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Estimation of gene action, heterosis, genetic advance and other components in brinjal (*Solanum melongena* L.)

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Abstract
Twelve generations, namely P_1, P_2, F_1, F_2, B_1, B_2, B_{11}, B_{12}, B_{21}, B_{22}, B_1s and B_2s of three crosses of brinjal *viz.,* JBG-10-208 x GOB-1 (cross 1), NSR-1 x GBL-1 (cross 2) and JB-12-06 x Pant Rituraj (cross 3) were transplanted at Instructional Farm, Junagadh Agricultural University, Junagadh during late *kharif* 2016-17 to study the gene effect, heterosis, inbreeding depression, heritability in narrow sense and genetic advance using Compact Family Block Design (CFBD) with three replications. The observations were recorded on yield and yield related components. Generation mean analysis using ten parameters (m, [d], [h], [i], [j], [k], [l], [w], [x], [y] and [z]) was carried out to assess the presence of inter-allelic interaction and to estimate the importance of various gene effects. The crosses and the traits which were found significant digenic interaction (weighted least square technique) subjected to trigenic ten-parameter model. The trigenic ten-parameter model was found significant χ^2 values with two degrees of freedom for all the traits in all the three crosses showing the presence of higher order epistasis and /or linkage. Besides this, all ten-parameters were significant for fruit weight, plant spread and fruit borer infestation in all the crosses. The heterosis over better parent was significant for days to opening of first flower, number of fruits per plant, plant height, total fruit yield per plant, plant spread and fruit borer infestation in all the crosses. A high degree of inbreeding depression was found in JB-12-06 x Pant Rituraj (10.65%) indicated the exploitation of heterosis in this cross. Narrow sense heritability was observed high for fruit weight and plant height in all the crosses. The high heritability estimates followed the trend of high genetic advance in all the three crosses for most of the characters.

Keywords: Brinjal, generation mean analysis, heterosis and inbreeding depression

1. Introduction
Brinjal (*Solanum melongena* L.) is one of the major vegetable crops in India, China and several other countries of Asia, Africa and Europe. Brinjal is grown in almost all parts of India except higher altitude. In India, it is grown in an area of 6.63 lakh ha with production of 12.51 million tones and productivity of 18868 kg/ha (Anon., 2016) [2]. The major objective in most brinjal breeding programme is to improve the genetic potential for fruit yield. The knowledge about nature and magnitude of fixable and non-fixable type of gene effects, in the control of components of yield, is essential in order to achieve the genetic improvement in this crop. The information on the nature of gene action could be helpful in predicting the effectiveness of selection in a segregating material. A distinct knowledge of the type of gene effect, its magnitude and composition of genetic variance are of fundamental importance to a plant breeder. The efficient partitioning of genetic variance into its components *viz.,* additive, dominance and epistatis help in formulating an effective and sound breeding programme. Improvement of quantitative traits through selection depends upon the nature and magnitude of gene effects involved in inheritance of that particular trait. Generation mean analysis is a simple and useful technique for characterizing gene effects for quantitative traits (Hayman, 1958 and Gamble, 1962) [12, 10].

To boost productivity, the trend has been directed into evolving hybrids for exploiting heterosis. The exploitation of heterosis has become a potential tool in the improvement of the brinjal yield. Nagai and Kida (1926) [19] were the first to observe hybrid vigour in brinjal. The commercial exploitation of this phenomenon has been possible in the brinjal because of the low cost of F_1 seed production and the low seed requirement per unit area.

Information on the magnitude of heterosis in different cross combination is a basic requisite for identifying crosses that exhibit high degree of exploitable heterosis.

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Hence, the present study was undertaken with an objective of studying the nature of gene action and extent of heterosis in different crosses and its confirmation through inbreeding depression in F_2 generation and then utilization in future crop improvement programmes.

Materials and Methods
The field experiment was conducted at Instructional Farm, Junagadh Agricultural University, Junagadh during late *kharif* 2016-17. Geographically, Junagadh is situated at 21^0N latitude and 70.5^0E longitude with an altitude of 60 meters above the mean sea level. Temperature ranges from 36.6°C to 10.2°C in winter. The experimental material consists of twelve generations *viz.,* P_1, P_2, F_1, F_2, B_1, B_2, B_{11}, B_{12}, B_{21}, B_{22}, B_1s and B_2s derived from following three crosses of brinjal. The details of the parents are as given in Table 1.
1. Cross-1: JBG-10-208 × GOB-1
2. Cross-2: NSR-1 × GBL-1
3. Cross-3: JB-12-06 × Pant Rituraj

Table 1: Source and salient features of females and males of brinjal used in study

Females				
Sr No	Entries	Pedigree	Source	Salient Features
1.	JBG-10-208	Selection from material collected from Porbandar district	J.A.U., Junagadh	Spreading plant habit. Fruits are big round and attractive due to shining of bright purple colour.
2.	NSR-1	Selection from Surati Ravaiya	N.A.U., Navasari	Plants are non-spiny and spreading type. Fruits are pink medium round.
3.	JB-12-06	JBGR-6-15 x JBGR-1	J.A.U., Junagadh	Early fruit picking. Erect plant with green round fruits.
Males				
Sr No	Entries	Pedigree	Source	Salient Features
1.	GOB-1	Selection from local material	A.A.U., Anand	Lower incidence of jassids. Early fruit picking. Fruits are black and medium oblong.
2.	GBL-1	Pusa Purple Cluster x Pusa Kranti	J.A.U., Junagadh	Fruits are purple long and born in cluster. Spreading plant habit.
3.	Pant Rituraj	Selection from breeding line	G.B.U.A.T, Pant Nagar	Plants are semi erect with dark green foliage. Early fruit picking. Fruits are round purple and slightly tapering toward bottom.

On the basis of parental characteristics and performance of field grown F_1 plants, three crosses were selected. The seeds of F_1 of three crosses were used to prepare F_2, B_1, B_2, B_{11}, B_{12}, B_{21}, B_{22}, B_1s and B_2s generations during *kharif* 2015-16 and evaluated at Instructional Farm, College of Agriculture, Junagadh Agricultural University, Junagadh. The twelve generations of the three crosses were raised in compact family block design (CFBD) with three replications during late *kharif* 2016-17. Each replication was divided in to three compact blocks, each consists of single cross and blocks were consisted of twelve plots of twelve basic generation of each cross. The crosses were assigned to each block and twelve generations of a cross were relegated to individual plot within the block. Each block was comprised of nineteen rows consisting single row each of P_1, P_2, F_1, B_1 and B_2; two rows of F2, B_{11}, B_{12}, B_{21}, B_{22}, B_1s and B_2s generations. Each hybrid and parents represented single rows of 8.5 meter length spaced at 90 cm between rows and 60 cm between plants. Recommended agronomic practices and plant protection operations were followed to raise good crop. Fertilizers were applied at the rate of 100 kg N/ha, 50 kg P_2O_5/ha and 50 kg K_2O/ha. P_2O_5 and K_2O were applied as basal dose with 50 kg of nitrogen before one week of transplanting, while, remaining 50 kg nitrogen was top dressed at the time of flowering.
Data was recorded on randomly selected five competitive plants from P_1, P_2 and F_1; 10 plants from B_1 and B_2; 20 plants from F_2, B_{11}, B_{12}, B_{21}, B_{22}, B_1s and B_2s generations in each replication for twelve characters *viz.,* days to opening of first flower, days to first picking, fruit length (cm), fruit girth (cm), fruit weight (g), number of fruit per plant, number of branches per plant, plant height (cm), total fruit yield per plant (kg), plant spread (cm), total soluble solids and fruit borer infestation (%). Mean and variances were calculated for each generation using the data recorded on individual plants in each replication.

Statistical Analysis
Generation mean
Data were subjected to individual scaling test as given by Mather (1949) [17] and Hayman and Mather (1955) [13], who devised four simple scaling test *viz.*, A, B, C, and D, for the detection of presence or absence of epistasis. Further, simple scaling tests B11, B12, B21, B22, B1s and B2s (Hill, 1966) [14] and X and Y (Van Der Veen, 1959) [25] were also computed. Cavalli (1952) [6] joint scaling test was used for the precise estimates of different parameters. When the simple additive-dominance model failed to explain variation among generation means, a six parameter perfect fit model involving digenic interaction parameter proposed by Hayman (1958) [12] was applied. Various gene effects including first order and second order epistasis were estimated using ten-parameter model as suggested by Hill (1966) [14]. The degree of freedom (d.f.) equals to number of generation means used (n) minus the number of parameters (p) estimated. The significance of parameters was tested with related standard errors at 1% and 5% probability levels.
The A and B scaling tests provide the evidence for the presence of additive x additive (i), additive x dominance (j) and dominance x dominance (l) types of gene interaction. The C scaling test provides the test for (l) type of epistasis. The D scaling test provides the test for (i) type of epistasis.

Heterosis and Inbreeding Depression
Heterosis for each trait was worked out by utilizing the overall mean of each hybrid over replications for each trait.
a. **Relative heterosis** (MP) (mid parent value) was estimated as per cent deviation of hybrid value from its mid parental value as per Briggle (1963) [5].

$$MP\ (\%) = \frac{\overline{F_1} - \overline{MP}}{\overline{MP}} \ X\ 100$$

b. Heterobeltiosis (BP): Heterosis over better parent was calculated as per Fonseca and Patterson (1968) [9].

$$Heterobeltiosis\ (\%) = \frac{\overline{F_1} - \overline{BP}}{\overline{BP}} \ X\ 100$$

c. Inbreeding depression (ID) in F_2 generation was calculated as per Allard (1960) [1].

$$ID\ (\%) = \frac{\overline{F_1} - \overline{F_2}}{\overline{F_1}} \ X\ 100$$

Where,

$\overline{F_1}$ = Mean performance of F_1,

$\overline{BP}$ = Mean value of better parent of respective cross combination,

$\overline{MP}$ = Mid parental value *i.e.,* $(\overline{P}_1 + \overline{P}_2)/2$.

The standard error and calculated 't' values for heterosis (H) and inbreeding depression were computed as below:

S.E. for (MP) = $\sqrt{V_{\overline{F_1}} + V_{\overline{MP}}}$

S.E. for (BP) = $\sqrt{V_{\overline{F_1}} + V_{\overline{BP}}}$

S.E. for (ID) = $\sqrt{V_{\overline{F_1}} + V_{\overline{F_2}}}$

The test of significance for heterosis and inbreeding depression was done by usual t-test.

Heritability in narrow sense and genetic advance
The narrow sense heritability (h^2_{ns}) was calculated by the formula suggested by Warner (1952) as follows:

$$h^2_{ns} = \frac{2VF_2 - (VB_1 + VB_2)}{VF_2}$$

where,
VF_2, VB_1 and VB_2 are the variances of F_2, B_1 and B_2 generations, respectively. The above heritability estimate is based on the assumption that epistasis is absent.
The genetic advance and genetic advance as percent of mean were calculated as per Allard (1960) [1] as under:

Genetic advance (GA) = $i.6_p. \ h^2_{(ns)}$

Genetic advance as per cent of mean (GA%) = $\frac{GA}{\overline{X}} \ x\ 100$

Where,
I = Selection intensity at 5% selection (K = 2.06)
6_P = Phenotypic standard deviation
$h^2_{(ns)}$ = Heritability in narrow sense
$\overline{X}$ = Mean of a character

Results and Discussion
The analysis of variance between families (crosses) revealed that the mean squares due to crosses were significant for all the characters under study. The analysis of variance among progenies within each family indicated significant differences among twelve generation means for all the characters studied in all the three crosses (data not shown). Hence, further genetic analysis of generation means and calculation of heterosis and inbreeding were done.

a. Gene action (table 2)
The results of simple scaling tests revealed significant values of A, B, C, D, B_{11}, B_{12}, B_{22}, B_1s, B_2s and Y (cross 1); A, B, C, D, B_{11}, B_{21}, B_{22}, B_1s, B_2s and Y (cross 2) and A, B, C, B_{11},

B_{12}, B_{21}, B_{22}, B_1s, B_2s, X and Y (cross 3) for days to opening of first flower; A, B, C, D, B_{11}, B_{12}, B_{22}, B_1s, B_2s, X and Y (cross 1); A, B, C, D, B_{11}, B_{21}, B_{22}, B_1s, B_2s, X and Y (cross 2) and A, B, C, D, B_{11}, B_{21}, B_{22}, B_1s, B_2s and Y (cross 3) for days to first pocking; A, B, C, D, B_{11}, B_{21} and B_1s (cross 1); C, B_{12}, B_{22}, B_1s and X (cross 2) and B_{11}, B_1s, X and Y (cross 3) for fruit length (cm); C, D and B_2s (cross 1); B_{21}, B_{22}, B_1s and Y (cross 2) and only D (cross 3) for fruit girth (cm); B_{11}, B_{12}, B_{22}, B_1s, B_2s and X (cross 1); B, C, D, B_{11}, B_{12}, B_{22}, B_1s and Y (cross 2) and B_{12}, B_{22} and X (cross 3) for fruit weight (g); A, B, C, B_{11}, B_{21} B_{22}, B_1s, B_2s, X and Y (cross 1); A, B, C, D, B_{11}, B_{21}, B_{22}, B_1s, B_2s and X (cross 2) and A, B, C, D, B_{11}, B_{12}, B_{22}, B_1s, B_2s, X and Y (cross 3) for number of fruits per plant; B_1s, B_2s and X (cross 1); B_1s, B_2s and Y (cross 2) and B_{12}, B_2s and X (cross 3) for number of branches per plant; B, D, B_{22} and X (cross 1); C, D, B_{12}, B_1s and Y (cross 2) and A, B, B_{12}, B_{21}, B_{22}, B_2s, X and Y (cross 3) for plant height (cm); B, C, B_{21}, B_{22}, B_1s, B_2s and X (cross 1); C, D, B_1s and B_2s (cross 2) and A, B, C, B_{11}, B_{22}, B_1s, B_2s and Y (cross 3) for total fruit yield per plant (kg); A, B, C, D, B_{11}, B_{12}, B_{21}, B_{22}, B_1s, B_2s and Y (all the three crosses) for plant spread; B_{21}, B_2s and Y (cross 1); B_{22} and B_1s (cross 2) and B_{22} and B_2s (cross 3) for total soluble solids (°B) and A, B, C, D, B_{11}, B_{12}, B_{21}, B_{22}, B_1s, B_2s, X and Y (cross 1); C, D, B_{12}, B_{21}, B_{22}, B_1s, B_2s, X and Y (cross 2); A, B, C, D, B_{11}, B_{12}, B_{22}, B_1s, B_2s, X and Y (cross 3) for fruit borer infestation (%). (data not shown).

The additive-dominance model was not found adequate for any traits in the present study. The failure of additive-dominance model was attributed mainly to the epistasis. The results obtained from six parameter model of Hayman (1958) [12] revealed that 'm', [d], [h] and digenic ([i], [j] and [l]) were significant in all the crosses for days to opening of first flower, days to first picking, fruit weight, number of fruits per plant and plant spread; fruit length in NSR-1 x GBL-1 (cross 2) and JB-12-06 x Pant Rituraj (cross 3), total fruit yield per plant in JBG-10-208 x GOB-1 (cross 1) and NSR-1 x GBL-1 (cross 2), total soluble solids in JBG-10-208 x GOB-1 (cross 1) and fruit borer infestation in JBG-10-208 x GOB-1 (cross 1) and NSR-1 x GBL-1 (cross 2). The $\chi^2_{(2)}$ values were significant for all the traits in three crosses indicating inadequacy of digenic six-parameter model.
The 'm' gene effect found significant in all the three crosses of most of the traits i.e., fruit length, fruit weight, number of fruits per plant, number of branches per plant, total fruit yield per plant, plant spread, total soluble solids and fruit borer infestation. Based on ten-parameter model, it was observed that additive [d] gene effect was significant in all the crosses for days to first picking, fruit length, fruit girth, fruit weight, number of fruits per plant, plant spread and fruit borer infestation, while it was significant in two crosses for days to opening of first flower, total fruit yield per plant and total soluble solids. The additive [d] gene effect was also found significant in one cross only for number of branches per plant. Dominance [h] gene effect was significant for days to opening of first flower, days to first picking, fruit length, fruit weight, number of fruits per plant, total fruit yield per plant, plant spread, total soluble solids and fruit borer infestation in all the crosses; fruit girth and number of branches per plant in two crosses. Rai and Asati (2011) [21] were observed preponderance of both additive and non-additive gene effects for yield and its contributing characters.
Among the digenic interactions, additive × additive [i] gene effect found significant in all the crosses for days to opening of first flower, days to first picking, fruit girth, fruit weight,

number of fruits per plant, total fruit yield per plant, plant spread, total soluble solids and fruit borer infestation; in two crosses for number of branches per plant as well as in one cross only for plant height. Likewise, additive x dominance [j] gene effect was significant in all the crosses each for characters like days to first picking, fruit girth, fruit weight, total fruit yield per plant, plant spread and fruit borer infestation and two crosses each for days to opening of first flower, fruit length, number of fruits per plant, number of branches per plant and total soluble solids. Dominance x dominance [1] gene effect was significant for days to opening of first flower, days to first picking, fruit length, fruit weight, total fruit yield per plant, plant spread, total soluble solids and fruit borer infestation in all the crosses and fruit girth, number of fruits per plant and number of branches per plant in two crosses. Naulsri *et al*. (1988) [20] observed dominance x dominance [l] interaction for yield per plant. Lawande *et al.* (1992) [15] reported the impact of additive and additive x additive gene effects were more prominent for the number of fruits per plant, fruit weight and fruit yield per plant. Shinde *et al.* (2009) [23] indicated that epistatic component additive x additive and dominance x dominance were involved in the expression of fruit weight, fruit diameter, fruit girth, height of plant and seeds per fruit.

Triallelic epistasis was found to be significant in various crosses for different characters in the present study. Additive x additive x additive [w] gene effect was significant in all the crosses each for fruit girth, fruit weight, number of fruits per plant, plant spread, total soluble solids and fruit borer infestation; two crosses each for days to opening of first

flower, days to first picking, fruit length and total fruit yield per plant and one cross for number of branches per plant. Additive x additive x dominance [x] was observed to be significant for days to opening of first flower, days to first picking, fruit length, fruit girth, fruit weight, number of fruits per plant, total fruit yield per plant, plant spread, total soluble solids and fruit borer infestation in all the crosses each and number of branches per plant in two crosses. Whereas, Additive x dominance x dominance [y] gene effect was found significant in all the crosses each for fruit girth, fruit weight, number of fruits per plant, total fruit yield per plant, plant spread and fruit borer infestation; two crosses each for days to opening of first flower, fruit length, number of branches per plant and total soluble solids and one cross for days to first picking. In case of dominance x dominance x dominance [z] gene effect, it was significant in all the crosses each for days to opening of first flower, days to first picking, fruit length, fruit weight, number of fruits per plant, total fruit yield per plant, plant spread, total soluble solids and fruit borer infestation; two crosses each for fruit length and number of branches per plant and one cross for plant height.

All the types of digenic and trigenic interactions were significant in all the crosses for fruit weight, plant spread and fruit borer infestation and in cross 1 (JBG-10-208 × GOB-1) and cross 2 (NSR-1 × GBL-1) for number of fruits per plant; cross 1 (JBG-10-208 × GOB-1) and cross 3 (JB-12-06 × Pant Rituraj) for total fruit yield per plant, cross 2 (NSR-1 × GBL-1) and cross 3 (JB-12-06 × Pant Rituraj) for total soluble solids and only in cross 1 (JBG-10-208 × GOB-1) for fruit girth.

Table 2: Estimation of gene effects based on ten parameter model for various characters in three crosses of brinjal

| Gene effects | Days to opening of first flower | | | | | | Days to first picking | | | | | |
	JBG-10-208 × GOB-1 (Cross 1)		NSR-1 × GBL-1 (Cross 2)		JB-12-06 × Pant Rituraj (Cross 3)		JBG-10-208 × GOB-1 (Cross 1)		NSR-1 × GBL-1 (Cross 2)		JB-12-06 × Pant Rituraj (Cross 3)	
m	25.06**	± 2.26	-17.57**	± 2.53	-3.46	± 2.25	49.36**	± 2.26	56.26**	± 2.53	4.20	± 2.25
(d)	4.24*	± 1.78	-2.36	± 1.88	-9.66**	± 1.77	-15.96**	± 1.78	-8.69**	± 1.88	7.69**	± 1.77
(h)	175.98**	± 11.58	353.46**	± 13.11	357.14**	± 11.56	109.35**	± 11.58	-83.87**	± 13.11	389.82**	± 11.56
(i)	-24.40**	± 2.27	23.30**	± 2.53	56.00**	± 2.26	-47.99**	± 2.27	16.88**	± 2.53	63.58**	± 2.26
(j)	-28.59**	± 4.87	-0.13	± 5.21	-34.06**	± 4.92	48.77**	± 4.87	17.73**	± 5.21	-86.44**	± 4.92
(l)	-397.52**	± 17.95	-544.22**	± 20.21	-735.39**	± 17.85	-264.85**	± 17.95	337.84**	± 20.21	-810.45**	± 17.85
(w)	0.79	± 1.76	3.85*	± 1.88	9.58**	± 1.75	24.87**	± 1.76	3.62	± 1.88	-5.76**	± 1.75
(x)	113.81**	± 6.47	-30.06**	± 7.33	-215.47**	± 6.50	170.07**	± 6.47	23.75**	± 7.33	-240.03**	± 6.50
(y)	105.96**	± 4.68	-6.74	± 5.26	203.42**	± 4.70	6.96	± 4.68	4.48	± 5.26	279.63**	± 4.70
(z)	246.41**	± 8.90	254.85**	± 9.78	433.31**	± 8.77	170.16**	± 8.90	-295.92**	± 9.78	480.36**	± 8.77
χ^2 (2 df)	5770.18**		4139.89**		4479.22**		14727.65**		4986.64**		7944.75**	
Types of epistasis	Duplicate		Duplicate		Duplicate		Duplicate		Duplicate		Duplicate	

| Gene effects | Fruit length (cm) | | | | | | Fruit girth (cm) | | | | | |
	JBG-10-208 × GOB-1 (Cross 1)		NSR-1 × GBL-1 (Cross 2)		JB-12-06 × Pant Rituraj (Cross 3)		JBG-10-208 × GOB-1 (Cross 1)		NSR-1 × GBL-1 (Cross 2)		JB-12-06 × Pant Rituraj (Cross 3)	
m	54.38**	± 2.26	17.59**	± 2.53	23.98**	± 2.25	50.58**	± 2.26	27.74**	± 2.53	0.36	± 2.25
(d)	7.52**	± 1.78	-4.93**	± 1.88	-9.80**	± 1.77	6.39**	± 1.78	-8.68**	± 1.88	-15.57**	± 1.77
(h)	-152.81**	± 11.58	46.44**	± 13.11	-22.75*	± 11.56	-174.15**	± 11.58	-18.20	± 13.11	81.06**	± 11.56
(i)	-36.50**	± 2.27	-1.69	± 2.53	-3.13	± 2.26	-39.13**	± 2.27	-16.85**	± 2.53	15.23**	± 2.26
(j)	-7.65	± 4.87	19.60**	± 5.21	28.54**	± 4.92	-20.99**	± 4.87	26.01**	± 5.21	47.44**	± 4.92
(l)	200.50**	± 17.95	-68.44**	± 20.21	73.03**	± 17.85	250.12**	± 17.95	-5.98	± 20.21	-108.46**	± 17.85
(w)	-16.32**	± 1.76	2.42	± 1.88	8.18**	± 1.75	-9.83**	± 1.76	9.88**	± 1.88	15.88**	± 1.75
(x)	105.72**	± 6.47	-17.73*	± 7.33	14.53*	± 6.50	108.22**	± 6.47	24.93**	± 7.33	-40.25**	± 6.50
(y)	-3.17	± 4.68	-18.22**	± 5.26	-21.03**	± 4.70	21.00**	± 4.68	-47.34**	± 5.26	-29.49**	± 4.70
(z)	-77.87**	± 8.90	24.02*	± 9.78	-62.27**	± 8.77	-109.45**	± 8.90	8.44	± 9.78	38.57**	± 8.77
χ^2 (2 df)	65205.79**		64306.50**		60016.21**		23885.72**		36956.21**		25922.63**	
Types of epistasis	Duplicate		Duplicate		Duplicate		Duplicate		Complementary		Duplicate	

Gene effects	Fruit weight (g)						Number of fruits per plant					
	JBG-10-208 × GOB-1 (Cross 1)		NSR-1 × GBL-1 (Cross 2)		JB-12-06 × Pant Rituraj (Cross 3)		JBG-10-208 × GOB-1 (Cross 1)		NSR-1 × GBL-1 (Cross 2)		JB-12-06 × Pant Rituraj (Cross 3)	
m	16.45**	± 2.26	10.36**	± 2.53	16.54**	± 2.25	63.57**	± 2.26	89.43**	± 2.53	52.41**	± 2.25
(d)	-34.66**	± 1.78	-27.23**	± 1.88	-45.37**	± 1.77	12.16**	± 1.78	15.82**	± 1.88	-5.35**	± 1.77
(h)	-117.60**	± 11.58	-90.62**	± 13.11	-126.76**	± 11.56	-139.69**	± 11.58	-271.80**	± 13.11	-40.64**	± 11.56
(i)	24.83**	± 2.27	29.45**	± 2.53	37.71**	± 2.26	-50.25**	± 2.27	-81.25**	± 2.53	-39.58**	± 2.26
(j)	198.17**	± 4.87	168.72**	± 5.21	255.29**	± 4.92	-81.59**	± 4.87	-83.45**	± 5.21	-8.39	± 4.92
(l)	246.55**	± 17.95	212.54**	± 20.21	273.10**	± 17.85	161.69**	± 17.95	374.58**	± 20.21	-26.16	± 17.85
(w)	-6.30**	± 1.76	-12.18**	± 1.88	-7.72**	± 1.75	-12.94**	± 1.76	-13.18**	± 1.88	3.49*	± 1.75
(x)	-83.20**	± 6.47	-81.19**	± 7.33	-123.99**	± 6.50	94.41**	± 6.47	193.95**	± 7.33	39.61**	± 6.50
(y)	-213.92**	± 4.68	-198.66**	± 5.26	-269.88**	± 4.70	102.41**	± 4.68	97.26**	± 5.26	16.31**	± 4.70
(z)	-146.48**	± 8.90	-132.58**	± 9.78	-163.90**	± 8.77	-67.36**	± 8.90	-183.02**	± 9.78	41.98**	± 8.77
χ^2 (2 df)	9811.66**		9610.06**		11259.23**		61.15**		269.58**		7.96*	
Types of epistasis	Duplicate		Duplicate		Duplicate		Duplicate		Duplicate		Complementary	

Gene effects	Number of branches per plant						Plant height (cm)					
	JBG-10-208 × GOB-1 (Cross 1)		NSR-1 × GBL-1 (Cross 2)		JB-12-06 × Pant Rituraj (Cross 3)		JBG-10-208 × GOB-1 (Cross 1)		NSR-1 × GBL-1 (Cross 2)		JB-12-06 × Pant Rituraj (Cross 3)	
m	11.43**	± 2.26	5.32*	± 2.53	12.28**	± 2.25	4.10	± 2.26	6.72**	± 2.53	4.90*	± 2.25
(d)	-3.15	± 1.78	-8.23**	± 1.88	-1.43	± 1.77	-1.63	± 1.78	-2.17	± 1.88	-0.17	± 1.77
(h)	-28.46*	± 11.58	15.69	± 13.11	-32.39**	± 11.56	-14.06	± 11.58	-12.36	± 13.11	-13.96	± 11.56
(i)	-7.36**	± 2.27	-2.61	± 2.53	-8.24**	± 2.26	-2.17	± 2.27	-5.48*	± 2.53	-2.51	± 2.26
(j)	11.72*	± 4.87	19.25**	± 5.21	-1.32	± 4.92	6.96	± 4.87	5.79	± 5.21	2.12	± 4.92
(l)	44.11*	± 17.95	-23.20	± 20.21	48.90**	± 17.85	29.06	± 17.95	17.41	± 20.21	24.07	± 17.85
(w)	2.15	± 1.76	7.89**	± 1.88	1.80	± 1.75	0.61	± 1.76	1.98	± 1.88	0.21	± 1.75
(x)	23.09**	± 6.47	-7.23	± 7.33	20.08**	± 6.50	10.93	± 6.47	10.06	± 7.33	8.50	± 6.50
(y)	-11.60*	± 4.68	-17.38**	± 5.26	8.90	± 4.70	-7.79	± 4.68	-4.62	± 5.26	-0.18	± 4.70
(z)	-22.38*	± 8.90	5.05	± 9.78	-24.00**	± 8.77	-17.71*	± 8.90	-10.34	± 9.78	-13.78	± 8.77
χ^2 (2 df)	1125.76**		655.32**		286.82**		10712.48**		11916.74**		9920.92**	
Types of epistasis	Duplicate		Duplicate		Duplicate		Duplicate		Duplicate		Duplicate	

Gene effects	Total fruit yield per plant (kg)						Plant spread (cm)					
	JBG-10-208 × GOB-1 (Cross 1)		NSR-1 × GBL-1 (Cross 2)		JB-12-06 × Pant Rituraj (Cross 3)		JBG-10-208 × GOB-1 (Cross 1)		NSR-1 × GBL-1 (Cross 2)		JB-12-06 × Pant Rituraj (Cross 3)	
m	57.60**	± 2.26	39.76**	± 2.53	43.13**	± 2.25	14.68**	± 2.26	-280.98**	± 2.53	-257.65**	± 2.25
(d)	20.70**	± 1.78	-2.02	± 1.88	10.95**	± 1.77	68.34**	± 1.78	-13.08**	± 1.88	-82.67**	± 1.77
(h)	-197.16**	± 11.58	-83.23**	± 13.11	-156.75**	± 11.56	628.40**	± 11.58	1726.98**	± 13.11	1480.95**	± 11.56
(i)	-46.67**	± 2.27	-35.48**	± 2.53	-34.46**	± 2.26	19.02**	± 2.27	320.28**	± 2.53	307.47**	± 2.26
(j)	-70.25**	± 4.87	-11.37*	± 5.21	-30.54**	± 4.92	-68.85**	± 4.87	81.41**	± 5.21	290.63**	± 4.92
(l)	252.49**	± 17.95	78.04**	± 20.21	232.71**	± 17.85	-1445.26**	± 17.95	-2494.57**	± 20.21	-2195.22**	± 17.85
(w)	-24.93**	± 1.76	1.59	± 1.88	-7.35**	± 1.75	-96.11**	± 1.76	-16.24**	± 1.88	68.39**	± 1.75
(x)	114.42**	± 6.47	28.36**	± 7.33	86.84**	± 6.50	-643.53**	± 6.47	-1222.85**	± 7.33	-903.51**	± 6.50
(y)	72.10**	± 4.68	22.83**	± 5.26	42.66**	± 4.70	-23.50**	± 4.68	-109.78**	± 5.26	-58.98**	± 4.70
(z)	-99.13**	± 8.90	-30.21**	± 9.78	-114.98**	± 8.77	893.28**	± 8.90	1058.17**	± 9.78	1061.08**	± 8.77
χ^2 (2 df)	47999.11**		22035.08**		27521.31**		35581.70**		52493.84**		33353.57**	
Types of epistasis	Duplicate		Duplicate		Duplicate		Duplicate		Duplicate		Duplicate	

Gene effects	Total Soluble Solids (TSS)						Fruit borer infestation (%)					
	JBG-10-208 × GOB-1 (Cross 1)		NSR-1 × GBL-1 (Cross 2)		JB-12-06 × Pant Rituraj (Cross 3)		JBG-10-208 × GOB-1 (Cross 1)		NSR-1 × GBL-1 (Cross 2)		JB-12-06 × Pant Rituraj (Cross 3)	
m	53.70**	± 2.26	44.04**	± 2.53	39.45**	± 2.25	54.14**	± 2.26	87.84**	± 2.53	66.25**	± 2.25
(d)	3.49	± 1.78	10.89**	± 1.88	10.37**	± 1.77	-14.57**	± 1.78	-23.84**	± 1.88	-34.83**	± 1.77
(h)	-189.35**	± 11.58	-125.56**	± 13.11	-97.92**	± 11.56	-103.36**	± 11.58	-252.86**	± 13.11	-162.78**	± 11.56
(i)	-43.37**	± 2.27	-38.10**	± 2.53	-32.27**	± 2.26	-39.29**	± 2.27	-80.08**	± 2.53	-52.70**	± 2.26
(j)	1.05	± 4.87	-37.18**	± 5.21	-38.89**	± 4.92	16.67**	± 4.87	18.00**	± 5.21	85.48**	± 4.92
(l)	273.62**	± 17.95	167.79**	± 20.21	133.59**	± 17.85	118.07**	± 17.95	319.39**	± 20.21	205.33**	± 17.85
(w)	-5.23**	± 1.76	-10.37**	± 1.88	-9.17**	± 1.75	15.50**	± 1.76	21.70**	± 1.88	35.99**	± 1.75
(x)	94.86**	± 6.47	65.70**	± 7.33	60.10**	± 6.50	63.06**	± 6.47	152.50**	± 7.33	133.56**	± 6.50
(y)	-7.19	± 4.68	34.57**	± 5.26	50.63**	± 4.70	14.10**	± 4.68	41.73**	± 5.26	-26.47**	± 4.70
(z)	-127.24**	± 8.90	-80.41**	± 9.78	-69.01**	± 8.77	-49.96**	± 8.90	-138.57**	± 9.78	-89.86**	± 8.77
χ^2 (2 df)	16527.72**		15951.78**		31308.68**		998.74**		4501.42**		3356.97**	
Types of epistasis	Duplicate		Duplicate		Duplicate		Duplicate		Duplicate		Duplicate	

While fitting trigenic epistasis model, the $\chi^2_{(3)}$ value at two degrees of freedom was significant in ten-parameter model for all the traits in all the three crosses suggesting the non-adequacy of the trigenic interaction model of Hill (1966) [14] and Van Der Veen (1959) [25].

The opposite signs of either two or all the three gene effects *viz.*, dominance [h], dominance × dominance [l] and dominance × dominance × dominance [z] gene effects suggests the presence of duplicate type of epistasis. In present study, duplicate epistasis was observed in all the crosses for all the traits except for fruit girth in cross 2 (NSR-1 × GBL-1) and number of fruits per plant in cross 3 (JB-12-06 × Pant Rituraj). Ansari and Singh (2015) [3] observed duplicate dominance type of epistasis for six fruit characters in brinjal *viz.*, fruit length, fruit diameter, average fruit weight, total number of fruits per plant, early yield per plant and yield per plant.

b. Heterosis and inbreeding depression
In the present study, heterosis is reported over mid parent (relative heterosis) and over better parent (heterobeltiosis). Whereas inbreeding depression is estimated over F_2 generation and results of the present study are discussed for the fruit yield and its components traits with respect to heterosis and inbreeding depression simultaneously. The data observed for heterosis over mid parent and better parents as well as inbreeding depression for different traits are summarized in Table 3.

For the characters like days to opening of first flower, days to first picking and fruit borer infestation, the low scoring parent was taken as better parent. The degree of heterosis over better parent varied from cross to cross for all the twelve characters. The heterosis over mid as well as better parent were significant and negative for days to opening of first flower and days to first picking in all crosses. Significant and positive heterosis over better parent observed in all the three crosses for number of fruits per plant, plant height, total fruit yield per plant, plant spread and fruit borer infestation. Significant and positive heterosis over better parent was observed fruit length in cross 1 (JBG-10-208 × GOB-1) and cross 2 (NSR-1 × GBL-1), fruit weight in cross 1 (JBG-10-208 × GOB-1) and cross 2 (NSR-1 × GBL-1), number of branches per plant in cross 2 (NSR-1 × GBL-1) and cross 3 (JB-12-06 × Pant Rituraj) and total soluble solids in cross 1 (JBG-10-208 × GOB-1) and cross 3 (JB-12-06 × Pant Rituraj). The heterosis over mid parent was significant and positive for fruit length in cross 2 (NSR-1 × GBL-1), fruit weight in cross 2 (NSR-1 × GBL-1), number of fruits per.

Table 3: Estimates of observed heterosis over mid parent (MP), heterobeltiosis (BP) and inbreeding depression (ID) for twelve characters in three brinjal crosses

Crosses	Days to opening of first flower						Days to first picking					
	MP		BP		ID		MP		BP		ID	
JBG-10-208 × GOB-1	-12.47**	± 1.01	-6.80**	± 1.41	2.18**	± 0.53	-9.60**	± 0.75	-4.93**	± 1.10	3.05**	± 0.50
NSR-1 × GBL-1	-10.53**	± 1.08	-9.20**	± 1.29	0.12	± 0.49	-8.40**	± 1.05	-8.07**	± 1.06	-1.72	± 1.09
JB-12-06 × Pant Rituraj	-3.73**	± 0.49	-1.73**	± 0.58	4.65**	± 0.49	-2.73**	± 0.50	-0.73	± 0.58	4.65**	± 0.51
	Fruit length (cm)						Fruit girth (cm)					
JBG-10-208 × GOB-1	0.08	± 0.33	0.78*	± 0.37	1.00**	± 0.32	0.45	± 0.34	0.63	± 0.42	-0.42	± 0.36
NSR-1 × GBL-1	0.72*	± 0.29	2.03**	± 0.32	1.03**	± 0.31	-0.14	± 0.33	0.38	± 0.39	-0.54	± 0.35
JB-12-06 × Pant Rituraj	-1.63**	± 0.37	-0.63	± 0.39	-0.47	± 0.35	-0.49	± 0.35	-0.34	± 0.40	-0.69*	± 0.34
	Fruit weight (g)						Number of fruits per plant					
JBG-10-208 × GOB-1	-9.35	± 6.39	14.53*	± 5.73	-2.50	± 6.46	6.30**	± 0.55	7.53**	± 0.57	-6.30**	± 0.57
NSR-1 × GBL-1	32.05**	± 6.12	45.02**	± 5.65	-6.16	± 6.53	2.37	± 1.60	8.80**	± 1.50	-5.30**	± 1.51
JB-12-06 × Pant Rituraj	-12.94*	± 6.10	-3.34	± 5.63	-5.66	± 6.51	14.57**	± 0.56	16.07**	± 0.69	-3.48**	± 0.53

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

Table 3: Contd…

Crosses	Number of branches per plant						Plant height (cm)					
	MP		BP		ID		MP		BP		ID	
JBG-10-208 × GOB-1	0.50	± 0.50	0.80	± 0.52	0.25	± 0.49	13.64**	± 3.13	19.27**	± 3.34	2.65	± 3.22
NSR-1 × GBL-1	1.77*	± 0.66	1.93*	± 0.71	0.62	± 0.67	12.27**	± 2.87	18.77**	± 3.06	1.52	± 2.90
JB-12-06 × Pant Rituraj	1.43**	± 0.49	1.67**	± 0.56	0.17	± 0.49	14.80**	± 3.13	19.81**	± 3.34	10.65**	± 3.19
	Total fruit yield per plant (kg)						Plant Spread (cm)					
JBG-10-208 × GOB-1	0.47*	± 0.22	0.86*	± 0.26	-0.62*	± 0.25	25.08**	± 0.68	30.55**	± 0.67	5.77**	± 0.55
NSR-1 × GBL-1	0.89**	± 0.31	1.24**	± 0.32	-0.79*	± 0.33	18.04**	± 1.04	24.96**	± 1.00	2.13*	± 1.02
JB-12-06 × Pant Rituraj	1.03**	± 0.31	1.19**	± 0.34	-0.38	± 0.33	41.07**	± 0.48	45.80**	± 0.57	6.73**	± 0.53
	Total Soluble Solids (TSS)						Fruit borer infestation (%)					
JBG-10-208 × GOB-1	0.96*	± 0.44	1.64**	± 0.51	0.24	± 0.44	3.68**	± 0.54	5.12**	± 0.68	-8.31**	± 0.55
NSR-1 × GBL-1	0.11	± 0.45	0.27	± 0.51	0.04	± 0.45	5.63**	± 0.53	6.41**	± 0.64	-0.41	± 0.54
JB-12-06 × Pant Rituraj	0.33	± 0.49	1.19*	± 0.53	-0.18	± 0.44	6.87**	± 0.53	7.61**	± 0.62	-0.80	± 0.52

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

plant in cross 1 (JBG-10-208 × GOB-1) and cross 3 (JB-12-06 × Pant Rituraj), number of branches per plant in cross 2 (NSR-1 × GBL-1) and cross 3 (JB-12-06 × Pant Rituraj); plant height, total fruit yield per plant, plant spread and fruit borer infestation in all the three crosses, total soluble solids in cross 1 (JBG-10-208 × GOB-1). The rest of the estimates of calculated heterosis over mid parent and better parent were either smaller than their standard errors or not significantly larger than them. Das and Barua (2001) [7] exhibited significant heterosis for days to first flowering, days to 50 per cent flowering, fruit length, number of fruits per plant, fruit weight and yield per plant in brinjal. Bhakta *et al.* (2009) [4] recorded better parent and economic heterosis for fruit yield per plant and eight other attributes for brinjal.

The estimates for inbreeding depression were found significant and positive for days to opening of first flower and

days to first picking in cross 1 (JBG-10-208 × GOB-1) and cross 3 (JB-12-06 × Pant Rituraj), fruit length in cross 1 (JBG-10-208 × GOB-1) and cross 2 (NSR-1 × GBL-1), plant height in cross 3 (JB-12-06 × Pant Rituraj) and plant spread in all the crosses. The estimates for inbreeding depression were found significant but negative for fruit girth in cross 3 (JB-12-06 × Pant Rituraj), number of fruits per plant in all the crosses, total fruit yield per plant in cross 1 (JBG-10-208 × GOB-1) and cross 2 (NSR-1 × GBL-1) and fruit borer infestation in cross 1 (JBG-10-208 × GOB-1). It is desirable to have high, significant and positive heterosis with low inbreeding depression. All the crosses exhibited highly significant heterosis with low inbreeding depression for number of fruits per plant and plant spread. Gopinath and Madalageri (1986) [11] reported significant inbreeding depression for days to first picking, number of fruits per plant, fruit yield per plant, fruit length and breadth of fruit in brinjal.

Sao and Mehta (2010) [22] reported the high degree of inbreeding depression for fruit yield per plant and its related traits in brinjal.

c. Heritability and genetic advance (table 4)
Heritability is a good index of the transmission of characters from parents to their offspring (Falconer, 1981) [8]. Narrow sense heritability indicates the proportion of additive genetic variance to the total phenotypic variance. Additive variance is always fixable.

High estimates of heritability were recorded for days to opening of first flower and days to first picking in cross 1 (JBG-10-208 × GOB-1) and cross 2 (NSR-1 × GBL-1), fruit girth in cross 1 (JBG-10-208 × GOB-1), fruit weight in all the crosses, number of branches per plant in cross 3 (JB-12-06 × Pant Rituraj), plant height in all the crosses, total fruit yield

Table 4: Estimates of heritability in narrow sense (h^2) and genetic advance (GA) as per cent of mean (GA %) for twelve characters in three crosses in brinjal

Characters	JBG-10-208 × GOB-1 (Cross 1)		NSR-1 × GBL-1 (Cross 2)		JB-12-06 × Pant Rituraj (Cross 3)	
	h^2	GA%	h^2	GA%	h^2	GA%
Days to opening of first flower	56.07	5.51	60.59	6.67	(-)	(-)
Days to first picking	105.67	8.13	92.67	8.80	(-)	(-)
Fruit length (cm)	31.04	12.87	28.84	11.69	(-)	(-)
Fruit girth (cm)	80.84	49.46	(-)	(-)	2.84	1.38
Fruit weight (g)	98.39	47.46	64.63	33.22	65.10	32.45
Number of fruits per plant	(-)	(-)	(-)	(-)	(-)	(-)
Number of branches per plant	(-)	(-)	(-)	(-)	56.13	66.27
Plant height (cm)	111.27	55.14	66.25	31.52	67.99	34.37
Total fruit yield per plant (kg)	63.25	60.29	49.85	59.47	55.96	67.11
Plant Spread (cm)	(-)	(-)	(-)	(-)	46.85	4.28
Total Soluble Solids (TSS)	(-)	(-)	(-)	(-)	(-)	(-)
Fruit borer infestation (%)	48.43	12.16	80.77	24.18	32.67	7.39

(-) Estimates were found negative

per plant in cross 1 (JBG-10-208 × GOB-1) and cross 3 (JB-12-06 × Pant Rituraj) and fruit borer infestation in cross 2 (NSR-1 × GBL-1). Sidhu *et al.* (1980) [24] observed high heritability for number of fruits per plant, weight of fruits, fruit length, girth of fruit, number of flowers per cluster and days to flowering. Monpara and Kamani (2007) [18] recorded high magnitude of heritability for days to first flower, days to first picking, plant height, branches/plant, fruit length, fruit girth, fruit shape index, fruits/plant, fruit weight and fruit yield/plant in brinjal.

In general, the high heritability estimates followed the trend of high genetic advance in all the three crosses for most of the characters. Some cross had either low or medium heritability for different traits. It depends upon the cross. This may be due to either over estimation of non-additive components (dominance and epistasis) or under estimation of additive and additive x additive components. Similar type of observation was recorded by Madhavi *et al.* (2015) [16] for number of fruits per plant, average fruit weight, fruit yield per plant, fruit volume, fruits per cluster, number of pickings, flowers per cluster, fruit diameter and dry matter content in brinjal.

Conclusion
Finally, it can be concluded from the present study that fruit yield and its component traits recorded in three brinjal crosses were governed by additive, dominance and digenic and/or trigenic epistasis gene effects. All the three digenic epistatic effect *viz.*, additive x additive (i), additive x dominance (j) and dominance x dominance (l) or trigenic epistasis effect

viz., additive x additive x additive [w], additive x additive x dominance [x], additive x dominance x dominance [y] and dominance x dominance x dominance [z], their combination or even one of them were important for these traits. Hence, bi-parental mating or few cycles of recurrent selection followed by heterosis breeding may give fruitful results for improvement of these traits in brinjal.

References
1. Allard RW. Principles of Plant Breeding. John Wiley and sons. Inc., New York, 1960.
2. Anonymous. Area and production of horticulture crops-all India. Department of Agriculture Cooperation and Farmers Welfare. Available at http://agricoop.nic.in/ statistics/state-level >accessed 15 February, 2017, 2016.
3. Ansari AM, Singh YM. Gene action for important fruit characters in brinjal (*Solanum melongena* L.). Ann. Agric. Res. New Series. 2015; 36(4):339-344.
4. Bhakta RS, Patel DU, Patel SJ, Patel NK, Kodappully K. Hybrid vigour in eggplant (*Solanum melongena* L.). Res. on Crops. 2009; 10:357-361.
5. Briggle LW. Heterosis in wheat - A review. Crop Sci. 1963; 3:407-412.
6. Cavalli LL. An analysis of linkage in quantitative inheritance. In Quantitative Inheritance. Ed. E. C. R. Reeve and C. H. Waddington, HMSO, London, 1952, 135-144.

7. Das G, Barua SN. Heterosis and combining ability for yield and it's component in brinjal. Ann. Agric. Res. New Series. 2001; 22(3):399-403.
8. Falconer DS. Introduction to Quantitative Genetics, Second edition. Longman, New York, 1981.
9. Fonseca S, Patterson FL. Hybrid vigour in a seven parents diallel cross in common winter wheat (*T. aestivum* L.). Crop Sci. 1968; 8:85-88.
10. Gamble FE. Gene effects in corn (*Z. mays* L.) seperation and relative importance of gene effects for yield. Canadian J. Plant Sci. 1962; 42:339-348.
11. Gopinath G, Madalageri BB. Genetics of yield and its components in brinjal (*Solanum melongena* L.). Haryana J. Hort. Sci. 1986; 15:103-109.
12. Hayman BI. The separation of epistatic from additive and dominance variation in generation. Heredity. 1958; 12:371-390.
13. Hayman BI, Mather K. The description of genetic interactions in continuous variation. Biometrics. 1955; 11:69-82.
14. Hill J. Recurrent backcrossing in the study of quantitative inheritance. Heredity. 1966; 21:85-120.
15. Lawande KE, Gadakh SR, Kale PN, Joshi VR. Generation mean analysis in brinjal. J. Maharashtra Agric. Univ. 1992; 17: 62-63.
16. Madhavi N, Mishra AC, Om Prasad J, Naveen Bahuguna. Studies on variability, heritability and genetic advance in brinjal (*Solanum melongena* L.). Plant Archives. 2015; 15(1):277-281.
17. Mather K. Biometrical genetics, 1st Edn., Dover Publications, Inc., New York, 1949.
18. Monpara BA, Kamani JM. Components of variation and associations among yield attributing traits in segregating populations of brinjal (*Solanum melongena* L.). National J. Plant Imp. 2007; 9(2):106-110.
19. Nagai K, Kida K. An experiment with some varietal crosses in eggplant. Jap. J. Genet. 1926; 4:10-30.
20. Naulsri CC, Dhanasobhen C, Srinivas P. A Study on inheritance of some economically important characters in four cultivars of eggplant (*Solanum melongena va. Esculenta Nees.*). II Gene actions controlling the characters. Kesetsart J. 1988; 20:117-123.
21. Rai N, Asati BS. Combining ability and gene action studies for fruit yield and yield contributing traits in brinjal. Indian J. Hort. 2011; 62:212-215.
22. Sao A, Mehta N. Heterosis and inbreeding depression for fruit yield and its components in brinjal (*Solanum melongena* L.). Agric. Sci. 2010; 37(1):95-101.
23. Shinde KG, Warade SD, Kadam JH, Sanap PB, Bhalekar MN. Generation mean analysis in brinjal *(Solanum melongena* L.). Veg. Sci. 2009; 36:31-40.
24. Sidhu AS, Bhutani RD, Kalloo G, Singh GP. Genetics of yield components in brinjal (*Solanum melongena* L.). Haryana J. hortic. Sci. 1980; 9:160-164.
25. Van Der Veen JH. Test of non-allelic interaction and linkage for quantitative characters in generations derived from two diploid purelines. Genetica. 1959; 30:201-232.
26. Warner JN. A method for estimating heritability. Agron. J. 1952; 44:427-430.