

Genetic diversity in brinjal genotypes under eastern Indian conditions

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ABSTRACT

Brinjal or eggplant or aubergine (*Solanum melongena*) is the most popular and widely cultivated vegetable crop in the Central, Southern and in South-east Asia and in some African countries. The cultivated brinjal, *Solanum melongena*, is extremely variable in India. In the present study 40 genotypes of brinjal collected from different places in the country and abroad were evaluated for different morpho-physiological characters and genetic diversity was measured among the genotypes through D² statistics. All the nine characters under study differed significantly among the forty genotypes. The range of D² values varied from 8.13 to 8015.95 which revealed high variability among the genotypes. Based on the degree of divergence the genotypes were grouped into ten clusters among which cluster ten was the largest having 22 genotypes. The divergence within the cluster showed medium and consistent level of divergence in all the clusters except cluster ten which had highest intra cluster distance. The top two characters which contributed most towards the genetic divergence were fruit yield and fruit weight. Dendrogram among the genotypes also revealed high diversity along with strong intra and inter cluster relationships.

Key words: brinjal, genetic diversity, D² statistics.

INTRODUCTION

Brinjal or eggplant or aubergine (*Solanum melongena*) is the most popular and widely cultivated vegetable crop in the Central, Southern and in South-east Asia and in some African countries. It is cultivated throughout the tropics and as a summer annual in the warm subtropics. In India brinjal is the second widely cultivated vegetable crop after chilli. It is consumed in a great variety of ways in different regions of the country. Brinjal belongs to the very large genus *Solanum* which is American in distribution. Among the 22 Indian species under *Solanum* there is group of 5 related ones, all non tuber bearing, prickly and diploid with $2n = 2x = 24$. These are: *melongena*, *coagulans*, *xanthocarpum*, *indicum* and *macranthum* (Choudhury, 1). The cultivated brinjal, *Solanum melongena*, is extremely variable in India and so there is a vast opportunity for genetic improvement. Information on magnitude of variability is a pre requisite for starting any systematic breeding programme. Considering these points, a study on genetic variability in brinjal was taken up.

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MATERIALS AND METHODS

The experimental material consists of forty genotypes of brinjal comprising of 8 elite varieties, 4 stable breeding lines, 24 local cultivars and 4 exotic collections (*Uttara*, *Singhanath 666*, *China & Bangladesh round*) from Bangladesh (Table 2). Genotypes were evaluated for eight different morpho-physiological characters. Each observation was recorded using random five numbers of plants at the appropriate stage of the crop. Field experiment was conducted at Central Research Farm, Gayeshpur, Bidhan Chandra Krishi Viswavidyalaya (23°N latitude, 89°E longitude and 9.75 m MSL) in 2003-04 and 2004-05 crop season and pooled data were taken for statistical analysis. The layout of the experiment was Randomized Block Design with three replications. Each plot consisted of 20 plants spaced by 60 cm in 2 rows, each of which are 6 m long. D² statistics is used for assessing the genetic divergence between genotypes as suggested by Mahalanobis (2). Grouping of genotypes into various clusters was done following Tocher's method as described by Rao (5).

RESULTS AND DISCUSSION

All the eight characters under study varied

significantly among the forty genotypes (Table 1). The genotypes were dwarf to very tall with few to very high branching habit exhibiting five different growth habits. Plant canopy was loose to compact. High leaf production was a general characteristic of brinjal though wide variation existed. Among the fruit characters fruit length and fruit girth varied widely. Fruit weight and number of fruits per plant also varied most. Significant variation was also found in case of fruit yield. High to moderate genotypic coefficient of variation (GCV) was found for fruit weight and fruit yield per plant indicating the potential of simple selection for the improvement of these characters. High genetic advance coupled with high heritability was exhibited by number of leaves per plant and fruit weight suggesting predominance of additive gene action. Fruit length, fruit girth and fruit yield per plant showed high heritability but poor genetic advance. This is because fruit length and fruit girth are the typical genotypic features in brinjal and these two traits are difficult to improve or change through further selection.

D² values of each pair of genotypes showed high degree of divergence. The range of D² values varied from 8.13 between *Nawabganj Local* and *Orissa Local 2* to 8015.95 between *Bangladesh Round* and *Patakata* indicating a wide diversity available in the germplasm. The 40 genotypes were grouped as per Tocher's method (Rao, 7) into 10 clusters (Table 2). Cluster X was the largest having 22 genotypes while all the other clusters had 2 genotypes in each. The pattern of distribution of genotypes from diverse geographical region into different clusters was random. The relative divergence of each cluster from other clusters (Table 3) showed higher order of divergence between clusters VIII and X followed by clusters VI and X and clusters IX and X. Highly divergent genotypes deem to produce wide variability that may help further selection for genetic improvement. Hybrids developed from these genotypes within the limits of

Table 2. Cluster classification and source of collection of 40 genotypes of brinjal.

Cluster	Genotypes and their source
I	Bangladesh Round(Bangladesh), Patakata(Nadia, WB)
II	Chalimakra(Nadia, WB) , Ayub 2(Nadia, WB)
III	Pusa Anupam(IARI), Soila(Nadia, WB)
IV	SM 59(ANGRAU,AP), CH 207(CHES, Ranchi)
V	Makra round(Nadia, WB), Makra long(Nadia, WB)
VI	CH 204(CHES, Ranchi), Virso(Nadia, WB)
VII	Mukta(Orissa), Ayub 1(Nadia, WB)
VIII	Uttara(Bangladesh), Debjhuri(Nadia, WB)
X	Hisar Jamuni(Hissar), CH 204(CHES, Ranchi)
X	Nawabganj local (South Dinajpur, WB), Bholanath (Tripura), Nadia local 1(Nadia, WB), Bhangar (Nadia, WB), Orissa local 1(Orissa), Singhnath 666 (Bangladesh), China (Bangladesh), Duli(Nadia, WB), Orissa local 2 (Orissa), Green Rocket (Orissa), Makra round (Nadia, WB), Shyamala (ANGRAU,AP), Hisar Shyamal (Hissar), HE 12 (Hissar), Pusa Purple Cluster (IARI), CH 205(CHES, Ranchi), Pusa Purple Long(IARI), Nadia local 3(Nadia, WB), CH 165(CHES, Ranchi), Kanta Makra (Nadia, WB), Makra (Nadia, WB), JC 1(Assam)

compatibility of those clusters may manifest high heterosis or desirable transgressive segregants which would be beneficial for genetic improvement. Maximum intra cluster distance was observed in cluster X indicating existence of wide genetic divergence among the constituent genotypes in it. High degree of divergence among the genotypes within a cluster would produce more segregating breeding materials and selection within such cluster might be executed based on maximum

Table 1. Morpho physiological characters of the genotypes.

S. No.	Characters	Mean	Range	GCV	PCV	Heritability	GA
1.	Plant height(cm)	73.08 ± 1.32	56.5 - 89.5	11.63	12.04	0.93	16.91
2.	Primary branches/plant	13.525 ±1.00	5 - 18	14.22	19.11	0.55	2.95
3.	Terminal shoots/plant	36.45 ± 1.67	8 - 60	32.93	33.87	0.95	24.04
4.	Leaves/plant	254.45 ±7.89	82 - 405	29.75	30.23	0.97	153.48
5.	Fruits/plant	31.63 ± 2.88	2-110	72.72	74.415	0.955	46.31
6.	Fruit length(cm)	11.72 ± 0.63	5.5 - 22.5	27.72	29.24	0.9	6.34
7.	Fruit girth (cm)	6.55 ± 0.38	2.2 - 14.5	29.78	31.43	0.9	3.81
8.	Fruit weight (g)	125.22 ±3.56	25.6- 478.5	61.99	62.19	0.99	159.42
9.	Fruit yield/plant (kg)	2.77 ± 0.26	0.52-- 6.14	44.34	47.12	0.89	2.38

Table 3. Average intra and inter cluster D² values.

Cluster	1	2	3	4	5	6	7	8	9	10
I	8.13	24.46	385.36	348.00	213.17	541.97	27.25	574.42	444.18	506.76
II		15.39	461.32	476.58	207.23	699.01	60.29	674.95	603.24	554.20
III			15.83	155.57	356.21	131.48	381.10	50.28	226.05	669.53
IV				17.63	357.29	76.88	309.94	177.72	41.13	628.08
V					29.51	532.28	237.07	492.36	536.06	654.47
VI						34.67	498.66	100.54	71.47	767.66
VII							36.39	541.51	392.58	485.79
VIII								36.81	214.76	786.02
IX									39.37	699.62
X										943.59

mean value for the desirable characters. Intra cluster value was minimum in case of cluster I which indicates the effects of unidirectional selection which could lead to uniformity with less divergence between the genotypes. The top three characters which contributed most towards the genetic divergence (Table 4) were fruit yield followed by number of fruits per plant and fruit weight respectively. These characters may be used in selecting genetically diverse parents for hybridization programme to exploit either maximum heterosis or to execute efficient selection in the segregating generation.

The cluster means of 40 genotypes (Table 5) showed that the mean values of the clusters varied in magnitude for all the 9 characters. Cluster VIII was the highest yielder followed by cluster III. Regarding fruit weight cluster II showed highest mean performances followed by cluster V. Highest number of fruits per plant was produced by cluster VIII followed by cluster VI. Fruit length was highest in cluster III whereas fruit girth was highest in cluster II.

Table 4. Contribution of different characters (%) towards divergence.

Sl. No.	Characters	No. of first rank	(%) contribution
1.	Fruit yield per plant (kg)	322	41.28
2.	Fruit no. per plant	126	19.74
3.	Fruit weight (g)	115	16.41
3.	Leaves per plant	71	9.10
4.	Fruit girth	45	5.77
5.	Fruit length	24	3.08
6.	Plant height (cm)	23	2.95
7.	Terminal shoots per plant	13	1.67
8.	Primary branches per plant	0	0.00

In further study of dendrogram following Ward (4)'s method (Fig. 1) by using squared Euclidean distance, it became clearly evident that there was high diversity

Table 5. Cluster wise mean values of different morpho physiological characters.

Cluster	Plant height (cm)	Primary branches /plant	Terminal shoots/ plant	Leaves/ plant	Fruit length (cm)	Fruit girth (cm)	Fruits No./ plant	Fruit weight (g)	Fruit yield/ plant (kg)
I	76.92	13.50	31.67	227.00	12.92	9.00	8.11	146.87	1.03
II	83.13	13.17	34.00	225.17	13.05	9.23	8.5	164.12	1.42
III	80.02	15.83	48.17	304.33	14.43	7.05	21.36	86.02	3.71
IV	65.48	14.33	32.67	320.67	7.78	6.07	18.88	87.33	3.38
V	85.10	14.00	33.67	375.17	12.40	5.72	10.33	158.67	2.30
VI	65.93	13.83	37.50	311.67	11.05	4.23	25.6	53.58	2.64
VII	71.00	13.17	33.17	214.17	12.63	7.55	8.55	152.98	1.90
VIII	76.57	16.00	53.83	300.83	11.85	4.05	28.68	71.50	3.96
IX	61.42	12.33	32.50	283.83	6.20	5.07	24.5	66.32	2.81
X	72.37	13.12	35.62	229.65	12.01	6.64	15.65	137.92	2.94

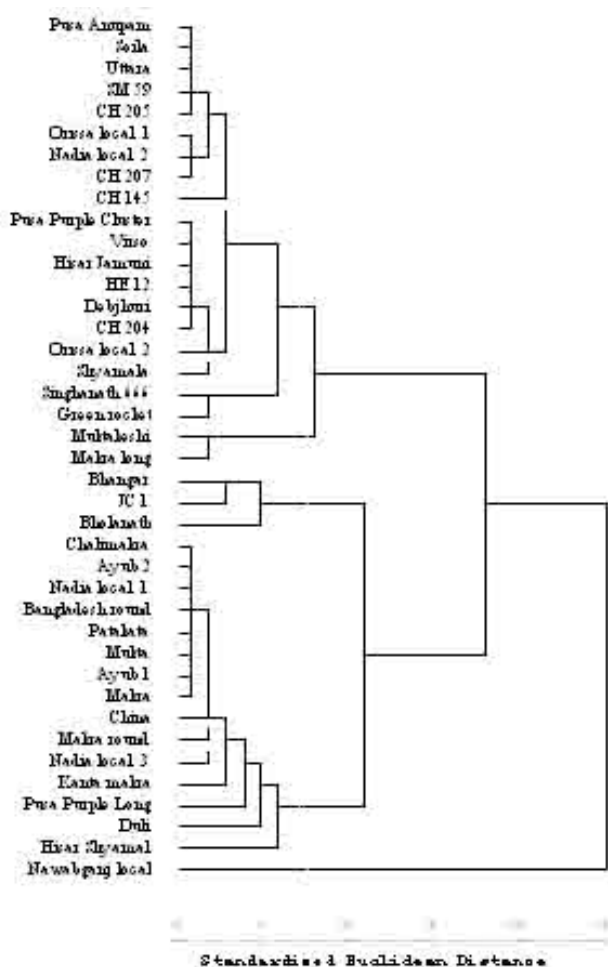


Fig. 1. Dendrogram of 40 genotypes of *Solanum melongena* following Ward's method

among the genotypes along with strong relationships among the genotypes.

So, it may be concluded that in brinjal there is a vast scope to develop new improved varieties with more yield potential and other attributes of economic importance by utilizing this present germplasm collection. To develop good varieties in long fruited group, selection from cluster III will be highly useful and to breed round fruited varieties, selection should be made from cluster II.

In general, the pattern of distribution of genotypes from diverse geographical region into different clusters was random. It might be due to free and frequent exchange of genetic material among the farmers and breeders of different region. Differential selection pressure according to regional preference also produced greater uniformity in the germplasm. In spite of huge diversity among the genotypes, relatively small number of clusters indicated either common character constellation or mutual balancing of characters among the genotypes (Sarma *et al.*, 6). The absence of relationship between genetic diversity and geographical distance indicates that forces other than geographical origin such as exchange of genetic stock, genetic drift, spontaneous mutation, natural and artificial selection are responsible for genetic diversity. Therefore, selection of genotypes for hybridization should be based on genetic diversity rather than geographic divergence (Mehta *et al.*, 3).

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Received: April, 2009; Revised: February, 2010
Accepted: August, 2010