GENETIC DIVERGENCE IN ROUND FRUITED BRINJAL (*SOLANUM MELONGENA* L.)

G. Kranthi Rekha* and V. A. Celine[1]

Horticulture Officer, Guntur (Andhra Pradesh), India.
[1]Department of Olericulture, Kerala Agricultural University, Vellayani - 695 522 (Kerala), India.

Abstract

A study of genetic divergence in 27 round fruited brinjal accessions for various biometric characters revealed substantial differences for all the traits. Based on D^2 values, the accessions were grouped into five clusters. Cluster I had the maximum number of accessions (20) followed by cluster IV (3). Cluster III had three accessions while clusters II and V had only one accession each. The inter cluster distance (D = 5911.80) was maximum between clusters II and V. The cluster IV recorded maximum intra cluster distance (D = 1266.45). Intercrossing among the genotypes belonging to cluster II, V and IV was suggested to develop high yielding varieties with other desirable characters or may be used as potential donors for future hybridization programme to develop superior brinjal variety with good consumer preference and high fruit yield.

Key words : Genetic diversity, brinjal (*Solanum melongena* L.), D^2 statistic.

Introduction

Brinjal (*Solanum melongena* L.), also known as aubergine or eggplant, is an important vegetable crop of central, south and south-east Asia and several African countries (Kalloo, 2002). In India, it is cultivated in an area of 5.66 lakh ha with an annual production of 95.95 lakh tons.

It is a good source of minerals and vitamins and has several medicinal properties (Khan, 1979). The area between India and Indochina is considered to be the centre of brinjal diversity (Vavilov, 1951). Hybridization between genetically divergent parents may result in heterotic and/or transgressive recombinants. More diverse the parents within a reasonable range, better are the chances of improving economic characters under consideration in the offspring. Mahalanobis D^2 statistic of multivariate analysis is recognized as a powerful tool in quantifying the degree of genetic divergence among the population. Therefore, the present study was undertaken to assess the genetic diversity among 27 accessions of round fruited brinjal and to identify suitable donors for a successful crop improvement programme. Similar studies have also been conducted in brinjal by Quamruzzaman *et al*. (2006).

Materials and Methods

Twenty seven round fruited brinjal accessions collected from different parts of country were evaluated in a randomized block design with two replications at the Department of Olericulture, College of Agriculture, Vellayani (Kerala), India; during 2010-2011. Thirty five days old seedlings were transplanted at a spacing of 75 cm between rows and 60 cm between plants in a ridge and furrow system. The crop received timely management practices as per package of practices recommendations of Kerala Agricultural University (KAU, 2007). Five plants were selected randomly for recording the observations on plant height (cm), canopy spread (cm), primary branches per plant, secondary branches, days to 50 per cent flowering, long and medium styled flowers (%), fruit length (cm), fruits per plant and yield per plant (g). Mahalanobis's generalized distance (D^2) was used to determine the degree of divergence and the group constellations were arrived by Tocher's methods described by Rao (1952).

Results and Discussion

The 27 accessions were grouped into five clusters (fig. 1) based on relative magnitude of D^2 values. Cluster I was the largest with twenty accessions, closely followed by cluster II with one genotype. Cluster V, cluster IV and cluster III had one, three and two accessions

---

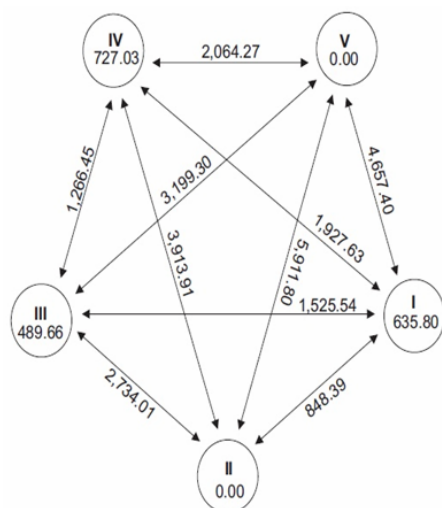****Author for correspondence:*** E-mail: kranthi.mscoleri@gmail.com

Fig. 1 : Cluster diagram.

Table 1: Clustering of brinjal accessions based on D^2 analysis.

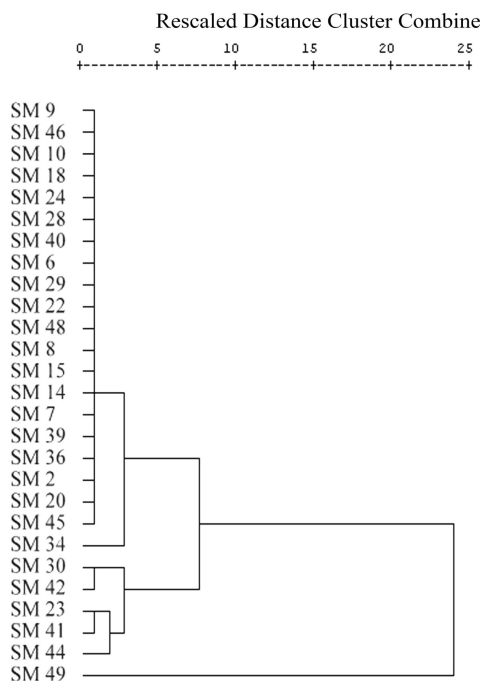| Clusters	Accessions
I	SM 2, SM 6, SM 7, SM 8, SM 9, SM 10, SM 14, SM 15, SM 18, SM 20, SM 22, SM 24, SM 28, SM 29, SM 36, SM 39, SM 40, SM 45, SM 46 and SM 48
II	SM 34
III	SM 30 and SM 42
IV	SM 23, SM 41 and SM 44
V	SM 49

Fig. 2 : Dendrogram of different brinjal accessions constructed using UPGMA hierarchial cluster analysis (between Groups) based on squared Euclidean dissimilarity.

for canopy spread (90.93) and cluster I had the minimum value. Cluster mean for number of primary branches was highest in cluster III (7.77) and lowest in cluster II (3.36). Cluster V exhibited the maximum values for secondary branches, percentage of long and medium styled flower,

Table 2 : Cluster means for nine biometric characters in brinjal.

Character	Clusters				
	I	II	III	IV	V
Plant height (cm)	65.22	75.63	58.33	76.31	94.65
Canopy spread (cm)	64.85	81.21	90.93	78.35	79.91
Primary branches	4.69	3.36	7.77	7.1	6.69
Secondary branches	6.59	4.17	5.61	9.01	9.69
Days to 50 per cent flowering	53.03	54.76	52.31	50.44	56.42
Long and medium styled flowers (%)	46.75	41.15	55.05	60.95	68.45
Fruit length (cm)	8.57	8.63	10.61	11.47	12.17
Number of fruits per plant	16.86	11.03	21.25	17.62	46.41
Yield per plant (g)	1297.56	661.66	2022.90	2607.19	3617.15

respectively. The clustering pattern is furnished in table 1. Dendrogram generated by UPGMA cluster analysis is shown in fig. 2.

Cluster means of the seven characters are presented in table 2. The highest mean for plant height (94.65 cm) was shown by cluster V, while lowest was seen in cluster III (58.33). Cluster III had the maximum cluster mean

fruits per plant and yield (9.69, 68.45, 46.41 and 3617.15) while cluster II had minimum values (4.17, 41.15, 11.03 and 661.66), respectively. Cluster mean for days to 50 per cent flowering was highest in cluster V (56.42) and lowest in cluster IV (50.44). The maximum value for fruit length was seen in cluster V (12.17) and minimum value in cluster I (8.57). This indicates superiority of these

Table 3 : Average intra and inter cluster distances (D values).

Clusters	I	II	III	IV	V
I	635.80	848.39	1525.54	1927.63	4657.40
II		0.00	2734.01	3913.91	5911.80
III			489.66	1266.45	3199.30
IV				727.03	2064.27
V					0.00

clusters with respect of those particular characters.

The average inter and intra cluster distances were estimated based on total D^2 values. The intra cluster (D value) distances varied from 0 to 727.03, whereas the inter cluster (D value) distances ranged from 848.39 to 5911.80. The intra cluster distances were lower than inter cluster distances. The maximum intra cluster distance was observed in cluster IV (727.03). Clusters II and V had only one genotype each and hence intra cluster distance was 0. The average intra and inter cluster distances are furnished in table 3.

The maximum inter cluster distance was noticed between cluster II and V (5911.80) meaning that these two clusters show the maximum genetic divergence which can be utilized in hybridization programmes to get heterotic advantage. Cluster I and cluster II with least inter cluster distance are genetically most similar. The intra cluster distances were seen to be lower than inter cluster distances there by suggesting homogeneity among the genotypes within a cluster and heterogeneity between clusters. Similar divergence analysis was reported in different accessions of brinjal by Kumar *et al.* (2008), Quamruzzaman *et al.* (2009), Polignano *et al.* (2010) and Islam *et al.* (2011).

References

Gunjeet, Kumar, B. L. Meena, Ranjan Kar, S. K. Tiwari, K. K. Gangopandhyay, I. S. Bisht and R. K. Mahajan (2008). Morpholigical diversity in brinjal (*Solanum melongena*) germplasm accessions. *Plant Genetic Resources: Characterisation and Utilisation*, **6** : 232-236.

Islam, M. A., N. A. Ivy, M. A. K. Milan, M. K. Shahadat and M. Shahjahan (2011). Genetic diversity in exotic eggplant (*Solanum melongena* L.). *Libyan Agric. Res. Center J. Int.*, **2** : 15-19

Kalloo, G., M. K. Banerjee, S. N. Singh and M. Singh (2002). Genetics of yield and its component characters in brinjal (*Solanum melongena* L.). *Veg. Sci.*, **29** : 24-26.

Khan, R. (1979). *Solanum melongena and its ancesteral forms*. In: Hawkes JG. Lester RN and Skelding AD (eds) *The Biology and Taxonomy of Solanaceae. Linnean Society Symposium, Series '7'*. London (GBR): Academic Press, pp. 629-636.

Polignano, G., P. Uggenti, V. Bisignano and C. D. Gatta (2010). Genetic divergence analysis in eggplant (*Solanum melongena* L.) and allied species. *Genet. Resour. Crop Evol.*, **57** : 171-181.

Quamruzzaman, A. K. M., M. A. Rashid, S. Ahmad and M. Moniruzzaman (2009). Genetic divergence analysis in eggplant. *Bangladesh J. Agric. Res.*, **34** : 705-712.

Rao, C. R. (1952). *Advanced Statistical Methods in Biometric Research*. Jhon Wiley and Sons Inc., Newyork, 390 p.

Vavilov, N. I. (1951). The origin, variation, immunity and breeding of cultivated palnts. *Chronica Botanica*, **13** : 1-364.