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Genetic divergence in Brinjal (*Solanum melongena* L.)

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Brinjal or egg plant (*Solanum melongena* L.) is one of the most common and principal vegetable crop grown in India. Fruit yield of brinjal is a polygenic in nature and is influenced by environmental factors. A great extent of divinity present in various quantitative traits among the genotypes of brinjal suggested good scope for improvement in economic traits through conventional breeding. In heterosis breeding programme, the diversity of parents is always emphasized. The D^2 statistics has been found to be powerful tool to estimate genetic divergence among populations (Sharma and Maurya 2004). Similarly the diversity of parental material is the basic requirement of any breeding programme. More diverse the parents within a reasonable range, better are the chances of improving economic characters under consideration, in the resulting off springs. It also helps to know the relative distances between these varieties for the characters under study. The aim of forming clusters and finding the intra and inter cluster divergence is to provide the base of selecting parents for a planned breeding programme. The present investigation was carried out to study the genetic divergence in promising brinjal germplasm.

Sixty five genotypes were collected from different agro-climatological regions of the country and maintained at All India Coordinated Research Project on Vegetable Crops, Mahatma Phule Krishi Vidyapeeth, Rahuri. The experiment was laid out during the year *Kharif* 2009-10 in a Randomized Block Design having 65 treatments replicated twice with a spacing of 90×60 cm. The gross plot size was 2.70×3.60 m. with 3 rows having 6 plants in each row. Number of plants per plot were 18 and from this randomly five plants were selected for observation purpose in each plot in each replication. Seedlings were transplanted in ridges and furrow layout. All the cultural practices to grow best crop were adopted. The genotypes were studied for fourteen quantitative characters viz. plant height (cm), plant spread (cm) (S-N and E-W), number of primary branches per plant, days to 50 percent flowering, days to first harvest, length of fruit (cm), breadth of fruit (cm), girth of fruit (cm), average weight of fruit (g), number of fruit per plant, yield per plant (kg), yield per hectare (q) and duration of harvest. The genetic divergence was assessed using Mahalanobis's (1936) D^2 Statistics. The genotypes were grouped according to the method described by Tocher (Rao, 1952).

Adequate diversity between the genotypes was observed with D^2 values ranging from 6.90 to 2850.23. The maximum D^2 value of 2850.23 was observed between the genotypes IAB-104 and Phule Harit, while the lowest D^2 value 6.90 was noted between genotypes Manjari Gota and JBR-1. The adequate diversity between various traits in brinjal was also reported by Yadav, 2008, Golani *et.al.* 2007, and Sharma and Mourya 2004.

The 65 genotypes from different sources were grouped into seven clusters. Based on D^2 values seven clusters were formed from sixty five genotypes. Out of these seven clusters, cluster A was the largest having thirty eight genotypes which was followed by cluster C which has ten genotypes and B and D clusters had seven genotypes, cluster E, F, G are unique containing only one genotype as solitary clusters (Table 1).

The aim of forming cluster and finding intra and inter cluster divergence is to provide the base for selecting parents for making crosses. The genotypes grouped in same cluster presumably vary little from each other and crossing between them is of no use as they should not give desired gene combination. Therefore, the crossing was made between genotypes of different cluster. It therefore appears logical to affect the crosses between strains belonging to diverse cluster. It is however, assumed that the statistical distance (D^2) is the index of genetic diversity. The clustering pattern obtained in present investigation revealed that geographic diversity did not seem to have a direct association with genetic diversity. Sharma and Mourya, 2004, Doshi *et.al.* 1998 and Golani *et.al.* 2007 were reported that geographical and genetic diversity were unrelated.

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Table 1: Distribution of 65 genotypes of brinjal in seven clusters.

Sr. No.	Cluster	Name of cultivars	Number of genotypes
1	A	Manjari Gota, Green Round, Kudachi, Krishna Kathi-1, IAB-22, JBR-1, RBH-743, JBR-2, IAB-32, RB-24, IVBR-1, CHRB-1, CHRB-2, PB-61, JBR-03-16-1, Black Beauty, APU-2, Kranti, IAB-20, IAB-107-1, IAB-104, RHR-1-6-8-1, JBR-2-23, Poona Selection, RB-26-1, IAB-107, KS-225, Sirasgaon Kata, Arka Navneet-2, IAB-83, Green Oval Brinjal, Aruna, Hissar-2, DBSR-52, DBSR-195, IVBR-1-1, Swarn Shree-2, RHR white	38
2	B	Swarn Mani, KS-224-2, ABH-1, Vaishali, Pragati, IAB-107-2, JBR-64	07
3	C	IAB-87, PB-60, RB-26, JB-14, CO-2, JB-13-1, Ruchira, Hissar-1, JB-24, Krishna Kathi-2	10
4	D	Swarn Shree-1, JB-13, JBR-03-16, IAB-104-1, Kranti-2, Arka Navneet-1, JB-19	07
5	E	Dorli	01
6	F	JBR-02-11	01
7	G	Phule Harit	01

The inter and intra cluster D^2 values and D values was presented in Table 2. The maximum inter cluster divergence was observed between cluster E and G (7.29), while it was lowest between cluster A and E (4.19). Intra cluster D values for the cluster A (3.60), B (3.66), C (3.99), D (4.34) suggested substantial and almost equal diversity within themselves, while cluster E, F, G comprising of a single genotype each had no intra cluster divergence.

The mutual relationship among various clusters based on generalized distance has been diagrammatically shown in Fig. 1. It is suggested that genotypes from more diverse groups and having high yield potential coupled with quality attributes might be useful in breeding programme. In addition to yield, incorporation of important quality oriented characters is equally important. Therefore taking into account the inter cluster divergence and the character means of genotypes and cluster means a precise breeding programme is suggested for high yield per plant. The yield per plant had highest cluster mean for cluster G (2.10) followed by F (1.80), B (1.73), D (1.42). The inter cluster distance between cluster G and F (6.62) and G and B (6.92) was high. So cross between the genotypes belonging to these clusters can be suggested on the basis of mean value for yield per plant among the genotypes included in these cluster, the crosses Phule Harit × JBR-02-11 and Phule Harit × Pragati were likely to give superior genotypes for high yield per plant. The crosses Dorli × Pragati and Dorli × JBR-02-11 likely to give superior genotypes for high number of fruits per plant. The crosses Phule Harit × Arka Navnet, Phule Harit × JBR-03-13, Phule Harit × JB-13 likely to give superior segregants for maximum fruit weight. By considering different character and genetic divergence the genotypes viz. JBR-02-11, Pragati, Dorli, Arka Navneet, JBR-03-11, and JB-13 should be exploited for further improvement. The cultivar Phule Harit, being a big size, can be exploited for roasting purpose for further improvement. In general, the information about the genotypes grouped in these clusters will be more meaningful in improving the yield and yield contributing characters.

Table 2: Average inter and intra cluster D^2 values and D values.

	A	B	C	D	E	F	G
A	13.01 (3.60)	24.06 (4.90)	20.01 (4.47)	19.93 (4.46)	17.58 (4.19)	21.78 (4.66)	43.08 (6.56)
B		13.44 (3.66)	32.12 (5.66)	34.90 (5.90)	23.81 (4.87)	20.11 (4.48)	47.95 (6.92)
C			15.99 (3.99)	25.65 (5.06)	28.20 (5.31)	22.05 (4.69)	43.53 (6.59)
D				18.87 (4.34)	24.34 (4.93)	32.51 (5.70)	42.74 (6.53)
E					0.00 (0.00)	29.56 (5.43)	53.21 (7.29)
F						0.00 (0.00)	43.85 (6.62)
G							0.00 (0.00)

Note: The values in bracket indicates inter and intra cluster D values.

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