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

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Genetic diversity of any vegetable crop including brinjal arises either due to geographical separation or due to genetic barriers to crossability. Whether differences in geographic origin (source) imply genetic distance in parental selection for hybridization is still a matter of controversy. Assessment of the diversity and relationships of the cultivated species facilitates the establishment of conservation strategies, the use of genetic resources in breeding programmes, and the study of the crop evolution. Keeping the importance of above facts, the present investigation was carried out to know genetic diversity in egg plant using 13 released and 17 pre-released variety representing 8 states of India

Thirty genetically diverse genotypes comprising 13 released and 17 pre released varieties of brinjal representing 8 states of India were grown at Instructional Farm, Mahatma GandhiChitrakoot Gramodaya Vishwavidyalaya,Chitrakoot, Satna (M.P) in the year 2009-10 to know genetic diversity among these genotypes. Twenty five days old seedlings were transplanted in the field at spacing of 60 cm within rows and 75 cm in between the rows in randomized block design with three replication consisting 30 plant in each replication.

The data an horticultural traits like Days to flowering, number of cluster per plant, number of fruits per cluster, fruit length (cm), fruit width (cm), number of fruits/ plant, average fruit weight (g), plant height (cm), plant spread (cm) and fruit weight /plant (kg) were recorded using standard procedures. Mean data was subjected for statistical analysis for ANOVA. Intra and inter cluster distances were calculated.

The effects of different scales of measurement for different quantitative traits were minimized by standardizing the data for each trait separately prior to cluster analysis; the STAND module of NTSYS-pc software was used to achieve the same. Pair-wise distance matrix was used as an input for analysis of clusters. UPGMA-based clustering was done using SAHN module of NTSYS-pc.

Analysis of variance revealed significant differences within the germplasm for all the traits studied. The mean performance for days to flowering varied from 76.33 to 61.00 Maximum days to flowering was recorded in Nurkee (76.33), followed by BR-114 (75.67), BB-85 (73.00) and minimum in Pusa Shyamla (61.00). The highest number of cluster per plant was recorded in Nurkee (34.93) followed by DRNKV-02-26 (34.33) and DBR-8 (34.20), whereas minimum was observed Jawahar Brinjal-64 (24.53). The high data were recorded in the genotypes BSS-464 (2.53) followed by Green Long (2.50), and Pusa Shyamla (2.33) and minimum showed in genotype BR-114 (1.03) for the trait number of fruits per cluster. Fruit length (cm) is an important quality trait; the genotype Green Long (15.00) was showed highest fruit length and minimum length show in genotype IBL-116-131 (3.87). The genotype Direct for visit-1 showed high fruit width 7.37 cm followed by IBL-116-131 (5.93) and BR-112 (5.77), whereas minimum was observed in Punjab Nageena (2.93). The high mean performance for the trait number of fruits per plant observed 35.20 in Pusa Shyamla followed by BR-112 (28.13) and Arka Shree (26.73), whereas minimum was observed in DBL-24 (23.00). The highest average fruit weight was recorded in DBR-8 (291.67g) followed by Direct for visit-1 (262.00) and Swarna Shyamali (211.00), whereas BSS-464 (31.67) was showed minimum weight. The highest plant height (cm) was recorded DRT-31 (93.47) followed by Collection No-4 (90.80) and Green Long (89.33) and minimum in Punjab Nageena (74.00). Plant spread is direct related to photosynthesis, the genotypes RB-9 non selection show high 76.73 cm followed by Pusa Shyamla (73.87) and JB-347 (62.67), whereas minimum plant spread was recorded in genotype DBR-8 (70.20). The genotype DBR-8 show highest fruit weight per plant (6.17 kg)

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Table 1. Distribution of 30 brinjal genotypes in different clusters

Cluster Number	Number of germplasm	Name of germplasm
I	18	TRB-9 non selection, BL-116-135, DBL-24, Arka Shree, Collection No-4, BCB-11, SB-1, Punjab Nageena, DRNKV-02-104, DRT-31, RPL-Nepal, Swarna Shyamali, Brinjal Selection-19, Jawahar Brinjal-64, JB-347
II	4	Pusa Shyamla, BR-112, Aruna, IBL-116-131
III	2	Direct for Visit-1, DBR-8
IV	3	IVBL-9, Nurkee, Green long
V	2	BB-85, BR-114
VI	1	BSS-464

followed by Direct for visit-1 (5.82kg) and BR-114 (5.26kg) and minimum was recorded in DRT-31 (1.12).

The genetic divergence existing in seventy brinjal germplasm collection was studied by employing non-hierarchical Euclidean cluster analysis for ten quantitative characters. The pseudo F-test revealed that six cluster arrangements were the most appropriate for this material. Therefore, the 30 genotypes were accepted to be grouped into six different non-overlapping clusters. The distribution of 30 egg plant lines in six clusters is given Table 1.

Thirty genotypes of eggplant were grouped into six clusters using clustering technique. The cluster I comprised eighteen genotypes, cluster II with four genotypes, cluster III had three genotypes while the clusters II and V and had two genotype genotypes each and cluster VI had only one genotype. The intra cluster distance ranged from 0.00 to 17.23. Cluster I showed minimum intra-cluster distance (12.45) and maximum intra-cluster distance was exhibited by cluster III (17.23) followed by cluster IV (16.44) (Table 2). Maximum inter cluster distance was found between clusters III and IV (49.18). This was followed by clusters I and III (35.69). Minimum inter cluster distance was observed between clusters I and VI (18.90). Selection of genotypes belonging to clusters with maximum inter cluster distance had also been proposed by Mehta *et al.,* (2004) and Shinde *et al*., (2012).

The taxonomic distance matrix of 10 quantitative traits for the 30 genotypes was employed for cluster analysis and a dendrogram was constructed; all the genotypes grouped into four major clusters. In the dendrogram, the longest branch separates in three genotype BB-85, Green Long and Pusa Shyamla from all the genotypes at a taxonomic distance of 0.00-0.28 and this genotype was the lone member of the cluster I.II and III, respectively. The fourth (cluster IV) major cluster consisted of two sub cluster; sub-cluster IV A consist 12 genotypes, viz., Swarna Shyamali, BSS-464, DRNKV-02-26, JB-6, Brinjal selection-19, Nurkee, BCB-11, IBL-116-131, Punjab Nageena, DBR-8, DRNKV-02-104, JB-347 and sub-cluster IV B has 15 genotypes, viz., BR-114, RPL-Nepal, BR-112, KS-356, SB-1, BL-116-135, Arka Shree, DRT-31, DBL-24, IVBL-9, Collection No-4, Direct for visit-1, Jawahar Brinjal-64, Aruna and TRB-9 non selection. Morphological/ qualitative data for cluster analysis is supported by earlier workers (Doshi *et al*., 1998; Tumbilen *et al*., 2011).

Table 2. Intra and Iner- cluser D2 and D values among 6 clusters in brinjal

Cluster number	1	II	III	IV	V	VI
I	154.97 (12.45)	467.96 (21.63)	1273.11 (35.68)	558.27 (23.63)	520.85 (22.82)	357.13 (18.90)
II		267.86 (16.370	532.88 (23.08)	1358.28 (36.85)	360.04 (18.97)	404.57 (20.11)
III			296.94 (17.23)	2419.06 (49.18)	654.53 (25.58)	1012.42 (31.82)
IV				270.28 (16.44)	12.06.07 (34.73)	1181.16 (34.37)
V					264.57 (16.27)	547.63 (23.40)
VI						0.00 (0.00)

*Bold figures represent intra cluster distance

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