

Full Length Research Paper

Genetic variability for quantitative and qualitative characters in Brinjal (*Solanum melongena* L.)

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In Brinjal significant variability is available in the land races and hybrids. They have several matchless characteristics of plant breeding significance with sufficient scope for added improvement to outfit the traditional growing conditions. Many land races also display heritable resistance and/or tolerance to some biotic stresses. The present study which consisted of 14 parents (10 land races, 4 commercial varieties) and 40 hybrids were evaluated in Randomized Complete Block Design replicated thrice at College Orchard, Agricultural College and Research Institute, TNAU, Madurai during 2009 to 2010. Fruit yield was kept as a dependent character and the results were analysed. Analysis of variance revealed that considerable variability among the genotypes for all the characters. High estimates of phenotypic and genotypic co-efficient of variation was observed in the parents and for fruit length, calyx length, number of fruits per plant, little leaf incidence, total phenol content and fruit yield per plant. The characters *viz.*, fruit length, calyx length, number of fruits per plant, little leaf incidence, total phenol content and fruit yield per plant also recorded high magnitude of heritability coupled with genetic advance. Therefore, these traits should be kept in mind for better planning of improvement programme in Brinjal. The study further reveals that simple phenotypic selection could be effective for the improvement of aforesaid traits.

Key words: Genetic analysis, eggplant, yield, pest, disease incidence.

INTRODUCTION

Brinjal (*Solanum melongena* L.) is native of India and widely grown during summer and winter seasons to fulfill the market demand. Yield of the brinjal varieties cultivated in India is less and size, shape and skin colour of brinjal varies in different locations. Improvement in fruit yield, colour, pest and disease resistances will certainly enhance the production and consumption of the crop (Islam and Uddin, 2009). India is the major producer of brinjal in the world and it is grown in an area of 0.61million ha with an estimated annual production of

13.37 million tonnes with a productivity of 17.3 tonnes per ha. In Tamilnadu, the production was 8.5 lakh tonnes with an area of 0.75 lakh ha (Anonymous, 2010). In the face of increasing population, there is a need for increased production and productivity levels of brinjal. In view of very high local preferences for colour, shape, taste, there are specific genotypes suited for specific locality. It is not possible to have one common cultivar to suit different localities and local preferences. It is therefore required to improve the yield potential of available land races through

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Table 1. Details of the parents used in the present study.

S/N	Name of the local types	Source	Symbol
1	Alavayal Local	Alavayal, Madurai D.t, Tamil Nadu	L ₁
2	Sedapatty Local (Green)	Sedapatty, Madurai D.t, Tamil Nadu	L ₂
3	Kariapatty Local	Kariapatty, Viradhunagar D.t, Tamil Nadu	L ₃
4	Alagarkovil Local	Alagarkovil, Madurai D.t, Tamil Nadu	L ₄
5	Palamedu Local	Palamedu, Madurai D.t, Tamil Nadu	L ₅
6	Melur Local	Melur, Madurai D.t, Tamil Nadu	L ₆
7	Keerikai Local	Sempatty, Dindigul D.t, Tamil Nadu	L ₇
8	Nilakottai Local	Nilakottai, Dindigul D.t, Tamil Nadu	L ₈
9	Singampunari Local	Singampunari, Sivagangai D.t, Tamil Nadu	L ₉
10	Sedapatty Local (Blue)	Sedapatty, Madurai D.t, Tamil Nadu	L ₁₀
11	Annamalai	Vegetable Research Station, Palur, Tamil Nadu	T ₁
12	KKM 1	Agricultural College and Research Institute, Tuticorin, Tamil Nadu	T ₂
13	Punjab Sadabahar	Tamil Nadu agricultural university, Coimbatore	T ₃
14	EP 65	Vegetable Research Station, Palur, Tamil Nadu	T ₄

The above 14 parents were crossed in possible combinations on LxT fashion to obtain 40 hybrids.

hybridization, may yield good hybrids or varieties (Ramesh Kumar et al., 2012). The success of any crop improvement programme largely depends upon the nature and magnitude of the genetic variability existing in breeding material with which plant breeder is working (Prabhu et al., 2009). Effectiveness of selection directly depends on the amount of heritability and genetic advance as percent of mean for that character (Prabakaran, 2010). Hence, an insight into the magnitude of variability present in available accessions and hybrids of brinjal is of utmost importance to a plant breeder for starting a judicious breeding programme. Therefore, in the present study, an attempt has been made to access the variability in brinjal hybrids and their parents.

MATERIALS AND METHODS

The present investigations were carried out at College Orchard, Agricultural College and Research Institute, Madurai during 2009 to 2010 which is situated at 9°5 latitude and 78°5 longitude and at an elevation of 147 m above MSL. The experimental material consists of forty hybrids and fourteen parents. All the parents and their hybrids (Table 1) were evaluated for its growth, yield and quality. The parental and hybrid seeds were sown in raised nursery bed and covered by the thin layer of sand and watered every day. Care was taken against damping off by drenching 0.1% of carbendazim. This study was carried out during April, 2010 to August, 2010. Forty hybrids along with 14 parents were raised in a randomized complete block design with three replications. Thirty days-old seedlings raised in the nursery beds were transplanted on the ridges adopting a spacing of 60 × 60 cm. Thirty plants were maintained for each hybrid and parent in each replication. Recommended cultural practices were followed uniformly to all the hybrids and parents as per TNAU Crop Production Guide (2013). Observations were recorded in five randomly selected plants in each replication. The data were analyzed by the methods outlined by Panse and Sukhatme (1967) using the mean values at random plots in each replication from all genotypes to find out significance

of genotypic effect. Genotypic and phenotypic coefficient of variation was calculated using the formulae suggested by Burton (1952). Broad sense heritability was calculated as per Lush (1949) and genetic advance was estimated by the method suggested by Johnson et al. (1955).

RESULTS AND DISCUSSION

The analysis of variance for fifteen characters is presented in Table 2. The results revealed that the parents and hybrids showed significant differences for all the characters indicating the existence of enormous amount of genetic variability for growth and yield attributes. Variability is the most important characteristic feature of any population. Estimation of variability is an important prerequisite for realizing response to selection as the progress in the breeding depends upon its amount, nature and magnitude. The genetic proportion of this variability measured in terms of genotypic coefficient of variation (GCV) alone represents the heritable component of total variability.

The higher the GCV, the more will be chance for exploitation of that particular character in a selection programme. The genetic variability in terms of GCV alone is not sufficient for determination of amount of heritable variability. In addition, estimation of heritability and genetic advance as percent of mean is also needed to assess the extent of genetic gain expected from effective selection. As heritability in broad sense includes both additive and epistatic gene effects, it will be reliable only when it is accompanied with high genetic advance (Burton, 1952; Johnson et al., 1955). In the present investigation, the variability available for the fifteen characters under study in a population of forty hybrids and fourteen parents were analysed using the

Table 2. Analysis of variance for yield and quality characters.

Source	df	PH ^a	DFF	NB/P	FL	FPL	FC	CL	NF/P	AFW	SBI	FBI	LLI	ACC	TPC	FY/P
Replication	2	226.8077	3.9454	12.6763	0.1768	0.0043	0.0770	0.0319	1.6104	6.4061	0.8644	0.3360	0.6058	0.0344	8.2018	0.0081
Genotype	53	354.0775**	51.0528**	17.4260**	6.3832**	1.7021**	10.4021**	2.5356**	129.5043**	214.0729**	53.7132**	58.1162**	98.9919**	10.8917**	820.4743**	0.5274**
Error	106	78.9549	3.4884	4.0873	0.0838	0.0256	0.3339	0.0347	2.5060	3.8861	0.7877	1.9757	0.8541	0.1464	3.6975	0.0105

** Significant at 1% level, ANOVA. ^aPH = Plant height (cm); DFF = Days to first flowering; NB/P = Number of branches per plant; FL = Fruit length (cm); FPL = Fruit pedicel length (cm); FC = Fruit circumference (cm); CL = Calyx length (cm); NF/P = Number of fruit per plant; AFW = Average fruit weight (g); SBI = Shoot borer infestation (%); FBI = Fruit borer infestation (%); LLI = Little leaf incidence (%); ACC = Ascorbic acid content (mg/100g); TPC = Total phenols content (mg/100g), and FY/P = Fruit yield per plant (kg).

above three parameters.

Genotypic (GCV) and phenotypic (PCV) coefficient of variation

A relatively high estimate of genotypic and phenotypic coefficient of variation (GCV of more than 20%) were observed for fruit length, calyx length, number of fruits per plant, little leaf incidence, total phenol content and fruit yield per plant (Table 3). Thus it could be inferred that, the selection for the improvement of these characters would be effective. This is in accordance with the findings of Prabakaran (2010) for fruit length and total phenol content. For fruit yield per plant the similar results were reported by Singh and Kumar (2005) and Moderate phenotypic and genotypic coefficient of variation (10 to 19%) were observed for plant height, number of branches per plant, fruit pedicel length, fruit circumference, average fruit weight, shoot and fruit borer infestation and ascorbic acid content. The results revealed that there is considerable scope for improving these characters in desirable direction through a selection programme.

This is in corroboration with the findings of Prabakaran (2010) in Brinjal. Low estimates of phenotypic and genotypic coefficient of variation were observed for the parameter days to first

flowering. Similar result was reported by Sharma and Swaroop (2000). In this study, the coefficient of phenotypic and genotypic variation in respect of all the characters do not differ much in their magnitude suggesting that the characters are not much amenable to environmental factors, thus the selection may be based very well on the phenotypic values.

Heritability and genetic advance as percent of mean

Heritability estimate in broad sense alone, does not serve as the true indicator of genetic potentiality of the genotype, since the scope is restricted by their interaction with environment. Hence, it is advisable to consider the predicted genetic advance as percent of mean along with heritability estimate as a reliable tool in selection programme (Johnson et al., 1955). Hence, both heritability and genetic advance as percent of mean were determined to get a clear picture of the scope for improvement in various characters through selection. The results of the present investigation showed that, the heritability values were quite high for all the characters, indicating that the major part of the variability was due to genotypic causes. High heritability also indicated that there was more number of additive genes for

these characters. The results are in line with the findings of Prabakaran (2010). High heritability coupled with high genetic advance was observed for fruit length, fruit pedicel length, fruit circumference, calyx length, number of fruits per plant, average fruit weight, shoot borer infestation, fruit borer infestation, little leaf incidence, ascorbic acid content, total phenol content and fruit yield per plant, which suggested that the selection among the genotypes can bring about significant improvement in the fruit yield and its component characters. This is in conformity with the findings of Pathania et al. (2002).

Further, high heritability combined with high expected genetic advance proved the involvement of additive genetic variance, therefore simple selection may be effective for improvement of these traits. Similar findings were reported by Chung-won et al. (2003). The qualitative trait ascorbic acid content had high heritability and high genetic advance, which confirms the predominance of additive gene action. Plant height and number of branches per plant exhibited moderate amount of heritability and genetic advance which indicated the presence of non-additive gene action for these traits and thus, improvement of these traits by selection was not possible. Days to first flowering had high heritability and low genetic advance which indicated the role of non-additive gene action that include dominance and epistasis.

Table 3. Variability parameters for different characters in Brinjal.

Character	PCV ^a	Mean	GCV	ECV	h ²	GA as % of mean
Plant height (cm)	13.93	91.97	10.21	9.47	53.74	15.42
Days to first flowering	5.70	80.30	5.18	2.49	81.46	9.64
Number of branches per plant	14.05	20.21	10.03	9.83	51.01	14.76
Fruit length (cm)	21.02	6.43	20.61	4.14	96.11	41.63
Fruit pedicel length (cm)	16.07	4.40	15.71	3.36	95.62	31.66
Fruit circumference (cm)	14.84	11.57	14.19	4.49	90.88	27.86
Calyx length (cm)	34.37	3.67	33.68	6.87	96.00	67.98
Number of fruit per plant	22.52	26.54	21.88	5.33	94.39	43.79
Average fruit weight (g)	15.93	50.38	15.51	3.65	94.74	31.10
Shoot borer infestation (%)	16.84	28.49	16.47	3.48	95.73	33.21
Fruit borer infestation (%)	12.41	41.89	11.86	3.64	91.36	23.36
Little leaf incidence (%)	26.57	26.49	26.32	3.65	98.10	53.71
Ascorbic acid content (mg/100 g)	15.13	11.38	14.83	2.99	96.07	29.95
Total phenols content (mg/100 g)	23.21	61.07	23.05	2.67	98.67	47.18
Fruit yield per plant (kg)	26.61	1.43	25.84	6.37	94.26	51.68

^a PCV = phenotypic coefficient of variation; GCV = genotypic coefficient of variation, h² = heritability and GA = genetic advance.

Conclusion

The genetic architecture of fruit yield is based on the balance or overall net effect produced by various yield components interacting with one another. Based on the studies on genetic variability, it may be concluded that, the characters fruit length, calyx length, number of fruits per plant, little leaf incidence, total phenol content and fruit yield per plant recorded high amount of genetic variability along with heritability and genetic advance. This reveals that there is a greater scope for improving these characters by simple phenotypic selection. Days to first flowering, which was found to be under the influence of non - additive gene action, suggested that heterosis breeding is the best to improve this trait.

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