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Inheritance of traits associated with shootfly resistance in *Rabi* Sorghum (*Sorghum bicolor* (L.) Moench)

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Abstract

Generation mean analysis involving six generations (P_1, P_2, F_1, F_2, B_1 and B_2) of four crosses associated with shootfly resistance was evaluated with the objectives to estimates the nature and magnitude of gene actions involved in control of the traits imparting to shootfly resistance in *rabi* Sorghum. Six diverse parents were selected and intermated to obtain six generations of four crosses *viz.*, BJV74 x RSV1093, RSV1006 x RSV458, RSV1098 x RSV1003 and RSV1006 x RSV1093 for shootfly tolerance. The joint scaling test for almost all the characters was found highly significant in all the crosses indicating inadequacy of additive-dominance model and presence of higher order interactions. Additive, and additive x additive as well as dominance x dominance gene interactions were found in control of number of eggs per plant, per cent plant having egg and per cent dead heart, while dominance and dominance x dominance gene interactions were found in control of number of plant height at maturity, number of leaves per plant and grain yield per plant traits associated with shootfly resistance. Dominance x dominance (l) interaction was predominantly made significant contribution for plant height at maturity, number of leaves per plant and grain yield per plant. The parent RSV1006 followed by RSV1098 (P_1) and RSV1093 followed by RSV458 (P_2) parents which could be considered in developing shootfly tolerant genotypes. The traits governed by additive gene action, simple selection would be effective for crop improvement, while for the traits governed by dominance gene action, the better option would be adoption of heterosis breeding. Duplicate type of epitasis observed allmost all the crosses as well as all the traits associated with shootfly resistance.

Keywords: Shootfly, generation mean analysis, *rabi* Sorghum, additive-dominance model

Introduction

Sorghum (*Sorghum bicolor* (L.) Moench) is the fifth major cereal crop of world following wheat, rice, maize and barley in terms of production and utilization. Sorghum grain is produced annually as dietary staple for millions of people in semi-arid areas of Asia (mainly India and China) and Africa. In India primarily in Maharashtra, Karnataka, Madhya Pradesh, Andhra Pradesh, Rajasthan and Tamil Nadu, it is grown as a dual purpose crop serving both grain and fodder requirements of the farming community. India has the largest share (17 %) of world sorghum area and ranks fourth in the production. In India, sorghum is cultivated both in *kharif and rabi* season on an area of 6.32 million hectare with a production of 6.01 million tones, having average productivity of 971 kg per hectare during 2014, which is much lower than world average productivity (1535 kg/ha) [1]. Maharashtra is a leading sorghum growing state in India. The national average productivity of sorghum is 971 kg ha^{-1} but it is only 567 kg ha^{-1} for *rabi* season in Maharashtra during 2011-12 [2].There are over 150 insect pests' species damaging sorghum crop from sowing to harvest. In Maharashtra more than 25 pests have been reported to damage sorghum crop, among these pests shoofly (*Atherigona soccata* Rondani) is one of the important. Shootfly is one of the major biotic factors which affect the productivity from 20 to 50 per cent in sorghum. Insect causes enormous loss in grain and forage yield of sorghum world-wide. Sorghum shootfly is one of the most destructive pests of sorghum in the semi-arid tropics of the world. Sorghum shootfly causes an average loss of 50% in India [7], but the infestation may be over 90%. The larvae of shootfly cuts the growing point of plant and feed on the decaying leaf tissue, resulting into wilting and drying of the central leaf known as 'dead heart'.

Materials and Methods

Based on the genetic diversity and various traits associated with shootfly tolerance six parents of sorghum *viz.*, BJV74, RSV1006 (Phule Revati), RSV1098 (Phule Suchitra), RSV458 (Phule Anuradha), RSV1093 and RSV1003, obtained from Senior Sorghum Breeder, All India Co-ordinated Sorghum Improvement Project, Mahatma Phule Krishi Vidyapeeth, Rahuri, were selected for generating six generations (P_1, P_2, F_1, F_2, B_1 and B_2) in four crosses for shootfly tolerant. Four crosses *viz*; BJV74 x RSV1093, RSV1006 x RSV458, RSV1098 x RSV1003 and RSV1006 x RSV1093 were affected by hand emasculation and pollination to study the genetics of traits imparting shootfly resistance. For raising parents during *rabi*, 2010-11 generating F_1 and selfing of F_1 generation and back crosses were affected to obtain enough self seed during *rabi*, 20011-12 at Sorghum Improvement Project and final evolutionary trial of six generations (P_1, P_2, F_1, F_2, B_1 & B_2) were conducted during *rabi*, 2012-13. The schematic details of different generations raised during regular *rabi*, season is given in Table 1.

The experiment material comprised of 24 treatments consisting of parents, F_1, F_2, B_1 and B_2, of four crosses *viz.*, BJV74 x RSV1093, RSV1006 x RSV458, RSV1098 x RSV1003 and RSV1006 x RSV1093. The sowing of P_1, P_2 and F_1 generations were done in a single row of 4.5m length with a spacing of 45 x 15 cm, whereas the sowing of F_2s, B_1s and B_2s were done in plot size of 4.5 x 3.6 m. accommodating 30 plants in each row. Recommended doses of fertilizers were applied @ 30 kg N/ha and 40 kg P_2O_5 / ha as a basal dose, done at the time of sowing and remaining half, 30 kg N / ha were applied after 30 days of sowing. Experimental plots were surrounded by non- experiments border rows to reduce the border effect.

Statistical analysis

To test the adequacy of additive dominance model A, B, C, and D scaling test were applied. Data collected on the mean of the individual plant for different characters were subjected to the weighted least square analysis i.e. joint scaling test [9, 4]. To provide information on the nature of gene action governing the traits under study all the six parameters of generation means were calculated by the method [6].

Results and Discussions

The estimates of *perse* performance of characters related to shootfly revealed that parent RSV1006 followed by RSV1098 (P_1) and RSV1093 followed by RSV1003 (P_2) exhibited superior average performance individually and in their cross combinations involving these parents for different traits imparting to shootfly resistance.

Table 1: Mean performance and standard error of six generations for traits associated with shoot fly resistance in four crosses of *rabi sorghum.*

Cross	Generations	Plant height at maturity	No. of leaves / plant	No. of eggs / plant	% Plant having eggs	% Dead heart	Grain Yield / plant
BJV74 x RSV1093	P_1	241.67 (2.71)	11.97 (0.29)	1.75 (0.07)	57.33 (1.80)	41.72 (0.59)	79.30 (1.30)
	P_2	224.90 (3.27)	11.00 (0.26)	1.05 (0.07)	35.97 (0.47)	26.47 (0.55)	50.23 (1.09)
	F_1	249.00 (2.37)	11.65 (0.28)	1.61 (0.08)	42.67 (0.77)	36.85 (0.56)	68.23 (0.99)
	F_2	246.33 (1.46)	11.52 (0.19)	1.53 (0.05)	44.60 (0.61)	38.69 (0.40)	65.10 (0.55)
	B_1	214.77 (1.45)	10.10 (0.18)	1.57 (0.04)	50.33 (0.61)	39.06 (0.38)	54.97 (0.55)
	B_2	245.00 (2.06)	11.45 (0.18)	1.42 (0.05)	40.00 (0.66)	34.39 (0.45)	60.70 (0.72)
RSV1006 x RSV458	P_1	235.33 (2.68)	11.77 (0.30)	1.68 (0.06)	47.67 (2.15)	36.99 (0.73)	92.70 (1.70)
	P_2	173.67 (1.68)	9.43 (0.27)	1.12 (0.07)	36.33 (0.73)	24.93 (0.70)	54.40 (1.08)
	F_1	241.00 (3.24)	11.37 (0.28)	1.53 (0.06)	40.33 (0.53)	34.51 (0.53)	66.60 (1.70)
	F_2	229.00 (1.54)	10.90 (0.21)	1.62 (0.05)	43.67 (0.19)	35.25 (0.43)	61.30 (0.96)
	B_1	217.33 (1.93)	9.50 (0.20)	1.61 (0.05)	47.67 (0.19)	36.27 (0.58)	55.35 (0.61)
	B_2	221.00 (2.41)	10.50 (0.20)	1.38 (0.05)	39.33 (0.19)	32.57 (0.87)	59.29 (0.67)
RSV1098 x RSV1003	P_1	205.27 (3.01)	10.60 (0.28)	1.76 (0.07)	49.17 (1.12)	37.37 (0.90)	72.40 (1.07)
	P_2	247.22 (2.02)	11.10 (0.28)	1.10 (0.07)	36.67 (0.35)	29.12 (0.95)	53.47 (1.09)
	F_1	236.26 (1.66)	11.52 (0.28)	1.35 (0.07)	40.70 (0.35)	34.35 (0.66)	66.37 (1.40)
	F_2	229.51 (1.70)	11.43 (0.21)	1.40 (0.05)	43.67 (0.63)	35.19 (0.50)	61.30 (0.55)
	B_1	198.15 (1.89)	9.00 (0.19)	1.74 (0.04)	44.33 (0.65)	36.85 (0.43)	56.14 (0.39)
	B_2	225.27 (1.89)	10.55 (0.22)	1.30 (0.05)	39.80 (1.10)	32.50 (0.40)	58.58 (0.42)
RSV1006 x RSV1093	P_1	236.67 (2.35)	11.68 (0.27)	1.64 (0.07)	46.77 (1.12)	36.53 (0.58)	94.27 (1.76)
	P_2	227.45 (2.24)	11.00 (0.29)	1.05 (0.07)	37.60 (0.91)	30.27 (0.53)	51.06 (0.90)
	F_1	245.33 (0.80)	11.60 (0.27)	1.23 (0.07)	38.75 (0.56)	33.39 (0.89)	76.90 (1.09)
	F_2	243.00 (1.38)	11.53 (0.18)	1.26 (0.04)	40.83 (0.27)	35.10 (0.64)	71.19 (0.42)
	B_1	228.67 (0.77)	10.30 (0.19)	1.51 (0.04)	48.57 (0.37)	36.24 (0.46)	65.77 (0.65)
	B_2	242.67 (1.22)	11.50 (0.19)	1.12 (0.05)	37.63 (0.29)	32.10 (0.38)	69.27 (0.81)

The F_1 and segregating generations evolve from cross combinations, RSV1006 x RSV1093 exhibited superior performance for the inheritance of number of eggs per plant, per cent plant having eggs, per cent dead heart and grain yield, whereas cross RSV1098 x RSV1003 and BJV74 x RSV1093, indicated superior performance for the inheritance of plant height at maturity and number of leaves per plant respectively. The substantial information obtained from the *perse* performance of parents and segregating generations the parent RSV1093 and RSV1003 could be considered in developing shootfly tolerant genotype. Depending on the results obtained from the present investigation, the crosses RSV1006 x RSV1093 most promising among the four crosses.

Analysis of variance indicated that all the characters associated with shootfly and drought tolerance exhibited highly significant difference, among the genotypes, indicated the considerable amount of variability in the experimental material. In all the four crosses for shootfly tolerance *viz.*, BJV74 x RSV1093, RSV1006 x RSV458, RSV1098 x RSV1003, RSV1006 x RSV1093 and RSV1098 x RSV458 respectively. The scaling test all or either ‘A’, ‘B’, ‘C’ and ‘D’ were highly significant, indicated the presence of all three types of non-allelic gene interaction effects *viz.*, additive x additive (i), additive x dominance (j) and dominance x dominance (l) and provided information about all six genetic parameters *viz.*, m, d, h, i, j and l. Further joint scaling test also resulted into high chi-square values for most of the characters, indicating inadequacy of additive-dominance model, for all the traits associated with shootfly tolerance.

Plant height at maturity (cm)

The scaling tests ‘A’, ‘B’, ‘C’ and ‘D’ in all the four crosses were highly significant in positive as well as negative direction and scaling test of ‘B’, ‘C’ and ‘D’ in all the four crosses were highly significant in positive direction for shootfly tolerance in the cross BJV74 x RSV1093, RSV1006 x RSV458, RSV1098 x RSV1003 and RSV1006 x RSV1093, indicated that inadequacy of additive-dominance model. However, the joint scaling tests were found highly significant in all the four crosses, indicating the presence of non-allelic interactions.

In the crosses BJV74 x RSV1093, RSV1006 x RSV458, RSV1098 x RSV1003 and RSV1006 x RSV1093, significantly negative additive (d) and dominance (h) components with higher magnitude in desirable direction of dominance (h) components, indicated the preponderance of dominance (h) gene effects for governing these traits. Parent BJV74 (P_1) and RSV1003 (P_2) were superior in contributing this trait. The magnitude of dominance gene effect was higher in desirable direction than additive gene effect, indicated predominance of non-additive gene action in the inheritance of these traits in all the crosses. Among the interaction effects significantly negative additive x additive (i) and additive x dominance (j) gene effects, while significantly positive dominance x dominance (l) gene effects indicated the presence of all these non-allelic interaction and predominance of dominance x dominance (l) gene effects played an important role in the expression of this character. As dominance (h) as well as dominance x dominance (l) gene effects was predominant and both had opposite sign, suggesting the duplicate gene action in the inheritance of this trait. However, dominance effects were significant and desirable direction, indicated exploitation of heterosis would be effective in improvement of plant height at maturity. This project the role of dominant gene action in the inheritance of this trait [8, 10, 12-14, 19].

Number of leaves per plant

The scaling test ‘A’, ‘B’, ‘C’ and ‘D’ in all the four crosses were highly significant for shootfly tolerance, indicated the inadequacy of additive-dominance model. Consequently dominance x dominance (l) and additive x additive (i) gene interaction effects as expected were greater and highly significant in positive direction for ‘l’ and negative direction for ‘i’. The significance of additive (d) and dominance (h) component in the crosses BJV74 x RSV1093, RSV1006 x RSV458, RSV1098 x RSV1003 and RSV1006 x RSV1093 indicated their importance in expression of number of leaves per plant. The significantly negative additive (d) and dominance (h) components with higher magnitude of dominance (h) components in desirable direction over the additive (d) components indicated the preponderance of dominance (h) gene effects for governing these traits. This project the role of dominant gene action in the inheritance of this trait. Parent BJV74 (P_1) and RSV1003 (P_2) were superior in contributing this trait.Among the interaction effects significantly negative additive x additive (i) and to additive x dominance (j) gene effects, while significantly positive dominance x dominance (l) gene effects indicated the presence of non-allelic interaction and predominance of dominance x dominance (l) gene effects played an important role in the expression of this character. As dominance (h) as well as dominance x dominance (l) gene effects was predominant and both had opposite sign, suggesting the duplicate gene action in the inheritance of this trait. The magnitude of dominance gene effect was higher in desirable direction than the additive gene effect indicated predominance of non-additive gene action in the inheritance of number of leaves per plant in all the crosses suggested that exploitation of heterosis would be more effective in improvement reported non additive gene action for these traits [8, 13, 12, 18].

Number of eggs per plant

Significance of scales ‘B’, ‘C’ and ‘D’ in the crosses BJV74 x RSV1093, RSV1006 x RSV458, RSV1098 x RSV1003 and RSV1006 x RSV1093 indicated inadequacy of additive-dominance model. Consequently dominance x dominance (l) and additive x dominance (j) gene interaction effects as expected were greater and highly significant in both the direction for ‘i’, ‘j’ and ‘l’. However, the joint scaling tests were found highly significant in all the four crosses, indicating the presence of non-allelic interactions. The additive (d) and dominance (h) gene action were negatively significant and additive (d) gene action had lower magnitude in desirable direction than dominance (h) indicating the preponderance of additive gene action in crosses BJV74 x RSV1093, RSV1006 x RSV458, RSV1098 x RSV1003 and RSV1006 x RSV1093 while among the interaction effects all three types of non-allelic interaction were significant along with predominant of additive x additive (i) interaction effects over additive x dominance (j) and dominance x dominance (l). In the cross RSV1006 x RSV458 and RSV1006 x RSV1093 exhibited significantly negative as well as positive type of digenic interaction, additive x additive (i) was negatively significant, while additive x dominance (j) and dominance x dominance (l) was positively significant gene effects with preponderance of additive x additive (i) in the expression of number of eggs per plant, indicated the opposite sign for dominance (h) and dominance x dominance (l) gene effects suggesting duplicate epistasis. However, in cross BJV74 x RSV1093 and RSV1098 x RSV1003 both additive as well as dominance gene action were positively as well as negatively significant along with preponderance of additive gene action with lower magnitude in desirable direction. In digenic interaction additive x additive (i) was negatively significant, whereas additive x dominance (j) and dominance x dominance (l) were significantly positive indicating the presence of all three types of non- allelic interaction gene effects with predominant additive type of inheritance for these traits, indicated that complementary gene action played an important role.

Table 3: Estimation of scaling test for detecting non-allelic interactions in four crosses for selected traits of shoot fly resistance in *rabi* sorghum

Sr. No.	Characters	Scaling tests	Crosses			
			BJV74 x RSV1093	**RSV1006 x RSV458**	**RSV1098 x RSV1003**	**RSV1006 x RSV1093**
1.	Plant height at maturity	A	-87.13**	-15.67**	-31.71**	-47.33**
		B	38.10**	87.33**	47.39**	12.89**
		C	36.77**	71.00**	113.89**	44.22**
		D	42.90**	-0.33	49.10**	39.33**
2.	No. of leaves / plant	A	-3.12**	-3.40**	-4.03**	-2.60**
		B	0.41**	2.80**	-0.10	0.40**
		C	-1.11**	1.27**	3.63**	2.07**
		D	0.80**	0.93**	3.88**	2.13**
3.	No. of eggs / plant	A	-0.23**	-0.03**	0.17**	0.02**
		B	0.12**	-0.29**	0.03**	-0.04**
		C	0.05**	-0.07**	0.26**	0.47**
		D	0.08**	0.13**	0.03**	0.24**
4.	% Plant having eggs	A	-5.27**	4.62**	-14.20**	-2.67**
		B	-14.57**	-2.08**	23.23**	-5.00**
		C	-23.83**	5.47**	3.43**	-21.00**
		D	-2.00**	1.47**	-2.80**	-6.67**
5.	% Dead heart	A	2.55**	0.78**	-2.24**	-3.87**
		B	1.47**	-3.06**	3.52**	-8.42**
		C	-6.15**	4.61**	-0.64**	-4.53**
		D	-5.08**	3.45**	-0.96**	3.88**
6.	Grain Yield / plant	A	-37.58**	-38.07**	-26.48**	-50.17**
		B	2.94**	7.23**	-2.67**	0.91**
		C	-5.60**	-16.15**	-13.39**	-33.32**
		D	14.52**	7.34**	7.88**	7.97**

The estimates of all three non-allelic interaction effects *viz.*, additive x additive (i), additive x dominance (j) and dominance x dominance (l) were significant, the predominant additive (d) and additive x additive (i) type of gene effect for the inheritance of number of eggs per plant indicated that additive gene action in desirable direction played an significant role and suggested that simple selection breeding would be rewarded in the improvement of this trait [3, 8] reported additive gene action for governing this trait.

Per cent plant having egg

The scaling test ‘A’, ‘B’, ‘C’ and ‘D’ in all the four crosses were highly significant in negative as well as positive direction for shootfly tolerance, indicated inadequacy of additive-dominance model. Consequently dominance x dominance (l) and additive x dominance (j) gene interaction effects as expected were greater and highly significant in positive direction for ‘j’ and ‘l’, while negative direction for ‘i’. However, the joint scaling tests were found highly significant in all the four crosses, indicating the presence of non-allelic interactions.The additive (d) component and dominance (h) component were negatively significant and additive (d) gene action had lower magnitude in desirable direction, indicating the preponderance of additive gene action in cross BJV74 x RSV1093, RSV1006 x RSV458 and RSV1006 x RSV1093 while among the interaction effects all three types of non- allelic interaction were significant along with predominant of additive x additive (i) dominance x dominance (l) interaction effects. In cross RSV1098 x RSV1003 significantly negative additive (d) as well as dominance (h) component with higher magnitude of additive gene effects, indicated the presence of both additive as well as dominance gene effects for governing this trait along with preponderance of additive gene action.

The crosses BJV74 x RSV1093, RSV1006 x RSV458 and RSV1006 x RSV1093 exhibited significantly positive as well as negative type of digenic interaction present, whereas additive x additive (i) and dominance x dominance (l) had significantly higher magnitude in desirable direction for the expression of per cent plant having egg, indicated the opposite sign for dominance (h) and dominance x dominance (l) gene effects suggesting duplicate gene action. In the cross combination RSV1098 x RSV1003 both additive as well as dominance gene action were negatively significant along with preponderance of additive gene action with lower magnitude in desirable direction. In digenic interaction additive x additive (i) was positively significant, whereas additive x dominance (j) and dominance x dominance (l) were negatively significant indicating the presence of all three types of non-allelic gene interaction with preponderance of dominance x dominance (l), with predominant additive type of inheritance with dominance x dominance (l) gene interaction. For these traits complimentary gene action played an important role. Above different estimates exhibited the importance of additive (d) and additive x additive (i) and dominance x dominance (l) gene effects over the dominant gene effect, suggested that simple selection would be effective in the improvement of this trait in crosses BJV74 x RSV1093, RSV1006 x RSV458, RSV1098 x RSV1003 and RSV1006 x RSV1093 [15, 5, 10, 8].

Per cent dead heart

Significance of scales ‘A’, ‘B’, ‘C’ and ‘D’ in both the direction for the crosses BJV74 x RSV1093, RSV1006 x RSV458, RSV1098 x RSV1003 and RSV1006 x RSV1093, indicated inadequacy of additive-dominance model. Consequently dominance x dominance (l) and additive x dominance (j) gene interaction effects as expected were greater and highly significant in positive as well as negative direction for ‘i’, ‘j’ and ‘l’. However, the joint scaling tests were found highly significant in all the four crosses, indicating the presence of non-allelic interactions. On the same line the simple selection for shootfly tolerance is appropriate in the cross BJV74 x RSV1093 and RSV1006 x RSV458. The genotype and cross combinations possess less number of shootfly eggs and dead heart percentage are more successful and tolerant to shootfly in *rabi* sorghum. Non-preference for oviposition is the fundamental mechanism for resistance to shootfly [17].

Significantly positive additive (d) component and significantly negative dominance (h) component, while additive (d) component had lower magnitude in desirable direction over the dominance (h) component, indicating the preponderance of additive gene action in crosses BJV74 x RSV1093, RSV1006 x RSV458, RSV1098 x RSV1003 and RSV1006 x RSV1093. Among the interaction effects all three types of non-allelic interaction were significant along with predominant of dominance x dominance (l) followed by additive x additive (i) interaction effects, indicating the presence of both additive (d) as well as dominance (h) gene action along with preponderance of additive (d) gene effects for the inheritance of this trait. However above four crosses predominant of additive (h) gene action and combine effect of dominance x dominance (l) and additive x additive (i) interaction with opposite sign indicated that duplicate gene action played an important role in the crosses BJV74 x RSV1093, RSV1006 x RSV458 and RSV1006 x RSV1093, while complementary gene action played an important role in the crosses RSV1098 x RSV1003 inheritance of per cent dead heart respectively. The magnitude of additive gene effect was higher in desirable direction than the dominance gene effect with preponderance of additive x additive (i) as well as dominace x dominance (l) interaction effect, suggested that additive gene action played an important role in the expression of this characters which, indicated predominance of additive gene action in the inheritance of per cent dead heart in all the crosses, suggested that simple selection would be more effective in improvement [3, 8].

Gene action for grain yield per plant

Significance of scales 'A', 'B', 'C' and 'D' in the cross BJV74 x RSV1093, RSV1006 x RSV458, RSV1098 x RSV1003 and RSV1006 x RSV1093, indicated inadequacy of additive-dominance model. Consequently dominance x dominance (l) and additive x dominance (j) gene interaction effects as expected were greater and significant in positive as well as negative direction for 'l', 'j' and 'i'. However, the joint scaling tests were found highly significant in all the four crosses, indicating the presence of non-allelic interactions. On the same line the exploitation of hybrid vigor and shootfly tolerance is an appropriate in the cross BJV74 x RSV1093 and RSV1006 x RSV458. The genotype and cross combinations possess less number of shootfly eggs, dead heart percentage was more successful for higher grain yield as well as tolerant to shootfly in *rabi* sorghum.

Table 4: Estimation of gene effects in four crosses of shoot fly resistance for the trait eggs per plant, per cent plant having egg and leaf glossiness.

Traits	Crosses	Genetic parameters						Type of Epistasis
		m	d	h	i	j	l	
Plant height at maturity	BJV74 x RSV1093	251.33** (1.46)	-4.23** (2.52)	-14.08** (8.33)	-18.80** (7.69)	-13.62** (3.29)	54.83** (13.26)	Duplicate
	RSV1006 x RSV458	229.00** (1.54)	-3.67* (3.09)	6.17* (9.45)	0.67 (8.73)	-11.50** (3.47)	-22.33** (15.58)	Duplicate
	RSV1098 x RSV1003	236.26** 1.70	-2.12* 3.00	-24.76** 9.41	-28.21** 9.08	-9.55** 3.51	82.53** (14.66)	Duplicate
	RSV1006 x RSV1093	245.33** (1.38)	-4.00* (1.44)	-7.22* (6.48)	-18.67** (6.23)	-8.11** (2.17)	43.11** (8.77)	Duplicate
No. of leaves / plant	BJV74 x RSV1093	11.20** (0.19)	-1.40** (0.26)	-1.55** (0.98)	-1.60** (0.92)	-1.76** (0.33)	4.31** (1.46)	Duplicate
	RSV1006 x RSV458	10.90** (0.21)	-1.87** (0.28)	-2.03** (1.08)	-1.87** (1.02)	-3.10** (0.35)	2.47** (1.57)	Duplicate
	RSV1098 x RSV1003	11.72** (0.21)	-1.55** (0.29)	-6.52** (1.08)	-7.77** (1.03)	-1.97** (0.35)	11.90** (1.59)	Duplicate
	RSV1006 x RSV1093	11.97** (0.18)	-1.20** (0.26)	-3.97** (0.96)	-4.27** (0.91)	-1.50** (0.33)	6.47** (1.45)	Duplicate
No. of eggs / plant	BJV74 x RSV1093	1.53** (0.05)	-0.15** (0.06)	0.13** (0.25)	-0.15** (0.23)	-0.18** (0.08)	0.26** (0.37)	Complem-entary
	RSV1006 x RSV458	1.46** (0.04)	-0.35** (0.07)	-0.45** (0.24)	-0.26** (0.22)	0.13** (0.08)	0.59** (0.36)	Duplicate
	RSV1098 x RSV1003	1.60** (0.05)	-0.31** (0.06)	-0.44** (0.25)	-0.07** (0.23)	0.07** (0.08)	-0.13** (0.36)	Complem-entary
	RSV1006 x RSV1093	1.62** (0.05)	-0.24** (0.07)	-0.43** (0.24)	-0.49** (0.23)	0.03** (0.08)	0.51** (0.36)	Duplicate
% Plant having eggs	BJV74 x RSV1093	39.67** (0.61)	-19.33** (0.90)	-26.05** (3.28)	4.00** (3.05)	4.65** (1.30)	15.83** (4.99)	Duplicate
	RSV1006 x RSV458	44.83** (0.27)	-8.93** (0.47)	-16.37** (1.70)	-2.93** (1.43)	3.35** (0.86)	0.40** (2.82)	Duplicate
	RSV1098 x RSV1003	43.7** (0.6)	-9.50** (1.3)	-10.60** (3.7)	5.60** (5.9)	-18.70** (3.6)	-14.60** (9.4)	Complem-entary
	RSV1006 x RSV1093	36.67** (0.19)	-9.33** (0.27)	8.17** (1.57)	13.33** (0.94)	1.17** (1.17)	-5.67** (2.83)	Duplicate
% Dead heart	BJV74 x RSV1093	36.69** (0.40)	-15.67** (0.59)	3.43** (2.24)	10.17** (2.00)	0.54** (1.01)	-14.18** (3.49)	Duplicate
	RSV1006 x RSV458	37.30**	-8.55**	-10.41**	-6.89**	1.92**	9.17**	Duplicate

		(0.64)	(0.60)	(2.97)	(2.81)	(0.72)	(3.99)	
	RSV1098 x RSV1003	35.89** (0.50)	-5.75** (0.59)	-11.47** (2.51)	1.92** (2.33)	-2.88** (0.88)	-3.20** (3.61)	Complem-entary
	RSV1006 x RSV1093	34.51** (0.43)	-12.00** (1.05)	-15.80** (2.80)	-7.76** (2.70)	2.27** (1.16)	20.05** (4.76)	Duplicate
Grain Yield / plant	BJV74 x RSV1093	65.10** (0.55)	-5.73** (0.91)	-25.58** (3.14)	-29.04** (2.85)	-20.26** (1.25)	63.68** (4.99)	Duplicate
	RSV1006 x RSV458	71.19** (0.42)	-3.50** (1.04)	-11.33** (3.07)	-14.68** (2.68)	-22.65** (1.45)	45.51** (5.39)	Duplicate
	RSV1098 x RSV1003	61.30** (0.55)	-2.44** (0.51)	-12.33** (2.91)	-15.76** (2.44)	-11.90** (0.92)	44.91** (4.39)	Duplicate
	RSV1006 x RSV1093	61.30** (0.96)	-3.94** (0.91)	-22.01** (4.69)	-15.94** (4.26)	-25.54** (1.34)	65.20** (6.58)	Duplicate

In the crosses BJV74 x RSV1093, RSV1006 x RSV458, RSV1098 x RSV1003 and RSV1006 x RSV1093 for shootfly tolerance, significantly negative additive (d) components and dominance (h) components with higher magnitude dominance (h) components in desirable direction over the additive (d) components. Presence of additive (d) as well as dominance (h) gene effects along with the preponderance of dominance (h) gene effects in negative direction and the parent RSV1006 (P_1) and RSV1093 (P_2) showed superior performance in inheritance for grain yield per plant. However, in entire four crosses dominant x dominant (l) component was significantly positive with higher magnitude, followed by both additive x additive (i), additive x dominance (j) component, which was significantly negative exhibited duplicate type of epistasis. The relatively low magnitude effects than additive x additive (i) component, revealed that grain yield was influenced by dominance (h) and dominance x dominance (l) interaction effects. Dominance gene effects was more pronounced and duplicate type of epitasis for the inheritance of grain yield per plant in all the four crosses *viz.*, BJV74 x RSV1093, RSV1006 x RSV458, RSV1098 x RSV1003 and RSV1006 x RSV1093 suggested that the breeding progress shall be through exploitation of Heterosis [11, 14, 16, 8, 13, 18].

Conclusion

Both additive and non-additive gene effects were found to be important and playing an important role, while considering the gene effects simultaneously in the inheritance of all the traits associated with shootfly resistance in which either additive (d) or additive x additive (i) or dominance (h) or dominance x dominance (l) gene effects, in all the crosses were found to be quite appreciable. The importance of additive gene effects in these traits *viz.*, number of eggs per plant, per cent plant having egg and per cent dead heart suggested that selection would be effective in improvement. However, difficulty in isolating better performing lines is expected for some of these characters, whereas dominance or epistasis effects were also significant under such circumstances heterosis breeding would be effective for improvement of these traits. The character *viz.*, plant height at maturity, number of leaves per plant and grain yield per plant in which dominance effects with duplicate type of epistasis in which heterosis breeding have been suggested to break the undesirable linkage to accumulate favorable genes and to generate desirable recombinants.

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