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Generation mean analysis for fruit yield and its component traits in Brinjal (*Solanum melongena* L.)

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Abstract

The present investigation was undertaken with a view to generate genetic information on gene effects for 12 quantitative traits in brinjal through generation mean analysis. The experimental materials comprise of six basic generations *viz*., P_1, P_2, F_1, F_2, BC_1 and BC_2 of four crosses of brinjal *viz*, AB-8-14 x S. Mani Black (cross 1), AB-15-07 x Pant Rituraj (cross 2), JB-12-06 x GJB-3 (cross 3) and NBR-14-1 x GJLB-4 (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 [i], additive x dominance [j] and dominance x dominance [l] gene actions were equally important for days to first flowering in cross NBR-14-1 x GJLB-4, fruit length in cross NBR-14-1 x GJLB-4, fruit weight in crosses AB-15-07 x Pant Rituraj and NBR-14-1 x GJLB-4, plant spread in cross NBR-14-1 x GJLB-4, TSS in cross AB-8-14 x S. Mani Black. 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, bi-parental 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.

Keywords: Brinjal (*Solanum melongena* L.), epistasis, generation mean analysis and gene action

1. 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) [4]. 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) [1]. 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) [15]. It is popular among people of all social strata and hence, it is rightly called as "vegetable of masses" (Patel and Sarnaik, 2003) [9]. 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 variances. 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.

Material and Methods

The experimental materials comprise of six basic generations *viz*., P_1, P_2, F_1, F_2, BC_1 and BC_2 of four crosses of brinjal *viz,* AB-8-14 x S. Mani Black, AB-15-07 x Pant Rituraj, JB-12-06 x GJB-3 and NBR-14-1 x GJLB-4 were transplanted at Vegetable Research Station, Junagadh Agricultural University, Junagadh, Gujarat during late *kharif /rabi* 2018-19 to study the gene effect, adequacy of additive-dominance model, heterosis, inbreeding depression for fruit yield and its component traits. Experiment was laid-out in Compact Family Block Design (CFBD) with three replications. The observations were recorded on twelve characters *viz.*, days to opening of first flower, days to first picking, fruit length (cm), fruit girth (cm), fruit weight (g), number of fruits per plant, number of primary branches per plant, plant height (cm), fruit yield per plant (kg), plant spread (cm), total soluble solids (TSS) (ºB) and fruit borer infestation (%). Each hybrid and parent 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) [8] and joint scaling test (Cavalli, 1952) [3] were applied to test the adequacy of additive-dominance model. When the model was adequate, six parameter model (Cavalli 1952) [3] 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 number of primary branches per plant in AB-8-14 x S. Mani Black (cross 1). 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) [14] in brinjal. The estimates of gene effects and various contributing traits are given in Table 2. The estimates of means (m) were highly significant for all the traits studied in all crosses, which showed the significant differences among the crosses and traits studied.

Table 1: Scaling and joint scaling tests for fruit 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	1.53	4.20**	0.20	2.33	A	4.87**	1.87	1.87	-2.20*	A	0.60	1.05**	0.16	-1.68**
B	3.40**	2.67*	-0.07	3.67**	B	-2.73*	3.93**	3.93**	3.07*	B	0.95**	0.90**	0.84**	-0.64
C	7.00**	6.13**	4.93**	3.60*	C	-1.67	4.93*	4.93*	-1.33	C	0.19	3.02**	0.28	-0.20
D	1.03	-0.37	2.40*	-1.20	D	-1.90*	-0.43	-0.43	-1.10	D	-0.68*	0.54*	-0.36	1.06**
Joint scale	580.64**	496.64**	864.78**	448.74**	Joint scale	202.89**	247.23**	142.05**	420.21**	Joint scale	22.51**	15.54**	36.81**	23.68**
	Fruit girth (cm)					**Fruit weight**					**Number of fruits per plant**			
A	1.36**	0.79**	0.35	0.25	A	24.58	-52.34*	-47.12**	47.10**	A	0.34*	0.20*	-0.06	-0.10
B	1.74**	0.55*	1.56**	1.33**	B	22.35	-54.34*	-43.39**	-12.91	B	-0.03	-0.18*	0.08*	-0.01
C	3.11**	0.34	2.04**	1.51**	C	-295.26**	-66.55	-55.13	14.17	C	2.66**	-0.18	0.02	-0.50**
D	0.50	-0.50**	0.07	-0.03	D	-161.09**	20.07	17.69	-10.01	D	1.17**	-0.10	0.05*	-0.20**
Joint scale	160.56**	272.89**	149.32**	21.50**	Joint scale	120.68**	140.32**	320.64**	273.83**	Joint scale	286.32**	254.32**	432.43**	443.76**
	Number of primary branches per plant					**Plant height**					**Fruit yield per plant**			
A	0.20	1.80**	1.67**	0.80*	A	1.93	11.80**	-1.33	9.33**	A	0.17	-1.21**	-1.23**	1.05**
B	0.47	0.87*	1.13*	0.80*	B	7.41*	14.67**	-7.40*	6.27*	B	0.22	-1.13**	-0.89**	1.33**
C	1.47	1.93**	1.33**	2.07**	C	8.47	16.33**	-0.67	14.93**	C	-0.67	-1.69**	-1.08*	0.84**
D	0.40	-0.37	-0.73**	0.23	D	-0.44	-5.07*	4.03	-0.33	D	-0.53**	0.33	0.52*	-0.77**
Joint scale	2.11	11.33**	45.98**	21.77**	Joint scale	21.15**	50.64**	37.09**	20.86**	Joint scale	110.46**	320.23**	254.52**	482.69**
	Plant spread					**TSS content**					**Fruit borer infestation**			
A	-0.27	0.73	2.93	-4.53*	A	1.01**	1.01**	-0.38*	0.45**	A	-1.07	1.53*	-1.27*	0.60
B	2.67	2.40	9.27**	0.33	B	0.48*	0.48*	0.43*	-0.01	B	-0.73	0.73	-0.67	1.13
C	8.40*	17.47**	16.80**	12.67**	C	1.22**	1.22**	0.82**	0.00	C	-2.00*	3.60**	-1.20	2.07*
D	3.00	7.17**	2.30	8.43**	D	-0.14	-0.14	0.39**	-0.22*	D	-0.10	0.67	0.37	0.17
Joint scale	543.46**	423.79**	18.28**	543.72**	Joint scale	23.93**	113.73**	234.86**	65.42**	Joint scale	188.64**	48.64**	198.64**	30.69**

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

Table 2: Estimates of gene effects for fruit 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	62.10**	58.25**	59.68**	59.46**	m	76.35**	75.72**	75.00**	75.59**	m	3.86**	6.85**	5.48*	8.17**
(d)	0.16**	0.19	0.42	-0.65**	(d)	1.72**	1.55**	-0.33**	0.40	(d)	-0.06**	-0.21**	-0.04	0.003**
(h)	-4.95**	7.82**	1.147*	5.09**	(h)	-1.41**	0.86**	-3.71*	0.52**	(h)	4.62**	-1.36**	0.25	-6.68**
(i)	-3.67**	2.84	2.46**	4.43**	(i)	-15.0	-1.87	-3.29**	3.42	(i)	1.49**	-1.57**	0.68	-2.12**
(j)	4.89	6.42	3.43	3.86**	(j)	7.70**	13.7	4.24*	-4.99**	(j)	0.89**	0.34	0.42	-1.04**
(l)	-3.64	-7.14**	2.54	-4.55**	(l)	-84.62**	64.72	-0.66**	-5.64	(l)	-3.17**	-0.42	-0.84*	4.44**
Epistasis	C	D	C	D	Epistasis	C	D	C	D	Epistasis	D	C	D	D
	Fruit girth (cm)					**Fruit weight (g)**					**Number of fruits per plant**			
m	3.86**	3.83**	4.48**	4.59**	m	77.80*	414.06**	410.90**	392.60**	m	5.94**	4.06**	60.96**	3.70**
(d)	0.18*	-0.04**	0.43**	0.75**	(d)	-0.35	-3.99*	86.69	-0.40*	(d)	-0.14**	0.08*	5.03**	-0.005**
(h)	3.97**	3.48**	2.51**	2.05**	(h)	631.30*	-32.3**	-47.30	8.56*	(h)	-4.17**	-0.01*	158.30**	0.20**
(i)	0.06	1.02	0.342	1.64	(i)	310.98**	22.32*	64.64	48.6*	(i)	-2.34**	0.03	18.86	0.23**
(j)	0.04	0.42	-1.20**	-1.09**	(j)	66.42	24.64*	58.44	50.56**	(j)	0.37*	0.36**	-23.13	0.04
(l)	-3.26**	-2.41**	-1.95**	-1.54**	(l)	-325.96**	88.34**	75.77**	46.46*	(l)	2.03**	-0.45	-56.40	- 0.03
Epistasis	D	D	D	D	Epistasis	D	D	D	C	Epistasis	D	C	D	D
	Number of primary branches per plant					**Plant height (cm)**					**Fruit yield per plant (Kg)**			
m	-	3.28**	2.25**	3.79**	m	56.38**	51.40**	60.93**	58.25**	m	2.99**	4.58**	5.19**	2.46**
(d)	-	-0.20**	0.16	-0.12**	(d)	4.54**	1.71*	1.47*	0.50**	(d)	0.01**	0.39**	-0.23**	0.22**
(h)	-	2.23**	5.38**	-2.07**	(h)	10.84**	35.65**	7.60**	-15.75	(h)	2.40**	-1.35**	-2.84**	6.01**
(i)	-	1.21	1.47**	1.65	(i)	1.21	9.82*	8.86	1.21	(i)	1.07**	0.42	-0.92*	1.55**
(j)	-	0.21	1.11	1.43	(j)	0.21	1.11	-23.13	7.96	(j)	0.41	0.64	0.23	1.13
(l)	-	-2.17**	-4.23**	-1.80**	(l)	-7.96*	-35.65**	-56.40	-15.34**	(l)	-1.48*	1.88**	2.92**	-3.89**
Epistasis		D	D	C	Epistasis	D	D	D	C	Epistasis	D	D	D	D
	Plant spread (cm)					**Total soluble solids (^{0}B)**					**Fruit borer infestation (%)**			
m	72.33**	78.71**	70.03**	89.96**	m	4.77**	5.12**	5.08**	4.54**	m	10.86**	12.75**	11.13**	10.98**
(d)	2.24**	-0.20**	-0.36	1.09**	(d)	-0.31**	-0.16**	0.40**	-0.06	(d)	-0.17	-0.21**	0.03**	0.47*
(h)	5.70*	-9.38	15.39**	-39.84**	(h)	1.41**	-0.01**	-0.04**	1.26*	(h)	-1.05*	-2.80	-0.93*	1.29**
(i)	-4.09*	-9.06**	3.98	-17.02**	(i)	1.32*	0.20*	-0.43**	0.44*	(i)	2.65	-1.79**	0.84	0.32
(j)	2.42	2.34	-7.16*	2.65**	(j)	0.57*	0.82*	-0.80**	0.45*	(j)	1.46	0.41	0.48	0.41
(l)	1.67	-1.64	-14.49**	20.47**	(l)	1.38**	0.64**	0.32**	-0.88*	(l)	1.92*	1.24	1.54*	-1.87*
Epistasis	C	C	D	D	Epistasis	C	D	D	D	Epistasis	D	D	D	D

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

Gene action

Days to opening of first flower: In cross 1 ‘m’, additive [d], dominance [h], additive x additive [i] gene effects were significant. Same signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested complementary type of epistasis for this trait. While, in cross 2, ‘m’, dominance [h] and dominance x dominance [l] found significant. The opposite sign of dominance [h] and dominance x dominance [l] components estimates observed in cross 2 suggested presence of largely duplicate type of epistasis. In cross 3, gene effect ‘m’, dominance [h], additive x additive [i] were significant. Same signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested complementary type of epistasis for this trait. In cross 4, gene effect ‘m’, additive [d], dominance [h], additive x additive [i], additive x dominance [j] and dominance x dominance[l] were found significant. Opposite signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested duplicate type of epistasis for this trait. Similar results were in trend with Bhakta *et al.* (2009) [2].

Days to first picking: In cross 1, ‘m’, additive [d], dominance [h], additive x dominance [j] and dominance x dominance [l] found significant. The same sign of dominance [h] and dominance x dominance [l] components estimates observed in cross 1 suggested presence of largely complementary type of epistasis. In case of cross 2, all three main effect ‘m’, additive [d], dominance [h] were significant, three interaction additive x additive [i], additive x dominance [j] and dominance x dominance [l] found non- significant. The opposite sign of dominance [h] and dominance x dominance [l] components estimates observed in cross 2 suggested presence of largely duplicate type of epistasis. In cross 3, all the gene effects were found significant. In cross 4, ‘m,’ dominance [h] and additive x dominance [j] were found significant. The same sign of dominance [h] and dominance x dominance [l] components estimates observed in cross 3, suggested presence of complementary type of epistasis. Similar results were in trend with Shinde *et al.* (2009) [14].

Fruit length: In cross 1, ‘m’, additive [d], dominance [h], additive x additive [i], additive x dominance [j] and dominance x dominance [l] were found significant. Opposite signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested duplicate of epistasis for this trait. In cross 2, gene effect ‘m’, additive [d], dominance [h] and additive x additive [i] were found significant. Same signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested complementary type of epistasis for this trait. In cross 3, ‘m,’ and dominance x dominance [l] were found significant. Opposite signs associated with additive [d] and additive x additive [i] components in this cross suggested duplicate type of epistasis for this trait. In cross 4, gene effect ‘m’, additive [d], dominance [h] additive x additive [i] additive x dominance [j] and dominance x dominance [l] were significant. Opposite signs associated with dominance [h] and dominance x dominance [l] component in this cross suggested duplicate type of epistasis for this trait. Similar results were in trend with Kathiria *et al.* (1981) [7].

Fruit girth: In cross 1, gene effect ‘m’, additive [d], dominance [h], and dominance x dominance [l] were significant. Opposite signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested duplicate type of epistasis for this trait. In cross 2, ‘m’, additive [d], dominance [h] and dominance x dominance [l] gene effects found significant. Opposite signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested duplicate type of epistasis for this trait. In cross 3, ‘m’, additive [d], dominance [h], additive x dominance [j] and dominance x dominance [l] gene effects found significant. Opposite signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested duplicate of epistasis for this trait. In cross 4, ‘m,’ additive [d], dominance [h], additive x dominance [j] and dominance x dominance [l] were found significant, opposite signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested duplicate of epistasis for this trait. Similar results were in trend with Patil *et al.* (2003) [10].

Fruit weight: In cross1,’m’, dominance [h], additive x additive [i] and dominance x dominance [l] were found significant. Opposite signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested duplicate type of epistasis for this trait. In cross 2, ‘m’, additive [d], dominance [h], additive x additive[i], additive x dominance [j] and dominance x dominance [l] gene effects found significant, opposite signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested duplicate type of epistasis for this trait. In cross 3, ‘m’, dominance x dominance [l] were significant, while ‘m’, were found significant, opposite signs associated with dominance [h] and dominance x dominance [l] component in this cross suggested duplicate type of epistatis for this trait. In cross 4, all the gene effects ‘m’, additive [d], dominance [h], additive x additive [i], additive x dominance [j] and dominance x dominance [l] were found significant, same signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested complementary type of epistasis for this trait. Similar results were in trend with Sao and Mehta (2010) [11].

Number of fruits per plant: In cross 1, gene effect ‘m’, additive [d], dominance [h], additive x additive [i], additive x dominance [j] and dominance x dominance [l] found significant, opposite signs associated with dominance [h] and dominance x dominance [l] component in this cross suggested duplicate type of epistasis for this trait. In cross 2, gene effect ‘m’ and additive [d], dominance [h] additive x dominance [j] significant, same signs associated with dominance [h] and dominance x dominance [l] component in this cross suggested complementary type of epistasis for this trait. In cross 3, ‘m’, additive [d] and dominance [h] were significant, opposite signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested duplicate type of epistasis for this trait. In cross 4, ‘m’, additive [d], dominance [h], additive x additive [i] gene effect were significant, opposite signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested duplicate type of epistasis for this trait. Similar results are in trend with Vaidvel and Babu (1993) [16].

Number of primary branches per plant: Non- significant chi-square value of the joint scaling test in the cross 1 indicated that the three parameter model is sufficient to explain the variations between the generations. In cross 2, ‘m’, additive [d], dominance [h] and dominance x dominance [l] were found significant, opposite signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested duplicate type of epistasis for this trait. In cross 3, ‘m’, dominance [h], additive x additive [i] and dominance x dominance [l] were found significant, opposite signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested duplicate type of epistasis for this trait. In cross 4, ‘m’, additive [d], dominance [h] and dominance x dominance [l] were found significant, same signs associated with dominance [h] and dominance x dominance [l] component in this cross suggested complementary type of epistasis for this trait. These results were in agreement with Sharaf *et al.* (2015) [13].

Plant height: In cross 1, ‘m’, additive [d], dominance [h] and dominance x dominance [l] were significant. In cross 2 ‘m’, additive [d], dominance [h], additive x additive [i] and dominance x dominance [l] were significant, opposite signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested duplicate type of epistasis for this trait. In cross 3, gene effect ‘m’, additive [d], dominance [h], were significant, opposite signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested duplicate type of epistasis for this trait. In cross 4, gene effect ‘m’, additive [d], and dominance x dominance [l] were significant, same signs associated with dominance [h] and dominance x dominance [l] component in this cross suggested complementary type of epistasis for this trait. Similar results were found by Bhakta *et al.* (2009) [2].

Fruit yield per plant: In cross 1, gene effect ‘m’, additive [d], dominance [h], additive x additive [i], dominance x dominance [l] were significant, opposite signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested duplicate type of epistasis for this trait. In cross 2, ‘m’ additive[d], dominance [h] and dominance x dominance [l] components were positive and significant, opposite signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested duplicate type of epistasis for this trait. In cross 3, ‘m’ additive [d], dominance [h], additive x additive [i], dominance x dominance [l] gene effect found significant, opposite signs associated with dominance [h] and dominance x dominance [l] component in this cross suggested duplicate type of epistasis for this trait. In cross 4, gene effect ‘m’, additive [d], dominance [h], additive x additive [i], and dominance x dominance [l] were significant, opposite signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested duplicate type of epistasis for this trait. Similar results were in trend with Gulamuddin *et al.* (1997) [5].

Plant spread: In cross 1, gene effect ‘m’, additive [d], dominance [h] and additive x additive [i] were significant, same signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested complementary type of epistasis for this trait. In cross 2, ‘m’, additive [d], additive x additive [i] were significant, same signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested complementary type of epistasis for this trait. In cross 3, gene effect ‘m’, dominance [h], additive x dominance [j] and dominance x dominance [l] were significant, opposite signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested duplicate type of epistasis for this trait. In cross 4, gene effect ‘m’, additive [d], dominance [h], additive x additive [i], additive x dominance [j] and dominance x dominance [l] were significant, opposite signs associated with dominance [h] and dominance x dominance [l] component in this cross suggested duplicate type of epistasis for this trait. Similar results were agreement with Savaliya (2017) [12].

Total soluble solids: In cross 1, gene effect ‘m’ additive [d], dominance [h], additive x additive [i] additive x dominance [j] and dominance x dominance [l] were significant, similar signs associated with dominance [h] and dominance x [l] components in this cross suggested complimentary type of epistasis for this trait. In cross 2, all the gene effects ‘m’, additive [d], dominance [h], additive x additive [i], additive x dominance [j] and dominance x dominance [l] were significant, opposite signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested duplicate type of epistasis for this trait. In cross 3, all the gene effects m’, additive [d], dominance [h], additive x additive [i], additive x dominance [j] and dominance x dominance [l] were found significant, opposite signs associated with additive [d] and additive x additive [i] components in this cross suggested dupicate type of epistasis for this trait. In cross 4, ‘m’, dominance [h], additive x additive [i], additive x dominance [j] and dominance x dominance [l] were found significant, opposite signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested duplicate type of epistasis for this trait. Similar results were observed by Joshi and Chadha (1994) [6].

Fruit borer infestation: In cross 1, ‘m’, dominance [h] and dominance x dominance [l] effects found significant, opposite signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested duplicate of epistasis for this trait. In cross 2, ‘m’, additive [d], and additive x additive [i] were found significant, opposite signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested duplicate type of epistasis for this trait. In cross 3, ‘m’, additive [d], dominance [h] and dominance x dominance [l] were significant, Opposite signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested duplicate type of epistasis for this trait. In cross 4, ‘m’, additive [d] and dominance [h] found significant, opposite signs associated with dominance [h] and dominance x dominance [l] components in this cross suggested duplicate type of epistasis for this trait. These findings were in agreement with Savaliya (2017) [12].

Conclusion

Overall, it can be concluded from the present study that fruit yield per plant and its component traits 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 were 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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