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Genetic Analysis for Fruit Yield and Its Component Characters in Brinjal (*Solanum melongena* L.)

Raju Shyadambi[*], M.H. Sapovadiya, S.B. Chaudhari, N. C. Ghadage and D. Dinesh Varma

Department of Genetics and Plant Breeding, Junagadh Agricultural University, Junagadh, Gujarat (India) - 362 001

*Corresponding author

A B S T R A C T

The present investigation was undertaken with a view to generate genetic information on gene effects for 14 quantitative traits in brinjal through generation mean analysis. The experimental material consists of six generations, namely P_1, P_2, F_1, F_2, B_1 and B_2 of four crosses in brinjal *viz.,* AB-15-07 x GJLB-4 (cross 1), JBR-14-07 x Pant Rituraj (cross 2), NSR-01 x Swarnmani Black (cross 3) and NBR-14-05 x GJB-03 (cross 4). The results indicated that the magnitude and type of gene effects differed for the same trait in different cross combinations. Therefore, for the improvement of particular trait, segregating generations of individual crosses should be handled according to the gene action involved in its inheritance. Additive [d], dominance [h], additive x additive, dominance x dominance gene actions were equally important for days to opening of first flower, fruit length (cross 1 and cross 2), fruit girth, number of fruits per plant (except cross 4), plant height, days to last picking (except cross 1), average fruit weight (except cross 4), fruit yield (except cross 4), number of picking (except cross 3), total phenol, total soluble solids (except cross 2) and fruit borer infestation. Classification of gene action showed importance of duplicate type of gene action for most of the characters in most of the crosses. Breeding procedure involving multiple crosses, biparental crosses may be restored to get transgressive segregants. This is especially important to develop inbred lines having superiority in different characters. Such lines can give better hybrids. While in case of complementary type of epistasis, material can be utilized directly in breeding programme.

Introduction

Vegetables are certain parts of plants that are consumed by humans as food as part of a savory meal. It can be eaten either raw or cooked and play an important role in human nutrition, being mostly low in fat and carbohydrates, but high in vitamins, minerals and dietary fiber. India is the second largest producer of vegetables in the world, next to China. Brinjal is one of the most important tender fruit vegetable crops of our country grown during rainy (*kharif*), winter (*rabi*) and spring (*summer*) seasons.

Brinjal or eggplant (*Solanum melongena* L.) originated in India which is also considered as center of diversity (Genebus, 1963). It is an

important solanaceous vegetable crop widely grown in the tropical and sub- tropical regions of the world. Brinjal shares 8.1 per cent in total vegetable production of India, it is grown in an area of 7.29 lakh ha with production of 12.61 million tons and productivity of 18868 kg/ha (Anon., 2017).

The crop has a somatic chromosome number of $2n=2x=24$ and comprises of three botanical varieties *viz*., var. *esculentum*, with round or egg shaped fruits, var. *serpentinum* with long slender fruits and var. *depressum* having dwarf stature. Brinjal is highly productive and usually finds its place as the poor man's vegetable (Som and Maity, 2002). It is popular among people of all social strata and hence it is rightly called as "vegetable of masses" (Patel and Sarnaik, 2003). Its immature fruits are used as vegetable and extensively used in various culinary preparations. Due to its quick growth, short duration and photo insensitive in nature, it enables the geneticists and plant breeders to raise two crops in a year, thereby reducing the period for improvement of yield. India being a center of origin, brinjal has a huge genetic diversity in our country which offers much scope for improvement through heterosis breeding.

The ultimate aim 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. Among different biometrical techniques, six parameter model for generation means analysis is the technique which estimate the additive, dominance and epistatic variance. In view of this, in the present investigation, an attempt has been made to detect and quantify the genetic interaction for yield and its component traits.

Materials and Methods

The experimental materials comprised of six basic generations *viz*., P_1, P_2, F_1, F_2, B_1, and B_2 of four crosses. Eight parents *viz*., AB-15-07, GJLB-4, JBR-14-07, Pant Rituraj, NSR-01, Swarnmani Black, NBR-14-05 and GJB-03 of brinjal were selected from diverse genetic stocks available at the Vegetable Research Station, Junagadh Agricultural University, Junagadh for crossing purpose. Six basic generations *viz*., P_1, P_2, F_1 ($P_1 \times P_2$), F_2 (F_1selfed), B_1 ($F_1 \times P_1$) and B_2 ($F_1 \times P_2$) derived from the four crosses namely, AB-15-07 x GJLB-4(cross 1), JBR-14-07 x Pant Rituraj (cross 2), NSR-01 x Swarnmani Black (cross 3) and NBR-14-05 x GJB-03 (cross 4). Experiment was laid-out in Compact Family Block Design (CFBD) with three replications during late *kharif,* 2018-19 at Vegetable Research Station, Junagadh Agricultural University, Junagadh. The observation were recorded on five randomly selected plants of P_1, P_2 and F_1, twenty plants from F_2 and ten plants from B_1 and B_2 generations in each replication for fourteen characters *viz.,* days to opening of first flower, days to first picking, fruit length (cm), fruit girth (cm), number of fruits per plant, number of primary branches per plant, plant height (cm), days to last picking, average fruit weight (g), fruit yield per plant (kg), number of pickings, total phenol (mg GAE/ g FW), total soluble solids (^0B) and fruit borer infestation (%). Each hybrid and parents represented single rows of 6 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. The individual scaling tests (Mather, 1949) and joint scaling test (Cavelli, 1952) were applied to test the adequacy of additive-dominance model. When the model was adequate, six parameter model (Hayman 1958) was used to estimate components of different parameters *viz.,* [m], [d], [h], [i], [j] and [l].

Results and Discussion

Results of individual scaling test A, B, C, D and joint scaling test (Table 1) were non-significant, the additive-dominance model was found adequate for description of variation in generation means for days to first picking (cross 1and cross 4), number of fruits per plant (cross 4), number of primary branches per plant (cross 1 and cross 4), days to last picking (cross 1), average fruit weight (cross 4), fruit yield per plant (cross 4) and total soluble solids (cross 2). For remaining crosses either all four or any one individual scaling test (A, B, C and D) were found significant. This was also confirmed by significant chi-square values of joint scaling test, indicating involvement of digenic interaction parameters in the inheritance of the characters. These findings were also in consonance with Shinde *et al.,* (2009) in brinjal.

The estimates of gene effects and various contributing traits are given in table 2. The estimates of mean (m) were highly significant for all the traits studied in all crosses which showed the significant difference among the crosses and traits studied.

Gene action

Days to opening of first flower: In cross AB-15-07 x GJLB-4the gene effects *viz.,* 'm', additive [d], dominance [h], additive x additive [i] and dominance x dominance [l] were found significant. The sequence of genetic effects in the decreasing order of their magnitudes was [l]>[i]>[h]> [d] indicating the predominance of non-additive gene action over additive gene action. While in case ofJBR-14-07 x Pant Rituraj all the six parameter found significant to explain the variations in this cross. In NSR-01 x Swarnmani Black there was significant digenic parameters like [l]>[i]>[h] were adequate to explain the variations, meanwhile

in crossNBR-14-05 x GJB-03the gene effects *viz.,* 'm', additive [d] and dominance x dominance [l] were found significant. The magnitude of their genetic effects was found more in [l]as compared to [d].The sign of [h] and [l] were found opposite in all the four crosses indicated the predominance of duplicate type of gene interaction. Similar results were found by Rai *et al.,* (2005) and Dhameliya *et al.,* (2009).

Days to first picking: As the scaling test results were non-significant, three parameter model analysis revealed that, significant dominance [h] gene action was noticed in cross 4 and non-significant in cross 1. The magnitude of dominance [h] was higher than additive [d] indicating more importance of dominance gene effects in the inheritance of this trait. Additive and dominance gene action for trait was also reported by Singh *et al.,* (2002). However, in remaining crosses *i.e.,* JBR-14-07 x Pant Rituraj and NSR-01 x Swarnmani Black showed the presence of significant scaling test for days to first picking was confirmed by joint scaling test indicated the existence of non-allelic gene interactions. The gene effects *viz.,* 'm', dominance [h] and additive x additive [i] were found significant and magnitude of genetic effect found more in [h] as compared to [i] indicating the predominance of non-additive gene action with complementary type of gene action in cross 2 meanwhile the gene effects *viz.,* 'm' and additive x dominance [j] were found significant in cross 3 with duplicate type of gene action to explain the variations for the said trait. These findings were in agreement with Rai *et al.,* (2005) and Dhameliya *et al.,* (2009).

Fruit length (cm): The components of gene action observed significant in cross 2 in desirable direction for all the components *viz.,* [m], [d], [h], [i], [j] and [l] indicating importance of additive, dominance and epistatic interactions for expression of this

character, meanwhile in cross 1 except [j] all the remaining digenic parameters found significant indicating the predominance of non-additive gene action in both cross 1 and 2.In cross 3the gene effects *viz.,* 'm', additive [d] and additive x additive [i] were found significant with higher magnitude of [i] as compared to [d], similarlythe gene effects *viz.,* 'm', additive [d] and additive x dominance [j] were found significant. The magnitude of genetic effect found more in [d] as compared to [j] indicating the predominance of additive gene action in both cross 3 and 4. The sign of [h] and [l] were found opposite in all the four crosses indicated the predominance of duplicate type of gene interaction to explain the variations for this trait. These findings were in agreement with the results of Prasad *et al.,* (2010).

Fruit girth (cm): In cross AB-15-07 x GJLB-4the gene effects *viz.,* 'm', dominance [h] and additive x additive [i] were found significant with higher magnitude of [i] indicating the importance of additive along with complementary type of gene action to explain the variations in this cross. In cross 3 the gene effects *viz.,* 'm', dominance [h], additive x additive [i] and additive x dominance [j] were found significant with sequence of genetic effects in the decreasing order of their magnitudes *i.e.,* [h]>[i]>[j] with complementary gene interaction. In case of cross 2 except [j] all the remaining digenic components found significant and depicted the importance of non-additive gene action, similarly in cross 4all the gene effects were found significant with the predominance of non-additive type of gene interaction in this cross. The sign of [h] and [l] were found opposite in cross 2 and 4 indicated the predominance of duplicate type of gene interaction to explain the variations for this trait. These results were in agreement with the results of Singh *et al.,* (2002) and Prasad *et al.,* (2010).

Number of fruits per plant: The scaling test results were non-significant, three parameter model analysis revealed that, significant additive [d] gene action was noticed in cross 4indicating more importance of additive gene effects in the inheritance of this trait. Additive and dominance gene action for trait was also reported by Singh *et al.,* (2002). The components of gene action observed significant in cross 2 and 3 in desirable direction for the components *viz.,* [m], [d], [h], [i] and [l] indicating importance of additive, dominance and epistatic interactions for expression of this character mean-while in cross 1the gene effects *viz.,* 'm', additive [d] and additive x dominance [j] were found significant with higher magnitude of [j] as compared to [d] indicating the predominance of non-additive gene effect. The sign of [h] and [l] were found opposite in cross 1, 2 and 3 indicated the predominance of duplicate type of gene interaction to explain the variations for this trait. These findings were in agreement with Rai *et al.,* (2005) and Dhameliya *et al.,* (2009).

Number of primary branches per plant: As the scaling test results were non-significant, three parameter model analysis revealed that, significant [h] and [d] gene action was noticed in cross 1and 4 and non-significant [d] in cross 4. The magnitude of dominance [h] was higher than additive [d] indicating more importance of dominance gene effects in the inheritance of this trait. Additive and dominance gene action for trait was also reported by Singh *et al.,* (2002). However, in remaining crosses *i.e.,* JBR-14-07 x Pant Rituraj and NSR-01 x Swarnmani Black showed the presence of significant scaling test for the trait was confirmed by joint scaling test indicated the existence of non-allelic gene interactions, the gene effect 'm', additive [d] and additive x dominance [j] were found significant, with higher magnitude of [j] as compared to [d] indicating the importance of

non-additive gene effect along with complementary gene interaction to explain the variations in number of primary branches per plant. The similar results were reported by Gauravkumar *et al.,* (2004) and Ahmed *et al.,* (2006).

Plant height (cm): The χ^2value of joint scaling test was significant which supported the findings of simple scaling tests. In cross 1 all the gene effects were found significant with non-additive gene effect along with the predominance of duplicate type of interaction in this cross. In cross 2 the gene effects *viz.,* 'm', dominance [h], additive x additive [i] and dominance x dominance [l] were found significant. The sequence of genetic effects in the decreasing order of their magnitude was [l]>[h]>[i], similarly in cross 3 the gene effects *viz.,* 'm', dominance [h], additive x additive [i], additive x dominance [j] and dominance x dominance [l] were found significant. The sequence of genetic effects in the decreasing order of their magnitudes was [l]>[h]>[i]>[j] indicating the importance of non-additive gene effect with duplicate type of interaction for the trait. In case of cross 4 the gene effect *viz.,* 'm', additive [d] and additive x dominance [j] were found significant. The magnitude of gene effect found more in [j] as compared to [d] which depict the importance of complementary type of interaction. These results were in agreement with the results of Singh *et al.,* (2002), Gauravkumar *et al.,* (2004) and Prasad *et al.,* (2010).

Days to last picking: In cross 1, none of the individual scaling tests was found significant. This result also supported by non-significant χ^2value derived from joint scaling test. Thus, the additive-dominance model was fitted very well. All the gene effects *viz.,* 'm', additive [d] and dominance [h] gene effects were observed significant. In cross 2 the gene effect *viz.,* 'm' and additive x dominance [j]

were found significant, indicating the importance of non-additive gene action. In case of cross 3 the gene effects *viz.,* 'm', additive [d], dominance [h], additive x additive [i] and dominance x dominance [l] were found significant with non-additive gene action. On the other hand cross 4 depicted the predominance of additive gene action with the significant gene effects *viz.,* 'm', additive [d], dominance [h], additive x additive [i] and additive x dominance [j] were found significant in this cross. The sign of [h] and [l] were found opposite in cross 2, 3 and 4 indicated the predominance of duplicate type of gene interaction to explain the variations for this trait. These findings were in agreement with Rai *et al.,* (2005) and Dhameliya *et al.,* (2009).

Average fruit weight (g): As the scaling test results were non-significant, three parameter model analysis revealed that, significant [h] and [d] gene action was noticed in cross 4 with more effect of additive gene action. Additive gene action for trait was also reported by Singh *et al.,* (2002). In cross 1the gene effects *viz.,* 'm', additive [d] and additive x dominance [j] were found significant with higher additive effect along with complementary gene action in this cross. In cross 2the gene effects *viz.,* 'm', dominance [h], additive x additive [i] and dominance x dominance [l] were found significant. The sequence of genetic effects in the decreasing order of their magnitudes was [l]>[i]>[h], similarly in cross 3the gene effects *viz.,* 'm', additive [d], dominance [h], additive x additive [i] and dominance x dominance [l] were found significant. The sequence of genetic effects in the decreasing order of their magnitudes was [l]>[h]>[i]>[d] indicating the predominance of duplicate type of interaction in cross 2 and 3 to explain the variations for the said trait. The results were in agreement with Shinde *et al.,* (2009) and Prasad *et al.,* (2010).

Table.1 Scaling and joint scaling tests for yield and yield attributing traits in brinjal

Scale	Cross 1	Cross 2	Cross 3	Cross 4	Scale	Cross 1	Cross 2	Cross 3	Cross 4	Scale	Cross 1	Cross 2	Cross 3	Cross 4
Days to opening of first flower					**Days to first picking**					**Fruit length (cm)**				
A	-0.60	5.07**	-1.13*	3.07**	A	-0.27	3.93*	-4.20*	1.73	A	2.01**	-2.55**	-0.31	0.40
B	0.53	-1.00	-1.07	3.33**	B	1.40	5.67**	1.00	2.20	B	3.53**	-0.75	-0.57	1.62**
C	7.40**	27.00**	9.93**	5.47**	C	1.27	15.67**	-0.87	1.33	C	0.35	-0.61	-2.55**	2.58**
D	3.73**	11.47**	6.07**	-0.47	D	-0.93	3.03*	1.17	0.70	D	-2.60**	1.34**	-0.84*	0.28
Joint scale	42.35**	553.61**	176.09**	47.22**	Joint scale	5.67	49.24**	8.31*	5.80	Joint scale	45.46**	40.16**	13.93**	20.50**
Fruit girth (cm)					**Number of fruits per plant**					**Number of primary branches per plant**				
A	-7.28**	-2.45*	-7.62**	3.47**	A	13.53**	-3.60	-6.80**	-2.33	A	-0.13	0.27	-0.60	0.80
B	-7.31**	-0.65	-1.78	6.78**	B	1.53	-8.87**	-4.60	-0.47	B	-0.67	-1.60**	1.40	0.40
C	-24.41**	2.87	-14.46**	2.87	C	24.47	13.73*	7.80*	-3.67	C	-0.67	-1.13	1.00**	-0.60
D	-4.91**	2.98**	-2.53*	-3.69**	D	4.70	13.10**	9.60**	-0.43	D	0.07	0.10	0.10	-0.60
Joint scale	200.40**	18.70**	81.80**	44.43**	Joint scale	18.19**	37.51**	32.69**	0.70	Joint scale	2.07	9.43**	9.85**	4.34
Plant height (cm)					**Days to last picking**					**Average fruit weight (g)**				
A	21.80**	3.67	0.60	7.00	A	1.33	-1.60	1.40	-3.00**	A	-12.35*	4.79	41.16**	7.79
B	-1.40	14.00*	15.00**	-28.00**	B	-0.13	11.80**	4.00**	2.40**	B	5.58	6.64	19.79**	2.19
C	-8.47	-11.53	-2.00	-22.93**	C	5.33	13.60**	0.00	-5.40*	C	-23.88*	-90.86**	-6.34	-0.01
D	-14.43**	-14.60**	-8.80*	-0.97	D	0.57	1.70	-2.70**	-2.40*	D	-8.56	-51.15**	-33.64**	-4.99
Joint scale	26.79**	13.31**	13.83**	69.92**	Joint scale	7.59	258.4**	15.44**	42.87**	Joint scale	14.16**	78.89**	27.85**	2.83
Fruit yield per plant (kg)					**Number of pickings**					**Total phenol (mg GAE/ G FW)**				
A	0.90**	-0.47	0.21	0.15	A	-1.07**	-1.00**	-0.73	-1.33**	A	-9.59**	39.38**	100.15**	-40.40**
B	0.53*	-0.59*	-0.41*	-0.08	B	0.60	-0.20	-1.20**	0.27	B	-76.51**	126.31**	146.12**	-42.47**
C	0.48	-2.40**	0.67*	0.05	C	0.53	-1.80**	-2.00**	-1.53**	C	10.89	-43.38*	209.53**	41.98**
D	-0.48*	-0.66**	0.43**	-0.01	D	0.50*	-0.30	-0.03	-0.23	D	48.49**	-104.54**	-18.37**	62.43**
Joint scale	31.36**	38.57**	27.02**	1.12	Joint scale	33.28**	15.77**	13.31**	20.67**	Joint scale	1321.84**	8469.24**	11199.97**	459.32**
Total soluble solids (^{0}B)					**Fruit borer infestation (%)**									
A	-0.45**	-0.03	-1.10**	0.02	A	0.04	1.00**	1.15**	1.68**					
B	-0.64**	0.37	-0.13	-0.57**	B	0.85**	0.53**	0.52**	0.80**					
C	-0.33	0.07	-0.13	-0.74**	C	11.89**	12.73**	14.26**	10.66**					
D	0.38**	-0.18	0.55**	-0.09	D	5.50**	5.60**	6.29**	4.09**					
Joint scale	16.360**	5.51	43.15**	16.72**	Joint scale	104.18**	171.89**	289.50**	333.43**					

*, ** Significant at 5 and 1 per cent level, respectively

Table.2 Estimates of gene effects for yield and yield attributing traits in brinjal

	Cross 1	Cross 2	Cross 3	Cross 4		Cross 1	Cross 2	Cross 3	Cross 4		Cross 1	Cross 2	Cross 3	Cross 4
	Days to opening of first flower					Days to first picking					Fruit length (cm)			
m	52.21**	53.81**	53.93**	52.11**	m	72.53**	75.20**	74.96**	75.86**	m	8.64**	8.28**	8.18**	9.17**
(d)	1.36**	1.10**	0.13	-2.30**	(d)	0.76	0.70	-0.23	-1.56**	(d)	-0.91**	-0.41*	-0.99**	-0.92**
(h)	-5.40**	-24.80**	-11.70**	0.90	(h)	0.12	-7.03**	-0.43	-5.15**	(h)	5.01**	-2.48**	0.08	0.85
(i)	-7.46**	-22.93**	-12.13**	0.93	(i)		-6.06*	-2.33	-	(i)	5.20**	-2.68**	1.68*	-0.56
(j)	-0.56	3.03**	-0.03	-0.13	(j)	-	-0.86	-2.60*	-	(j)	-0.76	-0.90 **	0.13	-0.61*
(l)	7.53**	18.86**	14.33**	-7.33**	(l)	-	-3.53	5.53	-	(l)	-10.74**	5.97**	-0.80	-1.46
Epistasis	D	D	D	D	Epistasis	-	C	D	-	Epistasis	D	D	D	D
	Fruit girth (cm)					Number of fruits per plant					Number of primary branches per plant			
m	15.32**	20.40**	18.01**	19.14**	m	36.00**	37.03**	28.30**	29.46**	m	4.36**	4.06**	3.88**	3.50**
(d)	-0.72	-2.65**	-0.90	-2.70**	(d)	5.50**	7.56**	-3.06*	7.09**	(d)	0.35**	0.76**	-0.86**	0.22
(h)	8.49**	-5.56**	6.27**	8.33**	(h)	-0.50	-19.80**	-23.23**	-1.91	(h)	0.70**	0.96	-0.13	0.87**
(i)	9.81**	-5.96**	5.06*	7.38**	(i)	-9.40	-26.20**	-19.20**	-	(i)	-	-0.20	-0.20	-
(j)	0.01	-0.90	-2.92**	-1.65*	(j)	6.00**	2.63	-1.10	-	(j)	-	0.93**	-1.00**	-
(l)	4.77	9.06**	4.33	-17.64**	(l)	-5.66	38.66**	30.60 **	-	(l)	-	1.53	-0.60	-
Epistasis	C	D	C	D	Epistasis	C	D	D	-	Epistasis	-	C	C	-
	Plant height (cm)					Days to last picking					Average fruit weight (g)			
m	61.08**	55.61**	58.08**	55.93**	m	151.60**	155.55**	154.85**	154.90**	m	81.66**	68.65**	91.02**	88.80**
(d)	6.40*	2.83	-3.36	15.16**	(d)	4.69**	-1.40	1.60**	-1.50**	(d)	-12.72**	-8.19	15.01*	-12.03**
(h)	47.00**	32.20**	22.43**	11.26	(h)	2.78*	0.70	6.50**	4.20*	(h)	-2.10	99.82**	68.84**	6.68 **
(i)	28.86**	29.20**	17.60*	1.93	(i)	-	-3.40	5.40**	4.80*	(i)	17.11	102.29**	67.28**	-
(j)	11.60**	-5.16	-7.20**	17.50**	(j)	-	-6.70**	-1.30	-2.70**	(j)	-8.96**	-0.92	10.68	-
(l)	-49.26**	-46.86**	-33.20**	19.06	(l)	-	-6.80	-10.80**	-4.20	(l)	-10.34	-113.73**	-128.2**	-
Epistasis	D	D	D	C	Epistasis	-	D	D	D	Epistasis	C	D	D	-
	Fruit yield per plant (kg)					Number of pickings					Total phenol (mg GAE/ G FW)			
m	2.62**	2.41**	2.61**	2.45**	m	12.23**	12.10**	12.10**	11.93**	m	99.04**	83.93**	129.29**	114.94**
(d)	0.06	0.29*	0.22*	0.21*	(d)	-0.43**	-0.10	0.43*	-0.30	(d)	36.30**	-2.62**	-4.25**	-0.98
(h)	1.28**	1.85**	-1.02**	0.21*	(h)	-0.80	1.10**	0.06	0.90	(h)	-43.90**	210.51**	36.37**	-120.37**
(i)	0.95**	1.32**	-0.87**	-	(i)	-1.00*	0.60	0.06	0.46	(i)	-96.98**	209.08**	36.73**	-124.85**
(j)	0.18	0.06	0.31**	-	(j)	-0.83**	-0.40*	0.23	-0.80**	(j)	33.45**	-43.46**	-22.98**	1.03
(l)	-2.39**	-0.26	1.06**	-	(l)	1.46	0.60	1.86	0.60	(l)	183.07**	-374.77**	-283.1**	207.73**
Epistasis	D	D	D	-	Epistasis	D	C	C	C	Epistasis	D	D	D	D
	Total soluble solids (^{0}B)					Fruit borer infestation (%)								
m	5.78**	5.67**	5.98**	5.79**	m	13.48**	13.98**	14.63**	13.63**					
(d)	0.05	0.02	-0.33**	0.20*	(d)	-0.39**	0.14**	0.23**	0.59**					
(h)	-0.91**	-0.08	-0.45	0.01	(h)	-9.85**	-10.06**	-11.48**	-7.58**					
(i)	-0.76**	-	-1.10**	0.18	(i)	-10.99**	-11.19**	-12.58**	-8.18**					
(j)	0.09	-	-0.48**	0.29**	(j)	-0.40**	0.23**	0.31**	0.44**					
(l)	1.84**	-	2.33**	0.36	(l)	10.10**	9.66**	10.90**	5.70**					
Epistasis	D	-	D	C	Epistasis	D	D	D	D					

*, ** Significant at 5 and 1 per cent level, respectively

Fruit yield per plant (kg): Among the crosses studied, in cross 4 none of the scales were significant for fruit yield per plant indicating that adequacy of additive dominance model and absence of non-allelic interactions between the genes. Hence, three parameter model analysis revealed that in cross 4 significant [d] and [h] gene action was noticed with low positive magnitude for inheritance of this trait. The results in cross 4 were also supported by similar findings of Prasad *et al.,* (2010). In cross 1 the gene effects *viz.,* 'm', dominance [h], additive x additive [i] and dominance x dominance [l] were found significant, depict the non-additive gene action. In cross 2 the gene effects *viz.,* 'm', additive [d], dominance [h] and additive x additive [i] were found significant in this cross. In cross 3 the gene effects *viz.,* 'm', dominance [h], additive x additive [i], additive x dominance [j] and dominance x dominance [l] were found significant, depict the non-additive gene action. The sequence of genetic effects in the decreasing order of their magnitude was [h]>[l]>[i]>[j], depict the non-additive gene action. The sign of [h] and [l] were found opposite indicated the predominance of duplicate type of interaction in cross 1, 2 and 3. These results were in agreement with the results of Singh *et al.,* (2002) and Prasad *et al.,* (2010).

Number of pickings: In cross 1 the gene effects *viz.,* 'm', additive [d], additive x additive [i] and additive x dominance [j] were found significant revealed the importance of additive gene effect along with duplicate type of gene interaction in this cross. Similarly in cross 2 the gene effect 'm', dominance [h] and additive x dominance [j] were found significant. The magnitude of genetic effect found more in [h] as compared to [j] indicating the importance of non-additive gene action in this cross. In case of cross 3 the results of simple scaling tests revealed significant values of B and C indicating

presence of digenic gene interaction. The χ^2 value of joint scaling test was significant which supported the findings of simple scaling tests. But in Hayman's six-parameter model the gene effects *viz.,* 'm' and additive [d] were found significant and remaining found non-significant indicated that there may be presence of linkage. Similarly in cross 4 gene effects *viz.,* 'm' and additive x dominance [j] were found significant. The sign of [h] and [l] were found same (+) indicated the predominance of complementary type of interaction in cross 2, 3 and 4. The similar results were reported by Gauravkumar *et al.,* (2004) and Ahmed *et al.,* (2006).

Total phenol (mg GAE/ g FW): The χ^2 value of joint scaling test was significant which supported the findings of simple scaling tests. In cross 1, 2 and 3 all the gene effects were found significant with greater magnitude of non-additive gene effect along with the predominance of duplicate type of interaction in these crosses. In cross 4 the gene effects *viz.,* 'm', dominance [h], additive x additive [i], and dominance x dominance [l] were found significant. The sequence of genetic effects in the decreasing order of their magnitude was [l]>[i]>[h] depict the predominance of non-additive gene action for the said trait. These results were in agreement with the results of Singh *et al.,* (2002) and Prasad *et al.,* (2010).

Total Soluble Solids (^0B): Among all the scaling tests none of the individual scaling test was found significant in cross 2 indicating the absence of epistasis for this trait which was supported by non-significant χ^2 value derived from joint scaling test. Thus, the additive-dominance model was fitted very well. On the other hand in cross 1 the gene effects *viz.,* 'm', dominance [h], additive x additive [i] and dominance x dominance [l] were found significant with the predominance

of duplicate type of interaction. In cross 3 the gene effects *viz.,* 'm', additive [d], additive x additive [i], additive x dominance [j] and dominance x dominance [l] were found significant. The sequence of genetic effects in the decreasing order of their magnitudes was [l]>[i]>[j]>[d] indicated the importance of non-additive gene action along with duplicate type of gene interaction. Similarly in cross 4 the gene effects *viz.,* 'm', additive [d] and additive x dominance [j] were found significant. The magnitude of gene effects found more in [j] as compared to [d] indicating the importance of non-additive gene effect along with complementary interaction to explain variations in this cross. These findings were in agreement with Rai *et al.,* (2005) and Dhameliya *et al.,* (2009).

Fruit borer infestation (%): The results of simple scaling tests revealed the presence of digenic gene interaction. Further, the χ^2 value of joint scaling test was significant which supported the findings of simple scaling tests. According to six-parameter model all the gene effects were found significant. The sequence of genetic effects in the decreasing order of their magnitudes was [i]>[l]>[h]>[j]>[d] depicting the presence of additive gene effect along with duplicate type of gene interaction to explain the variations in all the four crosses for fruit borer infestation. These results were in agreement with the results of Singh *et al.,* (2002), Gauravkumar *et al.,* (2004) and Prasad *et al.,* (2010).

Overall, it can be concluded from the present study that fruit yield per plant and its component traits recorded in four brinjal crosses were governed by additive, dominance and digenic epistasis gene effects along with duplicate type of gene action. When additive as well as non-additive effects are involved, a breeding scheme efficient in exploiting both types of gene effects should be employed. Hence, bi-parental mating or

few cycles of recurrent selection may give fruitful results for genetic improvement of these traits in brinjal.

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