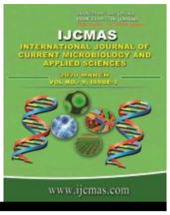
Int.J.Curr.Microbiol.App.Sci (2020) *9*(3): 2768-2773

International Journal of Current Microbiology and Applied Sciences
ISSN: 2319-7706 **Volume 9 Number 3 (2020)**
Journal homepage: http://www.ijcmas.com



Original Research Article https://doi.org/10.20546/ijcmas.2020.903.317

Breeding Potential of Brinjal (*Solanum melongena* L.) Genotypes using D^2 Analysis under Hill Zones of Karnataka, India

Devaraju*, K. M. Indiresh, V. Srinivasa, D. Lakshmana, T. H. Singh, V. Devappa and R. Venugopalan

Department of Vegetable Science, College of Horticulture, Bangalore, University of Horticultural sciences, Bagalkot, Karnataka, India

**Corresponding author*

ABSTRACT

In order to assess genetic divergence among thirty genotypes of brinjal, Mahalanobis D^2 statistics was applied. The analysis of variance revealed significant differences among the genotypes for all the traits. Based on divergence analysis thirty genotypes were grouped into 10 clusters. Cluster II was the largest having nine genotypes followed by cluster III (8) and cluster I (6). Clusters IV, V, VI, VII, VIII, IX and X are solitary with one genotype each. Among the ten clusters, cluster III with eight genotypes showed maximum intracluster distance followed by cluster II and cluster I. Based on inter-cluster distances, maximum divergence was observed between cluster VII and VIII followed by cluster II and cluster VIII indicating that the genotypes in these clusters could be utilized as parents in hybridization programme to develop high heterotic hybrids and to identify superior transgressive segregants in segregating population. The maximum cluster mean was observed in cluster IV followed by cluster II for fruit yield/plant and fruit yield (t/ha). These clusters could be useful sources of genes for improvement of yield component traits. Fruit diameter(49.43) contributed towards genetic divergence followed by fruits per plant (11.72%).

Keywords

Diversity,
Clustering pattern,
Cluster mean,
Transgressive

Article Info

Accepted:
22 February 2020
Available Online:
10 March 2020

Introduction

Brinjal (*Solanum melongena L.*) is an important vegetable crop, belongs to the family Solanaceae, having a chromosome number of 2n=24. It is originated in Indo-Burma region (Vavilov, 1928), Bangladesh and Myanmar region is believed to be the center of diversity (Isshiki *et al.*, 1994). According to Zeven and Zhukovsky (1975) brinjal is said to be originated in India and spread to China, which became a secondary center of origin. Brinjal fruit (unripe) is essentially consumed as cooked vegetable in various forms and the dried shoots are used as fuel in rural areas. The recent nutritional and medicinal findings proved that eggplant is highly nutritious and possesses excellent medicinal properties and excellent remedy excellent remedy for those who are suffering from diabetic and liver complaints (Shukla and Naik, 1993).

Recombination of different desirable traits spread over in diverse genotypes is essential for the improvement of yield and its related traits in any crop. The effectiveness of the technique like Mahalanobis D^2 statistics is to analyze the genetic diversity of the population and has been proved useful. Hence, the information on genetic variability and diversity present in a crop is essential to have a sound breeding program (Prabhu *et al.*, 2009). Selecting genetically diverse parents will enable the expansion of genetic base and development of superior plant types. In this regard, Mahalanobis (1936) generalized distance (D^2 technique) has been extensively used to measure the genetic divergence of the germplasm. Intercrossing between highly divergent parents is expected to generate a broad spectrum of variability and selection can be adopted in the segregating generations. The present study was planned to generate information on genetic diversity present in thirty diverse genotypes of brinjal under the hill zone of Karnataka so as to help the breeder in selecting promising and genetically diverse parents for bringing the desired improvement.

Materials and Methods

The experimental materials comprised of thirty indigenous genotypes of brinjal collected from different parts of India and were evaluated at Department of Vegetable Science, College of Horticulture, Mudigere, Karnataka, India. The thirty genotypes were tested in a Randomized Complete Block Design (RCBD) with two replications during *Rabi* 2016. Each treatment (genotypes) in each replication was represented by a plot size of 3.0 ×2.0 m with the spacing of 75 cm between rows and 60 cm between plants within the rows. Five weeks old seedlings were transplanted to the main field from the nursery, and planting was done by adopting ridges and furrow method. Standard agronomic practices were followed in time (Chattopadhyay *et al.*, 2007). Five plants were chosen at random from each plot for recording observations on branches/plant, days to first flowering, days to 50% flowering, flowers per cluster, fruits per cluster, per cent fruit set, fruits per plant, fruit length (cm), fruit diameter (mm), Fruit yield per plant (kg) Fruit yield (t/ha). The D^2statistic (Mahalanobis, 1936) was used to assess genetic divergence for various quantitative traits. Grouping of populations was done using Tocher’s method as described by Rao (1952).

Results and Discussion

The analysis of variance revealed highly significant differences among the different genotypes for all the traits studied indicating the existence of wide genetic divergence among the genotypes. By following Tocher’s method, thirty genotypes were grouped into ten clusters using estimated D^2 values like square of the generalized distance. The distribution of genotypes into various clusters is given in (Table 1). The grouping pattern of genotypes was random, indicating geographical diversity, and genetic divergence, unrelated (Mohanty and Prusti, 2001). Cluster II was the largest having nine genotypes followed by cluster III (8) and cluster I (6). Clusters IV, V, VI, VII, VIII, IX and X are solitary with one genotype each indicated genotypes from these clusters might have originated across the geographical location in breeding programs.

Among the ten clusters, cluster III with eight genotypes showed maximum intracluster distance of 512.53 followed by cluster II

(477.61) and cluster I (353.28) (Table 2). The clusters IV, V, VI, VII, VIII, IX and X had no intra-cluster distance as they possessed single genotype in each cluster. The maximum intra-cluster distance showed by cluster III indicated that genotypes included in this cluster are very diverse due to both natural and artificial selection forces operates among the genotypes

Based on distances between clusters (*i.e.* inter-cluster distances), maximum divergence was observed between cluster VII and VIII (5348.02) followed by cluster II and cluster VIII (4660.48), cluster VI and VIII (4269.95), cluster VII and cluster IX (4234.23), cluster V and VII (3917.72) and cluster II and IX (3756.32). Maximum inter-cluster D^2 values occurred between clusters VII and VIII indicating genotypes in these clusters can be used as parents in hybridization to identify desirable recombinants either in F_1 or subsequent generations Rathi *et al.*, (2011). The least inter-cluster value was recorded between cluster VI and VII (306.15) followed by cluster V and VIII (320.09) indicating a close relationship among genotypes.

Cluster means of genotypes (Table 3) indicated mean values of clusters varied in magnitude for all characters. The maximum cluster mean was in cluster IV followed by cluster II for fruit yield/plant andfruit yield (t/ha).

Table.1 Grouping of thirty brinjal genotypes into different cluster by Tocher's method

Clusters	Total number of genotypes in each cluster	Genotypes included in the cluster
I	6	Poluru vange, Madurai-3, Mritunjaya, Udupi Mattigulla, Kaateri Vange, Pusa Bindu,
II	9	Bethapudi Local, Arka Keshav, Arka Kusumakar, Kashi Prakash, Rampura Local WF, Uthkal Anushree, Swetha SarparamVanga, Bhagyamathi
III	8	Harita, Hiriyur Local, Kashi Taru, Punjab Sadabahar, Pusa Shymala, Surya, Raydurga Badane, Uthkal Kesari,
IV	1	Rampura Local PF
V	1	Dommeru Vanga
VI	1	Pusa Kranthi
VII	1	Pusa Purple Long
VIII	1	CARI- I
IX	1	Pusa Utham
X	1	Arka Neelkanth

Table.2 Average intra (bold) and inter cluster D^2 distance for ten different characters in thirty genotypes of brinjal

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X
Cluster I	**353.28**	2147.96	912.021	1204.92	663.12	2090.15	2693.26	1013.45	560.94	830.89
Cluster II		**477.61**	1141.65	817.91	3087.27	1371.16	1165.93	**4660.48**	3756.32	1334.14
Cluster III			**512.53**	1005.15	1499.28	717.85	1110.36	2489.64	1904.60	752.36
Cluster IV				**0.00**	2214.45	1800.27	1658.34	3262.45	1898.63	448.67
Cluster V					**0.00**	2900.69	3917.72	320.09	935.35	1658.82
Cluster VI						**0.00**	306.15	**4269.95**	3527.14	1347.98
Cluster VII							**0.00**	**5348.02**	4234.23	1602.84
Cluster VIII								**0.00**	737.75	2360.05
Cluster IX									**0.00**	1024.65
Cluster X										**0.00**

Table.3 Cluster mean values of ten characters in thirty brinjal genotypes

Character	**Clusters**									
	I	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**	**IX**	**X**
Branches per plant	7.55	8.74	8.29	9.10	9.00	7.64	7.00	7.40	5.70	8.10
Days to first flowering	69.67	56.56	57.38	61.50	70.50	42.50	37.00	68.00	70.00	48.50
Days to fifty per cent flowering	74.25	63.50	64.8	68.50	78.50	52.50	48.00	75.50	78.50	57.50
Flowers per cluster	2.29	4.35	3.09	5.45	1.00	2.75	3.38	1.00	3.55	5.19
Fruits per cluster	1.82	3.25	1.74	2.40	1.00	1.00	1.68	1.00	1.00	1.76
Per cent fruit set	54.87	76.94	55.72	44.02	100.00	36.38	48.64	100	28.18	33.95
Fruits per plant	14.04	26.95	18.26	16.60	18.40	19.80	11.60	12.20	7.50	19.55
Fruit length (cm)	7.30	12.61	10.50	14.78	9.95	15.00	20.55	8.73	10.34	7.73
Fruit diameter (mm)	56.73	34.11	44.45	33.17	63.73	39.15	40.40	84.50	62.96	43.69
Fruit yield per plant (kg)	1.17	1.43	1.30	1.45	1.29	1.30	1.06	1.26	1.24	1.34
Fruit yield (t/ha)	26.04	31.90	28.82	32.23	28.67	28.78	23.56	28.00	27.56	29.67

Table.4 *Per cent* contribution of various characters towards total divergence in brinjal genotypes

Sl. No.	Characters	Per cent contribution	Number of times ranked first
1	Branches per plant	4.83	21
2	Days to first flowering	0	0
3	Days to fifty per cent flowering	0	0
4	Flowers per cluster	8.05	35
5	Fruits per cluster	9.89	43
6	Per cent fruit set	4.37	19
7	Fruits per plant	11.72	51
8	Fruit length (cm)	7.13	31
9	Fruit diameter (mm)	49.43	215
10	Fruit yield per plant (kg)	4.6	20
11	Fruit yield (t/ha)	0	0

These clusters could be useful sources of genes for yield component traits. The lowest cluster mean was in cluster VII followed by cluster VI for the traits days to first flowering and days to 50% flowering. Early flowering could be helpful for breeding an early plant type. A high yielding, early flowering, type could be bred through utilizing the genotypes from cluster VI and VII as parents (Kumar *et al.*, 2013 and Ravali *et al.*, 2017).

These clusters have been formed based on the contribution of different characters towards divergence (Table 4). Among the characters, fruit diameter (49.43 %), contributed maximum to the total genetic diversity followed by fruit diameter (11.72 %), fruits per cluster (9.89%), flowers per cluster (8.05%), fruit length (7.13), days to first flowering (4.83%), fruit yield per plant (4.60) and per cent fruit set (4.37 %). No contribution towards total genetic divergence from days to fifty per cent flowering, branches per plant and fruit yield per hectare. Thus the three characters *viz.*, fruit diameter, fruits per clusterand flowers per cluster are the major traits contributing towards genetic divergence and hence selection for divergent parents based on these traits will be useful for exploitation of hybrid vigour in brinjal.

Emphasis should be given on number of fruit/plant, fruit weight, and yield/plant for selecting high yielding genotypes in brinjal. Based on genetic diversity, and average performance for fruit yield and other traits, genotypes Swetha, followed by Surya, Pusa Shymala, Uthkal Anushree and Uthkal Kesari are good donors for utilization in breeding. Crossing between these genotypes could produce desirable recombinants either in F_1 or segregating generations.

References

Chattopadhyay, A., Dutta, S., Bhattacharya, I., Karmakar, K., and Hazra, P. 2007. Dolichos bean, In: Technology for Vegetable Crop Production, Published by All India Coordinated Research Project on Vegetable Crops. BCKV, Nadia, West Bengal, India, pp. 218-230.

Isshiki, S., Okubo, H. and Fujieda, K., 1994, Genetic control of isozymes in eggplant and its wild species. *Euphytica*80**:** 145-150.

Kumar, Ramesh S., Arumugam, T., and Ananda kumar, C.R. 2013. Genetic diversity in eggplant (*Solanum melongena*L.). *Plant Gene and Trait*. 4(2): 4-8.

Mahalanobis, P.C., 1936, On the generalized distance in statistics. *Proc. Natl. Acad. Sci.*, 2: 55-79.

Prabhu, M., Natarajan, S. and Pugalendhi, L., 2009, Variability and heritability studies in F_5 and F_6 progenies of brinjal. *Am-Eur. J. Sustain. Agric.*, 3(3): 306-309.

Rao, C.R. 1952. Advanced statistical methods in biometrical research. Jhon Wiley and Sons Inc. NewYork, pp. 236-272.

Rathi, S., Kumar, R., Munshi, A.D., and Verma, M. 2011. Breeding potential of brinjal genotypes using D2 analysis. *Indian J. Hort.* 68(3): 328-331.

Ravali, B., Reddy, K. R., Saidaiah, P., and Shivraj, N. 2017. Genetic diversity in brinjal (*Solanum melongena*L.). *Int.J.Curr.Microbiol.App.Sci*. 6(6): 48-54. Vavilov, N.I. 1928. Proceedings 5th International Congress of Genetics, New York. pp. 42-369.

Shukla, V. and Naik, L.B., 1993, Agro-techniques of solanaceous vegetables, in 'Advances in Horticulture', Vol. 5, Vegetable Crops, Part 1 (Ed. Chadha, K. L. and Kalloo, G.), Malhotra Publishers, House, New Delhi, pp. 365.

Vavilov, N.I. 1928. Proceedings 5th International Congress of Genetics, New York. pp. 42-369

Zeven A.C., and Zhukovsky P.M. 1975. Dictionary of cultivated plants and their centre of diversity. Wageningen, Netherlands. P. 219.

How to cite this article:

Devaraju, K. M. Indiresh, V. Srinivasa, D. Lakshmana, T. H. Singh, V. Devappa and Venugopalan. R. 2020. Breeding Potential of Brinjal (*Solanum melongena* L.) Genotypes using D^2 Analysis under Hill Zones of Karnataka, India. *Int.J.Curr.Microbiol.App.Sci.* 9(03): 2768-2773. doi: https://doi.org/10.20546/ijcmas.2020.903.317