



P-ISSN: 2349-8528

E-ISSN: 2321-4902

IJCS 2019; 7(6): 730-733

© 2019 IJCS

Received: 10-09-2019

Accepted: 12-10-2019

VR Gurve

PG Scholar, College of
Agriculture, Vasantao Naik
Marathwada Krishi Vidyapeeth,
Parbhani, Maharashtra, India

DP Waskar

Director of Research, Vasantao
Naik Marathwada Krishi
Vidyapeeth, Parbhani,
Maharashtra, India

VS Khandare

Research Officer, Horticulture
Research Scheme (Vegetable),
Vasantao Naik Marathwada
Krishi Vidyapeeth, Parbhani,
Maharashtra, India

SP Mehtre

Soybean Breeder & officer
Incharge, AICRP on Soybean,
Vasantao Naik Marathwada
Krishi Vidyapeeth, Parbhani,
Maharashtra, India

Corresponding Author:**VR Gurve**

PG Scholar, College of
Agriculture, Vasantao Naik
Marathwada Krishi Vidyapeeth,
Parbhani, Maharashtra, India

Genetic diversity studies in brinjal (*Solanum melongena* L.)

VR Gurve, DP Waskar, VS Khandare and SP Mehtre

Abstract

Genetic divergence among 20 genotypes of brinjal for 25 characters was evaluated in a breeding programme aimed at improving yield potential by using Mahalanobis D^2 statistics. The genotypes were grouped into three clusters suggesting considerable amount of genetic diversity in the material. The cluster I had maximum 18 genotypes followed by II and III having each single genotypes respectively. These clusters having maximum number of genotypes, reflecting narrow genetic diversity. The highest intra-cluster distance was observed for cluster I (110.60). The highest inter-cluster distance was observed between cluster II and III (452.85). Noteworthy is that cluster II and III reflected high cluster means for plant height, plant spread NS and EW, days to first harvest, days to 50% flowering, number of flower per cluster, days to last harvest, fruiting span, fruit length, fruit yield per plant, fruit yield per plot, ascorbic acid, total phenolic content, flavonoid content and low percent of fruit and shoot borer infestation and these clusters can be successfully utilized in hybridization programmes to get desirable transgressive segregants.

Keywords: Brinjal, clusters, diversity, intra and inter cluster distance

Introduction

Brinjal (*Solanum melongena* L., $2n = 24$), a member of the Solanaceae family, is the most common and popular vegetable crop of India. It can be grown in almost all parts of India year round and is a major source of income for small and marginal farmers. It is being grown extensively in India, Bangladesh, Pakistan, China and Philippines. India is the second major producer of brinjal in the world after China (Ravali *et al.*, 2017) [15]. Due to its highest production potential and availability of the produce to consumers, it is also called as poor man's vegetable (Kumar *et al.*, 2014) [6]. India is a major producer of brinjal in the world and it is grown in area of 648 thousand hectares with estimated annual production of 12,303 thousand metric tonnes with a productivity of 18.98 metric tonnes per hectare. In Maharashtra, it is grown in an area of 35,859 hectare, with an annual production of 667,640 metric tonnes and productivity of 18.61 metric tonnes per hectare which is less than the national average (Anon., 2016-17) [2]. A large indigenous biodiversity exists in eggplant with variation in plant type, stem colour, leaf size, leaf tip, midrib colour, fruit size, fruit shape, fruit colour, fruit yield, fruit quality, cooking quality, and tolerance to pests and diseases (Ullah *et al.*, 2014) [18]. An improvement in brinjal is normally achieved by selecting the genotypes with desirable character combination existing in the germplasm or by hybridization. Genetic diversity is an important factor for any heritable improvement. Knowledge of genetic diversity, its nature and degree is useful for selecting desirable genotypes from a germplasm for the successful breeding programme. Genetic diversity can be worked out with the help of D^2 analysis which has given by Mahalanobis (1936) [9]. For the first time use of this technique for assessing the genetic variability in plants was suggested by Rao (1952) [14]. 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) [17, 16, 19]. In view of these facts, the present study was under taken to measure the magnitude of genetic diversity and characters contributing to genetic diversity among brinjal accessions for a planned breeding programme.

Material and methods

A field experiment to investigate the genetic diversity in 20 genotypes of brinjal (*Solanum melongena* Department of Horticulture, College of Agriculture, VNMKV, Parbhani, during the

kharif 2017-18. The experimental material comprised of twenty genotypes collected from IIVR, Varanasi and VNMKV, Parbhani. The 42 days old healthy seedlings of each genotype were transplanted with a spacing of 75cm x 60cm. The recommended package of practices was adopted for raising the crop. Observation were recorded in five randomly selected plants for twenty five characters *viz.* plant height (cm), number of branches per plant, plant spread (cm), days to first flowering, days to 50% flowering, number of flower per cluster, number of fruit per cluster, fruit setting (%), number of fruit per plant, days to first harvest, days to last harvest, fruiting span, fruit length (cm), fruit diameter (cm), fruit pedicel length (cm), ascorbic acid (mg/100g), total phenolic content (mg/100g), flavonoid content (mg/100g), average fruit weight (g), fruit yield per plant (g), fruit yield per plot (kg), fruit yield per hectare (qt), shoot borer infestation (%), fruit borer infestation (%) and little leaf of brinjal (%). The per cent shoot infestation were calculated using the following formula:

$$\text{Percent shoot infestation} = \frac{\text{Number of damaged shoots}}{\text{Total number of brinjal shoots}} \times 100$$

Incidence of fruit borer was recorded in terms of percentage of fruit damage by weight as well as number at each picking with the help of following formula.

$$\text{Percent fruit borer infestation (Number basis)} = \frac{\text{Total number of borer affected fruits}}{\text{Total number of fruits harvested}} \times 100$$

$$\text{Percent fruit borer infestation (Weight basis)} = \frac{\text{Total weight of borer affected fruits}}{\text{Total yield}} \times 100$$

Based on the mean infestation throughout growing season, the brinjal cultivars were categorized as per the grade index of Subbaratnam and Butani (1981).

Grade index for shoot and fruit infestation/damage by *Leucinodes orbonalis*

Grade	Percent infestation of shoot	Percent infestation of fruit
Tolerant	< 2.0	< 15
Moderately tolerant	2.1-3.0	16-25
Susceptible	3.1-5.0	26-40
Highly susceptible	> 5.0	> 40

Incidence of little leaf disease was recorded in terms of percentage of disease plant with the help of following formula.

$$\text{Percent disease incidence} = \frac{\text{Number of disease plant}}{\text{Total number of plant examined}} \times 100$$

Genetic diversity was studied following Mahalanobis's (1936)^[9] generalized distance (D²) extended by Rao (1952)^[14]. Based on the D² values, the genotypes were grouped into clusters following the method suggested by Tocher (Rao, 1952)^[14]. Statistical analyses were carried out using INDOSTAT software.

Results and discussion

The clustering based on D² statistics grouped genotypes into three clusters, indicating the presence of wide range of genetic diversity among the genotypes under investigation (Table 1) and (fig 1). Some of genotypes were so divergent in all the characters, hence each single genotype formed a separate cluster. Thus three clusters *viz.*, II and III were solitary with one genotype in each cluster and cluster I was biggest accommodated 18 genotypes. The clustering pattern obtained in present investigation revealed that accessions collected from the same region did not fall in a same cluster, indicating that there was no relationship between genetic divergence and geographical distribution of the accessions. Rahman *et al.* (2014)^[13] and Ravali *et al.* (2017)^[15] 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 Kumar *et al.* (2012)^[5] and Ajjaplavara (2009)^[11].

Average intra and inter cluster D² values are given in (Table 2). The intra cluster D² value was ranged from 0.00 (Cluster III) to 110.60 (Cluster I) and the cluster I had the maximum D² value (110.60) respectively. 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 of the three clusters revealed that highest inter cluster generalized distance (452.85) was between cluster II and cluster III, indicating wide genetic distance between these clusters, while the lowest (201.51) was between cluster I and cluster II, suggesting that the lowest degree of divergence and close genetic makeup of the genotypes included in these clusters. Similar observations were reported by Muniappan *et al.*, (2010)^[11], and Lokesh *et al.*, (2013)^[8]. 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)^[3]. The comparison of cluster means revealed considerable differences among the clusters of different characters (Table 3). Cluster I had highest cluster mean for number of branches per plant (6.17), number of fruit per cluster (1.99), fruit setting % (55.63), number of fruit per plant (35.21), fruit diameter (4.87) and lowest mean for days to 50% flowering (66.50) and days to last harvest (149.08). Cluster II had good mean value for plant spread NS (92.60) and EW (96.70), ascorbic acid (11.46), total phenolic content (646.79), flavonoid content (39.31) and lowest percent of shoot borer infestation (12.21) and days to first flowering (49.50) which is an important selection criteria for earliness. Cluster III had highest mean values for plant height (83.30), days to 50% flowering (73.50), number of flower per cluster (3.60), days to first harvest (74.0), days to last harvest (153), fruiting span (79), fruit length (21.39), fruit pedicel length (5.85), fruit yield per plant (2189.59), fruit yield per plot (61.80) and very less percent of shoot borer infestation (0.78). Similar findings have been also reported by Mehta *et al.*, (2004)^[10], Quamruzzaman *et al.*, (2009)^[12], Islam *et al.*, (2011)^[4] and Kumar *et al.*, (2013)^[4] 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 II and III showed

maximum inter cluster distance and crossing of genotypes DMU-1 and Kashi Taru from cluster II and cluster III suggested for improving plant spread NS and EW, ascorbic acid, total phenolic content, flavonoid content and lowest percent of shoot borer infestation (12.21), days to first flowering (49.50), plant height, days to 50% flowering, number of flower per cluster, days to first harvest, days to last harvest, fruiting span, fruit length, fruit pedicel length, fruit yield per plant, fruit yield per plot and shoot borer infestation. 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 is clustered with the varieties of other geographical region which is due to of selection pressure and genetic drift. This indicates that there is no parallelism between genetic diversity and geographical region except in some cases. It must be noted that in breeding

programmes, geographic diversity alone should not be considered as an index of genetic diversity for selection of parents. Generally crosses involving parents belonging to most divergent clusters are expected to give maximum heterosis and create wide variability in genetic architecture. However, for a practical plant breeder, the objective is not only obtaining high heterosis but also to achieve high level of production with the shortest possible time. In the present study, the maximum distances existed between cluster II and cluster III. Considering group distance and other agronomic performance, the inter-genotypic crosses between the members of cluster II with cluster III would exhibit high heterosis and is also likely to produce new recombinants with desired traits. Therefore, more emphasis should be given on cluster II and III in selecting inbreds for crossing in eggplant hybridization programmes.

Table 1: Cluster classification of brinjal genotypes

Cluster	No. of genotypes	Genotypes
I	18	VR-2, KKM-1, Punjab Sadabahar, Pusa Upkar, Aussey, Utkal keshari, PBNB-9, PBNB-1, PBNB-10, SBJH-691, PBNB-6, PBNB-5, JBH-3, BH-2, JB-262, Utkal Jyoti, BRLVAR-4, JKGEH-6012.
II	1	DMU-1
III	1	Kashi Taru

Table 2: Average intra (bold) and inter-cluster D^2 values for three clusters in brinjal genotypes

Clusters	I	II	III
I	110.60	201.51	284.08
II		0.00	452.85
III			0.00

Table 3: Mean values of clusters for twenty five characters in brinjal genotypes

Cluster	Plant height (cm)	Number of branches per plant	Plant spread (cm) NS EW	Days to 1 st flowering	Days to 50% flowering	Number of flowers per cluster	Number of fruit per cluster	Fruit setting %	No. of fruit per plant	Days to first harvest	Days to last harvest	Fruiting span	Fruit length (cm)
I	75.40	6.17	84.88 87.66	55.28	66.50	3.59	1.99	55.63	35.21	76.83	149.08	72.25	9.83
II	75.70	4.80	92.60 96.70	49.50	71.50	2.60	1.40	53.93	31.20	78.50	152.00	73.50	7.02
III	83.30	5.60	86.50 94.60	50.50	73.50	3.60	1.90	52.67	25.20	74.00	153.00	79.00	21.29

Cluster	Fruit diameter (cm)	Fruit pedicel length (cm)	Average fruit weight (g)	Ascorbic acid (mg/100g)	Total phenolic content (mg/100g)	Flavonoid content (mg/100g)	Fruit yield per plant (g)	Fruit yield per plot (kg)	Fruit yield per hector (qt.)	Shoot borer infestation (%)	Fruit borer infestation (%)	Little leaf of brinjal (%)
I	4.87	5.14	65.72	11.25	437.43	35.44	2083.04	52.64	580.45	1.76	32.69	0
II	4.68	4.55	52.94	11.46	646.79	39.31	1654.90	38.49	427.59	0.89	12.21	0
III	3.87	5.85	86.98	7.64	130.73	35.00	2189.59	61.80	686.67	0.78	36.71	0

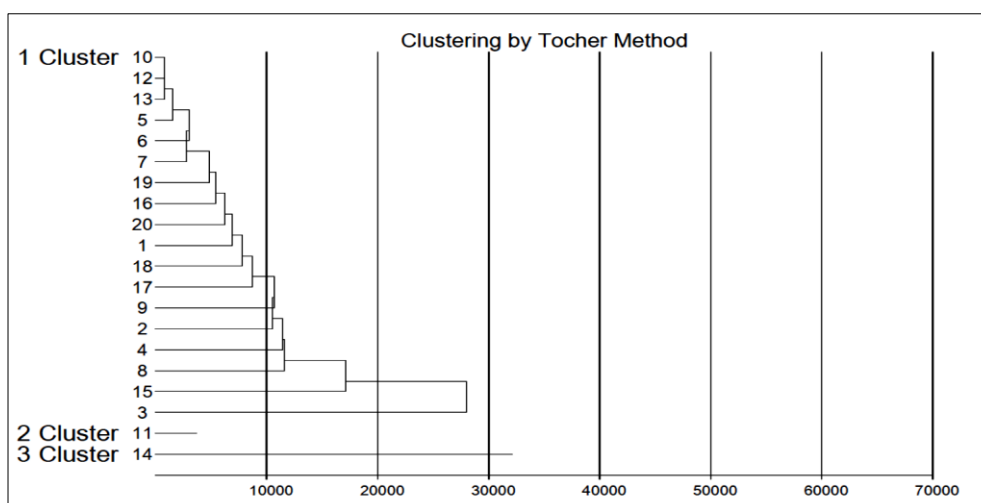


Fig 1: Dendrogram showing clustering pattern in divergence of brinjal genotypes

Acknowledgement

Authors wish to acknowledge ICAR-IIVR, Varanasi, India and VNMKV, Parbhani, India for providing genetic materials and partial financial support to conduct this study.

19. Vidhya C, Kumar N. Genetic divergence in brinjal (*Solanum melongena* L.). *EcSCAN*, Special issue. 2014; 6:197-200.

References

1. Ajjaplavara PS. Genetic diversity in chilli (*Capsicum annuum* L.). *The Asian Journal of Horticulture*. 2009; 4(1):29-31.
2. Anonymous. Indian Horticulture Database, 2017. <http://www.nhb.gov.in>.
3. Arunachalam V. Genetic distance in plant breeding. *Indian J Genet Plant Breed*. 1981; 41:226-236.
4. Islam MA, Ivy NA, Mian MAK, Shahadat MK, Shahjahan M. Genetic diversity in exotic eggplant (*Solanum melongena* L.). *Libyan Agric. Res. Cent. J Int*. 2011; 2(1):15-19.
5. Kumar SR, Arumugam T, Premalakshmi V. Evaluation and variability studies in local types of brinjal for yield and quality (*Solanum melongena* L.). *Electronic Journal of Plant Breeding*. 2012; 3(4):977-982.
6. Kumar R, Anjali K, Singh AK, Maurya S. Screening of bacterial wilt resistant accessions of brinjal for Jharkhand region of India. *The EcSCAN*. 2014; 8(1-2):67-70.
7. Kumar SR, Arumugam T. Variability, heritability and genetic advance for fruit yield, quality and pest and disease incidence in eggplant. *Vegetable Science*. 2013; 40(1):111-113.
8. Lokesh B, Reddy PS, Reddy RVSK, Sivaraj N. Genetic divergence in brinjal (*Solanum melongena* L.). *J Res. ANGRAU*. 2013; 41(1):79-82.
9. Mahalanobis PC. On generalized distance in statistics. *Proceedings of National Institute of Science*. 1936; 2:49-55.
10. Mehta DR, Golani IJ, Pandya HM, Patel RK, Naliyadhara MV. Genetic diversity in brinjal (*Solanum melongena* L.). *Veg. Sci*. 2004; 31(2):142-145.
11. Muniappan S, Saravanan K, Ramya B. Studies on genetic divergence and variability for certain economic characters in eggplant (*Solanum melongena* L.). *Electronic journal of plant breeding*. 2010; 1(4):462-465.
12. Quamruzzaman AKM, Rashid MA, Ahmad S, Moniruzzaman M. Genetic divergence analysis in eggplant (*Solanum melongena* L.). *Bangladesh J Agril. Res*. 2009; 34(4):705-712.
13. Rahman MO, Rabbani MG, Yesmin R, Garvey EJ. Genetic diversity of brinjal (*Solanum melongena* Linn.) through multivariate analysis. *International Journal of Natural and Social Sciences*. 2014; 1:85-93.
14. Rao CR. *Advanced statistical methods in biometrical research*. John Wiley and Sons, inc., New York, 1952, 357-363.
15. Ravali B, Ravinder Reddy K, Saidaiah P, Shivraj N. Genetic Diversity in Brinjal (*Solanum melongena* L.). *Int. J Curr. Microbiol. App. Sci*. 2017; 6(6):48-54.
16. Shinde D, Smita Chavan, Jadhav BD. Study on genetic divergence in sweet sorghum [*Sorghum bicolor* (L.) Moench]. *Bioscan*. 2013; 8(1):135-138.
17. Shinde KG, Birajdar UM, Bhalekar MN, Patil BT. Genetic divergence in brinjal (*Solanum melongena* L.). *Veg. Sci*. 2012; 39(1):103-104.
18. Ullah Smi, Usman Ijaz, Tahir Iqbal Shah, Muhammad Najeebullah. Association and Genetic Assessment in Brinjal. *European Journal of Biotechnology and Bioscience*. 2014; 2(5):41-45.