

Original Research Article

<https://doi.org/10.20546/ijcmas.2018.706.196>

Genetic Divergence Studies in Brinjal (*Solanum melongena* L.) under Subtropical Plains of North-Western Himalayan Region

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ABSTRACT

Twenty five diverse genotypes of brinjal (Ten hybrids and fifteen open pollinated varieties) were evaluated for 20 different quantitative, qualitative and biotic stress traits in the experimental field of Division of Vegetable Science & Floriculture, FOA, Chatha, SKUAST, Jammu during 2013-14 and 2014-15. The genotypes were grouped into six diverse clusters on the basis of D² statistics. The clustering pattern suggested no association between genetic diversity and geographical diversity. Cluster VI accommodated maximum number of genotypes (7), followed by cluster III (5), cluster IV (4) and cluster V (4). Cluster III had maximum intra cluster distance (12.636), followed by cluster II (7.303) and cluster I (6.044), suggesting considerable genetic divergence among the genotypes of the respective clusters and the genotypes from within the clusters can be chosen as parents for any hybridization programme. The inter-cluster distance depicts greater divergence among the clusters and maximum inter-cluster was recorded between cluster IV and cluster VI (53.430) followed by cluster III and cluster IV (51.078) and cluster I and cluster III (36.610), suggesting greater diversity between genotypes belonging to respective pairs of clusters. For cluster mean values, the genotypes in cluster IV were having highest values for days to 50 % flowering (55.39), days to first picking (77.14), number of fruits per plant (46.87), number of leaves per plant (56.98), number of primary branches (6.22), marketable yield per plant (1.70), fruit yield per plant (1.92), fruit yield per hectare (202.95), ascorbic acid content (13.55), total phenol content (1.25) and least mean values for shoot borer infestation (8.73), fruit borer infestation (8.06), spider mite infestation (4.51), little leaf incidence (2.60) and phomopsis blight (8.86). Cluster III registered highest mean value for average fruit weight (141.78) and fruit diameter (7.71), cluster VI registered highest mean values for fruit length (18.62) and plant height (90.69), whereas cluster II had least mean value for unmarketable yield per plant (0.11). Five traits namely fruit weight (44.67), ascorbic acid content (37.00), number of leaves per plant (6.33 %), fruit diameter (6.00 %) and fruit length (3.00 %), contributed 97 % towards total genetic diversity.

Keywords

Brinjal, D² clustering, genetic diversity, *Solanum melongena*, intra and inter-cluster distance

Article Info

Accepted:
18 May 2018
Available Online:
10 June 2018

Introduction

Brinjal (*Solanum melongena* L.), belonging to the angiospermic family 'Solanaceae', is an often cross-pollinated crop with cross-pollination reported as high as 48% (Madhavi, 2015). A great diversity in forms, shapes and colours of brinjal are found throughout Indian subcontinent, suggesting that this area is an important centre of variation and possibly of origin (Vavilov, 1951). It is one of the most popular and versatile vegetable crop adapted to different agro-climatic regions of India and can be grown throughout the year right from sea level to snowline. India is the second largest producer of brinjal in the world next to China and produces 13557.8 '000 MT from an area of 711.3 '000 ha (NHB, 2014). Brinjal crop is under constant assault by biotic agents including various pathogens and insect herbivores, with enormous economic and ecological impact and the most extensive damage to brinjal fruit yield is caused by fruit & shoot borer and diseases like phomopsis blight and little leaf which reduces the yield and inflicts colossal loss in production. There is an utmost need for development of high yielding varieties and hybrids for specific environments (Vaddoria *et al.*, 2009).

Selection of parents identified on the basis of divergence analysis would be more promising for a hybridization programme (Ahmad *et al.*, 2014). It was observed that more diverse the parents, greater is the chances of obtaining high heterotic F_1 's and broad spectrum of variability in the segregating generation (Arunachalam, 1981). Genetic divergence plays a pivotal role in assessment of diversity and establishing relationships among cultivated species and thus facilitates the establishment of conservation strategies, the use of genetic resources in breeding programmes, and the study of crop evolution (Mishra *et al.*, 2013). Therefore, brinjal having a greater variation with regard to fruit yield

and its component traits, genetic divergence based on Mabalnobis D^2 technique as described by Rao (1952) appears to be a fruitful approach which is based on multivariate analysis and serves to be a good index of genetic diversity. Existence of large variability among the genotypes necessitates further analysis of genetic divergence (Mehta *et al.*, 2004).

Materials and Methods

The experimental field of Division of Vegetable Science and Floriculture, SKUAST, Jammu is situated at 32° 40'N latitude and 74° 58' E longitude and has an elevation of 332 m above mean sea level. Agro-climatically, the location represents Zone V of Jammu and Kashmir and is characterized by subtropical climate. The place experiences hot dry summer, hot and humid rainy season and cold winter months, the maximum temperature goes up to 45° C during summer (May to June) and minimum temperature falls to 1° C during winters. The mean annual rainfall is about 1000-1200 mm.

The experimental material comprised of 25 diverse brinjal genotypes including 10 F_1 hybrids namely, Rajni, PPL-74, Nav Kiran Improved, Sandhya, MH-80, Chhaya, PBH-3, Nisha Improved, Shamli, and Abhishek, and fifteen open pollinated varieties namely Punjab Sadabahar, Arka Shirish, Arka Kusumkar, Arka Keshav, Arka Nidhi, Arka Neelkanth, Pusa Shyamala, Pusa Kranti, Pusa Ankur, Pusa Uttam, Pusa Purple Long, Pusa Purple Round, Pusa Purple Cluster, BR-14 and Puneri Kateri collected from different parts of the country. The experimental material was tested under six environments comprising of three sowing seasons spreading across two years during 2013-2014 and 2014-2015 *i. e.*, E_1 -autumn-winter, 2013; E_2 - spring-summer, 2014; E_3 -rainy, 2014; E_4 - autumn-winter, 2014; E_5 - spring-summer, 2015 and E_6 -rainy,

2015. The individual experiment was conducted in Randomized Block Design with three replications. The uniform, healthy seedlings were transplanted on ridges maintaining inter and intra row spacing of 90 cm x 60 cm, respectively. All the recommended package of practices for raising a healthy crop were followed. Observations were recorded on five randomly selected plants of each genotype in each replication for various traits. The data thus obtained was analyzed as per method given by Mahalanobis, 1936. Criteria Toucher (Rao, 1952) was used for determining the groups and clustering was done accordingly. Average inter and intra cluster distances were estimated as per method given by Singh and Chaudhary, 1985.

Results and Discussion

Twenty five diverse genotypes (15 open pollinated varieties and 10 hybrids) were grouped into six clusters on the basis of D^2 values, suggesting adequate genetic diversity for selecting superior and diverse parents which can be suitable exploited for any brinjal improvement programme. The perusal of data (Table 1) depicted that cluster VI had maximum number of genotypes (7) namely Arka Shirish, Arka Kusumkar, Pusa Shyamla, Pusa Purple Long, Pusa Purple Cluster, Puneri Kateri and Arka Neelkanth, followed by cluster III (5 genotypes) namely Rajni, Sandhya, PBH-3, Pusa Kranti and Pusa Ankur, cluster IV (4 genotypes) and cluster V (4 genotypes).

No association between genetic diversity and geographical diversity was indicated by the clustering pattern. The results are in accordance with the earlier work of Madhavi *et al.*, 2015; Ahmed *et al.*, 2014; Kumar *et al.*, 2013; Mishra *et al.*, 2013; Rathi *et al.*, 2011 and Mehta and Sahu, 2009 in brinjal. The genotypes that originated in one region had

been distributed into different clusters, indicating that genotypes with same geographic origin could have undergone change for different characters under selection. This could be due to selection pressure, genetic drift and introduction, which help in creating more diversity rather than genetic distance.

The intra and inter cluster values (Table 2) depicted that cluster III had maximum intra cluster distance *i. e.*, 12.636, followed by cluster II (7.303) and cluster I (6.044), suggesting considerable genetic divergence among the genotypes of the respective clusters and the genotypes from within the clusters can be chosen as parents for any hybridization programme. The relative distance of each cluster from the other cluster *i. e.*, inter-cluster distance depicts greater divergence among the clusters. In the present study maximum inter-cluster distance (Table 2) was recorded between cluster IV and cluster VI (53.430) followed by cluster III and cluster IV (51.078) and cluster I and cluster III (36.610), suggesting greater diversity between genotypes belonging to respective pairs of clusters. The genotypes between the respective farthest clusters can be exploited for hybridization programme.

The cluster means of genotypes revealed considerable genetic difference between the groups (Table 3). The genotypes in cluster IV were having highest mean values for days to 50 % flowering (55.39), days to first picking (77.14), number of fruits per plant (46.87), number of leaves per plant (56.98), number of primary branches (6.22), marketable yield per plant (1.70), fruit yield per plant (1.92), fruit yield per hectare (202.95), ascorbic acid content (13.55), total phenol content (1.25) and least mean values for shoot borer infestation (8.73), fruit borer infestation (8.06), spider mite infestation (4.51), little leaf incidence (2.60) and phomopsis blight (8.86).

Table.1 Clustering pattern of 25 genotypes of brinjal based on D² statistics

Cluster	Number of genotypes	Genotypes	Source
I	3	Pusa Uttam PPR BR-14	IARI, New Delhi IARI, New Delhi IIVR, Varanasi
II	2	PPL-74 Shamli	Century Seeds Seminis Seeds
III	5	Rajni Sandhya PBH-3 Pusa Kranti Pusa Anku	Nunhems Seeds Nunhems Seeds PAU, Ludhiana IARI, New Delhi IARI, New Delhi
IV	4	Nisha Improved Punjab Sadabahar ArkaKeshav ArkaNidhi	Century Seeds PAU, Ludhiana IIHR, Bangaluru IIHR, Bangaluru
V	4	Navkiran Improved MH-80 Chhaya Abhishek	Sungrow Seeds Mahycco Seeds Nunhems Seeds Nunhems Seeds
VI	7	ArkaShirish ArkaKusumkar Pusa Shyamla PPL PPC PuneriKateri ArkaNeelkanth	IIHR, Bangaluru IIHR, Bangaluru IARI, New Delhi IARI, New Delhi IARI, New Delhi Safal Seeds Co., Jalna IIHR, Bangaluru

Table.2 Average intra (bold) and inter cluster distance values among clusters in brinjal (*Solanum melongena* L.)

Cluster	I	II	III	IV	V	VI
I	6.044					
II	18.999	7.303				
III	36.610	33.909	12.636			
IV	14.763	31.874	51.078	3.108		
V	10.841	16.379	16.791	22.257	0.000	
VI	33.710	24.187	26.203	53.430	29.462	0.000

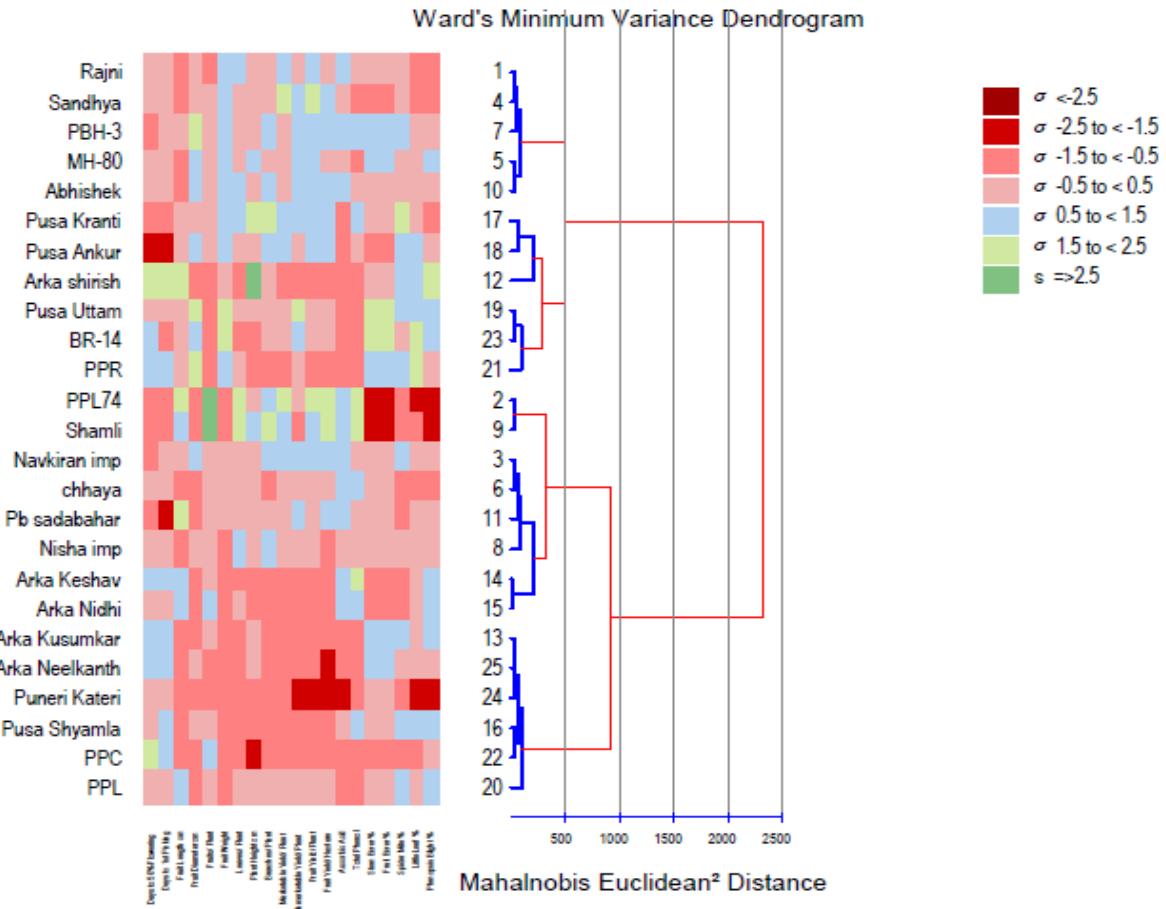
Table.3 Cluster means for various quantitative, qualitative and biotic stress traits in 25 genotypes of brinjal (*Solanum melongena* L.)

S No.	Traits	Cluster Means					
		I	II	III	IV	V	VI
1.	Days to 50% flowering	60.94	65.31	59.67	55.39	55.78	72.72
2.	Days to first picking	85.31	90.50	83.45	77.14	85.22	99.44
3.	Fruit length (cm)	12.67	7.18	9.01	14.39	8.98	18.62
4.	Fruit diameter (cm)	2.43	3.39	7.71	2.55	7.14	2.99
5.	Number of fruits/plant	16.38	11.58	10.41	46.87	15.79	6.78
6.	Average fruit weight (g)	55.67	40.80	141.78	40.46	90.61	104.67
7.	Number of leaves per plant	34.79	33.80	38.47	56.98	33.86	29.62
8.	Plant height (cm)	67.37	68.56	73.40	77.87	73.84	90.69
9.	Number of primary branches per plant	4.54	4.72	5.34	6.22	5.71	4.91
10.	Marketable yield per plant (kg)	0.74	0.39	1.13	1.70	1.16	0.57
11.	Unmarketable yield per plant (kg)	0.17	0.11	0.31	0.18	0.30	0.15
12.	Fruit yield per plant (kg)	0.91	0.47	1.45	1.92	1.46	0.74
13.	Fruit yield (Q/ha)	94.55	46.36	135.28	202.95	136.89	77.07
14.	Ascorbic acid content (mg/100g)	13.26	9.52	10.35	13.55	12.70	7.90
15.	Total phenol content (mg/100g)	1.14	0.85	0.90	1.25	0.87	0.74
16.	Shoot borer infestation (%)	15.53	17.82	20.02	8.73	18.41	16.58
17.	Fruit borer infestation (%)	14.79	17.27	19.07	8.06	17.60	16.07
18.	Spider mite infestation (%)	5.38	10.37	13.40	4.51	14.58	14.93
19.	Little leaf incidence (%)	5.47	6.30	8.02	2.60	6.94	10.07
20.	Phomopsis blight incidence (%)	18.45	17.71	17.13	8.86	17.17	23.85

Table.4 Per cent contribution of various traits to total divergence in brinjal (*Solanum melongena* L.)

S. No.	Trait	% contribution
1	Days to 50% Flowering	0.00
2	Days to 1st Picking	0.67
3	Fruit Length (cm)	3.00
4	Fruit Diameter (cm)	6.00
5	No. of Fruits/ Plant	0.67
6	Fruit Weight (kg)	44.67
7	No. of Leaves/ Plant	6.33
8	Plant Height (cm)	0.00
9	No. of Branches/ Plant	0.00
10	Marketable Yield/ Plant (kg)	0.67
11	Unmarketable Yield/ Plant (kg)	0.00
12	Fruit Yield/ Plant (kg)	0.00
13	Fruit Yield/ Hectare (q)	0.00
14	Ascorbic Acid (mg/100g)	37.00
15	Total Phenol (mg/100g)	0.67
16	Shoot Borer infestation (%)	0.00
17	Fruit Borer infestation (%)	0.00
18	Spider Mite infestation (%)	0.00
19	Little Leaf incidence (%)	0.00
20	Phomopsis Blight incidence (%)	0.33

Fig.1 Ward's Minimum Variance Dendrogram



Cluster III registered highest mean value for average fruit weight (141.78) and fruit diameter (7.71), cluster VI registered highest mean values for fruit length (18.62) and plant height (90.69), whereas cluster II had least mean value for unmarketable yield per plant (0.11). From the present investigation it can be concluded that intercrossing of genotypes from these diverse clusters may result in wide array of variability for having effective selection for these characters.

These results are in consonance with the findings of the earlier work of Madhavi *et al.*, 2015; Ahmed *et al.*, 2014; Kumar *et al.*, 2013; Mishra *et al.*, 2013; Rathi *et al.*, 2011 and Mehta and Sahu, 2009 in brinjal. Inter crossing of divergent groups would lead to

greater opportunity for crossing over, which may release hidden variability by breaking linkage (Thoday, 1969). Hence these genotypes can be used in singly as well as multiple crossing programmes for the development of promising hybrids.

Per cent (%) contribution of various traits towards total genetic diversity (Table 4) revealed that maximum contribution was of fruit weight (44.67), followed by ascorbic acid content (37.00), number of leaves per plant (6.33 %), fruit diameter (6.00 %) and fruit length (3.00 %), contributing 97 % of the total genetic diversity. The observations were in conformity with the results obtained by Madhavi *et al.*, 2015 and Kumar *et al.*, 2013 in brinjal.

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How to cite this article:

Anil Bhushan, R. K. Samnotra and Sanjeev Kumar. 2018. Genetic Divergence Studies in Brinjal (*Solanum melongena* L.) under Subtropical Plains of North-Western Himalayan Region. *Int.J.Curr.Microbiol.App.Sci*. 7(06): 1647-1653.
doi: <https://doi.org/10.20546/ijcmas.2018.706.196>