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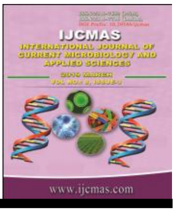

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Genetic Variability for Quantitative and Qualitative Characters in Brinjal (*Solanum melongena* L.)

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ABSTRACT

Keywords

Brinjal, Genotypic coefficient of variation, Phenotypic coefficient of variation, *Solanum melongena*, Fruit borer infestation

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In brinjal, lower marketable yield could be attributed to susceptibility of genotypes to shoot and fruit borer. The present investigation in brinjal (*Solanum melongena* L.) was undertaken during *kharif* season of 2016 for high marketable yield and fruit borer resistance. Hundred brinjal genotypes along with two checks were evaluated in Augmented design in University of Horticultural and Agricultural Sciences, Shivamogga. Analysis of variance revealed high significant differences among genotypes for fifteen out of nineteen characters studied. High estimates of PCV, GCV, heritability coupled with high genetic advance were observed for fruit weight, number of fruits per cluster and shoot borer infestation. Hence indicating high variability for these traits and selection for these traits may be effective.

Introduction

India, being the primary centre of origin has accumulated wide range of variation in this crop. A great genetic variation with regard to colour, maturity, fruit shape, vegetative characters and spinyness of the plants exists among the indigenous material. The wide range of variability was observed in respect of morphological traits. The genetic variance of any quantitative trait is composed of additive variance (heritable) and non-additive variance (non-heritable). Therefore, it becomes necessary to partition the observed phenotypic variability into its genotypic (partly heritable) and environmental (non-heritable) components with suitable parameters, such as phenotypic and genotypic coefficient of variation and heritability in broad sense. Effectiveness of selection directly depends on the amount of heritability and genetic advance as per cent mean of the character. Thus, the improvement in yield is possible only through selection of the desired component characters.

Materials and Methods

In the proposed research work conducted at ZAHRS Navile, Shivamogga during Kharif 2016-17, among the local germplasm collected from Organic forming research institute (OFRC) 100 superior germplasm lines were identified. The experiment was laid out in Augmented design, tray sowing was carried out in 6 June 2016. The seedlings were transplanted in main field 25 days after sowing with the spacing of 60×45 cms in Augmented design along with 2 checks. All the recommended cultural practices and plant protection measures were followed, observations were recorded for 100 genotypes along with 2 checks viz., leaf area, Days to first flowering, Days to 50 per cent flowering, Days to first fruit maturity, Plant height, Plant spread, No. of primary branches, Fruit length, Fruit diameter, Fruit length-diameter ratio, Fruit length of peduncle, Fruit length of calyx, Fruit length of pistil scar, No. of fruits per cluster, No. of fruits per plant, Average fruit weight, Total yield per hectar, fruit and shoot borer infestation on fruit, fruit and shoot borer infestation on shoot.

Results and Discussion

Totally 102 genotypes were evaluated to know the amount of variability for yield and yield contributing characters. The analysis of variance (Table 1) indicated highly significant differences among genotypes for most of the characters *viz*., plant height, plant spread, number of primary branches, days to first flowering, days to 50 per cent flowering, days to first fruit maturity, fruit length, fruit diameter, fruit length/diameter ratio, fruit size of calyx, fruit diameter of pistil scar, number of fruits per cluster, fruit weight, yield and shoot borer infestation. It indicated that sufficient variability existed for all the characters and considerable improvement could be achieved in most of these characters by selection.

One of the ways in which the variability of these characters assessed is through a simple approach of examining the range of variation. Range of variation observed for all the traits (Table 2) indicated the presence of sufficient amount of variation among the genotypes for all the characters studied. The range in the values reflects the amount of phenotypic variability which is not very reliable since it includes genotypic, environmental and genotype x environmental interaction components and does not reveal as which component is showing higher degree of variability.

In the present investigation, high genotypic coefficient of variation and phenotypic coefficient of variation (>20%) were observed for leaf area and number of primary branches. Similar results were also obtained by Kumar *et al.,* (2011), Shekar *et al.,* (2012) and Karak *et al.,* (2012) Lokesh *et al.,* (2013a) and Nayak and Nagre (2013). It indicated the presence of high variability in the germplasm for selection and even the differences between PCV and GCV values were minimum, indicating that traits under study were less influenced by environment. Hence, these characters can be relied upon and simple selection can be practiced for further improvement.

Low GCV and PCV were recorded for days to 50 per cent flowering. These findings are in close agreement with the results obtained by Muniappan *et al.,* (2010), Sao and Dahatonde *et al.,* (2010), Kumar *et al.,* (2011), Shekar *et al.,* (2012) and Arunkumar *et al.,* (2013) Das *et al.,* (2002), Mishra *et al.,* (2008), Sabeena *et al.,*(2011) and Vandana *et al.,* (2014). Low GCV and PCV indicated the narrow genetic base therefore selection for such traits may not give desirable results. Moderate GCV and PCV were observed for days to first flowering and days to first fruit maturity indicating the little influence of environment. Therefore, phenotypic variability may be a good measure of genotypic variability. The findings of Ramesh *et al.*, (2013), Abul *et al.*, (2015) and Gavade and Ghadage (2015) are in conformity with the present findings.

High heritability coupled with moderate genetic advance as percentage over mean was recorded for days to fifty per cent flowering indicating that the expression of this character as governed by non-additive gene action and could be exploited through heterosis breeding. This view was supported by Vandana *et al.*, (2014), Lokesh *et al.*, (2013a) and Akpan *et al.*, (2016).

High heritability coupled with high genetic advance as percentage over mean was recorded for days to first flowering and days to first fruit maturity indicating that the heritability is due to additive gene effects and selection may be effective. This view was supported by Sherly and Shanthi (2008), Sabeena *et al.*, (2011) and Abul *et al.*, (2015).

In the present study, very high heritability (>60%) along with high genetic advance as per cent over mean (>20%) was recorded for the growth parameters *viz.*, plant height, plant spread number of primary branches and leaf area. These results suggested that the inheritance of such characters is governed mainly by additive gene effects and therefore, selection based on phenotypic performance may prove useful. Similar results were also reported by Muniappan *et al.*, (2010), Karak *et al.*,(2012), Kumar *et al.*, (2012), Arunkumar *et al.*, (2013), Lokesh *et al.*, (2013a), Vandana *et al.*, (2014) and Akpan *et al.*, (2016).

Moderate estimates of GCV and PCV (11-20%) were observed for plant height and plant spread. Several workers *viz.*, Dahatonde *et al.*, (2010), Kumar *et al.*, (2011), Sabeena *et al.*,(2011), Karak *et al.*, (2012) and Ramesh *et al.*, (2013), reported similar findings. These results suggest that influence of environment was low or little. Therefore, phenotypic variability may be a good measure of genotypic variability.

High (>20%) GCV and PCV were observed for most of yield traits *viz.*, fruit size of calyx, fruit diameter of pistil scar, fruit length, fruit diameter and fruit length-diameter ratio. These results indicated the existence of sufficient variability in genetic stock studied and the environmental role is negligible. Hence, there is ample scope for improving these characters with direct selection. Several workers like Kumar *et al.*, (2012), Arunkumar *et al.*, (2013), Ramesh *et al.*, *(*2013), Lokesh *et al.*, (2013), Gavade and Ghadage (2015), Nayak and Nagre (2013), Sharmin *et al.*,(2010), Vandana *et al.*, (2014), Abul *et al.*, (2015), Vidhya and Kumar (2015) and Akpan *et al.*, (2016) reported similar findings.

High (>20%) GCV and PCV were observed for most of yield traits *viz.*, number of fruits per cluster, fruit weight, number of fruits per plant, and yield per hectare. These results indicated the existence of sufficient variability in genetic stock studied and the environmental role is negligible. Hence, there is ample scope for improving these characters with direct selection. Several workers like Dahatonde*e t al.*, (2010), Das *et al.*, (2010), Muniappan *et al.*, (2010), Kumar *et al.*, (2012), Arunkumar *et al.*, (2013), Lokesh *et al.*, (2013), Nayak and Nagre (2013) and Abul *et al.*, (2015) reported similar findings.

High heritability (>60%) estimates along with high GAM (>20%) was recorded for number of fruits per cluster, fruit length, fruit diameter, fruit length/diameter ratio, fruit weight, yield per hectare indicating predominance of additive gene component. Thus, there is ample scope for improving these characters with direct selection. In the existing germplasm stock, the *per se* performance of genotypes M-1, N-2, MS-2 and B-2 for fruit weight and B-1, M-6, B-3 and P-2 for yield per plant indicated that these genotypes could be used for further improvement. Similar findings were also reported by several investigators like Dahatonde *et al.*, (2010), Das *et al.*, (2010), Muniappan *et al.*, (2010), Kumar *et al.*, (2012), Arunkumar *et al.*, (2013), Lokesh *et al.*, (2013) Ramesh *et al.*, (2013), Vandana *et al.*, *(*2014), Nayak and Nagre (2013) and Vidhya and Kumar (2015).

Moderate (11-20%) GCV and PCV were observed for fruit length of peduncle indicating presence of moderate amount of variability for these traits. Selection for such traits may not give desired results. Similar results were also obtained by Ramesh *et al.*, *(*2013).

High (>20%) GCV and PCV were observed for most of yield traits *viz*., fruit borer infestation (%), shoot borer infestation (%). These results indicated the existence of sufficient variability in genetic stock studied and the environmental role is negligible. Hence, there is ample scope for improving these characters with direct selection. Several workers like Lokesh *et al.*, (2013a), Nayak and Nagre (2013), reported similar findings. High heritability (>60%) estimates along with high GAM (>20%) was recorded for fruit borer infestation (%), shoot borer infestation (%), indicating predominance of additive gene component.

Table.1 Analysis of variance in brinjal genotypes for various quantitative traits

SL. No.	Source	Treatment	Checks	Checks+Va vs. Var	Block	Entries	Varieties	Checks v varieties	Error
	Degrees of freedom	101	1	100	4	101	99	1	4
1.	Leaf area (cm^2)	911.71	1552.27 *	905.30	1884.17	983.45	978.19	935.02	176.92
2.	Days to first flowering	35.14 **	9.03 *	35.40 **	128.75	40.18	40.87	3.41	0.77
3.	Days to 50 per cent flowering	32.35 **	23.10 **	32.45 **	112.67	36.78	36.84	44.44 **	0.77
4.	Days to first fruit maturity	116.91 **	929.30	108.78 **	560.16	138.73 **	130.26 **	187.21 **	5.14
5.	Plant height (cm)	76.35 *	183.53 *	75.27 *	395.93	91.86 *	91.42 *	43.35	10.30
6.	Plant spread (cm)	120.70 **	93.40 **	120.97 **	835.07	153.65 **	155.80 **	1.15	3.62
7.	Number of primary branches	4.65 *	90.0	3.80	6.31	4.87 *	3.88	17.39 **	0.73
8.	Fruit length (cm)	4.47 **	5.99	4.45 **	7.53	4.76	4.71	8.61	0.07
9.	Fruit diameter (cm)	0.95 *	0.10	0.95 *	1.48	1.01 *	1.01 *	0.39	0.13
10.	Fruit length/diameter ratio	0.17 **	0.06 *	0.17 **	0.65	0.20 **	0.20 **	0.30 **	0.01
11.	Fruit length of peduncle (cm)	0.58	2.53 *	0.56	0.23	0.59	0.56	0.91	0.14
12.	Fruit size of calyx (cm)	0.65 *	2.02 *	0.64 *	0.05	0.65 *	0.64 *	0.33	0.10
13.	Fruit diameter of pistil scar (c	0.17 **	0.23 **	0.17 **	0.04	0.17 **	0.16 **	1.18	0.01
14.	Number of fruits per cluster	0.11 **	0.01	0.11 **	0.20	0.11	0.12	0.11	0.01
15.	Number of fruits per plant	77.20	110.89	76.86	15.78	77.60	74.80	321.20 *	22.30
16.	Fruit weight (g)	456.35 **	439.30	456.52 **	351.87	470.09	466.13	893.14	3.70
17.	Fruit yield (q/ha)	4364.71 *	48991.57	3918.44	5871.88	4567.53 *	4151.31	1349.57	741.87
18.	Fruit borer infestation (%)	510.22	196.25	513.36	952.09	539.27	546.55	161.56	171.14
19.	Shoot borer infestation (%)	119.40 *	129.81*	119.30 *	410.08	134.1 **	135.47 **	4.29	9.77

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

Table.2 Estimates of genetic parameters in brinjal genotypes for various quantitative characters

SL. No.	Character	Mean	Range		GCV (%)	PCV (%)	h^2 (%)	GAM (%)
			Min	Max				
1.	Leaf area (cm^2)	98.32	67.86	268.71	27.85	30.94	81.03	51.64
2.	Days to first flowering	54.63	41.40	65.80	11.27	11.38	98.01	22.98
3.	Days to 50 per cent flowering	66.78	54.20	80.80	8.73	8.84	97.79	17.80
4.	Days to first fruit maturity	98.79	80.40	117.60	10.97	11.21	95.83	22.12
5.	Plant height (cm)	61.63	49.28	90.22	14.19	15.12	88.14	27.45
6.	Plant spread (cm)	61.88	41.64	90.52	19.38	19.62	97.54	39.42
7.	Number of primary branches	7.04	4.20	11.80	24.57	27.42	80.28	45.34
8.	Fruit length (cm)	6.78	3.52	15.14	30.81	31.06	98.41	62.96
9.	Fruit diameter (cm)	4.41	2.42	9.20	20.64	22.20	86.44	39.53
10.	Fruit length/diameter ratio	1.56	0.92	3.17	27.50	27.84	97.55	55.94
11.	Fruit length of peduncle (cm)	4.06	2.24	6.88	15.64	18.11	74.63	27.84
12.	Fruit size of calyx (cm)	2.38	0.72	4.24	30.04	32.87	83.52	56.56
13.	Fruit diameter of pistil scar (cm)	1.34	0.64	2.15	28.12	28.92	94.59	56.34
14.	Number of fruits per cluster	1.11	1.00	2.46	29.69	29.87	99.51	61.15
15.	Number of fruits per plant	33.38	13.40	46.00	21.12	25.46	68.94	36.15
16.	Fruit weight (g)	49.07	24.62	121.20	42.40	42.58	99.16	86.98
17.	Fruit yield (q/ha)	269.37	143.46	419.26	21.06	23.36	81.25	39.10
18.	Fruit borer infestation (%)	23.33	5.74	44.77	40.05	48.78	67.41	67.73
19.	Shoot borer infestation (%)	11.46	3.59	23.14	92.38	47.78	92.38	94.59

GCV = Genotypic coefficient of variance PCV =Phenotypic coefficient of variance; h^2 = Heritability (broad sense)GAM = Genetic advance (per cent mean)

Thus, there is ample scope for improving these characters with direct selection. Similar findings were also reported by several investigators like Lokesh *et al.*, (2013a), Nayak and Nagre (2013), Ramesh *et al.*, (2013), Vidhya and Kumar (2015).

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