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Studies on genetic divergence for yield and its component traits in brinjal or eggplant (*Solanum melongena* L.)

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Abstract
The analysis of variance for the design of experiment indicated highly significant differences among the genotypes for all the traits. Cluster and cluster II had eight highest number of genotypes followed by cluster III, IV and VI. The intra cluster D^2 value I to cluster VI 74.86 (cluster V) to 169.6 (cluster). Maximum inter cluster distance was observed between cluster 1 to cluster VI (1527.7) suggested that cluster is genetically very diverse to each other. Cluster first showed maximum mean values for the fruits per plant, early yield per plant and yield per plant followed by cluster third.

Keywords: D^2m eggplant, *Solanum melongena*, genetic diversity

Introduction
Brinjal or eggplant (*Solanum melongena* L.) is one of the most important solanaceous vegetable crop having diploid chromosome number 2n=2x=24. It is grown in the tropics and subtropics of India and other parts of the world. It is called Brinjal in India and Aubergine in Europe. It is extensively grown in India, Japan, Indonesia, China, Bulgaria, Italy, France, USA, Pakistan, Bangladesh, Philippines and several African countries. Due to high productivity and wife adoptability, usually finds its place as the poor man's crop.

D^2 analysis grouped the all 30 genotypes into six clustures 10.5. maximum intra cluster distance was found among the genotypes of cluster VII (169.603). while maximum inter cluster distance of wasted estimated between cluster I and cluster VI (1527.354) and minimum between cluster II and V (219.76).

Brinjal being most important to growers and consumer, there is pressing need to increase its productivity to fulfill the increasing demands throughout the year. The information usually needed for developing high yield varieties in a particular species pertains to the extent of genetic variability for desirable train in the available germplasm. Evaluation of germplasm is the basic tool for identification of important genotypes. The great extent of natural variation present in various characters among the genotypes suggests good scope of improvement genetic diversity, is of paramount significance in formulating an appropriate breeding strategy aimed at exploiting the inherent variability of the original population.

As it helps in the assessment of genetic diversity among the genotypes and the contribution of each character to the total diversity Greater the genetic distance better are the chances of obtaining desirable hybrids or segregates after hybridization between diverse groups entitled.

Materials and Methods
The present investigation entitled was executed at Main Experiment, Station of Department of Vegetable Science, Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Faizabad, during *Kharif* 2010, to assess genetic divergence. The experimental field had sandy loam soil, low in organic carbon, nitrogen, medium in phosphorus, potash, and slightly alkaline in nature with pH 8.5.The mechanical composition of soil was 60.9 percent, 27.8 percent silt and 11.3 percent clay. Experimental material for the study consisted of 30 genotypes including six checks (Arka Nidhi, NDB-2, SM 6-6, Pant Rituraj, KS-224 and S. Mani). The experiment was conducted in Randomized Complete Block Design with three replications. Each treatment consisted 20 plant in two row, having spacing of 60 × 45 cm with net plot size of 4.5 × 1.2 m^2. Observations were recorded on 9 quantitative characters *viz.*, days to 50% flowering, primary branches per plant, plant height (cm), Fruit weight (g), fruit circumference (cm), polar length of fruit (cm), fruits per plant, early yield per plant (g) and yield per plant.

Analysis of variance was computed using suggested by Panse and Sukhatme (1967) [22] and D^2 analysis was done using method suggested by Mahalanobsis (1928) [13].

Results and Discussion

The analysis of variance for different character is presented n table 1. The mean sum of square due to replication was highly significant for all the characters. In other words, the performances of the genotypes with respect of these character were statistically different; suggesting that, these exists ample scope for selection present in different traits for brinjal improvement.

The studies of genetic divergence among 30 genotype of brinjal were carried out by using Manalanobis D^2 statistics. In present investigation 30 genotypes of brinjal were grouped in six distinct non-over lapping clusters (table 2). This presence of considerable diversity in the genotype. The major clusters in the above mentioned genetic divergence analysis contained frequently the genotypes of heterogeneous origin. Although the genotypes of same origin or geographic region were also found to be grouped together in the same cluster. The instances of groping of genotypes of different origin or geographic region in same clusters were frequently observed. This suggested that there is no parallelism between and geographic diversity.

Perusal of Table 3 reveals that cluster II and VI had maximum number of genotype (8) followed by clusters III, IV, VI (4) and cluster I (2). The intra cluster D^2 values ranged from 74.86 (cluster V) to 169.60 (cluster VI). The maximum inter cluster diversity was observed between cluster I to cluster VI (1527.35) which suggested that these two clusters are genetically very diverse to each other the inter clusters distance between cluster I and cluster V distance was observed between cluster II and (1216.89) cluster I to IIV (842.83) and cluster III to cluster VI (810.10) were. The minimum inter cluster V (219.76) followed by cluster II and cluster III (244.23). The higher inter cluster distance indicated greater genetic diver genes between the genotypes of those clusters, while lower inter values between the cluster suggested that the genotype of the cluster were not much genetically diverse from each other. The intra clusters means for different characters has been presented in Table 3. The entire cluster from I to VI had in general medium mean performance to most of the character. Cluster I showed the maximum means values for the fruits per plant, early yield per plant and yield per plant where as cluster IV and V had minimum mean values. Similar finding were also recorded by Chaudhry *et al.* (2007) [4]; Golani *et al*. (2007); Thirumurugan *et al*. (2007); Bansal and Mehta (2007) [2]; Dutta *et al.* (2009) [6]; and Hazara *et al.* (2010).

Table 1: Clustering pattern of thirty two genotypes of brinjal on the basis of Mahalanobis D^2 statistics

Cluster number	No. of genotypes	Genotypes
I	2	NDB-5, NDB-15
II	8	NDB-6, NDB-11, NDB-4, NDB-8, NDB-17, NDB-12, NDB-10, NDB-24
III	4	NDB-7, NDB-14, Arka Nidhi, SM-6-6
IV	4	NDB-13, NDB-16, NDB-29, NDB-2
V	8	NDB-9, NDB- 26, NDB-27, NDB-19, NDB-21, NDB-22. NDB- 23, S-Mani-8
VI	4	KS-224, NDB-28, NDB-20, Pant Rituraj

Table 2: Average intra and inter clusters D^2 values for six clusters in brinjal germplasm

Cluster number	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V	Cluster-VI
Cluster-I	137.067	750.969	400.079	842.829	1296.806	1527.354
Cluster-II		86.544	244.225	256.395	219.376	369.340
Cluster-III			111.277	256.400	475.975	816.096
Cluster-IV				128.809	329.416	576.471
Cluster-V					74.860	259.429
Cluster-VI						169.603

Table 3: Intra cluster group mean for ten characters in brinjal germplasm

Characters / Cluster Number	Days to 505 flowering	Primary branches per plant	Plant height (cm)	Fruit weight (cm)	Fruit circumference (cm)	Polar length of fruit (cm)	Fruits per plant	Early yield per plant (kg))	Yield per plant (kg)
Cluster-I	52.667	4.050	67.517	106.33	12.400	17.867	14.753	0.703	1.370
Cluster-II	54.625	4.037	76.050	167.875	19.417	14.883	4.962	0.328	0.822
Cluster-III	49.665	4.808	60.408	93.250	13.817	18.552	8.054	0.312	0.732
Cluster-IV	51.417	4.825	80.908	134.833	14.742	21.058	4.533	0.287	0.670
Cluster-V	57.833	6.096	64.492	208.167	23.271	16.204	2.460	0.359	0.5814
Cluster-VI	52.917	4.000	84.775	335.750	29.242	16.317	2.523	0.550	0.812

Conclusion

Significant differences were revealed by Mahalanobis D^2 statistic. The varieties were grouped into six clusters. There was no consistent relationship between genetic divergence and geographical distribution but the result suggested that crosses between selected genotypes from widely separated clusters are most likely to give desitable recombinants.

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