Vegetable Science (2018) 45(2) : 277-280

Short Communication

Genetic divergence studies in green fruited brinjal (*Solanum melongena* L.)

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Received: June 2018 / Accepted: January 2019

Brinjal (*Solanum melongena* L.) is widely cultivated as one of the most important vegetables in both subtropical and tropical regions of India. It is a popular vegetable in India, China, Turkey, Japan, Syria, Egypt, Indonesia, Philippines, Thailand, France, Italy and USA. It is an important source of fibre (1.3 g/100g), protein (1.4 g/100g), vitamin-A (124 I.U) and potassium (200 mg/100g) and it is recommended even for patients with diabetes, asthma, cholera and bronchitis. Being primary centre of origin, India has accumulated wide range of variability in this crop. In spite of large number of varieties available in India, only few are promising. This fact draws the attention of plant breeder for its improvement. Any plant breeding programme needs clear understanding of existing genetic divergence in the available population. Genetic diversity plays a very important role for selecting the suitable parents for hybridization programme resulting in superior hybrids and desirable recombinants.The information on genetic divergence of various traits particularly of those that contribute to yield, quality and pest resistance would be of most useful in planning the breeding programme. Brinjal is grown almost in all the districts of Tamil Nadu and extensively in Dindigul, Theni and Madurai districts. In these districts consumers prefer only green coloured fruits than other coloured fruits. To meet the consumers' preference of these districts, it is necessary to develop green fruited variety or hybrids. As a first step of the breeding programme, collection and evaluation of genotype is important to know the yield potential, quality and shoot and fruit borer resistance characters of the selected genotypes. The selected genotypes can be released as a variety otherwise used for further breeding programmes. D^2 statistics developed by Mahalanobis (1936) provides a measure of magnitude for divergence between two genotypes under comparison. It considers the variation produced by any character and their consequent effect on other characters.Considering the above point of view, present investigation was undertaken to work out genetic divergence among green fruited genotypes based on twenty two important traits of brinjal, to help the breeders in selecting promising and genetically diverse parents for crop improvement.

The present investigation was carried out at the Department of Vegetable Crops, Faculty of Horticulture, Tamil Nadu Agricultural University, Coimbatore during 2016 which is situated at 11° N latitude and 77° E longitude and at an elevation of 426.6 m above MSL.The experimental materials for the present study consisted of 30 genotypes of green fruited brinjal. Out of 30 genotypes, twelve (IC 261786, IC 354546, IC 111033, IC 090907, EC 316201, EC 315014, IC 249344, IC 354721, IC 383345, IC 454561, IC 310889 and IC 111013) from NBPGR, New Delhi; one (ABSR -2) from IIVR Varanasi; fifteen local types (Notchidaipatti, Namakkal, Karur, Patteswaram, Mathukadipattu, Sathirampatti, Kumbakonam, Kurumbapatti, Devachinnampatti, Swamimalai, Ottanchathiram, Andipatti, Thirchy, Mettupalayam and Musuri) and two (Arka Kusumakar and Arka Shirish) from IIHR, Bangalore were collected and evaluated in a randomized block design with two replications for two seasons. Forty five days old seedlings were transplanted on the ridges adopting a spacing of 60 x 60 cm. Cultural practices were followed as per the package of practices recommended for Tamil Nadu.Twenty five plants were maintained for each hybrid in each replication. The average values were computed as treatment mean under each replication for 22 traits *viz.,* plant height (cm), number of branches per plant, days to first flowering, days to 50 per cent flowering, days to first harvest,

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pedicel length (cm), calyx length (cm), fruit length (cm), fruit girth (cm), single fruit weight (g), number of fruits/ plant, fruit yield per plant (kg), shoot infestation (%), fruit infestation on number basis (%), fruit infestation on weight basis (%), marketable yield per plant (kg), protein content (mg 100g^{-1}), ascorbic acid (mg 100g^{-1}), total phenol (mg g^{-1}), total sugars (mg g^{-1}) (FW), polyphenol oxidase (changes in OD min^{-1} g^{-1}of sample) and solasodine (%). The genetic divergence was estimated using Mahalanobis' D^2 statistics and genotypes were grouped in clusters according to Tocher's method as described by Rao (1952). The inter- and intra-cluster distances were worked out as per method suggested by Murthy and Arunachalam (1967).

The D^2 statistics has been found as a powerful tool to estimate genetic divergence among populations. Similarly, the diversity of parental material is the basic requirement of any breeding programme. More diverse the parents within a reasonable range, better are the chances of improving economic characters under consideration, in the resulting off springs. The nature and magnitude of genetic distance among the genotypes also serve as an indication for hybridization to exploit maximum heterosis. In the present investigation, based on D^2 analysis thirty genotypes were classified into seven clusters (Table 1). Out of these seven clusters, cluster I had large population of fifteen genotypes followed by cluster II and IV with five genotypes each and cluster VI with two and in remaining clusters *viz.,* cluster III, V and VII had one genotype each.The clustering pattern of genotypes was observed to be random indicating that geographical diversity and genetic divergence were unrelated. Further, it was observed that genotypes belonging to the same origin not only appeared in the same cluster but many of them also distributed in different clusters, which may be due to preferential selection of ideotypes suitable for various vegetable purposes. These findings clearly demonstrated that there was no parallelism between the geographic origin and genetic diversity in brinjal. Therefore, the selection of genotypes for hybridization should be based on genetic divergence rather than geographical diversity. The present results are in accordance with the findings of Shinde et al. (2012) and Krishnapatel et al. (2014).

The absence of relationship between genetic diversity and geographical distance indicates that forces other than geographical origin, such as exchange of genetic stocks, genetic drift, spontaneous variation, natural and artificial selection are responsible for genetic diversity. It may also be possible that causes for clustering pattern were much influenced by environment and genotype x environment interaction resulting in differential gene expression. Another possibility may be that estimates might not have been sufficient to account for the variability caused by some other traits of physiological or biochemical nature which might have been important in depicting the total genetic diversity in the population.The intra- and inter-cluster D^2 values among 30 genotypes presented in Table 2 revealed that cluster VI having lowest intra-cluster D^{2}value (142.37), whereas, highest intra-cluster D^2 value (215.06) was recorded by cluster IV indicated that genotypes included in this cluster are very diverse and due to natural and artificial selection forces among the genotypes.

Table 1: Clustering pattern of thirty genotypes of brinjal based on D^2 analysis

Clusters	Number of genotypes	Name of the genotypes
I	15	Karur Local, Andipatti Local, IC 383345, Kurumbapatti Local, EC 316201, Namakkal Local, Notchidaipatti Local, Ottanchathiram Local, IC 090907, Musuri Local, IC 454561, Arka Shirish, IC 354721, IC 111013 and IC 310889
II	5	Patteswaram Local, IC 111033, IC 261786, Kumbakonam Local, Swamimalai Local
III	1	Arka Kusumakar
IV	5	Trichy Local, IC 249344, EC 315014, IC 354546 and Mettupalayam Local
V	1	Mathukadipattu Local
VI	2	ABSR-2 and Devachinnampatti Local
VII	1	Sathirampatti Local

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

Clusters	I	II	III	IV	V	VI	VII
I	179.53	253.73	214.82	274.54	213.12	235.96	242.89
II		186.78	334.32	290.82	273.13	341.73	229.05
III			0.00	237.01	324.25	285.86	275.75
IV				215.06	371.23	381.41	296.33
V					0.00	204.27	293.04
VI						142.37	340.61
VII							0.00

Table 3: Cluster mean for yield and quality traits of thirty brinjal genotypes

Cluster	Plant height (cm)	Number of branches per plant	Days to first flowering	Days to 50% flowering	Days to first harvest	Pedicel length (cm)	Calyx length (cm)	Fruit length (cm)	Fruit girth (cm)	Single fruit weight (g)	Number of fruits per plant	Fruit yield per plant (kg)
I	97.42	8.22	45.70	57.31	67.81	3.39	2.54	7.87	10.06	40.03	44.80	1.77
II	91.78	6.66	47.84	60.00	70.74	3.31	2.66	8.08	14.81	65.66	22.45	1.46
III	121.65	7.75	40.95	51.15	63.95	3.40	2.50	10.65	7.15	37.85	57.90	2.19
IV	76.25	6.36	49.07	60.79	70.83	3.38	2.60	7.34	12.88	55.28	25.26	1.45
V	102.55	7.30	45.40	56.75	68.40	2.65	2.10	7.75	10.40	35.45	36.10	1.28
VI	89.50	9.40	41.23	52.15	64.38	2.42	2.08	6.40	9.93	40.00	64.35	2.57
VII	114.75	8.65	43.50	55.55	66.85	3.15	2.75	6.45	10.70	35.10	48.45	1.70

Table 3 continued

Cluster	Shoot infestation (%)	Fruit infestation on number basis (%)	Fruit infestation on weight basis (%)	Marketable yield per plant (kg)	Protein content (mg $100g^{-1}$)	Ascorbic acid (mg $100g^{-1}$)	Total phenol (mg g^{-1})	Total sugars (mg g^{-1}) (FW)	Polyphenol oxidase (changes in OD min^{-1} g^{-1} of sample)	Solasodine (%)
I	11.77	22.56	22.85	1.39	16.02	14.19	1.46	12.45	0.65	0.04
II	13.45	25.22	24.59	1.10	16.34	13.22	1.47	11.54	0.42	0.04
III	13.50	21.84	22.45	1.70	16.56	14.76	1.53	9.50	0.94	0.04
IV	13.45	27.03	28.74	1.07	14.64	13.57	1.48	11.96	0.49	0.03
V	14.80	24.86	21.26	0.96	15.03	12.74	1.45	14.60	0.65	0.04
VI	8.95	15.26	14.04	2.19	16.98	14.79	1.59	7.95	1.12	0.03
VII	11.05	24.89	24.77	1.28	17.11	11.26	1.32	15.30	0.90	0.05

However, the cluster III, V and VII having single genotype had no intra cluster distance.

The minimum inter-cluster D^2 value was observed between the clustersVand VI (204.27) indicated close relationship among the genotypes included in these clusters. Maximum inter-cluster D^2 values was observed between the clusters IV and VI (381.41) followed by cluster IV and V (371.23), cluster II and VI (341.73), cluster VI and VII (340.61) and cluster II and III (334.32) indicated that the genotypes included in these clusters can be used as a parent in hybridization programme to get higher heterotic hybrids from the segregating population. It is suggested that genotypes from more diverse groups and having high yield potential coupled with quality and pest resistance attributes might be useful in breeding programme. Similar results were revealed by Saurabh et al. (2011). Overall inter cluster distances were found to be much higher than that of intra cluster distances, indicating the homogeneous and heterogeneous nature of the genotypes within and between the clusters. The cluster means of thirty genotypes for 22 characters were presented in table 3.The highest mean value are desirable for plant height, number of branches per plant, fruit length, fruit girth, single fruit weight, number of fruits per plant, fruit yield per plant, marketable yield per plant, protein content, ascorbic acid, total phenol, polyphenol oxidase and solasodine, whereas lowest values for days to first flowering, days to 50 % flowering, days to first harvest, pedicel length, calyx length, shoot infestation, fruit infestation on number basis, fruit infestation on weight basis and total sugars.

The cluster VI registered the best cluster mean value for number of branches per plant (9.40), pedicel length (2.42 cm), calyx length (2.08 cm), number of fruits per plant (64.35), fruit yield per plant (2.57 kg), shoot infestation (8.95 per cent), fruit infestation on number basis (15.26 per cent), fruit infestation on weight basis (14.04 per cent), marketable yield per plant (2.19 kg), ascorbic acid (14.79 mg $100g^{-1}$), total phenol (1.59 mg g^{-1}), total sugars (7.95 mg g^{-1}) and polyphenol oxidase (1.12 Changes in OD min^{-1} g^{-1}). The cluster III was identified best for plant height (121.65 cm), days to first flowering (40.95 days), days to 50 per cent flowering (51.15 days), days to first harvest (63.95 days) and fruit length (10.65 cm). The cluster II had highest mean value for fruit girth (14.81 cm) and single fruit weight (65.66 g). Cluster VII recorded the highest mean values for protein content (17.11 mg $100g^{-1}$) and solasodine (0.05 per cent).The information on cluster mean value for brinjal genotypes were also available from the studies of Arun kumar *et al.* (2013), Balaji Lokesh *et al.* (2013) and Vidhya (2015). Among the genotypes spread over seven clusters, the mean values were scored across the clusters for all the twenty two characters. The cluster mean values served as a parameter for selection of parents for recombination breeding. None of the traits in cluster IV and V showed the highest cluster mean values and this might be due less *per se* values of genotypes in these clusters. In brinjal breeding programme aimed to get higher yield and shoot and fruit borer resistance, the genotypes from cluster VI can be selected as parent for hybridization showing highest fruit yield per plant, yield contributing characters and shoot and fruit borer resistance. The genetic divergence studies in green fruited brinjal using 30 genotypes suggests that intra-cluster distance was the lowest in cluster VI and the highest in cluster IV. The maximum distance at intercluster value was between clusters IV and VI followed by cluster IV and V, cluster II and VI which may serve as a potential genotypes for hybridization programme to get higher heterotic hybrids from the segregating population.The cluster mean for yield and its contributing characters was found to be the highest in cluster VI followed by cluster III. The genotypes having high mean for yield characters and high inter cluster distance may lead to express greater heterotic expression in brinjal.

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