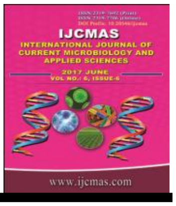
Int.J.Curr.Microbiol.App.Sci (2017) *6*(6): 48-54

International Journal of Current Microbiology and Applied Sciences
ISSN: 2319-7706 **Volume 6 Number 6 (2017) pp. 48-54**
Journal homepage: http://www.ijcmas.com



Original Research Article

https://doi.org/10.20546/ijcmas.2017.606.005

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

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ABSTRACT

Genetic divergence among 35 genotypes of brinjal for 19 characters was evaluated in a breeding programme aimed at improving yield potential by using Mahalanobis D2 statistics. The genotypes were grouped into ten clusters suggesting considerable amount of genetic diversity in the material. The cluster V had maximum 10 genotypes followed by II and IV having 6 and 4 genotypes, respectively. These clusters having maximum number of genotypes, reflecting narrow genetic diversity. The intra-cluster D2 value ranged from 21.71 to 52.61 while, inter-cluster D2 value ranged from 39.09 to 103.59. The maximum intra cluster distance was exhibited by cluster II followed by cluster V and cluster X. The maximum inter-cluster D2 value was observed between VIII and IX. Maximum contribution towards the total divergence was exhibited by fruit yield per plant (30.57%) followed by average fruit weight (29.90%) and ascorbic acid content (15.51%). Noteworthy is that cluster VIII and X reflected high cluster means for fruit yield per plant, average fruit weight, number of fruits per plant and these clusters can be successfully utilized in hybridization programmes to get desirable transgressive segregants.

Keywords

Brinjal,
Clusters,
Diversity, Genetic divergence,
Intra and inter cluster distance.

Article Info

Accepted:
04 May 2017
Available Online:
10 June 2017

Introduction

Brinjal (*Solanum melongena* L.), a member of the Solanaceae family, is the most common and popular vegetable crop in India. India is the major producer of brinjal in the world and it is grown in an area of 0.71 million ha with an estimated annual production of 13.55 million tonnes with a productivity of 19.1 tonnes per ha. In Telangana, the production was 0.30 million tonnes from 0.015 million ha of area (NHB, 2014-15). A large indigenous biodiversity exists in eggplant with variation in plant type, stem color, leaf size, leaf tip, midrib color, fruit size, fruit shape, fruit color, fruit yield, fruit quality, cooking quality, and tolerance to pests and diseases (Ullah *et al.*, 2014). Improvement in eggplant can be achieved by exploiting available sources of variability (Prabakaran, 2010). In any crop improvement programme, genetic diversity plays a very important role as it helps in selecting the suitable parents for hybridization programme resulting is superior hybrids and desirable recombinants (Rathi *et al.,* 2011). Genetic diversity can be worked out with the help of D2 analysis which has given by Mahalanobis (1936). For the first time use of this technique for assessing the genetic variability in plants was suggested by Rao (1952). It is a very potent technique of measuring genetic divergence. Now it is reliably and extensively used in plants for measuring genetic divergence (Shinde *et al.,* 2012; Shinde *et al.,* 2013; Vidhya and Kumar, 2014). In view of these facts, the present study was undertaken with the aim of examining the magnitude of genetic diversity and characters contributing to genetic diversity among brinjal genotypes for a planned breeding programme.

Materials and Methods

A field experiment to investigate the genetic diversity in 35 genotypes of brinjal (*Solanum melongena* L.) was laid out in randomized block design (RBD) with three replications at PG Research Block, Department of Vegetable Science, SKLTSHU, Rajendranagar, Hyderabad, during rabi 2015-16. The experimental material comprised of thirty five genotypes collected from NBPGR, Hyderabad. Planting of each genotype was done in a double row plot of 5m length accommodating 10 plants in a row with inter and intra row spacing of 50 cm x 50 cm. Observations were recorded on five randomly selected plants in each plot on nineteen different traits. Plot means over the replications were used for the statistical analysis. Genetic diversity was studied following Mahalanobis's (1936) generalized distance (D2) extended by Rao (1952). Based on the D^2 values, the genotypes were grouped into clusters following the method suggested by Tocher (Rao, 1952). Intra and inter cluster distances were calculated by the methods of (Singh and Chaudhury, 1985). Statistical analyses were carried out using GENRES software.

Results and Discussion

The clustering based on D^2 statistics grouped genotypes into ten clusters, indicating the presence of wide range of genetic diversity among the genotypes under investigation (Table 3). Among the ten clusters, cluster V was the largest, comprising of 10 genotypes followed by cluster II with 6 genotypes, cluster IV with four genotypes, cluster I with three genotypes and clusters III, VI, VII, VIII, IX, X with two genotypes each. The clustering pattern obtained in present investigation revealed that geographic diversity did not seem to have a direct association with genetic diversity. Bansal and Mehta (2007) and Mehta and Sahu (2009) reported that geographical and genetic diversity was unrelated.

It means the overall genetic similarity was found in the germplasms were presented within the cluster and the pattern of distribution of genotypes in different clusters exhibited that geographical diversity was not related to genetic diversity as genotypes of same geographical region were grouped into different cluster and vice-versa, as supported by earlier finding of Vidhya and Kumar (2014). The possible reason for grouping of genotypes of different places into one cluster could be free exchange of germplasm among the breeder of different region or unidirectional selection practiced by breeder in tailoring the promising cultivar for selection of different region (Verma and Mehta, 1976).

Table.1 Average intra (bold) and inter-cluster D^2 values for 10 clusters in 35 genotypes of brinjal

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X
I	**41.508**	57.985	60.628	70.564	51.294	50.06	53.67	82.385	55.539	68.504
II		**52.614**	41.129	54.318	52.877	52.34	70.12	57.343	75.343	52.531
III			**21.711**	46.242	51.633	52.575	70.124	39.098	79.964	42.103
IV				**45.782**	54.315	47.857	79.594	60.315	77.522	45.899
V					**46.958**	43.178	57.695	71.47	61.388	54.163
VI						**30.721**	57.103	73.172	51.574	55.347
VII							**38.097**	95.286	50.874	82.116
VIII								**38.833**	103.597	53.87
IX									**46.337**	83.184
X										**46.629**

Table.2 Mean values of clusters for nineteen characters in 35 brinjal genotypes

Cluster	Plant height (cm)	No. of branches per plant	Days to first flowering	Days to 50 % flowering	No. of flower clusters per plant	No. of flowers per cluster	No. of fruits per cluster	No. of fruits per plant	Days to first harvest	Days to last harvest	Fruit length (cm)	Fruit width (cm)	Average fruit weight (kg)	Fruit yield per plant (kg)	Ascorbic acid content (mg/ 100g)	Total phenol content (mg/ 100g)	Shoot and fruit borer infestation (%)	Cumulative wilt incidence (%)	Little leaf incidence (%)
I	95.23	13.81	42.43	47.88	19.31	3.01	2.32	27.28	65.00	161.33	7.28	3.67	0.07	1.70	6.43	42.48	0.06	0.00	0.00
II	93.88	13.40	44.84	50.16	16.92	2.81	1.94	23.31	63.50	156.83	13.26	5.76	0.11	2.40	6.30	55.65	0.11	0.00	0.00
III	101.82	12.60	48.27	54.33	16.66	3.10	1.55	21.83	65.50	156.33	14.56	5.92	0.10	2.28	6.43	58.00	0.13	0.00	0.00
IV	98.86	13.69	38.38	44.25	16.27	3.38	1.96	17.23	60.25	142.33	14.08	6.27	0.12	2.15	6.74	40.03	0.13	0.00	0.00
V	91.26	13.94	40.56	46.76	16.74	2.78	1.75	18.64	62.52	148.90	11.67	4.62	0.09	1.61	5.65	45.21	0.08	0.00	0.00
VI	93.49	13.55	40.05	45.66	20.88	1.94	1.22	17.94	67.16	146.16	12.23	5.07	0.08	1.50	8.37	39.41	0.08	0.00	0.00
VII	94.07	11.44	53.38	58.33	15.21	2.66	1.83	17.44	66.33	149.33	12.17	4.38	0.05	0.86	6.13	55.21	0.04	0.00	0.00
VIII	94.91	14.16	46.10	52.16	18.38	3.60	2.22	18.62	63.83	160.16	13.01	7.10	0.15	2.77	6.57	58.10	0.15	0.00	0.00
IX	93.40	13.88	44.05	49.83	18.55	2.60	1.94	25.94	57.33	137.66	6.05	3.82	0.04	1.12	7.86	36.57	0.04	0.00	0.00
X	103.3	14.05	37.60	41.83	21.16	2.88	1.60	20.44	64.50	143.66	13.50	4.81	0.12	2.46	4.36	35.56	0.12	0.00	0.00

Table.3 Cluster classification of 35 genotypes in brinjal

Cluster	No. of genotypes	Genotypes
I	3	IC-136260, BHAGYAMATHI, GULABI
II	6	IC-136017, IC-136251, IC-135912, IC-215018, IC-203602, IC-136311
III	2	IC-136461, IC-136006
IV	4	IC-136181, IC-136041, IC-136298, IC-215022
V	10	IC-136093, IC-136237, IC-135997, IC-136481, IC-13098, IC-136299, IC-136248, IC-136266, IC-136251, IC-136303
VI	2	IC-127018, IC-136455
VII	2	IC-136300, IC-136188
VIII	2	IC-144518, IC-90178
IX	2	IC-136293, IC-127023
X	2	IC-136098, IC-144516

Table.4 Percent contribution of different characters towards genetic divergence in 35 genotypes of brinjal

	Source	Times Ranked 1st	Contribution (%)
1	Plant height (cm)	4	0.6723
2	No. of branches per plant	0	0.0000
3	Days for first flowering	4	0.6823
4	Days for 50 % flowering	1	0.1681
5	No. of flower clusters per plant	0	0.0000
6	No. of flowers per cluster	0	0.0000
7	No. of fruits per cluster	0	0.0000
8	No. of fruits per plant	5	0.8403
9	Days to first harvest	3	0.5042
10	Days to last harvest	48	7.6120
11	Fruit length (cm)	4	0.6723
12	Fruit width (cm)	13	2.1849
13	Average fruit weight (kg)	182	29.9076
14	Fruit yield per plant (kg)	186	30.5798
15	Ascorbic acid content (mg/100g)	86	15.6134
16	Total phenol content (mg/100g)	12	1.8487
17	Shoot and fruit borer infestation (%)	45	8.7227
18	Cumulative wilt incidence (%)	0	0.00
19	Little leaf incidence (%)	0	0.00

Average intra and inter cluster D^2 values are given in (Table 1). The intra cluster distance ranged from Cluster III (21.71) to Cluster II (52.61). Among the ten clusters, the intra cluster distance was maximum in cluster II followed by cluster V (157.41) and cluster IV (150.10), while it was minimum in cluster I (23.06) followed by cluster II (46.95). The intra cluster values are lesser than the inter cluster values which indicates the homogenous and heterogenous nature of the genotypes within and between the clusters. The inter cluster D2 values was maximum between the cluster VIII and IX (103.59) indicating wide genetic distance between these clusters. The genotypes belonging to the clusters with maximum inter cluster distance show high genetic diversity and hybridization between genotypes of divergent clusters is likely to produce wide variability with desirable segregants (Arunachalam, 1981). The minimum inter cluster distance was observed between cluster III and VIII (39.09) suggesting the lowest degree of divergence and close genetic makeup of the genotypes included in these clusters. Similar observations were reported by Senapati *et al.*, (2009), Muniappan *et al.*, (2010), Islam *et al.*, (2011) and Lokesh *et al.*, (2013).

The comparison of cluster means revealed considerable differences among the clusters of different characters (Table 2). Cluster I had highest cluster mean for number of fruits per cluster (2.32), number of fruits per plant (27.28), days to last harvest (161.33) and second lowest cluster for shoot and fruit borer infestation (0.06). Cluster II had good mean value for number of fruits per plant (23.31), fruit length (13.26) and average fruit weight (0.11). Cluster III had highest mean values for fruit length (14.56) and good value for plant height (101.82) and total phenol content (58.00). Cluster IV had second highest values for days to first flowering (38.38), days to 50% flowering (44.25), number of flowers per cluster (3.38), days to first harvest (60.25), fruit length (14.08), fruit weight (6.27) and average fruit weight (0.12). Cluster V had good value for number of branches per plant (13.94), days to first flowering (40.56). Cluster VI highest cluster mean for ascorbic acid content (8.37) and second highest cluster mean for flower cluster per plant (20.88). Cluster VII has lowest value for shoot and fruit borer infestation (0.04). Cluster VIII having 2 genotypes exhibited highest value for number of branches per plant (14.16), number of flowers per cluster (3.60), fruit width (7.10), average fruit weight (0.15), fruit yield per plant (2.77), total phenol content (58.10) and good value for number of fruits per cluster (2.22) and days to last harvest (160.16). Cluster IX having 2 genotypes showed high cluster mean for days to first harvest (57.33) and lowest value for shoot and fruit borer infestation (0.04) and good value for number of fruits per plant (25.94) and ascorbic acid content (7.86). Cluster X had highest mean value for plant height (103.30), days to first flowering (37.60), number of flower clusters per plant (21.16), days to 50% flowering (41.83) and had second highest value for number of branches per plant (14.05), average fruit weight (0.12) and fruit yield per plant (2.46). Similar findings have been also reported by Lokesh *et al.*, (2013) and Sadarunissa *et al.*, (2015) reflected probability of getting better segregants and primary recombinants expected to more, in case if the genotypes of these clusters will be used in hybridization programme. Cluster VIII and IX showed maximum inter cluster distance and crossing of genotypes IC-90178 and IC-144518 from cluster VIII with genotypes from cluster IX suggested for improving days to first harvest, fruit width, average fruit weight, fruit yield per plant, total phenol content and shoot and fruit borer infestation to enhance the yield and chances of getting better recombinants in segregating generations. Noteworthy is that cluster VIII and X reflected high cluster means for number of branches per plant, average fruit weight and fruit yield per plant and Jagadev *et al.*, (1991) reported that the character contributing maximum to the divergence should be given greater emphasis for deciding the type of cluster for purpose of further selection and the choice of parents for hybridization. The maximum contribution towards the total divergence (Table 4) was exhibited by fruit yield per plant (30.57%) followed by average fruit weight (29.90%) and ascorbic acid content (15.61%). Thus the characters which show more contribution (%) towards the total divergence should be considered during selection. Similar observations are reported by Kumar *et al.*, (2012) and Sadarunnisa *et al.*, (2015). Thus, it is evident from the present finding that substantial genetic divergence was envisaged in genetic stock of brinjal. The varieties of same geographical region clustered with the varieties of other geographical region due to selection pressure and genetic drift. This indicates that there is no parallelism between genetic diversity and geographical region except in some cases. Hybridization between the genotypes of different clusters can give high amount of hybrid vigour and good recombination. Fruit yield per plant, average fruit weight, days to first flowering, days to 50% flowering were important components and these should be taken into account while breeding in brinjal.

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How to cite this article:

Ravali B., K. Ravinder Reddy, P. Saidaiah and Shivraj, N. 2017. Genetic Diversity in Brinjal (*Solanum melongena* L.). *Int.J.Curr.Microbiol.App.Sci.* 6(6): 48-54.
doi: https://doi.org/10.20546/ijcmas.2017.606.005