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Genetic divergence studies in brinjal [*Solanum melongena* (L.)] genotypes under northern dry zone of Karnataka

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Abstract

Seventeen diverse genotypes of brinjal were evaluated for 16 different qualitative and quantitative traits in brinjal and investigation was carried out at Department of Horticulture, College of Agriculture, Vijayapura during *kharif* season of 2018. The genotypes were grouped into Six diverse clusters on the basis of D^2 statistics and maximum number of genotypes (4) was found in clusters I and II with the maximum intra-cluster distance was recorded in cluster V ($D^2=3998.63$). The maximum inter-cluster distance was observed in clusters III and cluster VI ($D^2=46,144.38$). Hence, genotypes belonging to these clusters may be utilized for involving in hybridization programme for crop improvement. The characters like fruit diameter (61.76%), number of fruits per plant (22.06%) and yield per plant (12.50%) contributed more for genetic divergence.

Keywords: Brinjal, D^2 statistics, genetic diversity and cluster analysis

Introduction

Brinjal (*Solanum melongena* L.) belongs to the family Solanaceae, is an important and popular vegetable crop of India and it is native to Indo-Burma region and China (Vavilov, 1926). In India it is cultivated in an area of 730 Thousand Hectares and producing 12801 Thousand Metric tonnes with a productivity of 17.5 MT per hectare (Anon., 2018) [2]. It is considered as brain food and poor man's caviar. It is warm season vegetable grown under wide range of soil and climatic and tolerant to heat and drought conditions. As a often cross pollinated crop sometimes certain percentage of cross pollination also noticed, herbaceous plant having erect or semi spreading growth habit. The immature fruit is primarily used for cooking and used in preparation of various dishes in different parts of the world.

Brinjal is quietly having high in nutritive value as compared to tomato (Choudhary, 1976). It is an important source of carbohydrate (4.0 g), protein (1.40 g), fibre (1.30 g), vitamin A (124 IU), phosphorus (47 mg), potassium (2.0 mg) and iron (0.3 mg) and recommended for diabetes, asthma, cholera, bronchitis and it protects the brain cell membranes from damage. It has more regional preferences for specificity of fruits trait ranging from round to long fruit with green, purple, pink, white and striped multicolours. Considering the potentiality of this crop, there is a prime need for improvement and to develop varieties suited to specific agro-ecological conditions and also for specific usage. Generally, diverse germplasms are expected to give hybrid vigour (Harrington, 1940) and hence, study of genetic divergence among the existing genetic stocks provides an opportunity for selecting the diverse parents for hybridization. Such parents are expected to produce superior segregants in combination with others and thus are most valuable for breeders. The D^2 statistics developed by Mahalanobis (1930) [10] provides a measure of magnitude of divergence between two genotypes under comparison. Grouping of genotypes based on D^2 analysis will be useful in choosing suitable parental lines for heterosis breeding which intern can help farmers by making available the elite varieties.

Material and Methods

The experiment was conducted at Department of Horticulture, College of Agriculture, Vijayapura under the University of Agricultural Sciences, Dharwad (Karnataka) during 2018. Seventeen different genotypes were evaluated in randomized block design with three replications. Ridges and furrows prepared at a spacing of 75cm and then a five week old 15 seedling of each genotype is transplanted in separate row by maintaining 60cm plant to plant spacing (Anon., 2012) [11].

Five randomly chosen plants in each replication of each genotype were labelled and used for recording the observations for the growth parameters *viz.*, plant height (cm), plant spread (cm), number of primary branches per plant and stem girth (cm) at 90 days after transplanting. Earliness parameters *viz.*, days to first flowering, days to 50 per cent flowering and days to first fruit maturity and yield parameters *viz.*, fruit length (cm), fruit diameter (cm), fruit length-diameter ratio, average fruit weight (g), number of fruits per cluster, number of fruits per plant, total yield per plant (kg), yield per hectare (tonns) and also quality parameters recorded. Total phenol content of brinjal fruits were estimated by Folin Ciocalteu Reagent (FCR) method (Sadasivam and Manickam, 2005) [18]. Analysis of variance was carried out as per the procedure given by Panse and Sukhatme (1967) [14]. The variability for different characters was estimated. Genotypic and phenotypic coefficients of variance (Burton and Devane, 1953) [3], broad sense heritability (Falconer, 1981) [6] and genetic advance as per cent over mean (Johnson *et al.*, 1955) [9] worked out. Genetic diversity was studied by Mahalanobis (1936) [10]. Based on the D^2 values, the genotypes were grouped into clusters following the method suggested by Tocher's (Rao, 1952) [17]. Intra and inter-cluster distance were calculated by the methods of Singh and Choudary (1977) [21]. Statistical analysis was carried out using WINDOSTAT software.

Results and Discussion

Genetic divergence

Clustering pattern

The classification of brinjal genotypes into different clusters based on D^2 value is given in Table 1. The material for present study includes 17 genotypes grouped into six clusters using Tocher's method. Of the six clusters, studied the clusters I and II were the largest having 4 genotypes followed by clusters III and V with 3 genotypes, cluster VI with 2 genotypes and cluster IV had one genotype. Genotypes usually did not cluster according to geographical distributions. The findings of Rameshbabu and Patil (2002) [6] and Sharma and Mourya (2004) [19] were similar. There is no any direct relationship between geographical distribution and genetic distance.

Intra and Inter-cluster distance

The averages D^2 values of intra and inter-cluster distance are given in Table 3. Intra-cluster distances revealed that cluster V with 3 genotypes showed maximum intra-cluster diversity ($D^2=3998.63$) followed by cluster VI ($D^2=2895.60$), cluster III ($D^2=2848.00$), cluster I ($D^2=2189.98$), cluster II ($D^2=1963.04$). The cluster IV had no intra-cluster distance ($D^2=0.00$) as they possessed single genotype. Maximum intra-cluster distance was observed in cluster V indicating existence of wide genetic divergence among the constituent genotypes in it as compared to other cluster. High degree of divergence among the genotypes within a cluster would produce more segregating breeding material and selection within such cluster might be executed based on maximum mean value for the desirable characters. Inter-cluster distances, the maximum divergence was observed between clusters III and cluster VI ($D^2=46,144.38$) followed by clusters III and IV ($D^2=24,550.78$), clusters II and III ($D^2=21,933.63$), cluster III and V ($D^2=17,142.64$), clusters I and VI ($D^2=16,926.97$), clusters IV and VI ($D^2=14,514.88$) and clusters V and VI ($D^2=13,786.45$). Maximum inter-cluster D^2 values was observed between the clusters III and VI indicating that the

genotypes in these clusters can be used as a parents in hybridization programme to get higher heterotic hybrids and segregating population contribution of characters. Similar results were reported by Rai *et al.* (1999) [15]. The cluster I had the least inter-cluster distance ($D^2=3818.09$) with the cluster IV indicating that close relationship and less divergence between the genotypes included in these clusters I and IV.

Contribution of characters to genetic divergence

These clusters have been formed based on the contribution of different characters to the divergence is given in Table 2. Among these characters, the fruit diameter contributed maximum (61.76%) to the genetic diversity followed by number of fruits per plant (22.06%), yield per plant (12.50%), plant spread at 90 DAT (2.94%) and days to first fruit maturity (0.74%). Characters like plant height at 90 DAT, number of primary branches at 90 DAT, stem girth at 90 DAT, days to first flowering, days to 50 per cent flowering, fruit length, fruit length-diameter ratio, average fruit weight, number of fruits per cluster, total yield per hectare and phenol content did not contribute to genetic divergence. Contribution of characters towards divergence *viz.*, fruit diameter number of fruits per plant, yield per plant, plant spread at 90 DAT, and days to first fruit maturity was also reported by Mehta *et al.* (2004) [12], Naik (2005) [13], Golani *et al.* (2007) [21], Das *et al.* (2010) [5] and Shekar *et al.* (2012) [20] by several workers.

Conclusion

The characters like fruit diameter, number of fruits per plant and total yield per plant were contributed major to the total genetic divergence. Therefore, these characters may be used in selecting genetically diverse parents for hybridization programme to exploit either maximum heterosis or execute efficient selection in the segregating generation.

Table 1: Classification of brinjal genotypes into different clusters based on D^2 value

Cluster number	Number of genotypes	Name of the genotype
I	4	G-4, G-5, G-8 and G-10
II	4	G-3, G-13, G-9 and G-12
III	3	G-2, G-7 and G-17
IV	1	G-6
V	3	G-14, G-15 and G-11
VI	2	G-1 and G-16

Table 2: Relative per cent contribution of different traits to the total divergence in brinjal genotypes

Sl. No.	Characters	No. of times ranked first	Per cent contribution
1.	Plant height at 90 DAT (cm)	0	0.00
2.	Plant spread at 90 DAT (cm)	4	2.94
3.	Number of primary branches at 90 DAT	0	0.00
4.	Stem girth at 90 DAT (cm)	0	0.00
5.	Days to first flowering	0	0.00
6.	Days to 50 per cent flowering	0	0.00
7.	Days to first fruit maturity	1	0.74
8.	Fruit length (cm)	0	0.00
9.	Fruit diameter (cm)	84	61.76
10.	Fruit length-diameter ratio	0	0.00
11.	Average fruit weight (g)	0	0.00
12.	Number of fruits per cluster	0	0.00
13.	Number of fruits per plant	30	22.06
14.	Phenol content (mg/100 g)	0	0.00
15.	Total yield per plant (kg)	17	12.50
16.	Total yield per hectare (t)	0	0.00

Table 3: Average intra and inter-cluster D² values of 6 clusters for 16 characters formed by 17 genotypes of brinjal

Clusters	I	II	III	IV	V	VI
I	2189.98	4995.07	12902.32	3818.09	6612.79	16976.97
II		1963.04	21933.63	5143.77	7028.04	7223.82
III			2848.00	24550.78	17142.64	46144.38
IV				0.00	12447.09	14514.88
V					3998.63	13786.45
VI						2895.60

Note: Bold and diagonal values indicate intra-cluster distances

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