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Research Article

Genetic analysis for fruit yield and its component traits in brinjal (*Solanum melongena* L.)

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Abstract

An investigation was undertaken with a view to study the nature and magnitude of gene action for 10 quantitative traits among five crosses of brinjal through generation mean analysis. The study involved six generation *viz.*, P_1, P_2, F_1, F_2, BC_1 and BC_2 of five crosses derived from six diversified parents. 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 primary branches per plant, fruit breadth, fruit weight, yield per plant and seeds per fruit in most of the crosses. The complimentary type of epistasis was detected for inheritance of days to first flowering and days to first fruit picking in BNDT x PPC, number of fruits per plant in PPC x BB 64, yield per plant in N-1007 x BB-64 and KASARALI x PPC, while duplicate type of epistasis was important for inheritance of remaining traits in all the crosses except in BNDT x PPC.

Key words
Gene action, additive, non-additive, generation mean, brinjal

Introduction

Among the vegetables, brinjal is one of the important vegetable crops and is grown round the year, in tropics and subtropics. India is the major producer of brinjal in the world and ranks second in production of brinjal next to China. Being the centre of origin, India has great potentiality in enhancing the productivity and for the development of varieties with desirable traits. 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 material under investigation comprised of six generations *viz.*, P_1 (Parent 1), P_2 (Parent 2), F_1 (P_1 x P_2), F_2 (selfing of F_1), BC_1 (F_1 x P_1), and BC_2, (F_1 x P_2) of five crosses *viz.*, BNDT x PPC, N-1007 x BB-64, M. Gota x BB-64, Kasral x PPC and PPC x BB-64 in brinjal. The experiment was laid out in a randomized block design with three replications during *rabi* 2013-14 at the research and educational farm, Department of Agricultural Botany, Dapoli. Four rows, each of P_1, P_2, F_1, BC_1, and BC_2 generations and eight rows of F_{2s} were planted in 3 m long plots with 60 x 60 cm. Spacing in each replication. Five competitive plants from each of the genotypes of parents (P_1 and P_2) and F_1, ten from BC_1, BC_2 and forty plants from each of F_{2s} were randomly selected from three replications and observations on 10 characters *viz.*, plant height (cm), number of branches, days to first flowering, days to first fruit picking, length of fruit (cm), breadth of fruit (cm), average fruit weight (g), number of fruits per plant, yield per plant (g) and seeds per fruit (g) were recorded. Recommended package of practices and plant protection measures were followed. The individual scaling tests (Mather, 1949 and Hayman and Mather, 1955) and joint scaling test (Cavelli, 1952) were applied to test the adequacy of additive-dominance model. When the model was adequate, six parameter model (Mather and Jinks 1982) was used to estimate components of different parameters *viz.*, [m], [d], [h], [i], [j] and [l].

Results and discussion

Results of individual scaling test and joint scaling test (Table 1) were non-significant for number of primary branches plant^{-1} in KASARALI x PPC, fruit breadth and number of seeds per fruit in BNDT x PPC indicating adequacy of additive dominance model and absence of epistasis. Therefore, these crosses showed simple type of inheritance, while epistasis contributed significantly for the inheritance of rest 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: Plant height: The additive gene action was found significant for plant height in cross, N 1007 x BB 64 and PPC x BB 64 while predominance of dominant gene action was found in cross BNDT x PPC, N 1007 x BB 64 and KASARALI x PPC. N 1007 x BB 64 exhibited both additive and dominant gene action. The digenic interaction, additive x additive [i], in cross BNDT x PPC and N-1007 x BB-64 whereas dominance x dominance [l] gene action was found significant in cross M. Gota x BB 64, KASRAL x PPC and PPC x BB 64 which indicated expression of plant height was governed by additive, dominance, additive x additive and dominance x dominance gene action in respective crosses. Opposite sign of dominance [h] and dominance x dominance [l] revealed that existence of duplicate epistasis in cross KASRAL x PPC for plant height. Thus, it suggests that the character governed by additive component could be improved through selection while in other cases selection in later generations of segregating population would be meaningful. These findings were in agreement with the results of Prasad *et al.* (2010), Thangavel *et al.* (2011) in brinjal.

Primary branches per plant: As the scaling test results were non-significant, three parameter model analysis revealed that, significant dominance [h] gene action was noticed 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 number of primary branches was also reported by Singh *et al.*, (2002). However, in remaining crosses *i.e* BNDT x PPC, N-1007 x BB 64 and M. Gota x BB 64 showed the presence of significant scaling test for number of branches plant^{-1} was confirmed by joint scaling test indicated the existence of non-allelic gene interactions. Additive [d] gene action was found significant in N-1007 x BB. Among the interactions, dominance x dominance [l] gene action was relatively more important for expression of this trait in cross M. Gota x BB 64 being significant. The roles of additive and digenic interaction for inheritance of number of primary branches were also in conformity with the Kamani *et al.* (2008) and Dhameliya *et al.* (2009).

Days to first flowering: The components of gene action observed significant but negative magnitude in BNDT x PPC 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. Positive and negative sign of additive x additive [i] interaction showed association and dispersion of alleles respectively. Therefore, negative significant value of [i] in cross BNDT x PPC and M. Gota x BB-64 showed dispersion of alleles in parents for days to 1st flowering whereas association of alleles in cross KASRAL x PPC and PPC x BB 64. It is interesting to note that, both the components, [h] and [l] values were significant having similar negative sign indicating presence of complimentary type of epistasis. The complimentary effect will produce new recombinants capable of improving yield. Therefore, improving of this character could be achieved through heterosis breeding. In cross KASRAL x PPC also all the components of gene action were significant indicating presence of additive, dominance and digenic interactions for inheritance of this character. The opposite signs of both, [h] and [l] components concluded duplicate type of epistasis for expression of this character. In remaining crosses *i.e.* N-1007x BB 64, digenic interactions [j] and [l], in cross M. Gota x BB 64, [i] and [l], in cross PPC and PPC x BB 64, [i] and [l] were found significant. As magnitude of non-additive gene effects were higher than additive, improvement of this character needs intensive selection through later generation. The results of the present investigation are in accordance with the earlier results of Rai, *et al.* (2005) and Dhameliya *et al.* (2009).

Days to first fruit picking: In cross BNDT x PPC showed significant but negative magnitude in desirable direction for all the components *viz.*, [m], [d], [h], [i], [j] and [l] depicted more importance of dominance and digenic [i, l] interactions for inheritance of this character than additive [d] gene effects. . It is interesting to note that, both the components, [h] and [l] values were significant having similar negative sign concluded presence of complimentary type of epistasis. In cross M. Gota x BB 64 also importance of dominance x dominance [l], additive x dominance [j] and additive [d] gene actions were noticed which indicate presence of additive, and digenic interactions for expression of this character while in cross KASRAL x PPC additive [d] and additive x dominance [j] remaining dominance [h], additive x additive [i] and dominance x dominance [l] components were found significant and played important role in expression of this trait. In the crosses, M. Gota x BB 64 and KASRAL x PPC the components [h] and [l] had opposite sign which suggest presence of duplicate type of epistasis which is responsible for inheritance of this trait. In cross N-1007 x BB 64 significant negative magnitude were found for both digenic [j] and [l] components while in cross KASRAL x PPC dominance [h] and additive x additive [i] components played important role in expression of this trait. Whereas, Gauravkumar *et al.* (2004), Rai, *et al.* (2005), Dhameliya *et al.* (2009) and Prasad *et al.* (2010) reported involvement of additive [d], dominance [h] and additive x dominance [j] gene effects were responsible for inheritance of this character.

Fruit length: Besides additive[d] and dominance [h], epistatic gene interactions *viz.*, [i], [j], [l] were found significant in all the crosses except additive[d], additive x additive [j] and dominance x dominance [l] in crosses, N-1007x BB 64, M. Gota x BB 64, KASRAL x PPC and PPC x BB 64, respectively. As compared to all six components, the higher magnitude of dominance x dominance [l] type of interaction was observed in most of the crosses. By in large both components [h] and [l] had opposite sign in all the crosses except in cross PPC x BB 64 presence of duplicate type of epistasis which concluded for inheritance of this character. The findings from present study were supported by findings of Gauravkumar *et al.* (2004), Ahmed *et al.* (2006), Shinde *et al.* (2009) and Prasad *et al.* (2010).

Fruit breadth: Among the crosses studied, none of the scales were significant in cross BNDT x PPC for fruit breadth indicating that adequacy of additive-dominance model and absence of non-allelic interactions. Therefore, three parameter model analysis revealed that in cross BNDT x PPC no epistatic effects found to be involved in the inheritance of this trait. Only dominance [d] gene action was found significant. The results in BNDT x PPC were supported by findings of Ahmed *et al.* (2006) and Kamani *et al.* (2008). The results obtained for significance of scaling and joint scaling tests for fruit breadth indicated the presence of epistatic gene interaction for its inheritance in remaining four crosses. In cross N-1007 x BB 64 and M. Gota x BB 64 all six components [m], [d], [h], [i], [j] and [l] except [d], [l] and [j] respectively were relatively more important as they possess higher magnitude value than [l] and [j] component. This suggested contribution of dominance [h] and digenic [i, l] gene interactions for inheritance of this character. Similarly, the components [h] and [l] had opposite signs, it clearly indicated involvement of duplicate type of epistasis in the inheritance of this character. Higher negative magnitude of dominant gene action and dominance x dominance gene interaction indicated the dominance towards the parents with lower fruit breadth and positive and higher ‘h’ indicated dominance towards the higher fruit breadth. While, the absence of significance in ‘d’ were indicating non- significant role of additive gene action. These results are in complete agreement with the results of Ahmed *et al.*, (2006), Dhameliya *et al.* (2009), Shinde *et al.* (2009) and Prasad *et al.* (2010).

Fruits per plant: Among all the five crosses, additive [d] and dominance x dominance [l] in crosses, BNDT x PPC , N-1007x BB 64 and PPC x BB 64 dominance [h] in cross KASRAL x PPC gene interactions were found non-significant indicating absence of [d], [h] and [l] type of gene interactions in these crosses for fruits per plant. Significant higher and more or less equal magnitude values of dominance [h] and additive x additive [i] component than other components in positive direction were recorded in all the crosses except in cross KASRAL x PPC indicating predominant role of [h] and [i] gene interactions in inheritance of this character. Besides these, dominance x dominance [l] epistatic interactions was also found significant gene interactions for inheritance of this trait in cross KASRAL x PPC and PPC x BB 64 both, had duplicate and complimentary type of epistasis respectively. Thus present investigation suggested that expression of the character, fruits per plant would governed by dominance and epistatic interactions with duplicate and complimentary epistasis. These results were in accordance with Gauravkumar *et al.* (2004) and Ahmed *et al.* (2006).

Fruit weight: Comparatively higher significant magnitude in positive direction was noticed in cross BNDT x PPC , for additive [d] and in cross , N-1007 x BB 64 and M. Gota x BB 64 for dominance x dominance [l]components while in cross 4 for dominance [h] and in cross PPC x BB 64 for additive x additive [i] components, indicating involvement of additive [d], dominance [h], additive x additive [i] and dominance x dominance [l] gene interactions were more important in inheritance of this character. In addition to this, the important component [h] and [l] had opposite signs which concluded presence of duplicate type of epistasis was found to be responsible for inheritance of this character in cross KASRAL x PPC and PPC x BB 64. These findings from present investigation were in accordance with Lawande *et al.* (1992), Patil *et al.* (2000), and Dhameliya *et al.* (2009).

Yield per plant: The relative contribution of dominance (h) and three epistatic interactions [i, j, l] were important as they possess significant higher magnitude than additive which indicated involvement of dominance and epistatic interactions for inheritance of this trait. Complementary type of epistasis was found significant for inheritance of this character in in cross N-1007x BB 64 and KASRAL x PPC as both the components, [h] and [l] had similar signs which suggest complimentary type of epistasis for inheritance of this character in in cross N-1007x BB 64 and KASRAL x PPC. These results were in agreement with those obtained by Lawande *et al.* (1992), Gauravkumar *et al.* (2004), Ahmed *et al.* (2006), and Thangavel *et al.* (2011).

Seeds per fruit: Among the crosses studied, in cross BNDT x PPC none of the scales were significant for seeds per fruit 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 BNDT x PPC significant additive [d] gene action was noticed with low positive magnitude for inheritance of this trait. The results in BNDT x PPC were also supported by similar findings of Dharmegowda *et al.* (1979), Prasad *et al.* (2010). In cross N-1007x BB 64, all the six components *viz.,* dominance [h], additive x additive [i], additive x dominance [j] and dominance x dominance [l] gene interactions were found significant higher magnitude than additive [d] and [l]. Remaining crosses indicated these dominance and digenic interactions were more important for expression of this character. Opposite signs of both components, [h] and [l] suggested presence of duplicate type of epistasis found to be responsible for expression of this character. In crosses, M. Gota x BB 64, KASRAL x PPC and PPC x BB 64 digenic [i], [j] and [l] epistatic interactions were found significant except [i] in cross M. Gota x BB 64 which indicated additive x additive [i], additive x dominance and dominance x dominance gene interactions were played important role towards governing this character. The findings from present study were in agreement with reports of Suneetha *et al.* (2008), Shinde *et al.* (2009), Sabolu *et al.* (2014).

Conclusion

Considering overall results, it is apparent that most of the characters in either of the crosses were found to be under the control of additive and non-additive gene effects coupled with complementary and duplicate type of epitasis. This indicated that heterosis breeding and use of population improvement, bi-parental mating, recurrent selection might be profitable in exploiting both additive and non-additive gene action to obtain desirable recombinants having the characteristics like early flowering, days to first picking and high yielding.

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

Characters	Crosses	Scales				Joint scale test
		A	B	C	D	
Plant height (cm)	C_1	1.27	4.47	24.33**	10.57**	17.97**
	C_2	0.27	18.11**	58.93**	20.54**	108.35**
	C_3	23.93**	18.40**	39.87**	1.23	27.88**
	C_4	3.73	14.33**	18.97*	18.52**	40.29**
	C_5	18.87**	18.87**	33.20**	2.27	26.46**
Primary branches/ plant	C_1	1.40	0.93	3.03*	0.35	7.68*
	C_2	0.27	1.73**	2.90**	0.45	15.56**
	C_3	1.47*	1.20	2.30*	0.18	11.34**
	C_4	1.07	0.27	1.37	0.02	4.00
	C_5	1.60*	1.53*	1.83	0.65	10.66**
Days to first flowering	C_1	12.93**	20.73**	51.97**	9.15**	165.78**
	C_2	13.40**	33.67**	49.70**	1.32	150.05**
	C_3	16.60**	29.60**	51.40**	2.60	96.56**
	C_4	15.47**	15.07**	18.57**	5.98**	59.64**
	C_5	28.47**	46.87**	64.70**	5.32**	248.83**
Days to first fruit picking	C_1	14.53**	21.60**	55.33**	9.60**	194.80**
	C_2	17.40**	32.40**	55.60**	2.90	181.38**
	C_3	22.00**	32.73**	58.30**	34.52**	274.15**
	C_4	16.73**	17.93**	24.60**	5.03*	108.97**
	C_5	28.00**	39.87**	65.73**	1.07	207.34**
Fruit length (cm)	C_1	4.66**	1.82*	4.48**	3.37**	42.48**
	C_2	2.14*	2.90**	1.50	1.76**	13.50**
	C_3	3.33**	2.46*	2.78*	4.28**	45.80**
	C_4	1.62	2.46*	5.96**	3.40**	35.121**
	C_5	2.04*	0.49	3.20**	0.82	16.80**
Fruit breadth (cm)	C_1	0.66	0.003	0.35	0.15	4.65
	C_2	1.04*	0.29	1.61*	1.18**	25.39**
	C_3	1.57**	0.66	0.20	1.01**	19.71**
	C_4	0.83	1.39**	0.48	0.04	19.24**
	C_5	0.91**	0.73	3.57**	0.96**	44.33**
Fruits/plant	C_1	11.07**	26.73**	66.90**	14.55**	196.25**
	C_2	9.00**	14.2**	48.07**	12.40**	489.20**
	C_3	9.53**	8.13**	35.43**	13.65**	1003.24**
	C_4	20.60**	31.60**	60.30**	4.05**	265.21**
	C_5	30.47**	11.67**	68.47**	13.17**	667.12**
Fruit weight (g)	C_1	0.40	17.20**	37.77**	10.08*	17.39**
	C_2	31.40**	16.80*	46.80**	0.70	29.03**
	C_3	48.40**	16.33**	35.57**	14.58**	57.77**
	C_4	16.13	56.93**	27.77*	34.28**	75.31**
	C_5	1.93	27.73**	3.43	11.18*	40.76**
Yield/plant (g)	C_1	479.67	808.87**	2983.4**	847.42**	125.87**
	C_2	1182.9**	1371.6**	4358.5**	902.0	916.37**
	C_3	630.80**	848.87**	3196.8**	858.55**	882.89**
	C_4	2060.7**	996.67**	4259.1**	600.87**	372.88**
	C_5	1528.3**	532.33**	4186.4**	1062.9**	954.93**
Seeds/fruit (g)	C_1	0.60	0.33	0.22	0.24	7.33
	C_2	0.33	1.93	6.90**	2.65**	90.35**
	C_3	1.67**	6.60**	8.50**	-0.12	92.55**
	C_4	2.57**	2.23**	3.50**	1.58**	58.96**
	C_5	0.60**	4.57**	6.40**	0.62**	76.80**

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

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

Traits	Crosses	[m]	[d]	[h]	[i]	[j]	[l]	Epistasis
Plant height (cm)	C_1	52.05**	-0.07	25.80**	21.13**	2.87	-17.93	-
	C_2	41.55**	11.09**	47.45**	41.08**	9.19**	-23.24	-
	C_3	44.33**	-2.90	4.00	- 2.47	-2.77	44.80**	-
	C_4	48.89**	-1.03	18.30**	37.03**	-5.03	-55.1**	D
	C_5	50.80**	4.27**	-12.33	- 4.53	-0.00	42.27**	-
Primary Branches/ plant	C_1	4.67**	0.33	1.83	0.70	-0.23	1.63	-
	C_2	4.09**	1.03**	1.40	0.90	0.73	1.10	-
	C_3	3.94**	0.03	- 0.20	- 0.37	-0.13	3.03**	-
	C_4	4.37**	-0.27	0.93**	-	-	-	-
	C_5	4.22**	0.13	-0.80	-1.30	-0.03	4.43**	-
Days to 1st flowering	C_1	60.14**	-7.00**	-27.53**	-18.30**	-3.90**	-15.37*	C
	C_2	61.63**	-1.67	-2.37	-2.63	-10.13*	-44.43**	-
	C_3	59.88**	0.38	-6.07	-5.20**	-6.50	-41.00**	-
	C_4	59.61**	-2.27*	17.10**	11.97**	0.20	-42.50**	D
	C_5	62.11**	-2.07	7.03	10.63**	-9.20	-85.97**	-
Days to 1st fruit picking	C_1	76.78**	-5.83**	-24.30**	-19.20**	-3.53**	-16.93*	C
	C_2	79.32**	-2.27	-9.03	-5.80	-7.50**	-44.00**	-
	C_3	77.09**	29.33**	-71.53**	-69.03**	27.37**	79.77**	D
	C_4	75.42**	-1.80	13.53**	10.07**	-0.60	-44.73**	D
	C_5	78.77**	-2.47	-3.73	2.13	-5.93**	-70.00**	-
Fruit length (cm)	C_1	11.41**	3.78**	9.30**	7.32**	3.24**	-10.15**	D
	C_2	9.21**	1.03	-3.57**	-3.53**	0.38	8.57**	D
	C_3	8.21**	0.63	8.09**	8.56**	0.44	-14.36**	D
	C_4	11.79**	0.13	-4.42*	-6.80**	2.04**	7.65**	D
	C_5	9.73**	-0.24	2.74**	1.64	-1.26**	-0.09	-
Fruit breadth (cm)	C_1	3.44**	0.50**	1.13	-	-	-	-
	C_2	4.33**	0.07	2.73**	2.36**	0.67**	-3.11*	D
	C_3	4.64**	-1.06**	- 1.69**	-2.02**	-0.45	4.25**	D
	C_4	4.00**	0.29	- 1.49*	0.07	-1.11**	-0.63	-
	C_5	3.73**	-1.03**	2.77**	1.92**	- 0.09	-0.28	-
Fruits/ plant	C_1	9.02**	0.53	31.87**	29.10**	7.83**	8.70	-
	C_2	4.63**	0.87	31.63**	24.80**	2.63**	-1.53	-
	C_3	4.66**	1.57**	29.33**	27.30**	4.07**	-19.17**	D
	C_4	6.64**	-2.73**	4.67	8.10**	5.50**	44.10**	-
	C_5	5.32**	-1.07	24.53**	26.33**	-9.40**	15.80**	C
Fruit weight (g)	C_1	64.04**	19.40**	-38.70**	-20.17**	- 8.40	2.57	-
	C_2	76.68**	4.00	3.43	- 1.40	- 7.30	49.60**	-
	C_3	75.61**	-15.17**	-11.23	-29.17**	-16.03**	93.90**	-
	C_4	72.46**	4.20	73.77**	68.57**	-36.53**	-109.5**	D
	C_5	66.37**	-34.13**	42.67**	22.37*	-14.83**	-48.17**	D
Yield/ plant (g)	C_1	520.5**	361.2**	1602.7**	1694.8*	164.6**	-406.30	-
	C_2	343.7**	93.10	2457.6**	1804.0**	94.33	750.53**	C
	C_3	342.5**	-71.0*	2145.0**	1717.1**	109.0**	-237.43	-
	C_4	454.7**	-191.9**	1328.9**	1201.7**	-532.0**	1855.6**	C
	C_5	320.8**	-493.9**	2637.0**	2125.8**	-497.9**	-65.20	-
Seeds/ fruit (g)	C_1	1.88**	0.47**	-1.067	-	-	-	-
	C_2	2.08**	-1.43**	4.30**	5.30**	2.27**	-3.70*	D
	C_3	2.43**	0.23	0.07	0.23	4.93**	8.03**	-
	C_4	1.38**	-0.05	1.12	3.17**	-4.80**	-2.83*	-
	C_5	1.37**	-0.98**	-0.63	1.23**	3.97**	3.93**	-

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