

Original Research Paper

Genetics of growth and yield attributing traits of brinjal (*Solanum melongena* L.) through six generation mean analysis

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ABSTRACT

Understanding gene action of different traits is of utmost importance for formulating successful breeding programs. The population was developed involving Arka Neelachal Shyama and CARI-1 to inquire the gene actions controlling the inheritance of several growth as well as yield attributing parameters through six-generation mean analysis. Three parameter model revealed the insufficiency of the simpler additive dominance model for the evaluated traits, referring to the existence of inter-allelic interactions. Six parameter model was implemented to better understand gene actions. Most of the yield and attributing traits under study except number of branches showed a high estimate of dominance as well as environmental variance, disclosing a lower extent of heritability. The number of branches was observed to be controlled by duplicate epistasis. Hence, for the fixation of this trait, the best strategy is to exercise minimal selection during advance generations, followed by intense selection during later generations (F_4 population onwards). The preponderance of the narrow sense type of heritability revealed that dominant effects were predominantly accountable for the existing genetic variation. Hence, recurrent selection followed by bi-parental mating and selection during the later stage of generations is advised to increase the occurrence of favorable alleles and accumulation of desirable genes.

Keywords: Brinjal, gene action, genetics, six-generation mean analysis and yield.

INTRODUCTION

Brinjal (*Solanum melongena* L.) is among the foremost important and popular vegetables consumed globally as well as in India. It consists of a significant amount of anthocyanin pigments (purple types), phenols, amide proteins as well as free reducing sugars. Brinjal is widely utilized for its medicinal properties and has also been prescribed for diabetic patients and liver complaints (Sabolu *et al.*, 2014). Although brinjal is one of the prime members of the Solanaceae family, minimal breeding attempts have been undertaken for the development of potential hybrids/hybrid as well as for crop improvement by the exploitation of local germplasm in comparison to the remaining Solanaceous crops. Yield being a highly complex trait gets fluctuated by genetic as well as environmental factors, (Foolad and Lin, 2001) and applied agro technical methods (Kaşıkavalcı, 2007).

The selection of suitable parental material is of utmost importance during crop improvement program to achieve the inherent yield potential of a crop (Koutsika-Sotiriou *et al.*, 2008). In brinjal, the number of marketable fruits per plant, the number of branches, and the average fruit weight are the major yield attributing traits. In brinjal, yield per plant directly correlates with average fruit weight and number of fruits (Kaffytullah *et al.*, 2011; Angadi *et al.*, 2017); and these traits are highly influenced by several genetic and environmental components (Karki *et al.*, 2020). The extent of the success achieved in a crop improvement program relies solely upon the accessibility to the information concerning nature as well as the measure of gene action governing the traits of commercial significance. Yield being a complex trait relying upon several other parameters along with their interactions, understanding the alliance of these traits with fruit yield will supplement the selection procedure



with enhanced accuracy and precision (Deb and Khaleque, 2009).

Keeping the above-mentioned points in view, the extent of hybrid vigour and inbreeding depression as well as the gene action governing various growth and yield attributing characters in brinjal was assessed through six generation mean analysis, as this is highly efficient technique providing the accurate evaluation of chief genetic components governing the manifestation of the quantitative traits (Mather and Jinks, 1982).

MATERIALS AND METHODS

Experimental site

The present research work was commenced during the period from 2018 - 2020 at CHES, IIHR-ICAR, Bhubaneswar, India. The experimental soil was red laterite soil with very low pH (4.4) containing organic carbon in a medium amount. The soil contained be 296 Kg/ha, 39.2 Kg/ha, and 157kg/ha of nitrogen, phosphorus and potassium, respectively.

Plant materials

For development of the population, two parents *viz*, Arka Neelachal Shyama (Large, round, green with purple stripes) and CARI-1 (Large, oblong, light green) were selected. Arka Neelachal Shyama was used as female parent, while CARI-1 was used as pollen parent. The two parents were artificially crossed for the production of F_1 hybrid. Subsequently, F_1 generation plants were selfed to obtain F_2 generation seeds as well as backcrossed with Arka Neelachal Shyama (P_1) and CARI-1 (P_2) to obtain B_1 and B_2 generations respectively.

Evaluation of populations under field growing conditions

The seeds of six generations including two parents, their F_1 hybrid, segregating F_2 population and backcross populations with each of the parents were sown and proper nursery management practices were followed. During the transplanting of the seedlings, a spacing of 60 x 60 cm² was adopted. The number of plants evaluated differed according to the generation. For the assessment of the inheritance of growth and yield attributing traits,

30 plants each of female and pollen parents and their F_1 's, 259 plants of F_2 population, 50 plants of B_1 population and 58 plants of B_2 population were planted in the open field. Recommended package of practices such as fertilizer application, intercultural operations, crop protection measures and irrigation were carried out for raising a successful crop.

Freshly harvested and marketable fruits of individual plants were utilized for genetic inheritance study. The mode of inheritance of various traits including plant height, number of branches, number of fruits and yield per plant, as well as average fruit length, girth, and weight were recorded.

Statistical analysis

In the current experiment, the scaling test was performed on means of each generation as per Mather and Jinks, 1982. The joint scaling test along with χ^2 test were utilized for the determination of the sufficiency of the additive-dominance model (Cavalli, 1952; Fowler *et al.*, 1998; Singh and Chaudhary, 1977). Similarly, the χ^2 values for all the traits were checked to fit into the three-parameter model (m, d, h) and significant values implicated the epistatic gene interaction. By exercising the six-parameter model, six gene components including mean (m), pooled additive component (d), dominance component (h), additive \times additive component (i), additive \times dominance component (j), and dominance \times dominance component (l) were calculated (Jinks and Jones, 1958). The magnitude of scales was estimated by the formulae: $A=2B_1 - P_1 - F_1=0$; $B=2B_1 - P_2 - F_1=0$; $C=4F_2 - 2F_1 - P_1 - P_2 = 0$ and $D = 2F_2 - B_1 - B_1=0$. Significance of any of these scales indicated the involvement of epistasis in governing the respective traits (Mather and Jinks, 1982). The estimate of heterosis over parents as well as mid-parent value was calculated as % increase or decrease of F_1 mean over the parental and mid-parental means, respectively. Heritability (narrow-sense) was calculated by method suggested by Warner (1952).

Potence ratio was estimated as per Smith (1952) to analyze the extent of dominance, which is given below:

$$P \text{ (relative potence of gene set)} = \frac{\text{mean of first filial generation} - \text{midvalue of the parents}}{0.5 \text{ (better parent mean} - \text{lower parent mean)}}$$

Where, $P = +1$, suggest complete dominance, $-1 < P < +1$ suggest partial dominance, except $P = 0$, which suggests non-existence of dominance. When potence ratio exceeds ± 1 ; it indicates over dominance. The signs (+/-) of the parents indicate the direction of dominance.

OP-STAT software was used for all the above statistical analysis (Sheoran *et al.*, 1998).

RESULTS

Heterosis and inbreeding depression

Heterosis over the mid-parent *i.e.*, relative heterosis (Table 1) was found to be significantly negative for all the traits. Only vegetative traits under study exhibited positive relative heterosis *i.e.*, 72.09 % in case of plant height and 2.82 % for the number of branches. Relative heterosis (-13.41%) and heterobeltios over P_1 (-18.39 %), along with positive inbreeding depression (33.55 %) were recorded for fruits per plant in this population. The higher magnitude of heterobeltiosis/over P_2 (-31.64 %) as well as relative heterosis (-17.80 %) in the negative direction was observed for fruit yield per plant. In the current study, negative relative heterosis for both fruit length (-19.36 %) and fruit girth (-6.24 %) were observed in this population. Negative relative heterosis (-6.24 %) as well as heterobeltiosis/over P_2 (-25.76 %) was observed for fruit weight. Similarly, inbreeding depression ranged from 0.12 % (fruit length) to 40.60 % (yield per plant).

Gene action

For the assessment of inheritance pattern and gene actions governing growth and yield attributing

traits, six generation mean analysis was implemented and the findings are presented in Table 2. Significant variability among the populations were recorded implicating the appropriate choice of the parents.

The significance estimates of three parameter model associated with joint scaling test for the means of generation of each parameter are shown in Table 3. Owing to the significant χ^2 value for all the traits, this test disclosed the constraints of the additive as well as dominance gene actions to describe the trait's inheritance. However, it expressed their cumulative effects on interaction. Hence, for the better interpretation the gene actions six parameter model was utilized (Table 4). Nonetheless, the inheritance of the studied traits could not be adequately elucidated through the normal additive-dominance model after obtaining the significant estimate of individual scales (A, B, C, or D) for the means of generations. The existence of epistasis was concluded upon the significant estimate of either of 'A', 'B', 'C' or 'D' components of the scaling test for all the traits under study.

Plant height

The highest and lowest plant height were recorded in F_1 (55.50 cm) and P_1 (29.10 cm), followed by F_2 (51.96), B2 (47.07 cm) and B1 (43.48 cm). Significant value of mean (m) was recorded, however additive (d) along with dominant (h) estimates appeared to be insignificant (Table 4). The additive x additive ($-i$) component contributed significantly towards the plant height similar to additive x dominance (j) component.

Table 1. Estimates of genetic parameter for plant vigor, yield and yield attributing traits in the cross between Arka Neelachal Shyama (P_1) and CARI-1 (P_2)

Traits	Heterosis (%)			Inbreeding depression (%)
	over P_1	over P_2	over mid parent	
Plant height (cm)	90.72	56.78	72.09	6.38
Number of branches per plant	10.98	-4.21	2.82	21.89
Yield per plant (g)	3.07	-31.64	-17.80	40.60
Number of fruits per plant	-18.39	-7.79	-13.41	33.55
Fruit length (cm)	-1.81	-31.59	-19.36	0.12
Fruit girth (cm)	-4.25	-8.15	-6.24	3.89
Fruit weight (g)	27.22	-25.76	-6.24	9.46

Table 2. Generation means (+/-SE) for fruit traits and yield per plant from the Arka Neelachal Shyama x CARI-1 derived population

Characters	Population					
	P ₁	P ₂	F ₁	F ₂	B ₁	B ₂
Plant height (cm)	29.10 ±1.36	35.40 ±1.62	55.50 ±2.22	51.95 ±0.61	43.48 ±2.10	47.06 ±1.17
Number of branches per plant	8.20 ±0.38	9.50 ±0.76	9.10 ±0.33	7.10 ±0.16	5.14 ±0.27	6.91 ±0.26
Number of fruits per plant	8.70 ±0.36	7.70 ±0.26	7.10 ±0.34	4.71 ±0.14	4.98 ±0.30	4.53 ±0.23
Yield per plant (g)	1472.00 ±61.78	2219.50 ±87.26	1517.25 ±86.31	901.28 ±30.16	1000.75 ±66.23	958.70 ±63.81
Fruit length (cm)	9.65 ±0.23	13.85 ±0.31	9.47 ±0.30	9.46 ±0.10	9.76 ±0.21	10.27 ±0.20
Fruit girth (cm)	23.55 ±0.39	24.55 ±0.39	22.55 ±0.35	21.67 ±0.14	21.40 ±0.39	21.98 ±0.34
Fruit weight (g)	169.27 ±1.61	290.08 ±11.88	215.34 ±9.49	194.97 ±3.80	200.45 ±8.80	210.23 ±7.40

Table 3. Joint scale test with three parameter model (*m*, *d* and *h*) for various traits in the cross of Arka Neelachal Shyama and CARI-1 population

	Plant height	Number of branches	Number of fruits per plant	Yield per plant	Fruit length	Fruit girth	Fruit weight
<i>m</i>	34.77 ±0.92**	6.68 ±0.28**	6.91 ±0.19**	1488.26 ±46.59*	11.17 ±0.17**	23.08 ±0.23**	188.20 ±28.17**
<i>d</i>	3.06 ±0.94**	0.51 ±0.27	-0.25 ±0.19	184.70 ±45.75*	1.52 ±0.16**	-0.50 ±0.24*	-60.40 ±5.99**
<i>h</i>	25.91 ±1.76**	0.48 ±0.50	-3.02 ±0.38**	-834.46 ±92.35*	-2.75 ±0.33**	-2.04 ±0.44**	-19.35 ±9.82**
χ^2	52.13**	100.83**	155.01**	188.79*	49.63**	39.81**	26.52**

*and **significant at p - “0.05” and “0.01”, respectively

The dominance x dominance (*l*) estimate showed superiority over additive x dominance (*j*), dominance (*h*) and additive x additive (*i*) estimates. The potence ratio of -7.381 was observed indicating overdominance in inheriting this trait.

Number of branches

P₂ (9.50) exhibited the highest number of branches, while B₁ exhibited the least number of branches (5.14), followed by F₁ (9.10), F₂ (7.11) and B₂ (6.91). Besides mean (*m*), a significant estimate of the additive (*-d*), dominance (*-h*), additive x additive (*-i*), and dominance

x dominance (*l*) components was noticed (Table 4). The estimate of dominance x dominance (*l*) component exhibited superiority over the additive x dominance (*j*), dominance (*h*) and additive x additive (*i*) estimates.

Number of fruits per plant

Plants of P₁ produced the highest average number of fruits, while the minimum fruit count was noticed in B₂ (4.53), accompanied by P₂ (7.70), F₁ (7.10) and B₁ (4.98). The mean (*m*) was shown to be significant, however non-significant value was recorded for additive (*d*) along with dominance (*h*), additive x

additive (i) as well as additive \times dominance (j) estimates (Table 4). In the current study, dominance \times dominance (l) played key role in the governance of this trait. The estimate of dominance \times dominance (l) was higher than dominance (h), additive \times dominance (j) and additive \times additive (i) estimates.

Yield per plant

The highest yield from individual plant was obtained from P_2 (2.22 kg), while the minimum yield per plant was procured from F_2 (0.90 kg), accompanied by F_1 (1.52 kg), P_1 (1.47 kg) and B_1 (1.00 kg). The mean (m), additive \times dominance (j) in addition to dominance \times dominance (l) components were recorded to be significant (Table 4), while non-significant values was reported for additive (d), dominance (h), additive \times additive (i) components. The higher estimate of dominance \times dominance (l) was observed in comparison with the additive \times dominance (j), additive \times additive (i), as well as dominance (h). The potence ratio of 0.87 was estimated suggesting partial dominance in the inheritance.

Fruit length

Fruit traits including fruit skin color varied significantly across the population (Fig 1). The mean maximum length was exhibited by the fruits of P_2 (13.85 cm) and the lowest fruit length was observed for F_2 (9.46 cm), succeeded by B_2 (10.27 cm), B_1 (9.76 cm) and P_1 (9.65 cm). The mean (m) was found to be significant, however non-significant estimates were observed for additive (d), dominance \times dominance (l) as well as dominance (h) components (Table 4). Besides additive \times additive (i) estimate, a significant estimate of additive \times dominance (j) components was also found for fruit length. The magnitude of additive \times dominance (j), was greater as compared to additive \times additive (i), dominance \times dominance (l) as well as dominance (h). The potence ratio of 1.083 was found stipulating overdominance in the trait's inheritance.

Fruit girth

The highest and lowest fruit girth were recorded in P_2 (24.55 cm) and B_1 (21.40 cm), followed by P_1 (23.55 cm), F_1 (22.55 cm) and B_2 (21.99 cm). Except the mean (m) and dominance \times dominance (l) components, the remaining estimates were estimated to be nonsignificant (Table 4). In the current study, the estimate of dominance \times dominance (l) was greater

than additive \times additive (i), additive \times dominance (j), and dominance (h). For fruit girth, the potence ratio of 3.00 was recorded referring towards overdominance in inheriting this trait

Average Fruit weight

The greatest and lowest individual fruit weight were exhibited by P_2 (290.08 g) and P_1 (169.27 g), followed by F_1 (215.3 g), B_2 (210.23 g) and B_1 (200.45 g). The significant value of mean (m) was recorded. The additive \times dominance (j) component was found to be significant, unlike the additive (d), additive \times additive (i), dominance (h) as well as dominance \times dominance (l) components (Table 4). The additive \times dominance (j) estimate was shown to be more in comparison with the additive \times additive (i), dominance \times dominance (l) and dominance (h) components. The potence ratio of 0.237 was observed indicating partial dominance in the inheritance of this trait.

DISCUSSION

Heterosis and inbreeding depression

The parameters pertaining to growth and vigor showed significantly positive relative heterosis. The greater estimates of positive heterotic effects and minimal inbreeding depression for plant height revealed that crop improvement programs through heterosis could be successfully implemented for growth and vigor in brinjal (Roy *et al.* 2009; Mistry *et al.* 2018). Relative heterosis as well as heterobeltiosis over P_1 in the negative direction recorded for fruits per plant in this population. Plant yield being a highly complex trait, is the sum total of various basic yield constituents. The greater estimate of heterobeltiosis/over P_2 along with relative heterosis in the negative direction suggested that instead of heterosis breeding, selection at the later stage of the segregating population may be the best way to obtain higher yield per plant in the population studied (Sao and Mehta, 2011; Patel *et al.*, 2013; Bagade *et al.*, 2020). Fruit length as well as fruit girth are regarded as essential characters considering the diversity observed in consumer preference especially in India, where eastern region prefer large round types as opposed to south region preferring long types. Hence, negative heterosis for these traits especially fruit length is desired. In the current study, desirable negative relative heterosis for both fruit length and fruit girth were observed in this population, which will have advantage in development of round type fruits.

Table 4. Estimates of gene effects for various traits in the cross between Arka Neelcalhal Shyama x CARI-1 derived population using six parameter model

	Characters						
	Plant height	Number of branches	Number of fruits per plant	Yield per plant	Fruit length	Fruit girth	Fruit weight
A	-9.40±3.32**	7.02±0.74**	5.84±0.79**	987.75±169.74**	-0.40 ±0.57	3.29±0.94**	-16.28±20.06
B	2.83±4.30	4.77±0.98**	5.73±0.64**	1819.33 ±177.06**	2.78±0.59**	3.12±0.87**	84.96±21.22**
C	-32.33±4.82**	7.46±1.26**	11.72±1.00**	3120.86±236.20**	4.59±0.82**	6.50±1.06**	110.16**±27.11
D	12.88±2.76**	2.16±0.49**	-0.07 ±0.48	-156.88 ±109.99	-1.10±0.35**	-0.04 ±0.59	-20.73±13.78
Mean (<i>m</i>)	51.95±0.78**	7.10±0.16**	4.71±0.14**	901.28±30.16**	9.46±0.10**	21.67±0.14**	194.97±3.80**
Additive (<i>d</i>)	2.96 ±2.27	-1.77±0.37**	0.44 ±0.38	42.04 ±91.96	-0.50 ±0.29	-0.58 ±0.52	-9.78±11.50
Dominance (<i>h</i>)	-2.51±5.81	-4.07±1.13**	-0.94 ±1.04	-14.72 ±242.28	-0.06±0.80	-1.40±1.27	27.14±29.77
Additive × additive (<i>i</i>)	-25.76±5.52**	-4.32±0.99**	0.15 ±0.96	313.77 ±219.98	2.21±0.71**	0.09 ±1.18	41.47±27.57
Additive × dominance (<i>j</i>)	12.23±5.01*	-2.24 ±1.14	-0.10 ±0.89	831.58±212.75**	3.18±0.70**	-0.16 ±1.18	101.25±25.94**
Dominance × dominance (<i>l</i>)	19.19±10.28	16.11 ±1.97**	11.41 ±1.84**	2493.31±437.17**	0.17 ±1.43	6.31 ±2.34**	27.21±53.40
<i>d+h</i>	0.45	-5.84	-0.49	27.31	-0.57	-1.98	17.36
<i>I+i+j</i>	5.66	9.54	11.46	3638.67	5.56	6.24	169.93
Magnitude of Gene Effect	> >h>i	> >h>i	> >h>h	> > >h	> > >h	> > >h	> > >h
Epistasis	-	Duplicate	-	-	-	-	-
Potence ratio (F ₁)	-7.38	-0.38	-2.20	0.87	1.08	3.00	0.23

*and **significant at p - “0.05” and “0.01” , respectively.

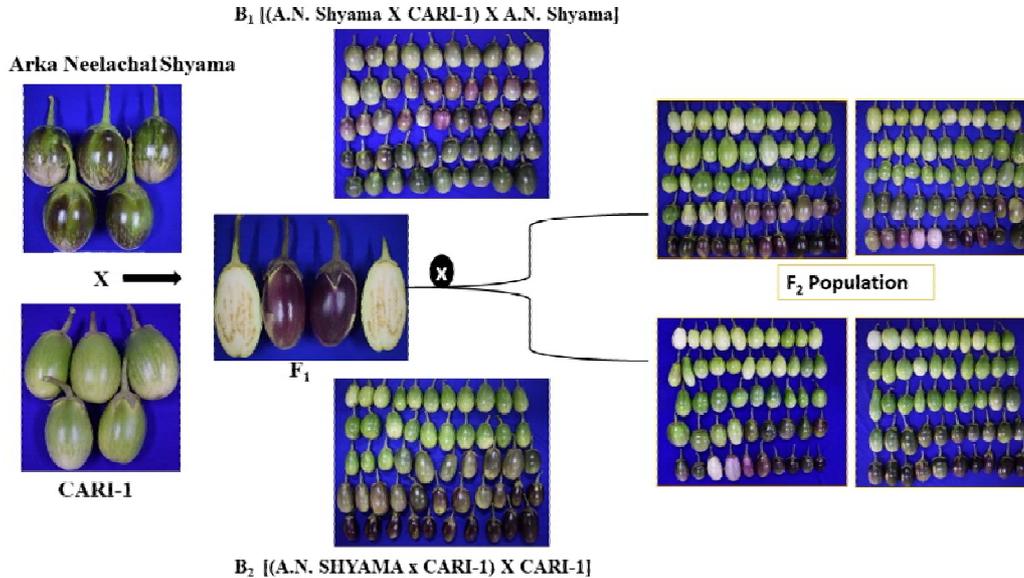


Fig 1. Segregation of fruit traits in populations derived from cross between Arka Neelchal Shyama x CARI-1

These results are consistent with the result obtained by Timmapur *et al.*, (2008), Chowdhury *et al.*, (2010), Sahajahan *et al.*, (2016) and Sujin and Karuppaiah (2018). Negative relative heterosis as well as heterobeltiosis/over P_2 were observed for fruit weight. The pronounced negative heterosis for fruit weight revealed dominance of negative alleles contributed by the lower scoring parent (Patil *et al.*, 2001; Das *et al.*, 2009).

East (1908) and Shull (1909, 1910) demonstrated that a decrease in heterozygosity results in a corresponding decline in vigour due to inbreeding (Crow, 1952), which also fully satisfies the dominance hypothesis. Inbreeding depression was resulted to the extent of 40.60 % (fruit yield per plant) in our brinjal population. However, the inbreeding depression reports of this research work is also supported by the findings of recent research workers like Sao and Mehta (2010), Singh and Rai (1990) and Kumar and Pathania (2003), who reported positive inbreeding depression for a number of traits of brinjal.

Gene action

Significant variability among the means of populations were recorded suggesting that the choice of parents was appropriate.

Plant height: Additive x additive (-i) component contributed significantly towards the plant height similar to additive x dominance (j) component, which suggested the preponderance of non-additive components; hence should be considered immensely in

the crop improvement programs. The magnitude of dominance x dominance (l) was higher than additive x dominance (j), dominance (h) and additive x additive (i), suggesting heterosis breeding is the best strategy to for improvement programs for enhancing plant height. Non-additive gene action governing the plant height trait in brinjal was also recorded by Singh *et al.* (2002) as well as Patel (2003).

Number of branches: The significant value of the additive (-d), dominance (-h) as well as additive x additive (-i) components pointed towards the existence of additive and non-additive gene actions controlling this trait. The contrasting signs of h and l showed the existence of duplicate epistasis interaction among the alleles. The estimate of dominance x dominance (l) component was superior to the additive x dominance (j), dominance (h) and additive x additive (i) components. Significant estimate of additive component in negative direction was observed, hence revealed that the trait could not be fixed via simple selection. The involvement of non-additive gene action in governing number of branches in brinjal was reported by Dharwad *et al.* (2011), Reddy and Patel (2014) and Sujin and Karuppaiah (2018). However, in our study, association of additive along with non-additive gene actions suggested that the population improvement through reciprocal recurrent selection should be considered as the best breeding scheme to increase the accumulation of favorable alleles (Ramalho *et al.*, 2001). Again, duplicate class of inter-allelic interrelationship is operating (Patel, 2003;

Mistry *et al.*, 2016) indicating the reduction in variability in segregating generations which obstruct the selection activity (Kumar and Patra, 2010). Hence, mild selection during earlier generations, followed by bi-parental mating and intense selection in the later generations should be done for improving the trait.

Number of fruits per plant: In the current study, dominance x dominance (*l*) was playing major role in the governance of this trait. For the given trait, additive gene action (Dixit *et al.*, 1982; Joshi and Chadha, 1994) and non-additive gene action (Rao 2003; Aswani and Khandelwal 2005) have been reported. The estimate of dominance x dominance (*l*) was higher than additive x additive (*i*), dominance (*h*) and additive x dominance (*j*). Thus, recombination breeding and hybridization accompanied by selection during early generations could be performed for the improvement of this trait. Non-significant value was recorded for additive (*d*) along with dominance (*h*), additive x additive (*i*) as well as additive x dominance (*j*) components.

Yield per plant: Additive x dominance (*j*) in addition to dominance x dominance (*l*) components were recorded to be significant. The higher estimate of dominance x dominance (*l*) was observed in comparison with the additive x dominance (*j*), additive x additive (*i*), as well as dominance (*h*). Thus, additive along with non-additive interactions were involved in governing the trait. Hence, trait improvement strategy consisting of recurrent selection as well as bi-parental mating could be highly fruitful for the accumulation of the favorable genes and/or to remove the existing undesirable and unfavorable linkages (Mistry *et al.*, 2016). Shafeeq *et al.* (2013) in their study involving genetic inheritance of yield and yield attributing traits found the similar report concluding the fruit yield per plant to be governed by both additive and non-additive gene actions. Non-significant value was found for additive (*d*), dominance (*h*), additive x additive (*i*) components.

Fruit length: Predominance of additive gene action was concluded owing to the significance of additive x additive (*i*) and additive x dominance (*j*) components. The magnitude of additive x dominance (*j*), was greater as compared to additive x additive (*i*), dominance x dominance (*l*) and dominance (*h*). Hence, selection would be the best strategy in the improvement of fruit length. This finding however was in contradiction to Mistry *et al.* (2016) who reported the

fruit length trait to be governed by additive-dominance interaction. The non-significant estimates were observed for additive (*d*), dominance x dominance (*l*) and dominance (*h*) components.

Fruit girth: In the current study, only dominance x dominance (*l*) components were observed to be significant and the estimate of dominance x dominance (*l*) was higher than additive x additive (*i*), additive x dominance (*j*), and dominance (*h*). For fruit girth, both additive gene action and non-additive gene action have been reported by the researchers (Kumar and Ram, 1987; Vaghasiya *et al.*, 2000; Rao, 2003; Patel, 2003). Thus, due to the involvement of the non-additive gene action, recombination breeding and hybridization accompanied by selection during later generations could be performed for the improvement of this trait (Mistry *et al.*, 2016). The non-significant estimate of additive (*d*), additive x additive (*i*), dominance (*h*) and additive x dominance (*j*) were recorded.

Fruit weight: The additive x dominance (*j*) component was found to be significant. The additive x dominance (*j*) estimate was shown to be more in comparison with the additive x additive (*i*), dominance x dominance (*l*) and dominance (*h*) components. Hence, reciprocal recurrent selection can be adopted. Meanwhile, selection process needs to be delayed until required homozygosity is achieved in the inbred lines (Mistry *et al.*, 2016). The additive (*d*) component in addition to additive x additive (*i*), dominance (*h*) as well as dominance x dominance (*l*) components, were recorded to be non-significant.

CONCLUSION

In the current study, the growth and yield attributing traits were identified/reported to be governed by additive and non-additive gene action along with the preponderance of combination of both the gene actions. A higher order of non-allelic interaction (involvement of more than 2 genes) was exhibited by most of the traits except number of branches in which duplicate type of epistasis was recorded. Due to the existence of a higher estimate of interactions, the frequency of the non-fixable gene effects was more as compared to the fixable gene effects. Of all the traits, only fruit length was reported to be governed by additive gene action, which can be fixed by simple selection. However, for the remaining traits combination of recurrent selection/ hybridization and bi-parental mating can be adopted followed by intense selection at later stage of segregating population.

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