Original Research Paper

Inheritance studies on different quantitative and qualitative fruit traits in brinjal (*Solanum melongena* L.)

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ABSTRACT

Generation mean analysis of brinjal lines, GL 401 × BR 104 (CROSS I), GL 401 × W 230 (CROSS II) and W 230 × RMO 1142 (CROSS III) six generation of three crosses *viz.* highlighted the involvement of epistatic interactions (duplicate) for most of the qualitative traits. However, the number of fruits per plant in CROSS I & III and fruit girth, calyx length, and yield per plant in CROSS II confirmed the occurrence of complementary epistasis. Mainly, additive effect for fruit girth, non-additive effect for calyx length, calyx width, peduncle girth, fruit weight, and fruit length, and both types for peduncle length, number of fruits /cluster, number of fruits/ plant, and yield/ plant were experienced. Additive × dominance or dominance × dominance type of interactions were more prevalent than additive × additive type of interactions for different traits. Cluster bearing was monogenic dominant and green color of calyx as well as peduncle was dominant over purple with the duplicate type of epistasis. Fruit shape was digenic with incomplete dominance. Fruit color displayed digenic control in CROSS I & II and tri-genic ratio in CROSS III with incomplete dominance of purple and green pigmentations producing variable color intensity in homozygous or heterozygous conditions.

Keywords: Additive effect, brinjal, dominance, epistasis, fruit color, inheritance

INTRODUCTION

Brinjal (*Solanum melongena* L., 2n=24) is known for its high diversity of fruit traits. India, being the centre of diversity, has primitive types of green, very small, bitter fruits with hard pulp and thick peel. Domestication, natural inter-crossing and hybridization among different species and cultivars, natural mutations, incessant selection have created broad fruit diversity in brinjal (Frary *et al*., 2007). India has enormous diversity in brinjal color (light to dark purple and almost black, green, white, variegated), shape (round, long, oblong, oval, pear type), size (big, medium, and small), bearing habit (solitary or in clusters) and other fruit traits (Swarup, 1995). There are many region-wise set preferences among the consumers based on these traits. From the marketing point of view, purple, dark purple or black varieties suitable for '*Bhartha*' are generally preferred in North India, while, long and green types are preferred in Bihar and Southern Karnataka. In brinjal, fruiting behaviour, fruits per plant and fruit weight are highly correlated and important indicators of high yield potential (Mangi *et al*., 2016).

For the improvement of market-oriented traits, a suitable breeding method with set objectives can aid in the selection of desired genotypes. The breeder can only proceed for genetic improvement of such traits with a confirmed knowledge about the mode of their inheritance. In previous studies, inheritance of fruit colour in brinjal was reported as monogenic, digenic, or tri-genic based on the colour of parents involved in the crosses (Kamini *et al*., 2007; Liu *et al*., 2016), while the others have reported polygenic inheritance with the fitment of additive-dominance-epistasis (Pang *et al*., 2008; Patidar, 2015). Fruit shape was under the control of a single gene with partial dominance of elongated or long fruits over round fruits and role of maternal effect in the expression of the trait as reported by Aravindakshan (2003). However, the involvement of one basic gene in complementation to the other three genes was also shown for fruit shape (Kamini *et al*., 2007). In contrast to this Qiao *et al*. (2011) reported the quantitative nature of fruit shape by fitting additive major gene + additive-dominant polygene model (D-2 model). Patidar (2015) reported the dominance of purple calyx over the green.

Although a few studies have been reported on the inheritance of fruit shape, color, bearing habit, a combined approach describing the genetics of all these traits is lacking. Because of the importance of these traits in the improvement of brinjal, the present investigation was planned to study the inheritance of various quantitative as well as qualitative fruit traits in brinjal.

MATERIALS AND METHODS

The present investigation was carried out at Vegetable Research Farm of Department of Vegetable Science, Punjab Agricultural University Ludhiana, Punjab, India with six generations of each for three crosses *viz*; GL 401 × BR 104 (Cross I), GL 401 × W 230 (Cross II) and W 230 × RMO 1142 (Cross III) attempted among four diverse parents in 2016-17. Each cross was used to develop F_2, BC_1P_1, and BC_1P_2 generations in summer 2017. Six generations (P_1, P_2, F_1, F_2, BC_1P_1, and BC_1P_2) of each cross were evaluated in a tri-replicated trial in randomized block design. Each replication of each cross carried 10, 50, and 100 plants for each parent and hybrid, each backcross and F_2, respectively. The crop was raised following recommended cultural practices. Each plant was observed for various qualitative and quantitative fruit traits related to consumer preference and yield potential. Generation means analysis for six generations in each cross was done using the software BMM (Singh, 1993) for estimating the gene effects. The scaling test (A, B, C) was used for checking the presence of epistasis (Mather, 1949). A three-parameter model or additive dominance model (ADM) was applied to estimate m, [d], and [h] and test goodness of fit (χ^2) in the absence of epistasis (Cavalli, 1952), and six parameter model was used to determine epistatic interactions between the alleles when the goodness of fit (χ^2) for Additive dominance model was significant. The goodness of fit of the models was tested from expected and observed frequencies for the parameters (three or six) under investigation. The significance of the parameters in each model was used to explain the inheritance of quantitative traits. For analysis of qualitative traits, Mendelian ratios of F_2 and backcross generations were tested through the χ^2 test and the inheritance pattern of such traits was confirmed.

RESULTS AND DISCUSSION

Inheritance of quantitative traits

The generation mean analysis of three different crosses for various quantitative traits in brinjal revealed the adequacy of the simple Additive dominance model for calyx width in *GL 401 × W 230*. In all the other traits, the significance of A, B, C scales and inadequacy of the Additive dominance model highlighted the influence of epistatic interactions for their expression (Table 1). Six parameter model (Table 2) unveiled significant additive genetic effects with or without additive × additive interactions for fruit girth, fruit weight, peduncle length, and the number of fruits per cluster in *GL 401 × BR 104*, for fruit girth, calyx length, calyx width, peduncle length, peduncle girth, and the number of fruits per plant in *GL 401 × W 230*. These traits from these specific crosses can be fixed in homozygous conditions easily by the selection of individuals based on their phenotype and carrying forward the progeny of selected individuals only. Therefore, the expression of these traits can easily be improved through the pedigree method as suggested in earlier reports of Yadav *et al*. (2017) and Santhosha *et al*. (2017) in brinjal.

The genetics of fruit length, number of fruits per plant and yield per plant in *GL 401 × BR 104*, fruit length, average fruit weight, number of fruits per cluster and fruit yield in *GL 401 × W 230* and fruit length, fruit girth, calyx width, peduncle girth, number of fruits per plant in *W 230 × RMO 1142* displayed highly significant dominant genetic effects along with the significance of different types of epistatic interactions. Between both genetic effects, the magnitude of dominance was on the higher side for most of these traits. As both the components cannot be easily fixed, these traits in specific crosses can further be improved through the reciprocal recurrent selection that involves phenotypic selection and inter-crossing and later on can be used in heterosis breeding to exploit non-additive gene effects. The importance of both additive and non-additive effects in the present study was substantiated with the findings of Santhosha *et al*. (2017) and Yadav *et al*. (2017) in brinjal.

Dominant effects as well as dominance × dominance type of interactions were highly significant with higher magnitude for calyx length, calyx width, peduncle girth, and average fruit weight in *GL 401 × BR 104*, for peduncle girth in *GL 401 × W 230,* and calyx

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Table 1 : Scaling and joint scaling test for fruit traits in brinjal

Trait	A	B	C	χ^2_{ADM}
Fruit length (cm)				
CROSS I	-1.50 ± 0.52**	0.89 ± 0.55	-2.91 ± 1.06**	18.66**
CROSS II	-1.71 ± 0.52**	2.11 ± 0.60**	-5.78 ± 0.84**	75.76**
CROSS III	-0.79 ± 0.27**	-1.79 ± 0.41**	-1.53 ± 0.53**	25.45**
Fruit girth (cm)				
CROSS I	0.34 ± 0.17*	-0.01 ± 0.20	0.76 ± 0.30*	9.15**
CROSS II	0.86 ± 0.16**	0.70 ± 0.19**	2.60 ± 0.30**	80.52**
CROSS III	0.30 ± 0.22	-1.72 ± 0.25**	-1.94 ± 0.36**	73.30**
Calyx length (mm)				
CROSS I	-3.91 ± 1.25**	-8.01 ± 1.53**	-12.55 ± 2.19**	41.20**
CROSS II	-2.53 ± 1.21*	-0.04 ± 1.36	-4.79 ± 2.02*	7.86*
CROSS III	-3.94 ± 0.92**	-10.23 ± 0.93**	-12.55 ± 1.60**	134.44**
Calyx width (mm)				
CROSS I	-3.29 ± 0.88**	-10.74 ± 1.14**	-12.84 ± 1.68**	95.10**
CROSS II	0.44 ± 0.61	0.40 ± 0.64	-2.09 ± 1.11	7.80
CROSS III	-1.88 ± 0.71**	-7.05 ± 0.85**	-9.12 ± 1.34**	72.12**
Peduncle length (mm)				
CROSS I	-3.89 ± 1.96*	-3.39 ± 1.99	-11.21 ± 3.05**	13.66**
CROSS II	-3.33 ± 1.40*	-0.29 ± 1.43	-8.40 ± 2.08**	18.11**
CROSS III	-13.15 ±1.01**	-13.52 ± 1.18**	-16.61 ± 1.79**	279.69**
Peduncle girth (mm)				
CROSS I	-0.75 ± 0.21**	-2.37 ± 0.32**	-1.84 ± 0.44**	61.54**
CROSS II	-0.29 ± 0.20	0.27 ± 0.23	1.20 ± 0.35**	19.49**
CROSS III	-0.24 ± 0.21	-0.95 ± 0.26**	-1.64 ± 0.39**	19.86**
Average fruit weight (g)				
CROSS I	-23.84 ± 9.53*	-5.78 ± 13.53	65.87 ± 18.99**	19.26**
CROSS II	-73.31 ± 7.34**	10.75 ± 7.20	-69.45 ± 9.26**	145.67**
CROSS III	-43.10 ± 5.91**	-123.47 ± 10.61**	-105.84 ± 11.22**	245.53**
Number of fruits per cluster				
CROSS I	-0.11 ± 0.05*	-0.02 ± 0.04	-0.35 ± 0.07**	37.63**
CROSS II	0.46 ± 0.09**	-0.17 ± 0.11	0.65 ± 0.16**	44.74**
CROSS III	-0.91 ± 0.10**	-0.33 ± 0.07**	-0.81 ± 0.15**	102.05**
Number of fruits per plant				
CROSS I	-2.01 ± 0.72**	4.91 ± 0.52**	4.36 ± 0.96**	109.66**
CROSS II	-0.84 ± 0.75	-2.54 ± 0.69**	-7.61 ± 1.12**	54.37**
CROSS III	-5.10 ± 1.09**	-3.07 ± 0.96**	-11.06 ± 1.53**	56.38**
Yield per plant (kg)				
CROSS I	-0.77 ± 0.17**	0.82 ± 0.23**	1.73 ± 0.27**	82.39**
CROSS II	-1.91 ± 0.17**	0.10 ± 0.15	-2.31 ± 0.21**	192.79**
CROSS III	-1.87 ± 0.13**	-2.42 ± 0.21**	-2.81 ± 0.28**	243.74**

*,** significant at 5% and 1% levels, respectively.   ADM- Additive Dominance Model, CROSS I-GL 401 × BR 104, CROSS II -GL 401 × W 230 and CROSS III-W 230 × RMO 1142

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Table 2 : Estimation of gene effects and inter-allelic interactions in the best fit model for fruit traits in brinjal

Trait	M	d	h	I	j	L	Type of epistasis
GL 401 × BR 104							
Fruit length (cm)	10.83 ± 1.16**	4.18 ± 0.11**	6.23 ± 2.76**	2.30 ± 1.15**	-2.40 ± 0.69**	-1.69 ± 1.69**	Duplicate
Fruit girth (cm)	7.05 ± 0.36**	-2.33 ± 0.04**	-1.65 ± 0.90	-0.44 ± 0.36	0.35 ± 0.25	0.11 ± 0.56	Duplicate
Calyx length (mm)	36.42 ± 2.03**	-0.14 ± 0.47	-8.95 ± 5.31	0.62 ± 1.98	4.10 ± 1.71*	11.30 ± 3.59**	Duplicate
Calyx width (mm)	22.79 ± 1.22**	-3.77 ± 0.37**	-17.11 ± 3.25**	-1.18 ± 1.16	7.45 ± 1.12**	15.21 ± 2.38**	Duplicate
Peduncle length(mm)	40.32 ± 2.59**	6.31 ± 0.58**	-1.00 ± 6.99	3.93 ± 2.53	-0.50 ± 2.27	3.34 ± 4.95	Duplicate
Peduncle girth (mm)	9.94 ± 0.43**	-2.11 ± 0.12**	-6.48 ± 1.08**	-1.30 ± 0.41**	1.61 ± 0.35**	4.43 ± 0.69**	Duplicate
Average fruit weight (g)	29.92 ± 24.55**	-44.51 ± 1.73**	-254.25 ± 60.98**	-95.44 ± 24.49**	-18.07 ± 16.44	125.03 ± 37.33**	Duplicate
Number of fruits/cluster	0.91 ± 0.05**	0.09 ± 0.02**	0.27 ± 0.15	0.22 ± 0.05**	-0.10 ± 0.06	-0.09 ± 0.11	Duplicate
Number of fruits/plant	20.37 ± 0.93**	4.10 ± 0.28**	-4.84 ± 2.41*	-1.47 ± 0.89	-6.92 ± 0.83**	-1.43 ± 1.56	Complementary
Fruit yield/plant (kg)	5.27 ± 0.35**	-0.02 ± 0.06	-4.56 ± 0.91**	-1.68 ± 0.34**	-1.59 ± 0.28**	1.63 ± 0.58**	Duplicate
GL 401 × W 230							
Fruit length (cm)	4.98 ± 0.98**	6.15 ± 0.11**	15.06 ± 2.52**	6.17 ± 0.97**	-3.82 ± 0.73**	-6.57 ± 1.63**	Duplicate
Fruit girth (cm)	5.38 ± 0.32**	-0.07 ± 0.05	-0.70 ± 0.80	-1.03 ± 0.32**	0.17 ± 0.23	-0.53 ± 0.51	Complementary
Calyx length (mm)	27.81 ± 1.85**	6.88 ± 0.34**	3.18 ± 4.87	2.21 ± 1.82	-2.49 ± 1.50	0.36 ± 3.36	Complementary
Calyx width (mm)	14.88 ± 0.16**	2.99 ± 0.16**	0.67 ± 0.34*	-	-	-	Incomplete dominance
Peduncle length(mm)	34.54 ± 2.39**	11.25 ± 0.52**	1.62 ± 6.16	4.78 ± 2.34*	-3.05 ± 1.94	-1.16 ± 3.88	Duplicate
Peduncle girth (mm)	6.82 ± 0.36**	0.85 ± 0.06**	-2.45 ± 0.91**	-1.15 ± 0.35**	-0.56 ± 0.27*	1.17 ± 0.59*	Duplicate
Average fruit weight (g)	97.02 ± 12.90**	51.07 ± 0.95**	-8.81 ± 33.95	6.89 ± 12.87	-84.06 ± 9.98**	55.68 ± 21.66**	Duplicate
Number of fruits/cluster	2.15 ± 0.19**	-0.57 ± 0.03**	-1.09 ± 0.47*	-0.36 ± 0.19	0.63 ± 0.14**	0.08 ± 0.30	Duplicate
Number of fruits/plant	21.47 ± 1.07**	-2.70 ± 0.26**	3.31 ± 2.79	4.23 ± 1.04**	1.71 ± 0.91	-0.85 ± 1.85	Duplicate
Fruit yield/plant (kg)	2.02 ± 0.26**	1.03 ± 0.04**	0.14 ± 0.70	0.51 ± 0.26**	-2.01 ± 0.22**	1.28 ± 0.45**	Complementary
W 230 × RMO 1142							
Fruit length (cm)	9.32 ± 0.61**	-3.27 ± 0.06**	-2.10 ± 1.58	-1.05 ± 0.61	0.99 ± 0.45*	3.63 ± 1.02**	Duplicate
Fruit girth (cm)	6.05 ± 0.39**	-2.10 ± 0.05**	-1.11 ± 0.99	0.47 ± 0.38	1.98 ± 0.29**	0.99 ± 0.66	Duplicate
Calyx length (mm)	31.71 ± 1.54**	-6.93 ± 0.28**	-16.24 ± 3.86**	-1.63 ± 1.52	6.29 ± 1.21**	15.80 ± 2.52**	Duplicate
Calyx width (mm)	16.60 ± 1.03**	-4.87 ± 0.31**	-7.73 ± 2.65**	0.19 ± 0.98	5.18 ± 0.90**	8.74 ± 1.86**	Duplicate
Peduncle length(mm)	44.26 ± 1.93**	-6.14 ± 0.40**	-42.83 ± 4.83**	-10.06 ± 1.88**	0.37 ± 1.46	36.73 ± 3.04**	Duplicate
Peduncle girth (mm)	5.91 ± 0.35**	-1.55 ± 0.11**	-0.34 ± 0.89	0.46 ± 0.34	0.71 ± 0.30*	0.73 ± 0.58	Duplicate
Average fruit weight (g)	209.74 ±15.83**	-96.17±0.82**	-303.60 ± 41.26**	-60.73±15.81**	80.36 ±11.89**	227.30 ±26.10**	Duplicate
Number of fruits/cluster	2.18 ± 0.16***	0.61 ± 0.03**	-2.08 ± 0.39**	-0.43 ± 0.16**	-0.59 ± 0.11**	1.67 ± 0.24**	Duplicate
Number of fruit/plant	18.21 ± 1.43**	7.30 ± 0.24**	6.33 ± 3.86	2.90 ± 1.41**	-2.03 ± 1.20	5.27 ± 2.69**	Complementary
Fruit yield/plant (kg)	3.92 ± 0.24**	-0.94 ± 0.05**	-5.71 ± 0.64**	-1.48 ± 0.24**	0.55 ± 0.20**	5.77 ± 0.45**	Duplicate

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

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length, peduncle length, average fruit weight, number of fruits per cluster and yield per plant in *W 230 × RMO 1142*. Therefore, these traits can be improved through the exploitation of heterosis breeding in these specific crosses as reported earlier by (Kumar and Arumugam, 2013 and Santhosha *et al*., 2017) in brinjal. In the present investigation, the negative sign of additive × additive interactions for fruit girth, calyx width, peduncle girth, average fruit weight, number of fruits per plant, and yield per plant in *GL 401 × BR 104*, for fruit girth, peduncle girth, and number of fruits per cluster in *GL 401 × W 230* and fruit length, calyx length, peduncle length, average fruit weight, number of fruits per cluster and yield per plant in *W 230 × RMO 1142* disclosed the presence of dissociated gene pairs, while the positive sign of [*i*] interaction in other traits in these crosses indicated the presence of associated gene pairs in parents. The associated gene pair from the parents will lead to faster improvement of the mentioned traits in particular crosses in brinjal. The negative values of the dominance for fruit girth, calyx length, calyx width, peduncle length, peduncle girth, average fruit weight, number of fruits per plant and yield per plant in *GL 401 × BR 104*, for peduncle girth, average fruit weight, and number of fruits per cluster in *GL 401 × W 230* and fruit length, fruit girth, calyx length, calyx width, peduncle length, peduncle girth, average fruit weight, number of fruits per cluster and yield per plant in *W 230 × RMO 1142* suggested the dominance of decreasing alleles and while the positive sign of [*h*] in other traits indicated the dominance of increaser alleles for the target traits. The dominance of increaser alleles will raise the expression of such traits in heterosis breeding.

Duplicate type of epistasis was noticed for most of the traits in different crosses suggesting selection should be mild in earlier generations and intense in later generations. However, the number of fruits per plant (*GL 401 × BR 104*), fruit girth, calyx length and yield per plant in *GL 401 × W 230*, and the number of fruits per plant in *W 230 × RMO 1142* highlighted the occurrence of a complementary type of epistasis. Duplicate and complementary types of epistasis were also following the statements of Dhameliya and Dobariya (2009) and Devmore (2016). In this study, non-significant interactions for peduncle length and fruit girth in *GL 401 × BR 104* and calyx length in *GL 401 × W 230* pointed toward the occurrence of

higher-order interactions or the presence of linkages. Therefore, more generations were required to be evaluated for the elucidation of genetic in these traits.

Inheritance of qualitative traits

The present investigation also explained the inheritance of various qualitative traits like fruit color and shape as well as pigmentation of calyx and peduncle from three crosses (Table 3). Light purple fruits in *GL 401 × BR 104* (green × dark purple) were segregated in F_2 into three phenotypic classes with 108, 53, and 39 plants bearing dark purple, green, and light purple fruits, respectively, and this segregation pattern was in agreement with the 9:3:4 ratio. However, BC_1P_1 and BC_1P_2 were segregated into 1:1 ratios for light purple: green fruits and light purple: dark purple fruits, respectively. It indicated digenic inheritance of fruit colour with supplementary gene interaction. However, the intensity of green and purple fruits varied due to incomplete dominance. In *GL 401 × W 230*, light green F_1 was segregated into 9:3:4 (supplementary) ratio for light green (105 plants), dark green (36 plants), and white (59 plants) in F_2. BC_1P_1 resulted in light green and dark green fruits and BC_1P_2 segregated into light green and white fruits in 1:1 proportion again confirmed digenic inheritance in this cross. However, the reduction in the intensity of green fruits suggested the incomplete dominance of the green colour of fruits. In *W 230 × RMO 1142* (white× reddish-purple), F_1 with light purple fruits segregated in F_2 progeny into 24:12:12:12:4 ratio for light purple (69 plants), reddish-purple (39 plants), dark purple (40 plants), whitish-green (36 plants), and white (16 plants) that suggested tri-genic inheritance of fruit colour in brinjal. BC_1P_1 progeny was segregated into 1:2:1 for whitish green, light purple, and white fruits and BC_1P_2 resulted from 1:2:1 ratio for light purple, reddish-purple, and dark purple fruits. The reduction in the intensity of fruit colour again suggested the incomplete dominance of purple and green colours. In earlier studies, digenic tri-genic, and polygenic inheritance was reported by Liu *et al*. (2016); Kamini *et al*. (2007) and Patidar (2015), respectively. Overall, the inheritance of fruit colour was complex in brinjal, but segregation behaviour of three crosses highlighted trigenic (purple, green, and white) control with supplementary effects, where the genes responsible for purple and green colour display incomplete dominance that led to a reduction in the intensity of colour in fruits. Therefore the homozygous and heterozygous condition of three genes in various combinations along

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Table 3 : Qualitative inheritance of different fruit traits in F_2, BC_1P_1, and BC_1P_2 progenies of variable crosses in brinjal

Trait	Cross	F_1	Progeny	Progeny size	Phenotypes	Observed frequencies	Expected frequencies	χ^2_{cal}	χ^2_{tab}	Phenotypic ratio
Calyx color	GL 401 × BR 104 (green ×purple)	Green	F_2	200	Green : Purple	184:16	187.5:12.5	1.04	3.84	15:3
			BC_1P_1	100	Green	100	-	-	-	-
			BC_1P_2	100	Green : Purple	69:31	75:25	1.92	3.84	3:1
Peduncle color	GL 401 × BR 104 (green × purple)	Green	F_2	200	Green : Purple	184:16	187.5:12.5	1.04	3.84	15:3
			BC_1P_1	100	100	Green	100	-	-	-
			BC_1P_2	100	Green : Purple	69:31	75:25	1.92	3.84	3:1
Fruit bearing habit	W 230 × RMO 1142 (clustered ×solitary)	Clustered	F_2	200	Clustered : Solitary	142:58	150:50	1.71	3.84	3:1
			BC_1P_1	100	Clustered	100	-	-	-	-
			BC_1P_2	100	Clustered : Solitary	54:46	50:50	0.64	3.84	1:
Fruit color	GL 401 × BR 104 (green ×dark purple)	Light purple	F_2	200	LP:DP:G	108:39:53	112.5:37.5:50	0.42	5.99	9:3:4
			BC_1P_1	100	LP:G	56:44	50:50	0.64	3.84	1:1
			BC_1P_2	100	LP:DP	54:46	50:50	0.64	3.84	1:1
	GL 401 × W 230 (green × white)	Light green	F_2	200	LG:DG:W	105:36:59	112.5:37.5:50	2.18	5.99	9:3:4
			BC_1P_1	100	LG:DG	43:57	50:50	0.36	3.84	1:1
			BC_1P_2	100	LG:W	56:44	50:50	0.64	3.84	1:1
	W 230 × RMO 1142 (white ×red purple)	Light purple	F_2	200	LP:RP:DP:WG:W	69:39:40:36:16	75:37.5:37.5:37.5:12	2.1	9.49	24:12:12:12:4
			BC_1P_1	100	LP:RP:DP	30:47:23	25:50:25	1.34	5.99	1:2:1
			BC_1P_2	100	WG:LP:W	22:62:26	25:50:25	0.48	5.99	1:2:1
Fruit shape	GL 401 × BR 104 (long ×big round)	Oblong	F_2	200	Oblong:Long:Round	108:57:35	112.5:50:37.5	1.32	5.99	9:3:4
			BC_1P_1	100	Long:Oblong	54:46	50:50	0.64	3.84	1:1
			BC_1P_2	100	Round:Oblong	44:56	50:50	1.44	3.84	1:1
	GL 401 × W 230 (long ×small oval)	Long	F_2	200	Long: Small oval	142:58	150:50	0.67	5.99	3:1
			BC_1P_1	100	Long	100	-	-	-	-
			BC_1P_2	100	Long : Small oval	46:54	50:50	0.64	3.84	1:1

Fruit color: LP-Light Purple, RP-Reddish Purple, DP- Dark Purple, G- Green, LG- Light Green, DG- Dark Green, WG- Whitish Green, and W-White CROSS I-GL 401 × BR 104, CROSS II -GL 401 × W 230 and CROSS III-W 230 × RMO 1142

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with interactions results in different shades of the fruits in brinjal. For the improvement of fruit colour in brinjal colour, specific contrasting parents can be selected along with other horticultural traits. The combination of dark or shining purple and white genotypes can give rise to the development of a variety of colours in F_2, but all these genotypes are not homozygous for colour at this stage. Therefore, the selection for this trait can be delayed to the F_3 or F_4 generation of selfing. The intensity of the purple colour can be increased by backcross with the dark coloured parent. For the development of white or green genotypes, parents involving these colours can be used.

The inheritance of fruit shape is also shown in three crosses (Table 3, Fig 1). In *GL 401 × BR 104* (Long× Big Round), oblong fruits of F_1 were segregated into three phenotypic classes of oblong (108), long (57), and round (35) fruits in the F2 that highlighted some kind of the interaction of two genes. The segregation pattern of this cross for fruit shape was following 9:4:3 ratio. However, BC_1P_1 & BC_1P_2 progenies were segregated into 1:1 ratios for long: oblong and round: oblong fruits, respectively. In *GL 401 × W 230* (long × small oval), long fruited F_1 produced a 3:1 ratio for long: oval fruits. BC_1P_1 plants had long fruits only, while BC_1P_2 resulted in long: oval fruits in a 1:1 ratio. In *W 230 × RMO 1142* (small oval× big oval), oval

GL-401 (P₁)   BR104 (P₂)   GL-401 ×BR-104   F₂- GL-401 ×BR-104

GL-401 (P₁)   W-230 (P₂)   GL-401 ×W-230   F₂- GL-401 × W-230

GL-401 (P₁)   RMO-1142 (P₂)   GL-401 ×RMO-1142   F₂- GL-401 ×RMO-1142

Fig. 1 : Inheritance of fruit colour and shape in brinjal

fruited F_1 did not segregate for fruit shape as both the parents were similar for fruit shape. Phenotypic ratio of the first cross indicated that both round and long fruit shape was controlled by two dominant genes, where the homozygous recessiveness of one gene allows full expression of the other gene and vice versa. However, the dominance of both genes produces oblong fruits. The phenotypic ratios of the second cross confirmed the monogenic control of fruit shape. Overall observation from all the crosses suggested that fruit shape was controlled by two genes with supplementary effects that resulted in oblong fruits. The size of fruits in segregating populations was affected by the type of parents involved in the hybridization. These findings for fruit shape were in agreement with Aravindakshan (2003) and Kamini *et al.* (2007). For the generation of F1 hybrids based on fruit shape, we should either select both the parents with oblong fruits or we can cross a parent with big round fruits to a parent with long fruits for the oblong type. Here, the size of the fruit also affects. The cross between long and oval should result in oblong fruits, but our result for this cross showed long fruit. This may have occurred due to variation in size. In quantitative inheritance also, fruit length and fruit breadth were strongly affec0ted by dominant genes. It means more length and breadth of the fruit in parents, as in cross I, is showing the dominance of both the traits. In contrast, a cross of parents with more length and less breadth is showing the dominance of fruit length only. Therefore, the involvement of both major and minor genes in the expression of the trait cannot be neglected. Our results were in accord with the findings of Kamini *et al.* (2007) and Qiao *et al.* (2011) regarding fruit shape in brinjal. For the improvement of fruit shape, length, and breadth specific parental genotypes such as long ×long, round × round, round × long, small round ×long can be crossed and selections can be practiced for the desired genotypes.
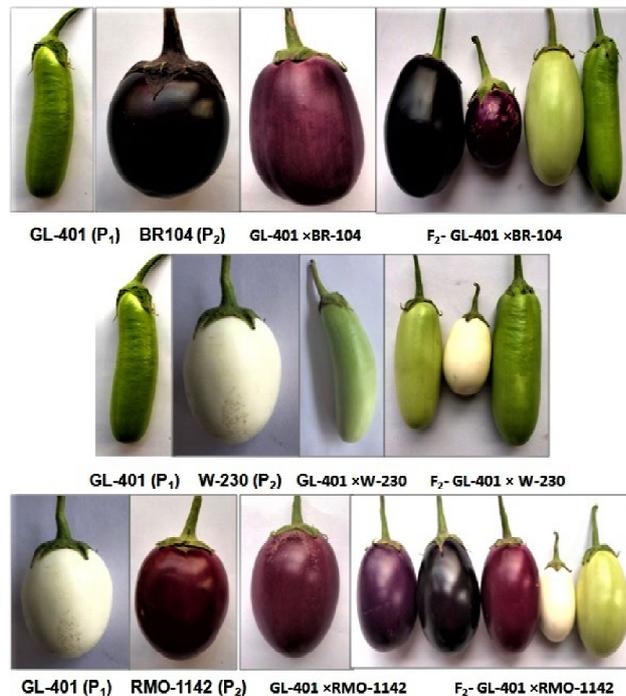
In brinjal, generally, three classes of calyx and peduncle pigmentation are common i.e. completely pigmented, partially pigmented, and green. In the present investigation, the inheritance of calyx and peduncle colour was elucidated from the *GL 401 × BR 104* (green × partially pigmented) (Table 3 and Fig 1). F_1 had green calyx as well as peduncle that segregated into 184 plants with green calyx as

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well as peduncle and 16 plants with purple pigmentation. It pointed toward the dominance of green colour for both the traits. The ratio obtained for calyx as well as peduncle colour was following the 15:1 ratio that suggested the digenic inheritance through duplicate factors. Backcross to the parent with pigmented calyx as well as peduncle resulted in a ratio of 3:1 for green and purple traits, while with a parent having green calyx and peduncle resulted in progenies bearing fruits with green calyx and peduncle only. In contrast, Patidar (2015) reported the dominance of purple calyx over the green. They might have selected completely pigmented calyx of one parent and green calyx of the other. Similarly, for fruit-bearing (single or in a cluster), *W 230 × RMO 1142* (cluster× single) produced clustered fruits and segregated into clustered type (142) and solitary bearing (58) in 3:1 ratio in F_2, all cluster bearing plants in BC_1P_1 and 1:1 proportion in BC_1P_2 that unveiled monogenic dominance of clustered fruits in brinjal. These findings were in agreement with the results of Rangaswamy and Kadambavanasundaram (1973).

CONCLUSION

It was concluded from the present investigation that epistatic interactions significantly influenced most of the traits in all crosses. All types of interactions were observed affecting different traits. The type of interactions affecting the expression of a particular trait varied in different crosses. The non-significance of interactions for peduncle length and fruit girth in CROSS I and calyx length in *GL 401 × W 230* pointed towards the occurrence of higher-order interactions or the presence of linkages for these traits. Among the qualitative traits in brinjal, clustered fruit bearing was the monogenic dominant, and the green colour of calyx and peduncle was dominant over purple with a duplicate type of epistasis. Fruit shape was controlled with two genes with incomplete dominance of both round and long fruits. However, in other crosses, long shapes remained dominant over small oval fruits. For the inheritance of fruit colour, dark purple × green and green × white crosses followed the 9:3:4 ratio with incomplete dominance of genes controlling purple and green pigmentation, respectively. However, in red-purple × white cross,

trigenic control (ratio of 24:12:12:12:4) was noticed along with incomplete dominance of the above two genes, where each class represented the variable intensity of colour due to homozygous or heterozygous condition of three genes in various combinations.

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