



Genetic variability and divergence studies for morpho-economic characters in brinjal (*Solanum melongena* L.)

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Abstract : Study on the genetic components was carried out to assess the variability, association, direct and indirect effects and divergence of eight morpho-economic characters in thirty four brinjal (*Solanum melongena* L.) genotypes. High PCV and GCV were recorded by the characters viz., number of branches per plant, fruit length, fruit breadth, number of fruits per plant, average fruit weight and fruit yield per plant. All the characters were accompanied by high heritability and high genetic advance except for the trait days to 50 per cent flowering. The characters were mostly controlled by additive gene action, hence, it could be inferred that simple selection will be effective for these characters. The characters such as number of branches per plant, fruit breadth, number of fruits per plant and average fruit weight exhibited positive and significant association with fruit yield per plant. Path analysis indicated that the number of fruits per plant and average fruit weight had high direct effects and were the major factors that determine fruit yield per plant. The selection of genotypes based on these analyzed parameters can be utilized for further improvement.

Key Words : Brinjal, Heritability, Genetic divergence, Correlation, Path analysis

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INTRODUCTION

Brinjal (*Solanum melongena* L.), also known as eggplant, is an important solanaceous vegetable crop grown round the year in India. It is grown for its immature, unripe fruits which are used in the variety of ways as cooked vegetable in curries. It is grown extensively in all parts of India except at higher altitude. It is popular among people of all social strata and hence, it is rightly called as vegetable of masses (Patel and Sarnaik, 2003). Brinjal was first cultivated in India which is regarded as the primary centre of origin/diversity. In India, brinjal cultivation is estimated in an area of 5,12,800 ha with an annual production of 84,50,200 tonnes and productivity of 16,478.50 kg ha⁻¹ (FAO, 2007). In Karnataka, the area is

estimated around 8006 hectares with an annual production of 97,550 tons (Anonymous, 2007). Genetic improvement programme depends on the existence, nature and extent of genetic variation available for manipulation within the species. Assessment of available genetic variability for important economic traits to develop high yielding varieties is an important function in crop breeding. This research paper reports about the level of genetic variation within and between 34 eggplant genotypes by assessing the variability, heritability, genetic advance, genetic advance as percentage of mean, correlation and path co-efficient analysis. The D² statistics which is an effective tool to estimate the genetic divergence among the genotypes of different eco-geographical origin has also been presented and discussed in this paper.

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MATERIAL AND METHODS

The collections of thirty four genotypes were sown in different rows on a raised bed nursery followed by recommended nursery practices. The experiment was laid out in a randomized complete block design with three replications at University of Agricultural Sciences, GKVK, Bengaluru. In each replication, the genotypes were planted in double rows of twelve meters length with the spacing of 60 cm between plants and 75 cm between the rows and followed the recommended agronomic practices to raise the health and good crop. Eight important characters *viz.*, days to 50 per cent flowering, plant height, number of branches per plant, fruit length, fruit breadth, number of fruits per plant, average fruit weight and fruit yield per plant were recorded from five randomly selected plants for each genotype. The individual plant observations were utilized for the conversion of mean values. These mean values were used for statistical analysis. Genotypic and phenotypic co-efficients of variations were computed according to Johnson *et al.* (1955). The estimation of mean, variance, co-efficient of variation, heritability, genetic advance and genetic advance as percentage of mean were calculated as described by Falconer (1989). The correlations were further partitioned into direct and indirect effects as suggested by Dewey and Lu (1959). Mahalonobis (1936) D² statistical analysis was used for assessing the genetic divergence among the genotypes.

RESULTS AND DISCUSSION

The results obtained from the present investigation as

well as relevant discussion have been summarized under following heads :

Analysis of variability :

The phenotypic co-efficient of variation ranged from 6.57 to 53.43 per cent and The GCV ranged from 6.17 per cent for days to 50 per cent flowering to 45.39 per cent for fruit yield per plant (Table 1). High GCV estimates were recorded for the characters *viz.*, number of branches per plant, fruit length, fruit breadth, number of fruits per plant, average fruit weight and fruit yield per plant indicating their greater role of contribution to the variability among the genotypes. Tambe *et al.* (1992) reported similar result. Low estimate of GCV and PCV was recorded by days to 50 per cent flowering. These results supported by the findings of Choudhary and Mishra (1989) and Kabir and Som (1993). A close correspondence between the estimates of GCV and PCV was noted especially in case of plant height, fruit length and average fruit weight indicating less environmental influence in the expression of these traits. The traits like number of fruits per plant and fruit yield per plant showing high PCV as compared to the GCV. The low genetic variance coupled with low genetic advance for the character fruit breadth (0.83 and 1.88, respectively). The heritability values ranged from 72.18 per cent for fruit yield per plant to 99.83 per cent for fruit length. All the estimates for heritability had very high value. The maximum genetic advance was observed in fruit yield per plant (219.06) whereas the characters fruit breadth and fruit length recorded the minimum genetic advance value of 1.88 and 2.26, respectively. The genetic advance as per cent of mean was noted maximum

Table 1 : Magnitude of variability for eight characters in 34 brinjal genotypes

Sr. No.	Characters	V _{th}	V _e	PCV (%)	GCV (%)
1.	Days to 50 per cent flowering	14.44	12.74	6.57	6.17
2.	Plant height	276.88	272.13	18.89	18.72
3.	Number of branches per plant	5.56	5.52	29.05	28.95
4.	Fruit length	1.23	1.21	22.37	22.24
5.	Fruit breadth	0.84	0.83	25.08	24.99
6.	Number of fruits per plant	48.79	36.69	50.42	43.73
7.	Average fruit weight	28.06	27.86	26.78	26.68
8.	Fruit yield per plant	21706.02	15667.42	53.43	45.39

Table 2 : Estimation of heritability and genetic advance

Sr. No.	Characters	h ² (%)	GA	Genetic advance as per cent mean
1.	Days to 50 per cent flowering	88.25	6.91	11.94
2.	Plant height	98.29	33.69	38.24
3.	Number of branches per plant	99.28	4.82	59.42
4.	Fruit length	99.83	2.26	45.54
5.	Fruit breadth	99.34	1.88	51.32
6.	Number of fruits per plant	75.19	10.82	78.12
7.	Average fruit weight	99.28	10.83	54.77
8.	Fruit yield per plant	72.18	219.06	79.44

for fruit yield per plant (79.44 %) (Table 2). Estimate of heritability and genetic advance in combination are more important for selection than heritability alone. High heritability combined with high genetic advance observed for plant height and fruit yield per plant indicated that these characters were controlled by additive gene effects and phenotypic selection would be highly effective. Average fruit weight revealed high heritability and medium genetic advance which might be due to predominance of non-additive gene action and / or less genetic variability for these traits in the present material.

Correlation :

Correlation studies provide better understanding of yield components which helps the plant breeder during selection (Table 3). Positive association of these yield attributing

characters with fruit yield per plant was also reported by Ponnuswami and Irulappan (1994). Fruit yield per plant was found to be significantly and positively correlated with number of branches per plant, fruit breadth, number of fruits per plant and average fruit weight, both at genotypic as well as phenotypic levels (Table 3). Inter correlation was positive and significant for days to 50 per cent flowering with fruit breadth and average fruit weight. Plant height showed significant positive association with number of branches per plant, fruit length, fruit breadth and average fruit weight which is in agreement with the findings of Ponnuswami and Irulappan (1994). Number of branches per plant showed significant association with average fruit weight, while the fruit length observed positive correlation with fruit breadth. Fruit breadth expressed significant positive association with average fruit

Table 3 : Phenotypic and genotypic correlation between various characters in brinjal genotypes

Characters		Days to 50 per cent flowering	Plant height	Number of branches per plant	Fruit length	Fruit breadth	Number of fruits per plant	Average fruit weight	Fruit yield per plant
Days to 50 per cent flowering	P	1.000	0.206*	0.066	0.112	0.299**	-0.052	0.255**	0.055
	G	1.000	0.109	-0.009	0.019	0.269**	-0.104	0.213*	0.025
Plant height	P		1.000	0.555**	0.366**	0.277**	-0.023	0.284**	0.066
	G		1.000	0.543**	0.340**	0.256**	-0.038	0.262**	0.054
Number of branches per plant	P			1.000	0.024	-0.060	0.149	0.306**	0.233*
	G			1.000	-0.001	-0.081	0.143	0.291**	0.228*
Fruit length	P				1.000	0.317**	0.105	0.214*	0.138
	G				1.000	0.300**	0.095	0.193	0.130
Fruit breadth	P					1.000	0.061	0.408**	0.234*
	G					1.000	0.053	0.396**	0.228*
Number of fruits per plant	P						1.000	0.061	0.879**
	G						1.000	0.052	0.879**
Average fruit weight	P							1.000	0.493**
	G							1.000	0.491**

* and ** indicate significance of values at P=0.05 and P=0.01, respectively
 P – Phenotypic correlation G – Genotypic correlation

Table 4 : Path co-efficient analysis for various characters in brinjal genotypes

Characters	Days to 50 per cent flowering	Plant height	Number of branches per plant	Fruit length	Fruit breadth	Number of fruits per plant	Average fruit weight	Fruit yield per plant
Days to 50 per cent flowering	0.0164	-0.00135	0.00018	0.00077	0.00322	-0.08965	0.09674	0.025
Plant height	0.00178	-0.01239	-0.01053	-0.01350	0.00306	-0.03280	0.11873	0.054
Number of branches per plant	-0.00016	-0.00672	-0.01941	0.00003	-0.00097	0.12283	0.13231	0.228*
Fruit length	0.00032	-0.00422	0.00002	-0.03964	0.00360	0.08217	0.0962	0.138
Fruit breadth	0.00441	-0.00317	0.00157	-0.01190	0.01198	0.04531	0.17992	0.228*
Number of fruits per plant	-0.00171	0.00047	-0.00277	-0.00378	0.00063	0.86198	0.02372	0.879
Average fruit weight	0.00350	-0.00324	-0.00566	-0.00765	0.00475	0.04504	0.42390	0.491*

Residual effect = 0.1646

weight and this is in similitude with the findings of Kumar *et al.* (1990) (Table 3).

Plant height showed positive significant association with number of branches per plant, fruit length, fruit breadth and average fruit weight. Fruit length recorded significant positive association with fruit breadth and average fruit weight. These results indicated that these are the major yield contributing characters in brinjal and a selection for these traits would possibly be helpful in getting a quantum jump in yield increase of this crop.

Path co-efficient analysis :

Path co-efficient analysis based on genotypic correlation revealed almost same pattern of direct and indirect influence of different characters on seed yield. Thus, the results based on genotypic correlations indicated that number of fruits per plant had large and positive direct effect on fruit yield per plant followed by average fruit weight. Average fruit weight had the positive and direct effect on number of fruits per plant followed by number of fruits per plant, fruit breadth and days to 50 per cent flowering. Whereas, fruit length had negative direct effect on fruit yield per plant. Similar results were reported by Patel and Sarnaik (2003). Fruit breadth had high direct effect in positive direction and it had positive indirect effects via, average fruit weight, number of fruits per plant, days to 50 per cent flowering and number of branches per plant resulting in positive association with fruit yield per plant. The positive direct effect of days to 50 per cent flowering was manifested through indirect positive effects via, average fruit weight, fruit breadth, fruit length and number of branches per

plant (Table 4).

Thus, for improving the seed yield and developing high yielding genotypes of brinjal due emphasis should be placed on number of fruits per plant, average fruit weight, fruit breadth and days to 50 per cent flowering. As all these traits had high heritability coupled with high to moderate genetic advance, it may be possible to have a rapid gain by mass selection. Since, late flowering beyond certain limit is not desirable, greater emphasis should be laid on early flowering genotypes.

Diversity analysis :

The analysis of variance revealed significant differences among the genotypes for all the traits studied. Based on D^2 statistics and Tocher's method as suggested by Rao (1952). 34 genotypes accessions were grouped into 7 clusters (Table 5). Cluster I had the maximum number with thirteen genotypes followed by cluster III with eleven genotypes. Cluster V with three genotypes, whereas the cluster II, IV and cluster VI with two genotypes. Cluster VII was solitary with single genotype indicating its distinctiveness from the germplasm accessions with respect to traits considered. Similar findings were reported by Mahto *et al.* (1995) in linseed. Average inter and intra cluster D^2 values among 34 genotypes (Table 6), revealed that the intra cluster distance ranged from 0.00 to 144.95. cluster III followed by V, I and VI had the maximum intra cluster values *viz.*, 144.95, 144.14, 128.80 and 110.65, respectively indicating existence of diverse genotypes that fell in these clusters. The inter cluster D^2 values ranged from 0.00 to 65237.45 (Table 6). Minimum inter cluster D^2 values were observed between cluster II and V (13635.14) indicating the close relationship

Table 5 : Composition of D^2 clusters for 34 brinjal genotypes

Cluster	Number of genotypes	Name of genotypes
I	13	SM-1, SM-2, SM-3, SM-4, SM-5, SM-6, SM-7, SM-8, SM-9, SM-10,
II	2	SM-25, SM-29
III	11	SM-13, SM-14, SM-15, SM-16, SM-17, SM-18, SM-19, SM-20, SM-21, SM-32, SM-34
IV	2	SM-27, SM-33
V	3	SM-23, SM-26, SM-30
VI	2	SM-28, SM-31
VII	1	SM-24

Table 6 : Average intra and inter cluster D^2 and D values for 34 brinjal genotypes

Cluster	I	II	III	IV	V	VI	VII
I	16591.21 (128.80)	22143.11 (148.81)	24342.32 (156.02)	13961.61 (118.16)	21891.17 (147.96)	25616.15 (160.05)	29037.37 (170.40)
II		2418.77 (49.18)	18224.99 (135.00)	19307.55 (138.95)	13635.14 (116.77)	18541.70 (136.17)	65237.45 (255.42)
III			21009.63 (144.95)	16821.92 (129.69)	23833.23 (154.38)	34920.28 (186.87)	48680.21 (220.64)
IV				5547.73 (74.48)	16726.76 (129.33)	22619.64 (150.40)	30624.30 (175.00)
V					20775.78 (144.14)	15470.70 (124.38)	53810.65 (231.97)
VI						12242.55 (110.65)	56306.80 (237.29)
VII							0.00 (0.00)

Note: Figures within the parenthesis represent intracluster distance

among the genotypes included in these clusters. Maximum inter cluster values were observed between clusters II and VII (65237.45) followed by clusters VI and VII (56306.80) which indicated that genotypes included in these clusters were genetically diverse and may give rise to high heterotic response in early generations if utilized repeatedly in the crossing programme, which in turn may release hidden variability by breaking tight linkages, if any, as reported by Thoday (1960).

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