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Breeding potential of brinjal genotypes using D^2 analysis

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ABSTRACT

The present investigation was carried out in *kharif* season of 2005-2006. All the genotypes were grouped into five clusters based on D^2 values, which exhibited no association between geographical and genetic divergence. The intra-cluster distance was minimum for cluster IV and maximum in cluster II. The maximum distance at inter-cluster level was between clusters I and clusters IV followed by II and IV which may serve as a potential genotypes for hybridization programme. On the basis of mean performance of different clusters, genotypes having high yield along with fruit diameter, fruit index and average fruit weight were observed in cluster V having genotypes like DBR-31 (Delhi), Green Long (Kalyani), KS-335 (Kalayanpur), G-190 (IARI, Delhi), DBR-8 (IARI, Delhi), SL-91-2 (Pantnagar), SL-190-10-12 (Panipat), Swarna Shree (Ranchi), ABR-1 (Anand) .

Key words: Breeding potential, genetic divergence, brinjal, multivariate analysis.

INTRODUCTION

Brinjal or eggplant a member of family Solanaceae is normally a self-fertilized annual or weak perennial. Varied forms, colours and shapes of brinjal are found throughout South and Southeast Asia, suggesting that this area is an important centre of variation and possibly of origin (Vavilov, 14). The eggplant originated in India but has secondary centre of variation in China (Zeven and Zhukovsky, 15). Brinjal is believed to have been domesticated in North-Eastern India where wild forms still grow (Kochhar, 5; Lester and Hasan, 6). India possesses a rich diversity of *Solanum melongena* and related species, differing widely in botanical and agronomic traits. Apart from a large number of high yielding cultivars many landraces and wild forms have also been reported (Rai and Gupta, 11).

In plant breeding genetic diversity plays a very important role as it helps in selecting the suitable parents for hybridization programme resulting in superior hybrids and desirable recombinants. Keeping in view the above facts present investigation was undertaken to work out genetic divergence among 30 genotypes based on eleven important traits of brinjal, to help the breeders in selecting promising and genetically diverse parents for desired improvement.

MATERIALS AND METHODS

The present investigation was carried out at the Research Farm of Division of Vegetable Science, IARI, New Delhi, during *kharif* seasons of 2005-2006. The experimental materials comprised of thirty indigenous genotypes of brinjal collected from different parts of India. The experiment was laid out in a randomized block design with three replications. Seeds were sown in the nursery bed on 10th June and transplanting was done on 15th July, 2006. A spacing of 75 cm × 60 cm was maintained and all the recommended agronomic package of practices along with plant protection measures were followed. The observations were recorded on five randomly selected plants per replication after discarding the border plants at both ends for each genotype on eleven quantitative characters: i) plant height (cm), ii) days to first flowering, iii) days to first fruit set, iv) days to first harvest, v) number of flowers per cluster, vi) number of fruits per plant, vii) average fruit weight (g), viii) fruit length (cm), ix) fruit diameter (cm), x) fruit index, and xi) yield per plant (kg). Mean across three replications were calculated for each trait and the analysis of variation was carried out as suggested by Snedecor and Cochran (13). The observations were recorded on five randomly selected plants per replication for each genotypes on eleven quantitative characters. Multivariate analysis was done utilizing Mahalanobis D^2 statistic (Mahalanobis, 7) and genotypes were grouped into different clusters following Tocher's method as described by Rao (12).

RESULTS AND DISCUSSION

On the basis of D^2 values, the 30 genotypes were grouped into five highly divergent clusters (Table 1). The cluster divergence was proved by the high intercluster and low intra-cluster D^2 values. The germplasm were so divergent, that only six genotypes were grouped in cluster III and five genotypes were grouped in cluster I. The genotypes Pusa Purple Round and KS-224 were so divergent in all the characters that they had to be given the status of separate cluster (Table 1).

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This cluster comprising of two genotypes with specific valuable traits and other genotypes falling in the highly divergent groups will help in broadening the existing genetic base and may produce new genotypes with hitherto unknown combinations. A perusal of the Table 1 clearly showed the genotypes usually did not cluster according to geographical distributions. This is an agreement with results of Pramanick *et al.* (10), Mehta *et al.* (8), Bansal and Mehta (2), and Mehta and Sahu (9). One of the possible reasons may be the fact that it is very difficult to establish the actual location of origin of a genotype. The free and frequent exchange of genetic material among the crop improvement programmes in the country makes it difficult to maintain the real identity of the genotypes. Moreover, breeding progenies incorporate genes from varied sources, thus losing the basic geographical identity of the genotype. The absence of relationship between genetic diversity and geographical distance indicates that forces other than geographical origin, such as exchange of genetic stocks, genetic drift, spontaneous variation, natural and artificial selection are responsible for genetic diversity. It may also be possible that causes for clustering pattern were much influenced by environment and genotype x environment interaction resulting in differential gene expression. Another possibility may be that estimates might not have been sufficient to account for the variability caused by some other traits of physiological or biochemical nature which might have been important in depicting the total genetic diversity in the population.

Considerable diversity was observed among the genotypes collected from IARI, New Delhi and Uttar Pradesh. This wide diversity can be attributed to the reason that these regions extend from far west to far east of India and have ecologically variable agro-climatic conditions. This is not the case when a plant population is restricted to small geographical areas with identical environmental pressure, which help to evolve adaptive gene complexes rather with little diversity. The intra- and inter-cluster D^2 values among 30 genotypes presented in Table 2 revealed that cluster IV showed minimum intra-cluster D^2 value (1.382), whereas, maximum intra-cluster D^2 value (2.362) was shown by cluster II indicated that genotypes included in this cluster are very diverse and was due to both natural and artificial selection forces among the genotypes. Minimum inter-cluster D^2 value was observed between the clusters I and II (2.781) indicated close relationship among the genotypes included in these clusters. Maximum inter-cluster D^2 values was observed between the clusters I and IV (5.788) followed by II and IV (4.909) indicated that the genotypes included in these clusters can be used as a parent in hybridization programme to get higher heterotic hybrids from the segregating population. Similar results were revealed by Babu and Patil (1), and Mehta *et al.* (8).

The cluster mean of 30 genotypes (Table 3) showed that the mean value of clusters varied in magnitude for all the 11 characters. Genotypes in cluster I showed maximum value for number of fruits per plant (30.12), while cluster II showed the highest value for fruit length (17.83 cm). Cluster III showed maximum values for days to first flowering (41.33) and number of flowers per cluster (2.72). Likewise, cluster IV showed highest mean values for plant height (101.48 cm), days to first fruit harvest (82.50) and days to first fruit set (54.33). Cluster V exhibited highest value for fruit diameter (7.84 cm), fruit index (86.28), average fruit weight (242.07 g) and yield per plant (2.10 kg). Depending upon the aim of breeding, the potential lines to be selected from different clusters as parents in a hybridization programme should based on genetic distance. In accordance to the findings, Edang *et al.* (3), and Hazra *et al.* (4) reported that the clustering pattern could be utilized in choosing parents for cross

Table 1. Cluster classification and source of collection of 30 genotypes based on D^2 analysis.

Cluster	No. of genotypes included	Genotypes
I	5	Kt-4 (IARI, Delhi), SL-195 (IARI, Delhi), KS-327 (Kalayanpur), DBSR-44 (IARI, Delhi), DBSR-91 (IARI, Delhi)
II	8	NDB-25 (Faizabad), DBL-21 (IARI, Delhi), Pusa Bhairav (IARI, Delhi), Long White Cluster (IARI, Delhi), Pusa Kranti (IARI, Delhi), DBL-11 (IARI, Delhi), KS-331 (Kalaynpur), Pusa Purple Long (IARI, Delhi)
III	6	Pusa Purple Cluster (IARI, Delhi), Aruna (Akola), JNDBL-1 (Jabalpur), APAU SL-2 (A.P.), SL-71-19 (Sabour), ABSR-1 (Anand)
IV	2	Pusa Purple Round (IARI, Delhi), KS-224 (Kalyanpur)
V	9	DBR-31 (Delhi), Green Long (Kalyani), KS-335 (Kalyanpur), G-190 (IARI, Delhi), DBR-8 (IARI, Delhi), SL-91-2 (Pantnagar), SL-190-10-12 (Panipat), Swarna Shree (Ranchi), ABR-1 (Anand)

Table 2. Intra- (bold) and inter-cluster distance among clusters in brinjal.

Cluster	I	II	III	IV	V
I	**2.020**				
II	2.781	**2.362**			
III	3.338	3.823	**2.269**		
IV	5.788	4.909	4.781	**1.382**	
V	4.595	3.616	4.484	2.917	**2.026**

Table 3. Cluster means of thirty brinjal genotypes for eleven traits.

Cluster	Plant height (cm)	Days to first flowering	Days to first fruit set	Days to first fruit harvest	No. of flowers per cluster	No. of fruits/ plant	Fruit length (cm)	Fruit dia. (cm)	Fruit index	Av. fruit wt. (g)	Yield/ plant (kg)
I	78.34	33.33	44.73	66.53	2.54	30.12	10.12	5.02	47.41	67.15	1.70
II	88.11	34.75	47.16	69.37	2.30	21.34	17.83	4.84	83.50	90.53	2.03
III	83.21	41.33	53.55	74.85	2.72	24.42	11.13	3.69	39.55	60.72	1.34
IV	101.48	40.33	54.33	82.50	1.98	5.66	9.83	7.46	72.98	224.90	1.32
V	87.86	37.63	51.48	79.92	2.34	8.72	11.24	7.84	86.28	242.07	2.10

combinations likely to generate the highest possible variability for various economic characters.

For breeding programme aimed at higher yield, the genotypes from cluster V can be selected as parent showing highest mean yield per plant along with higher fruit index and average fruit weight. To breed good varieties in small fruited group, selection from cluster IV will be highly useful and to breed long fruited varieties having some demand in specific region of our country, selection from cluster II will be useful. The genotypes of highly divergent cluster may also be utilized in a breeding programme for development of high yielding varieties with desirable attribute and can also be utilized in heterosis breeding programme for development of F_1 hybrids with superior yield and quality characters.

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