Genetic Investigation in Segregating Generation of Brinjal (*Solanum melongena* L.)

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Received: 3 October 2020 / Revised: 15 May 2021 / Accepted: 9 July 2021 / Published online: 27 September 2021
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Abstract The genetic variability studies indicated that the prevalence of sufficient genetic variation among the genotypes for all the characters. The high Genotypic co-efficient of variation and Phenotypic co-efficient of variation were observed for the number of primary branches and number of fruits per plant. High heritability coupled with high Genetic Advance as per cent of Mean was observed for plant height, number of primary branches, plant spread from North to South, plant spread from East to West, fruit length, fruit diameter, average fruit weight, number of fruits per plant, fruit yield per plant and Total Soluble Solids indicating that these characters are governed by additive gene action. Hence, direct selection may be followed for the improvement of brinjal by assessing these characters.

Keywords Brinjal · Variability · Heritability · Genetic advance

Significant Statement

The success of any crop improvement programme largely depends upon the nature and magnitude of the genetic variability existing in breeding material. So the experiment was conducted to study the genetic variability, heritability and genetic advance in F₂ segregating population of the cross Surya × Harita.

Introduction

Brinjal also known as eggplant or aubergine is a common vegetable crop grown in tropical and subtropical climates. It is not possible to have one common cultivar to suit different localities. It is therefore required to improve the yield potential of available land races through hybridization, which may yield good hybrids or inbreds. The success of any crop improvement programme largely depends upon the nature and magnitude of the genetic variability existing in breeding material. Effectiveness of selection directly depends on the amount of heritability and genetic advance as *per cent* of mean for that character. 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 program. Therefore, in the current study, an attempt has been made to access the variability in the segregating population of the brinjal hybrid, Surya × Harita.

Material and methods

The present investigation was carried out at the Vegetable Science Block in College of Horticulture, Mudigere, University of Agricultural and Horticultural Sciences,

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Shivamogga during the rabi season 2018–2019. The experiment consisted of 300 F_2 plants derived from the cross Surya $\times$ Harita along with their parents, F_1 hybrids and four checks viz., Arka Harshitha, Arka Keshav, Arka Kusumakar and Devanur Local which were evaluated for yield and yield components. The experiment was laid out in an Augmented Block Design and 30-days-old seedlings were transplanted in 60×45 cm spacing, and all the recommended agronomic package of practices were followed. Data were recorded on all the 300 F_2 plants, ten randomly selected plants in each of the checks, parents and F_1 hybrids for 16 characters viz., plant height (cm), number of primary branches, plant spread from North to South (cm), plant spread from East to West (cm), days to first flowering, number of flowers per cluster, number of fruits per cluster, fruit set percentage, days to first picking, fruit length (cm), fruit diameter (mm), average fruit weight (g), number of fruits per plant, fruit yield per plant (kg) and TSS ($^{\circ}$ brix). The genetic parameters of variability like grand mean, range, phenotypic and genotypic coefficient of variation [1], broad-sense heritability, genetic advance and genetic advance as percentage over mean [2] were calculated.

Estimation of Genetic Parameters

Genotypic, Phenotypic and Environmental Variances

Variance due to genotype, phenotype and environment were computed as follows.

$$\text{Genotypic variance}(\sigma^2g) = \frac{\text{Treatment MSS} - \text{Error MSS}}{r}$$

$$\text{Environmental variance}(\sigma^2e) = \text{Error mean sum of squares,}$$

$$\text{Phenotypic variance}(\sigma^2p) = \sigma^2g + \sigma^2e$$

where, r is the number of replications.

Phenotypic and Genotypic Coefficient of Variation

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for all the characters were calculated according to the formula provided by [1] based on the estimate of genotypic and phenotypic variance as follows:

(a)

$$\text{Phenotypic coefficient of variation(PCV\%)} = \frac{\sigma^2p}{\bar{X}} \times 100$$

(b)

$$\text{Genotypic coefficient of variation(GCV\%)} = \frac{\sigma^2g}{\bar{X}} \times 100$$

where, σ^2p = Phenotypic variance of F_2 , σ^2g = Genotypic variance of F_2 , $\bar{X}$ = Mean of F_2 population.

PCV and GCV were classified as 0–10% as Low, > 10–20% as Moderate and more than 20% and above as High.

Heritability (h^2 Broadsense)

Broad-sense heritability was estimated for all the traits using the following formula of [2]

$$h^2(\%) = \frac{\sigma^2g}{\sigma^2p} \times 100$$

where, h^2 = Heritability (broad sense) expressed in per cent, σ^2g = Genotypic variance of F_2 population, σ^2p = Phenotypic variance of F_2 population.

Heritability percentage was categorized, 0–30% as Low, > 30–60% as Moderate and more than 60% and above as High.

Genetic Advance (GA)

The extent of genetic advance expected through selection in the F_2 population for each character was estimated by using the following formula of [2].

$$GA = h^2 \times K \times \sigma_p$$

where, h^2 = Heritability estimate, K = Selection differential at given intensity (which is equal to 2.06 at 5 per cent intensity of selection), σ_p = Phenotypic standard deviation.

Genetic Advance as Per Cent over Mean Genetic advance as per cent over mean was worked out as suggested by [2].

Genetic advance as per cent over mean

$$= \frac{GA}{\text{Grand mean}} \times 100$$

The genetic advance as percent mean was categorized as 0–10% as Low, > 10–20% as Moderate and more than 20% and above classified as High.

Analysis of variance in F_2 segregating population of the cross Surya $\times$ Harita indicated a significant mean sum of squares attributable to ‘treatment’ (F_2 progenies + checks), ‘tests’ (F_2 progenies), ‘controls’ (checks) and ‘tests vs controls’ for all the traits studied (Table 1). Overall high variability existed for all the characters studied and considerable improvement could be achieved in most of the traits by selection.

The estimates of genetic parameters for growth and yield attributes in F_2 segregating population of the bi-parental cross Surya $\times$ Harita were presented in the Table 2 and Fig. 1. High value of GCV and PCV (> 20 per cent) were observed for number of primary branches per plant (22.10% & 24.91%) and number of fruits per plant

Table 1 Analysis of variance in F_2 segregating population of the bi-parental cross Surya $\times$ Harita for growth and yield parameters

Sl. no.	Source Degrees of freedom	Block 9	Treatment 303	Tests 299	Controls 3	Tests versus controls 1	Error 67	Total 379
1.	Plant height (cm)	35.16*	158.22**	145.86**	653.80**	2368.12**	15.68	60.01
2.	Number of primary branches	1.27**	3.13**	2.85**	28.42**	8.38**	0.34	5.07
3.	Plant spread from north to south (cm)	51.84	219.54**	220.58**	135.85**	159.50*	30.75	61.67
4.	Plant spread from east to west (cm)	54.43*	196.55**	197.91**	92.26**	102.54*	20.89	62.22
5.	Days to first flowering	0.59	14.77**	12.93**	44.05**	478.21**	0.51	59.48
6.	Number of flowers per cluster	0.52**	0.48**	0.42**	1.08**	14.00**	0.14	2.87
7.	Number of fruits per cluster	0.16*	0.29**	0.19**	1.15**	28.22**	0.07	1.55
8.	Fruit set percentage	90.97	246.65**	218.98**	221.31*	8594.05**	60.30	55.19
9.	Days to first picking	0.95	14.80**	12.94**	41.76**	490.45**	0.63	89.49
10.	Fruit length (cm)	1.40**	9.14**	5.20**	129.42**	828.87**	0.48	15.73
11.	Stalk length (cm)	0.06	0.69**	0.68**	1.11**	3.71**	0.20	5.93
12.	Fruit diameter (mm)	1.49	46.02**	39.87**	58.01**	1849.17**	2.30	31.20
13.	Average fruit weight (g)	13.45	129.90**	129.32**	105.44**	374.78**	11.73	52.21
14.	Number of fruits per plant	1.09	28.33**	27.86**	5.26**	239.54**	1.24	15.27
15.	Fruit yield per plant (kg)	0.01**	0.12**	0.11**	0.02**	1.01**	0.002	0.80
16.	Total soluble solids ($^{\circ}$ brix)	0.25	1.45**	1.35**	1.81**	30.98**	0.13	4.61

*Indicates significant @ 5% level, and **indicates significant @ 1% level

Table 2 Estimates of genetic parameters for growth and yield attributes in F_2 segregating population of the bi-parental cross Surya $\times$ Harita

Sl. no.	Characters	Mean	Range		GV	PV	GCV (%)	PCV (%)	h^2 (%)	GA	GAM (%)
			Min	Max							
1.	Plant height (cm)	60.00	21.00	95.00	65.09	80.76	13.45	14.98	80.60	19.32	32.20
2.	Number of primary branches	5.07	2.00	12.00	1.26	1.60	22.10	24.91	78.68	3.39	66.83
3.	Plant spread from north to south (cm)	61.67	26.00	100.00	94.92	125.66	15.80	18.18	75.54	23.85	38.67
4.	Plant spread from east to west (cm)	62.21	17.00	104.00	88.51	109.40	15.12	16.81	80.90	22.36	35.94
5.	Days to first flowering	59.48	55.00	67.00	6.21	6.71	4.19	4.36	92.55	6.26	10.53
6.	Number of flowers per cluster	2.86	1.20	5.80	0.14	0.28	13.08	18.50	50.00	1.59	55.60
7.	Number of fruits per cluster	1.54	1.00	3.60	0.06	0.13	15.91	23.41	46.15	1.20	78.20
8.	Fruit set percentage	55.19	25.00	99.12	79.34	139.64	16.14	21.41	56.82	24.91	45.14
9.	Days to first picking	89.49	85.00	97.00	6.16	6.78	2.77	2.91	90.85	6.27	7.01
10.	Fruit length (cm)	15.72	9.90	23.90	2.36	2.84	9.77	10.72	83.10	4.30	27.37
11.	Stalk length (cm)	5.92	3.70	8.10	0.24	0.44	8.28	11.21	54.54	1.91	32.30
12.	Fruit diameter (mm)	31.20	22.08	49.60	18.78	21.08	13.89	14.72	89.09	10.35	33.17
13.	Average fruit weight (g)	52.20	16.66	90.00	58.80	70.53	14.69	16.09	83.37	18.13	34.74
14.	Number of fruits per plant	15.27	8.00	38.00	13.31	14.54	23.89	24.97	91.54	8.77	57.44
15.	Fruit yield per plant (kg)	1.48	0.36	2.40	0.05	0.06	15.70	15.99	96.43	1.45	98.09
16.	Total soluble solids ($^{\circ}$ brix)	4.61	2.34	8.45	0.61	0.74	16.94	18.66	82.43	2.60	56.32

GV genotypic variance, GCV genotypic coefficient of variance, h^2 heritability (broad sense), PV phenotypic variance, PCV phenotypic coefficient of variance, GA genetic advance, GAM genetic advance as per cent of mean

(23.89% & 24.97%). The difference between PCV and GCV being very low for majority of the characters suggesting more prevalence of genetic governance of these characters and thus selection on phenotypic basis would

hold good. These findings are consistent with those of previous researchers [3–5].

High estimates of heritability coupled with higher genetic advance as per cent of mean were observed for

Fig. 1 Variability in F_2 segregating population of the bi-parental cross Surya $\times$ Harita

plant height (80.60% & 32.20%), number of primary branches (78.68% & 66.83%), plant spread from North to South (75.54% & 38.67%), plant spread from East to West (80.90% & 35.94%), fruit length (83.10% & 27.37%), fruit diameter (89.09% & 33.17%), average fruit weight (83.37% & 34.74%), number of fruits per plant (91.54% & 57.44%), fruit yield per plant (96.43% & 98.09%) and TSS (82.43% & 56.32%). This indicates the role of additive gene action in the expression of these characters. Hence, simple selection method can be employed for the improvement of these characters. These results are in agreement with earlier workers [6, 7].

Acknowledgements This study was carried out and financially supported by the College of Horticulture, Mudigere, University of Agricultural and Horticultural Sciences, Shivamogga to study the genetic investigation in segregating generation of brinjal (*Solanum melongena* L.). The author is very thankful to Devaraju and Srinivasa V from department of Vegetable Science, College of Horticulture, Mudigere for their support throughout the study.

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