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Study of genetic variability and heritability in brinjal (*Solanum melongena* L.)

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Abstract
The investigation was carried out at Vegetable Research Station, Junagadh Agricultural University, Junagadh (Gujarat) during late *kharif*/rabi 2018-19 in Randomized Block Design with three replications. The experimental material comprised of thirty five genotypes and five check varieties. The analysis of variance revealed that mean sum of square due to genotype was highly significant for all fourteen characters studied. High phenotypic and genotypic coefficients of variation, high heritability coupled with high genetic advance as per cent of mean were observed for fruit borer infestation, number of fruits per plant, fruit weight, fruit length, number of branches per plant, plant height and total fruit yield per plant.

Keywords: Genetic variability, heritability, GCV, PCV, brinjal

Introduction
Eggplant [*Solanum melongena* (L.) 2n=24] or aurbergine is a species of nightshade, belongs to family Solanaceae. The solanaceae family consists 75 genera and over 2000 species. The genus Solanum comprises approximately 200 tuber bearing and 1800 non-tuber bearing species.

Brinjal originated in India, which is also considered as a center of diversity (Genabus, 1963) [7]. It is classified as a self-pollinated crop. Natural out-crossing has also been reported which varies with the varieties and environments, the average being about 6-7% so, it is also said to be often cross-pollinated crop (Choudhary, 1976) [5].

To develop high yielding varieties for a systematic breeding programme, information on genetic variability is basic pre-requisite. The success of any breeding programme depends upon the amount of genetic variability present in the available germplasm of a particular crop. Wider the genetic variability, more are the chances of improvement through selection. Fruit yield are governed by polygenic system and are highly influenced by the fluctuations in the environments. Hence, selection of plants based directly on fruit yield would not be very much reliable in many cases. Therefore, the present study was conducted to estimate genetic variability, heritability and genetic advance for fruit yield and yield contributing characters.

Materials and Methods
The present investigation was carried out to assess the genetic variability in brinjal (*Solanum melongena* L.). The experiment was conducted at Vegetable Research Station, Junagadh Agricultural University, Junagadh during late *kharif/rabi* of 2018-19. The experimental material comprised of 35 genotypes and 5 check varieties. Five randomly selected plants were considered for different characters *viz.*, days to 50% flowering, days to first picking, days to last picking, number of pickings, fruit length (cm), fruit girth (cm), fruit weight (g), number of fruits per plant, number of branches per plant, plant height (cm), plant spread (cm), total fruit yield per plant (kg), total soluble solids (B°) and fruit borer infestation (%). The analysis of variance for randomized block design (RBD) was done for each character as per Panse and Sukhatme (1985) [9]. Phenotypic co-efficient variation (PCV) and genotypic co-efficient variation (GCV) was calculated as per the formula suggested by Burton and De Vane (1952) [4]. Heritability and genetic advance was estimated using the formula suggested by Allard (1960) [1].

Result and Discussion

Analysis of variance

The analysis of variance indicated that the mean sum of squares due to genotypes were significantly influenced by all traits and indicated presence of sufficient amount of variability among the genotypes for total fruit yield per plant and its components.These findings are in general agreement with the findings of Tripathi *et al.* (2009) [12] and Ravali *et al.* (2017) [11].

Genotypic and phenotypic coefficient of variation

The value of phenotypic coefficient of variation was higher than corresponding genotypic coefficient of variation indicating the influence of environmental factors. Fruit borer infestation (Ravali *et al.*, 2017; Bende *et al.*, 2019) [11, 3] exhibited the maximum values for genotypic and phenotypic coefficients of variation followed by number of fruits per plant (Rani *et al.*, 2017; Ravali *et al.*, 2017) [10, 11], fruit weight (Ravali *et al.*, 2017; Divya and Sharma, 2018) [11, 6], fruit length (Ravali *et al.*, 2017; Divya and Sharma, 2018) [11, 6], number of branches per plant (Muniappan *et al.*, 2010) [8], plant height (Divya and Sharma, 2018) [6] and total fruit yield per plant (Tripathi *et al.*, 2009; Ansari, 2010) [12, 2].

Heritability and genetic advance

In present study, high heritability coupled with high genetic advance expressed as percent of mean was recorded for fruit borer infestation, number of fruits per plant, fruit weight, fruit length, number of branches per plant, plant height, total fruit yield per plant, fruit girth and plant spread suggesting the existence of sufficient amount of heritable variation and wider scope for effective selection. These findings are in general agreement with the findings of Tripathi *et al.* (2009) [12], Munniappan *et al.* (2010) [8], Koundinya *et al.* (2017), Ravali *et al.* (2017) [11], Divya and Sharma (2018) [6] and Bende *et al.* (2019) [3].

Table 1: Analysis of variance showing mean squares for 14 characters in 40 genotypes of brinjal

Source	d.f.	Days to 50% flowering	Days to first picking	Days to last picking	No. of pickings	Fruit length (cm)	Fruit girth (cm)	Fruit weight (g)
Replications	2	0.18	2.28	1.96	1.26	1.20	0.24	0.74
Genotypes	39	121.34**	165.83**	92.40**	2.76**	21.83**	2.68**	2059.52**
Error	78	5.47	6.04	25.49	0.78	1.29	0.39	122.02

Source	d.f.	No. of fruits/plant	No. of branches/plant	Plant height (cm)	Plant spread (cm)	Total fruit yield/plant (kg)	Total soluble solids (B°)	Fruit borer infestation (%)
Replications	2	17.29**	0.13	60.11	34.59	0.0026	0.02	0.17
Genotypes	39	95.70**	1.74**	728.06**	476.69**	0.24**	0.78**	35.32**
Error	78	3.62	0.04	41.04	78.92	0.02	0.05	0.14

*, ** significant at 5% and 1% levels, respectively

Table 2: The estimates of genotypic and phenotypic variances and other genetic parameters for different characters in brinjal

Sr. No.	Characters	Range	Genotypic coefficients of variance (GCV %)	Phenotypic coefficients of variance (PCV %)	Heritability in broad sense (H^2_{bs}) (%)	Genetic advance (GA)	Genetic advance as % of mean (GAM %)
1	Days to 50% flowering	50.26 - 92.32	9.19	9.41	95.49	12.51	18.51
2	Days to first picking	66.12 – 101.25	9.26	9.43	96.36	14.76	18.73
3	Days to last picking	149.65 – 170.65	2.92	3.44	72.41	8.28	5.12
4	No. of pickings	8.99 – 12.99	6.90	8.15	71.77	1.42	12.04
5	Fruit length (cm)	5.17 – 15.08	27.12	27.96	94.10	5.24	54.20
6	Fruit girth (cm)	3.19 – 6.80	17.57	19.02	85.30	1.66	33.44
7	Fruit weight (g)	32.01 – 133.28	31.54	32.52	94.08	50.78	63.02
8	No. of fruits/plant	8.64 – 27.30	32.54	33.18	96.22	11.20	65.76
9	No. of branches/plant	2.00 – 5.40	23.71	24.01	97.43	1.53	48.20
10	Plant height (cm)	36.10 – 95.65	23.08	23.76	94.36	30.28	46.18
11	Plant spread (cm)	58.44 – 112.76	13.71	15.01	83.44	21.67	25.80
12	Total fruit yield/plant (kg)	0.86 – 1.85	21.57	22.64	90.82	0.53	42.35
13	TSS (B°)	4.19 – 6.56	8.76	9.09	93.00	0.98	17.41
14	Fruit borer infestation (%)	0.00 – 16.70	45.90	45.99	99.60	7.04	94.38

Conclusion

It can be concluded from the present investigation that high phenotypic and genotypic coefficients of variation, high heritability coupled with high genetic advance as percentage of mean were recorded for fruit borer infestation, number of fruits per plant, fruit weight, fruit length, number of branches per plant, plant height, total fruit yield per plant, fruit girth, plant spread, which indicated the predominance of additive gene action and better scope for improvement of these characters for effective selection of genotype.

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