



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

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Abstract: A study of genetic divergence in 40 brinjal (*Solanum melongena* L.) genotypes for various characters to study the diversity based on qualitative and quantitative characters. Significant variations were observed among the brinjal lines for all the parameters under study. Based on D^2 values, the accessions were grouped into seven clusters. Average intra- and inter-cluster D^2 values among 40 genotypes revealed that cluster II showed a minimum intra-cluster value of 3.793, indicating that the genotypes within this cluster were similar, while the cluster I showed maximum intra-cluster D^2 value (4.681) revealing the existence of diverse genotypes in these clusters. The inter-cluster D^2 values ranged from 4.657 to 7.174. The minimum inter-cluster D^2 value was observed between cluster III and IV (4.657), indicating the close relationship among the genotypes included in these clusters. The maximum inter-cluster value was observed between cluster V and II (7.174), indicating that the genotypes included in these clusters had maximum divergence. Hence, hybridization between the genotypes included in these different clusters may give high heterotic responses and thus better segregants are greatly suggested for selection and improvement of brinjal crop with good consumer preference and high fruit yield.

Keywords: Brinjal, D^2 statistic, Genetic diversity, *Solanum melongena* L.

INTRODUCTION

Brinjal (*Solanum melongena* L.) is the most important annual herbaceous self pollinated *solanaceous* vegetable crop grown throughout the world (Timmapur, 2007). It has been an important vegetable in our diet since ancient times and very commonly used in all households. Improvement in yield and quality is normally achieved by selecting genotypes with desirable character combinations existing in the nature or by hybridization. Selection of parents identified based on divergence analysis would be more promising for a hybridization programme. It was observed that more diverse the parents, greater is the chance of obtaining high heterotic F_1 s and broad spectrum of variability in the segregating generation (Kumar *et al.*, 2000).

Morphological characterization is the first step in the description and classification of germplasm collections (Smith *et al.*, 1989). The multivariate analysis is useful for characterization, evaluation and classification of plant genetic resources when a number of accessions are to be assessed for several characters of agronomic and physiological importance (Peters and Martinelli, 1989). The multivariate analysis can be used to develop new variety from assessed diverse genetic stock. The genetically diverse parents can be quantified through biometrical procedures successfully to choose for a hybridization program (Uddin *et al.*, 2014). Furthermore, Gupta *et al.* (2015) studied genetic diver-

sity and suggested that the assessment is important to recognize the basis of genes for a particular attribute within the accessible germplasm.

Different types of analysis such as cluster analysis can be used to obtain the idea about how to identify groups of accessions that have desirable traits for breeding and enlightening the patterns of variation in germplasm collection, to identify relationships among accessions and possible eggplant improvement can be attained by exploiting available sources of variability (Prabakaran, 2010) and Quamruzzaman *et al.* (2006). Keeping in view these facts, the present studies were carried out to investigate the degree of genetic diversity in brinjal (*Solanum melongena* L.).

MATERIALS AND METHODS

Forty brinjal accessions, collected from different parts of country were evaluated at Research Farm of the Department of Vegetable Science, CCS Haryana Agricultural University, Hisar (Haryana), India during autumn winter season 2015. The experiment was laid out in randomized block design, having 40 genotypes replicated thrice in a plot size of 1.5x5.4 m for each genotype. The experimental material was sown on raised beds nursery of 1.5x1 m dimension in lines six centimeter apart during the first week of July 2015. Seedlings of four-five weeks were transplanted in a well-prepared field. The seedlings were planted in a fashion accommodating 18 plants in each treatment at spacing of 75 cm line to line and 60 cm plant to plant.

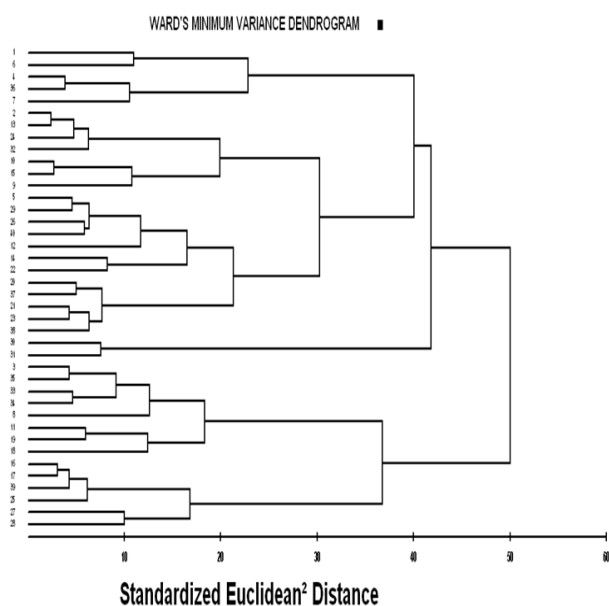


Fig.1. Dendrogram showing the clustering pattern of forty genotypes of brinjal.

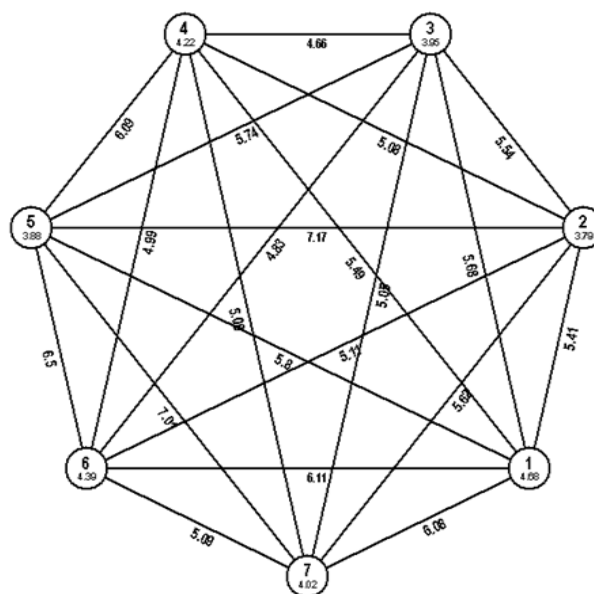


Fig.2. Intra- and inter-cluster distance for seven groups of forty brinjal genotypes.

The genotypes were randomly distributed to each row within each line and observations on ten randomly selected competitive plants were recorded. The packages of practice and plant protection schedule were given as per recommendations of the University for raising the healthy crop successfully. Mahalanobis's generalized distance (D^2) was used to determine the degree of divergence and the group constellations were arrived by Ward's methods described by Rao (1952).

RESULTS AND DISCUSSION

Group constellation: Seven major clusters were formed by grouping all the forty genotypes in such a way that genotypes within each cluster had smaller D^2 value than those between clusters as shown in Figure 1 (Table 1). Cluster pattern reveals that cluster IV consisting of 12 genotypes and cluster VI consisting of eight genotypes were the largest group, which was followed by cluster III (seven genotypes), cluster VII (six genotypes), cluster II (three genotypes), cluster V (two genotypes) and cluster I (two genotypes) Mehta and Sahu (2009), Shekar et al. (2012) and Gupta et al. (2015) also reported similar grouping of brinjal genotypes into different cluster.

Intra- and inter-cluster distance means: The cluster

means for thirteen quantitative characters in brinjal maintainer lines revealed considerable difference among all the clusters. Cluster wise mean and over all cluster mean for the characters are presented in Table 2. In support with the present results, Shekar et al. (2012) and Gupta et al. (2015) also revealed the same results. From the present study, it is evident that the highest mean value for number of branches per plant was possessed by cluster III (6.71) and lowest mean value by cluster V (5.33). Cluster VI (82.08) had the highest and cluster VII (58.44) the lowest mean value for plant height. For length of the peduncle, the cluster II (6.64) and V (4.40) revealed the maximum and minimum mean value, respectively. Cluster II (8.71) showed the highest mean value and cluster VII (5.18) the lowest mean value for number of fruits per plant. Cluster III (4.0) had the highest and cluster IV (2.69) the lowest mean value for number of flowers per cluster. Fruit length was the highest in cluster VII (15.55) and lowest in cluster IV (8.54). For fruit diameter, cluster V (106.06) divulged the highest mean value and cluster VII (41.92) the lowest mean value. Cluster VII (14.38) also revealed the highest mean value for days to 50 % flowering, whereas, cluster V had the lowest mean value (8.66). Cluster II (15.78) had the

Table 1. Distribution of forty brinjal genotypes in different clusters.

Cluster No.	Number of genotypes	Genotypes
Cluster I	2	HE-80, HALB
Cluster II	3	IC 545972, HE-109, HE-83
Cluster III	7	HE-81, HE-88, HE-98, HE-106, HE-85, HE-90, HE-84
Cluster IV	12	IC 433562, HE-103, HE-100, HE-113, HE-87, HE-89, HE-96, HE-94, HE-110, PR-4, HE-97, HE-111
Cluster V	2	HE-104, HE-105
Cluster VI	8	Swarnima, HE-108, BRL, HE-107, HE-83, HE-86, HE-93, PR
Cluster VII	6	HE-91, HE-92, HE-112, HE-99, HE-101, HE-102

Table 2. Cluster means analysis of forty genotypes of Brinjal.

Character clusters	1	2	3	4	5	6	7	8	9	10	11	12	13
Cluster 1	5.833	65.333	4.950	7.667	3.000	10.600	74.112	11.333	13.833	152.500	449.667	8.167	1.477
Cluster 2	5.556	74.667	6.643	8.711	2.889	9.867	42.977	12.667	15.789	58.222	299.778	9.641	1.44
Cluster 3	6.714	61.095	4.951	6.129	4.000	8.671	47.423	12.190	12.948	40.072	349.762	7.541	3.126
Cluster 4	5.417	65.333	4.825	5.311	2.691	8.544	43.836	12.667	14.526	50.722	403.667	8.431	2.486
Cluster 5	5.333	77.167	4.403	5.633	3.333	10.367	106.065	8.667	12.960	47.833	589.167	3.443	3.085
Cluster 6	5.833	82.083	5.820	5.833	3.833	12.990	42.863	13.625	13.504	36.208	443.708	9.963	2.467
Cluster 7	5.611	58.444	5.471	5.183	3.333	15.556	41.926	14.389	14.778	72.222	175.333	7.870	3.634
Mean	5.783	68.200	5.265	5.928	3.308	10.800	48.543	12.767	14.065	54.668	371.775	8.330	2.548

highest and cluster III (12.94) the lowest mean value for leaf length. Cluster I (152.50) showed the maximum mean value for fruit weight and cluster VI (36.20) showed the lowest mean value. Yield per plant was the highest in cluster V (589.16) and lowest in cluster VII (175.33). For leaf width cluster VI (9.98) divulged the highest mean value and cluster V (3.44) divulged the lowest mean value. Fruit length to width ratio had highest mean value in cluster VII (3.63) and lowest mean value in cluster II (1.44). These results confirm the earlier findings of Yadav *et al.* (1996), Doshi *et al.* (1998) and Polignano *et al.* (2010) in brinjal for the attributes *viz.* number of branches per plant, length of the peduncle, days to 50 % flowering, leaf length, number of fruits per plan, fruit length and fruit diameter, respectively.

The above comparison indicates that cluster V and cluster VII had the highest mean value for more characters. Therefore, cluster V and cluster VII were considered the most desirable for selecting genotypes for further breeding improvement. Similar results were reported by Tambe *et al.* (1993), Yadav *et al.* (1996) and Rekha *et al.* (2015). Quamruzzaman *et al.*, 2009; Islam *et al.* (2011) worked on divergence analysis in different accessions of brinjal and found similar results for D² statistics for number of branches per plant, length of the peduncle, days to 50 % flowering, leaf length, number of fruits per plan.

Intra- and inter-cluster distance: The intra- and inter-cluster distances are given in Table 1 (Fig. 2). A maximum difference among the genotypes within the same cluster was shown by cluster I (4.681). This was followed by cluster VI (4.386), cluster IV (4.219), cluster VII (4.017), cluster III (3.949), cluster V (3.883) and cluster II (3.793). When diversity within clusters was studied, it showed a range of 4.657 to 7.174. Cluster II and V showed maximum inter-cluster distance of 7.174, followed by that presented between cluster V and VII (7.012). The lowest inter-cluster distance was noticed between cluster IV and III (4.657), followed by that presented between cluster VI and III (4.833). The present results support the study of Gupta *et al.* (2015). The present study may be helpful to breeder to cope up with environmental variability and to reduce potentially deleterious effects of close relative. The genotypes used are diverse in nature. It is a primary basis for adaption and to identify the new genotypes in the face of use to future environmental uncertainty, which shows that the studied genotypes had a broad genetic base. The results may be used further to improve the yield of the brinjal crop and also as a parent material in future breeding works. Thus, the genotypes would be suitable for efficient hybridization program for exploitation of hybrid vigour in brinjal.

Conclusion

Average intra- and inter-cluster D² values among 40

Table 3. Analysis for Intra- and Inter-cluster distances for forty brinjal genotypes.

Cluster No.	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	4.681	5.413	5.679	5.489	5.795	6.109	6.077
Cluster II		3.793	5.544	5.084	7.174	5.114	5.617
Cluster III			3.949	4.657	5.742	4.833	5.054
Cluster IV				4.219	6.088	4.993	5.079
Cluster V					3.883	6.496	7.012
Cluster VI						4.386	5.086
Cluster VII							4.017

Diagonal values are intra-cluster distances.

genotypes revealed that cluster II showed a minimum intra-cluster value indicating that the genotypes within this cluster were similar, while the cluster I showed maximum intra-cluster D^2 value revealing the existence of diverse genotypes in these clusters. The minimum inter-cluster D^2 value was observed between cluster III and IV indicating the close relationship among the genotypes included in these clusters. The maximum inter-cluster value was observed between cluster V and II indicating that the genotypes included in these clusters had maximum divergence. Hence, hybridization between the genotypes included in these different clusters may give high heterotic responses and thus better segregants are greatly suggested for selection and improvement of brinjal crop.

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