doshi *et al.* 1998; Sarma *et al.* 2000) although, some genotypes collected/developed in the same place appeared in the same cluster. In fact, highly differential selection pressures according to regional preference might have caused greater genetic diversity of brinjal in India.

The data (Table 2) suggested medium and consistent level of intra-cluster divergence in all the clusters (D^2 19.36 to 24.07). Low intra-cluster divergence also suggested the proposition that common character constellation was expressed in the genotypes. Maximum inter-cluster distance existed between cluster 4 and 5 (D^2 104.70) followed by between 3 and 4 (D^2 95.44) and between 1 and 5 (D^2 83.33). The multivariate analysis has well been demonstrated for choosing parents for hybridization programme for greater realization of heterosis and higher expectation of large number of segregates in the advanced generations. Selection of desirable parents from 6 different clusters as per breeding objectives is suggested.

The cluster wise mean values for 18 characters showed appreciable variability (Table 3).

Genotypes belonging to cluster 3 were the highest yielding but fruit quality traits in them were manifested in negative direction and on the contrary, genotypes grouped in cluster 4 were the lowest yielding but the best in quality. It indicated inverse relationship between fruit yield and quality.

No character contributed overwhelmingly towards divergence of the genotypes (Table 4) which again suggested high mutual balancing of the characters during their expression in the genotype. The top 3 characters contributed towards genetic divergence most were fruit weight (7.03%), total phenol content of fruit (6.81%), plant height (6.52%) and primary branches/plant (6.34%). However, the estimated genetic divergence among the entries is related only to the variability existing in the characteristics used for their estimation, not allowing extrapolations to other non-analyzed characters.

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Table 1: Clustering pattern of 70 entries of brinjal based on pooled data for 18 characters

Cluster	Brinjal entries under the cluster
1	Bhagyamati (Hyderabad), CH 309 (Ranchi), Astrang Local (Orissa, LC), Kanta Makra (West Bengal, LC), Mukta (Orissa, LC), BR 112 (Hisar), Malapur Local (Karnataka, LC), BB 40(Orissa), Nilgiri Local (Orissa, LC), CH 166 (Ranchi), Coochbehar Local (West Bengal, LC), China (Bangladesh, LC), CO-2 (Tamil Nadu), Jafar's Black (Bangladesh, LC), Jessore Local (Bangladesh, LC), Makra (West Bengal, LC), Hisar Pragati (Haryana), CH 243 (Ranchi), SM 59 (Hyderabad), CH 671 (Ranchi), CH 165 (Ranchi), CH 668 (Ranchi), Orissa Muktakeshi (Orissa, LC), Muktakeshi (West Bengal, LC), Makra Long (West Bengal, LC), Pusa Purple Long (New Delhi), Duli (West Bengal, LC), Orissa Local (Orissa, LC), Hisar Shyamal (Haryana), Makra Round (West Bengal, LC), Orissa Green (Orissa, LC), BB 14 (Orissa), Chakdah Local (West Bengal, LC), CH 156 (Ranchi), Guli (West Bengal, LC), HLB 25 (Haryana), Bholanath (Tripura, LC), Bhangar (West Bengal, LC)
2	Haringhata Local (West Bengal, LC), Orissa Local (Orissa, LC), Puri Local (Orissa, LC), CH 225 (Ranchi), CH 207 (Ranchi), Hisar Jamuni (Haryana), KS 352 (Kalyanpur), NDBS-26-1 (Faizabad), NDBS-28-2 (Faizabad), PLR 1 (Tamil Nadu), KS 331 (Kalyanpur), Utkal Madhu (Orissa), Green Rocket (Orissa), DLB 11 (New Delhi), Tufanganj Local (West Bengal, LC), Nadia Local (West Bengal, LC), Sel 4 (Varanasi), Falakata Local (West Bengal, LC), Islampuri (West Bengal, LC), Uttara (Bangladesh), Melwanki Local (Karnataka, LC)
3	Pusa Purple Cluster (New Delhi), CH 204 (Ranchi), Pusa Anupam (New Delhi), Orissa Green (Orissa, LC), HE 12 (Punjab)
4	Nawabganj Local (West Bengal, LC), Singhnath Local (Tripura, LC)
5	Shyamala (Hyderabad)
6	Singnath 666 (Bangladesh)

Note: 1. Place of collection/development of the genotype in parenthesis; 2. LC denotes local cultivar; 3. Other entries are either improved varieties or breeding lines

Table 2: Average intra and inter-cluster distance (D^2 values)

Cluster	1	2	3	4	5	6
1	19.36					
2	42.86	22.16				
3	77.74	43.25	19.93			
4	33.44	61.66	95.44	24.07		
5	83.33	50.73	32.43	104.70	0.00	
6	56.93	39.41	50.07	70.74	55.82	0.00

Bold values in the diagonals denote intra-cluster D^2 distances

Table 3: Cluster wise mean values for 18 characters

Cluster	Plant height (cm)	Primary branches/plant	Terminal shoots/plant	Thickness of terminal shoot (mm)	Leaves/plant	Mean leaf area (cm ²)	Leaf area /plant (m ²)	Calyx length (cm)	Calyx diameter(cm)
1	72.25	13.65	36.25	3.85	248.06	128.31	3.27	2.93	3.30
2	73.02	13.71	42.68	3.66	261.10	124.73	2.96	2.55	2.75
3	65.67	13.62	40.81	3.27	285.09	107.29	3.07	2.10	2.06
4	58.36	8.00	11.97	4.25	68.71	226.28	4.99	3.24	3.47
5	67.67	16.90	86.20	2.50	330.33	58.43	1.95	1.43	1.45
6	98.47	14.00	27.83	3.23	201.83	152.20	3.01	4.05	1.76

Cluster	Fruit length(cm)	Fruit girth(cm)	Fruit weight(g)	Fruit number/plant	Moisture (%)	Crude protein (g/100g fresh weight)	Total sugar (%)	Phenol (mg/100g fresh fruit)	Fruit yield/plant (kg)
1	9.98	6.02	128.95	19.84	92.51	1.68	3.65	0.09	2.33
2	10.82	5.14	100.61	35.41	91.32	1.49	2.66	0.13	2.93
3	10.52	4.04	51.50	77.81	89.06	1.23	1.69	0.21	3.75
4	14.03	7.91	302.95	3.73	92.48	1.77	3.86	0.08	1.11
5	11.80	2.20	27.27	55.33	89.27	1.29	1.84	0.19	1.54
6	20.43	2.27	53.13	40.50	90.08	1.41	2.49	0.14	2.77

Table 4: Contribution of different characters towards divergence of the genotypes

Characters	Percent contribution
Plant height (cm)	6.52 (3)
Primary branches/plant	6.34 (4)
Terminal shoots/plant	2.85 (17)
Thickness of terminal shoot (mm)	5.52 (9)
Leaves/plant	5.40 (10)
Mean leaf area (cm ²)	5.63 (8)
Leaf area /plant (m ²)	6.11 (6)
Calyx length (cm)	5.24 (11)
Calyx diameter(cm)	5.12 (12)
Fruit length(cm)	5.09 (13)
Fruit girth(cm)	4.91 (14)
Fruit weight(g)	7.03 (1)
Fruit number/plant	4.01 (15)
Moisture (%) of fresh fruit	5.80 (7)
Crude protein (g/100g fresh weight)	3.32 (16)
Total sugar content (%)	1.39 (18)
Phenol content of fresh fruit(mg/100g fresh fruit)	6.81 (2)
Fruit yield/plant (kg)	6.26 (5)

Rank in the parenthesis