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Variability and Genetic Divergence Studies in Brinjal (*Solanum melongena* L.) Genotypes

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Abstract A field investigation was carried out with 60 genotypes of brinjal. High GCV and PCV (>20%) were observed for number of primary branches (at 90 and 120 DAT), number of fruits per cluster, average fruit weight, fruit length-diameter ratio, number of fruits per plant, total yield per plant, indicating the existence of broad genetic base, which would be amenable for further selection. High heritability coupled with high genetic advance over mean was observed for plant height (at 60, 90 and 120 DAT), days to first flowering, number of fruits per cluster, fruit length, fruit diameter, average fruit weight and total yield per plant indicates predominance additive gene action. Genetic divergence was studied with same genotypes and the maximum number of genotypes (36) was found in cluster 1 with intra-cluster distance of 20.79. The maximum inter-cluster distance was observed in between cluster III and cluster VII. Hence, genotypes belonging to these clusters may be utilized for involving in hybridization program for crop improvement. The characters of average fruit weight (52.32%), number of fruits per cluster (14.52%) and plant spread at 60 DAT (13.90%) contributed more for genetic divergence.

Keywords Variability, Heritability, Genetic diversity, D^2 statistics, Brinjal.

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Introduction

Brinjal (*Solanum melongena* L.) is an important and popular vegetable crop of India, belongs to the family Solanaceae and is native of Indo-Berma region and China [1]. Brinjal quite high in nutritive value as compared with tomato [2]. It is an important source of carbohydrate (4.0 g), protein (1.4 g), fiber (1.3 g), vitamin A (124 IU), phosphorus (47 mg),potassium (2.0 mg) and iron (0.3 mg) and recommended for diabetes, asthma, cholera, and it protects the brain cell membranes from damage.

Brinjal has more regional preferences for specificity of fruits trait ranging from round to long fruit with green, purple, pink, white and stripped multicolor. 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 use. The role of genetic variability in crops is of par amount importance in selecting the best genotypes for making rapid improvement in yield and related characters as well as to select the most potential parents for making the hybridization program successful. The success of any crop improvement program largely depends upon the nature and magnitude of the genetic variability existing in breeding material with which plant breeder is working [3].

Generally, diverse germplasms are expected to give hybrid vigor 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 [4], 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.

Materials and Methods

The experiment was conducted at the Research Block of Vegetable Section in Sector 1 under the University of Horticultural Sciences, Bagalkot (Karnataka) during the year, Sixty genotypes of brinjal were grown in randomized block design with three replications. Randomly chosen plants in each replication of each entry were labelled and used for observations for the growth parameters viz. plant height (cm), plant spread (cm), number primary branches per plant, stem girth (cm) and leaf area (cm^2) at 60, 90 and 120 days transplanting. Earliness parameters viz. days to first flowering, days to 50% days to first fruit maturity and yield parameters viz. fruit length (cm), fruit diameter (cm), length-diameter ratio, average fruit weight (g), number of fruits per cluster, number of plant, early yield per plant (first three pickings-kg), total yield per plant (kg), yield per plot and yield per hectare (t) were recorded. Data on qualitative characters were also recorded. Percent dry matter in fruit was found by drying the cut fruit samples in hot air oven at 60^0C, constant weight of samples was achieved over the two subsequent observations and dry of fruits was recorded and percent dry matter in fruit was worked. Total phenol content of brinjal fruits was estimated by folin ciocalteu reagent (FCR) method [5]. Analysis was carried out as per the procedure given by Panse and Sukhatme [6]. The variability for different characters was estimated. Genotypic and phenotypic coefficients of variance, sense heritability and genetic advance as percent over mean worked out. Genetic diversity studied following. Mahalanobis [7] generalized distance D^2 extended by Rao [8]. On the D^2 values, the genotypes were grouped into clusters following the method suggested Tocher's. Intra and inter cluster distance were calculated by the methods of Singh and Choudhary [9]. Statistical analysis was carried out using WINDOSTAT software.

Results and Discussion

Genetic variability studies

The estimates of genotypic and phenotypic coefficients of variation, heritability, genetic advance and genetic advance as percent of mean are presented in Table 1. The phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the traits. High GCV and PCV (>20%) were observed for number of primary branches (at 90 and 120 DAT), stem girth at 60 DAT, leaf area (at 60 and 90 DAT), number of fruits per cluster, number of fruits per plant, average fruit weight, fruit length-diameter ratio, total yield per plant, yield per plot, yield per hectare and phenol content [10-13] it indicates existence of broad genetic base, which would be amenable for further selection. Moderate GCV and PCV (10-20%) were observed for plant height (at 60, 90 and 120 DAT), plant spread at 60 DAT, stem girth (at 90 and 120 DAT), days to first flowering, fruit length, fruit diameter and percent dry matter in fruits [13, 14]. These results suggested that little influence of environment. Therefore, phenotypic variability may be a good measure of genotypic variability and hence selection for such traits would be rewarding GCV (<10%) and moderate PCV (10-20%) were observed for plant spread (at and 120 DAT), days to 50% flowering and days to first fruit maturity. These results indicate that apparent variation is not only due to genotypes but also due to the influence of environment on the expression of character. Selection for such traits may not give desirable results. Higher (>20%) values of genetic advance over mean (GAM) coupled with high

Table 1. Estimates of components of variance, heritability, genetic advance and genetic advance over mean for growth, earliness, yield and quality parameters in brinjal. Gv = Genotypic variance, PV = Phenotypic variance, GCV = Genotypic coefficient of variance, GA= Genetic advance, h^2=Heritability (broad sense), PCV=Phenotypic coefficient of variance, GAM = Genetic advance (per cent mean), DAT = Days after transplanting.

Sl. No.	Characters	GV	PV	GCV (%)	PCV (%)	h^2 (%)	GA	GAM (%)
A.	Growth parameters							
1.	Plant height at 60 DAT (cm)	49.66	50.01	12.98	3.08	99.31	14.46	26.64
2.	Plant height at 90 DAT (cm)	76.60	97.63	13.08	14.76	78.46	15.97	23.86
3.	Plant height at 120 DAT (cm)	80.36	101.11	12.21	13.69	79.48	16.46	22.42
4.	Plant spread as 60 DAT (cm)	56.91	57.21	12.57	12.60	99.47	15.49	25.83
5.	Plant spread at 90 DAT (cm)	46.17	91.08	9.73	13.66	50.70	9.96	14.27
6.	Plant spread at 120 DAT (cm)	42.89	86.37	8.87	12.59	49.66	9.50	12.83
7.	Number of primary branches at 60 DAT	0.49	1.62	14.31	25.97	30.38	0.79	16.25
8.	Number of primary branches at 90 DAT	2.67	2.83	24.56	25.29	94.31	3.26	49.14
9.	Number of primary branches at 120 DAT	2.40	2.56	21.40	22.08	93.93	3.09	42.73
10.	Stem girth at 60 DAT (cm)	0.08	0.09	21.02	21.46	95.99	0.59	42.44
11.	Stem girth at 90 DAT (cm)	0.05	0.11	12.94	18.54	38.73	0.33	18.61
12.	Stem girth at 120 DAT (cm)	0.05	0.11	12.65	18.14	48.66	0.33	18.18
13.	Leaf area at 60 DAT (cm^2)	1075.44	1087.67	34.26	34.46	98.88	67.17	70.19
14.	Leaf area at 90 DAT (cm^2)	2910.82	2990.38	36.92	37.42	97.34	109.65	75.04
B.	Earliness parameters							
15.	Days to firsts flowering	30.48	37.50	10.91	12.10	81.30	10.25	20.26
16.	Days to 50% flowering	29.18	34.78	9.35	10.21	83.89	10.19	17.65
17.	Days to first fruit maturity	18.53	22.36	5.78	6.35	82.87	8.07	10.84
C.	Yield parameters							
18.	Number of fruits per cluster	0.21	0.21	40.04	40.14	99.52	0.95	82.29
19.	Fruit length (cm)	1.95	2.42	18.73	20.87	80.53	2.58	34.63
20.	Fruit diameter (cm)	0.62	0.80	15.46	17.45	78.56	1.44	28.24
21.	Fruit length-diameter ratio	0.15	0.16	26.65	27.48	94.06	0.79	53.25
22.	Early yield per plant (kg)	0.03	0.04	24.45	28.04	76.05	0.32	43.93
23.	Average fruit weight (g)	784.45	785.79	34.57	34.60	99.83	57.64	71.16
24.	Number of fruits per plant	68.86	87.05	40.36	45.38	79.11	15.20	73.95
25.	Total yield per plant (kg)	0.14	0.17	25.12	28.29	78.86	0.68	45.96
26.	Yield per plot (kg)	28.27	35.30	24.44	27.31	80.09	9.80	45.05
27.	Yield per hectare (t)	62.03	77.46	24.44	27.31	80.09	14.52	45.05
D.	Quality parameters							
28.	Percent dry matter in fruits	3.58	4.19	15.84	17.14	85.48	3.60	30.18
29.	Phenol content (mg/100 g)	4922.21	4925.81	49.36	49.37	99.90	144.47	101.64

of heritability (>60%) were observed for the characters viz. plant height (at 60, 90 and 120 DAT), plant spread at 60 DAT, number of primary branches (at 90 and 120 DAT), stem 60 DAT, leaf area (at 60 and 90 DAT), days to first flowering, number of fruits per cluster, length, fruit diameter, fruit length-diameter ratio, average fruit weight, phenol content, yield per plant, total yield per plant, yield per plot, yield per hectare and percent dry fruits. These results indicated the predominant role of additive genetic component in these traits and improvement of these traits through direct selection would be rewarding.

Moderate (20-30%) value of genetic advance over mean (GAM) coupled with moderate estimates of heritability (30-60%) were observed plant spread (at

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

Cluster number	Number of genotypes	Name of the genotype
I	36	CBB-24, CBB-34, CBB-21, CBB-38, CBB-28, CBB-17, CBB-51, CBB-31, CBB-57, CBB-7, CBB-2, CBB-9, CBB-50, CO-2, CBB-20, CBB-32, CBB-35, CBB-42, CBB-25, CBB-36, CBB-44, CBB-29, CBB-22, CBB-26, CBB-18, CBB-30, CBB-54, CBB-56, CBB-47, CBB-55, CBB-37, CBB-58, CBB-41, CBB-52, CBB-33 and CBB-3.
II	14	CBB-6, CBB-16, CBB-40, CBB-4, CBB-23, CBB-5, CBB-27, CBB-1, CBB-10, CBB-48, CBB-14, CBB-45, CBB-49 and CBB-43.
III	6	CBB-13, CBB-19, CBB-46, CBB-12, CBB-15 and CBB-11
IV	1	CBB-8
V	1	CBB-39
VI	1	CBB-59
VII	1	CBB-53

90 and 120 DAT), number of primary branches at 60 DAT, stem girth (at 90 and 120 DAT). This indicates the importance of additive effects for this trait and selection may be rewarding [15].High heritability coupled with moderate genetic advance over mean were observed for days to 50% flowering and days to first fruit maturity, indicating non-additive gene action. The high heritability is being exhibited due to favorable influence environment rather than genotype and selection for such traits may not be rewarding.

Genetic divergence

Clustering pattern

The classification of brinjal genotypes into different clusters based on D^2 value is given in Table 2. The material for present study includes 60 genotypes grouped into seven clusters using Tocher's method. Of the seven clusters, studied the cluster 1 was the largest having 36 genotypes followed by clustar II

Table 3. Average intra and inter-cluster D^2 values of 7 clusters for 21 characters formed by 60 genotypes of brinjal. Bold and diagonal value indicate intra-cluster distance.

Clusters	I	II	III	IV	V	VI	VII
I	**20.79**	36.41	39.79	29.45	28.76	36.88	54.60
II		**23.64**	54.94	36.21	40.27	47.44	40.62
III			**27.63**	46.53	44.71	51.15	69.50
IV				**0.00**	46.76	35.33	64.09
V					**0.00**	43.44	43.19
VI						**0.00**	68.98
VII							**0.00**

Table 4. Relative percent contribution of different characters to the total divergence in brinjal genotypes.

Sl. No.	Character or source	No. of times ranked first	Percent contribution
1.	Plant height at 60 DAT (cm)	188	10.62
2.	Plant height at 90 DAT (cm)	0	0.00
3	Plant spread at 60 DAT (cm)	246	13.90
4.	Plant spread at 90 DAT (cm)	0	0.00
5.	Number of primary branches at 60 DAT	0	0.00
6.	Number of primary branches at 90 DAT	4	0.23
7.	Stem girth at 60 DAT (cm)	4	0.23
8.	Stem girth at 90 DAT (cm)	0	0.00
9.	Leaf area at 60 DAT(cm^{-2})	115	6.50
10.	Leaf area at 90 DAT (cm^2)	21	1.19
11.	Days to first flowering	1	0.06
12.	Days to 50% flowering	0	0.00
13.	Days to first fruit maturity	1	0.06
14.	Number of fruits per cluster	257	14.52
15.	Fruit length (cm)	0	0.00
16.	Fruit diameter (cm)	2	0.11
17.	Fruit length-diameter ratio	5	0.28
18.	Early yield per plant (kg)	0	0.00
19.	Average fruit weight (g)	926	52.32
20.	Number of fruits per plant	0	0.00
21.	Total yield per plant (kg)	0	0.00

with 14 genotypes, cluster III with 6 genotypes, cluster IV (CBB-9), cluster V (CBB-40), cluster VI (CBB-60) and cluster VII (CBB-54) had one genotype. Genotypes usually did not chuster according to geographical distributions [16]. There is no any direct relationship between geographical distribution and genetic distance.

Intra and inter cluster distance

The average D^2 values of intra and inter cluster distance are given in Table 3. Intra-cluster distances revealed that cluster III with 6 genotypes showed maximum intra-cluster diversity (D^2=27.63) followed by cluster II (D^2=23.64) and cluster I (D^2=20.79). The clusters IV, V, VI and VII had no intra-cluster distance (D^2=0.00) as they possessed single genotype. Maximum intra-cluster distance was observed in cluster III 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. Maximum inter-cluster D^2 values was observed between the clusters III and VII (D^2=69.50) indicating that the genotypes in these clusters can be used as a parents in hybridization program to get higher heterotic hybrids and segregating population contribution of characters. The cluster 1 had the least inter-cluster distance (D^2=28.76) with the cluster V indicating that close relationship and less divergence between the genotypes included in these clusters.

Contribution of characters to genetic divergence

Relative percent contribution of different characters to divergence is given in Table 4. Among these characters, the average fruit weight contributed maximum (52.32%) to the genetic diversity followed by number of fruits per cluster (14.52%), plant spread at 60 DAT (13.90%) and plant height at 60 DAT (10.62%) [17, 18]. Characters like plant height, plant spread, number of primary branches, stem girth (at 90 DAT), days to 50% flowering, fruit length, early yield per plant, number of fruits per plant and total yield per plant did not contribute to genetic divergence.

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