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Genetic Inheritance of Morpho-physiological trait associated with Shootfly resistance in post rainy season sorghum (*Sorghum bicolor* (L.) Moench)

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Abstract

The present investigation was conducted with 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 tolerance in post rainy season sorghum. 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, dominance and epistasis interactions were found operating in control of almost all the Morphophysiological traits associated with shootfly tolerance. Genetic analysis indicated that the additive gene effects with additive x additive (i) and dominance x dominance (l) were predominant for the inheritance of days to 50 per cent flowering, while dominance gene effects with dominance x dominance (l) were found important for trichome density and seedling vigor. However, both additive and dominance gene effects with additive x additive (i) were found important for leaf surface wetness. As regards the non-allelic interactions, additive x additive (i) and dominance x dominance (l) was found important for most of the characters. For 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 in almost all the crosses as well as all the traits associated with shootfly resistance. In the presence of both additive and dominance gene effects with equal magnitude, the reciprocal recurrent selection will be useful in the improvement of traits associated with shootfly tolerance.

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

Introduction

Shootfly (*Atherigona soccata* Rondani) 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. The monsoon sorghum though susceptible, escapes the incidence but winter sorghum is prone to attack due to high shootfly population. Sorghum shootfly causes an average loss of 50% in India (Jotwani and Shrivastava, 1982) [3], but the infestation may be over 90%. Sorghum production is affected by a wide array of biotic constraints, of which sorghum shoot fly (*Atherigona soccata*) is the most important pest, which severely damages the sorghum crop during the seedling stage. Grain yield on poor farmer field are generally low and insect pest are one of the major factors limiting sorghum production. 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 is one of the important, which causes major considerable damage. Host plant resistance is one of the most effective means of keeping shootfly population below economic threshold levels as it does not involve any cost input by the farmers. Present study aims to know genetics of traits imparting shootfly resistance in *rabi* sorghum.

Materials and Methods

Based on the genetic diversity and various morphophysiological 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. The evaluation trial of six generations (P_1, P_2, F_1, F_2, B_1 and B_2) were conducted during *rabi*, season at Botany Farm, Post Graduate Institute, Mahatma Phule Krishi Vidyapeeth, Rahuri. The experiment was conducted in a uniform piece of land by giving one ploughing and two harrowing in a randomized block design with three replications. The experiment material comprised of 24 treatments consisting of parents, F_1's, F_2's, B_1s and B_2's, 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. The growth of crop was uniform and satisfactory during the season. The experimental plots were surrounded by non-experiments border rows to reduce the border effect. The observations were recorded on days to 50 per cent flowering, trichome density (mm^2), leaf surface wetness (LSW) and seedling vigor (1 to 5 scale).

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 as outlined by Mather (1949) [6] and Cavali (1952). 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 outlined by Hayman (1958) [2].

Results and Discussion

The estimates of mean 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 tolerance. The F_1 and segregating generations evolve from cross combinations, RSV1006 x RSV1093 exhibited superior performance for the inheritance of trichome density, whereas cross RSV1098 x RSV1003 and BJV74 x RSV1093, indicated superior performance for the inheritance of trichome density, leaf surface wetness and seedling vigor. 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 could be most promising among the four crosses (Table 1).

Analysis of variance indicated that all the characters associated with shootfly 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 (Table 2).

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	Days to 50% flowering	Trichome density(mm^2)	Leaf surface wetness	Seedling vigor
BJV74 x RSV1093	P_1	78.67 (0.35)	6.53 (0.28)	3.33 (0.07)	3.50 (0.06)
	P_2	78.00 (0.40)	11.83 (0.33)	2.33 (0.06)	2.33 (0.05)
	F_1	74.00 (0.30)	8.83 (0.29)	2.83 (0.06)	3.00 (0.07)
	F_2	75.00 (0.21)	8.10 (0.20)	3.00 (0.04)	3.17 (0.04)
	B_1	75.67 (0.24)	7.83 (0.21)	3.17 (0.03)	3.67 (0.03)
	B_2	73.33 (0.24)	8.30 (0.22)	2.67 (0.04)	3.00 (0.03)
RSV1006 x RSV458	P_1	76.33 (0.35)	7.61 (0.31)	3.50 (0.06)	3.17 (0.06)
	P_2	69.33 (0.35)	10.90 (0.28)	2.50 (0.07)	2.67 (0.05)
	F_1	72.00 (0.30)	8.87 (0.29)	2.83 (0.04)	2.83 (0.07)
	F_2	71.67 (0.24)	8.70 (0.22)	3.00 (0.03)	2.67 (0.03)
	B_1	74.67 (0.24)	7.97 (0.22)	3.17 (0.02)	3.00 (0.04)
	B_2	70.00 (0.28)	8.50 (0.21)	2.67 (0.03)	2.50 (0.03)
RSV1098 x RSV1003	P_1	74.33 (0.31)	7.70 (0.29)	3.17 (0.05)	3.00 (0.05)
	P_2	71.33 (0.35)	11.30 (0.32)	2.17 (0.06)	2.17 (0.06)
	F_1	72.67 (0.35)	9.35 (0.31)	2.67 (0.07)	2.50 (0.05)
	F_2	72.90	9.02	2.67	2.50

		(0.27)	(0.25)	(0.03)	(0.03)
	B_1	73.33 (0.22)	7.87 (0.22)	2.83 (0.04)	3.00 (0.04)
	B_2	70.33 (0.22)	8.97 (0.20)	2.33 (0.04)	2.33 (0.03)
RSV1006 x RSV1093	P_1	76.87 (0.32)	7.67 (0.32)	3.33 (0.05)	3.17 (0.05)
	P_2	78.30 (0.41)	11.93 (0.29)	2.33 (0.07)	2.17 (0.05)
	F_1	74.83 (0.37)	8.35 (0.34)	2.83 (0.02)	2.67 (0.05)
	F_2	75.40 (0.24)	8.14 (0.19)	2.83 (0.03)	2.67 (0.03)
	B_1	77.07 (0.24)	7.80 (0.22)	3.00 (0.03)	3.00 (0.03)
	B_2	73.47 (0.23)	8.33 (0.22)	2.50 (0.02)	2.83 (0.03)

Table 2: 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.	Days to 50% flowering	A	-1.33**	1.00**	-0.33	2.43**
		B	-5.33**	-1.33**	-1.33**	-6.20**
		C	-4.67**	-3.00**	2.60**	-3.25**
		D	1.00**	-1.33**	2.13**	0.26
2.	Trichome density (mm^2)	A	0.30**	-0.37**	-0.73**	-0.43*
		B	-4.06**	-1.86**	-1.36**	-3.62**
		C	-3.63**	-1.90**	-0.45*	-3.76**
		D	0.07	0.17**	0.82**	0.14*
3.	Leaf surface wetness	A	0.12	0.01	-0.18**	0.01
		B	-0.17**	0.01	-0.51**	0.01
		C	0.15**	0.34**	-0.33**	0.34**
		D	0.16**	0.16**	0.18**	0.16**
4.	Seedling vigor	A	0.33**	-0.01	0.51**	0.16**
		B	-0.18**	-0.16**	-0.33**	0.82**
		C	-0.51**	-0.48**	-0.48**	-0.68**
		D	-0.33**	-0.16**	-0.33**	-0.83**

Table 3: Estimation of gene effects in four crosses of shootfly resistance.

Traits	Crosses	Genetic parameters						Type of Epistasis
		Mean m	**Additived d**	**Dominance h**	**a x a i**	**a x d j**	**d x d l**	
Days to 50% flowering	BJV74 x RSV1093	75.00** (0.21)	-2.33** (0.35)	-6.33** (1.16)	8.67** (1.09)	8.67** (0.44)	8.67** (1.80)	Duplicate
	RSV1006 x RSV458	71.67** (0.24)	-4.67** (0.37)	1.83** (1.29)	2.67** (1.23)	1.17** (0.45)	-2.33** (1.94)	Duplicate
	RSV1098 x RSV1003	72.90** (0.27)	-3.00** (0.31)	-3.48** (1.32)	-4.27** (1.25)	0.50* (0.39)	5.93** (1.85)	Duplicate
	RSV1006 x RSV1093	75.40** (0.24)	-3.60** (0.33)	-3.97** (1.25)	-0.52* (1.17)	4.32** (0.42)	4.49** (1.87)	Duplicate
Trichome density (mm^2)	BJV74 x RSV1093	8.10** (0.20)	-0.47** (0.30	-0.89** (1.06)	-0.13** (0.99)	2.18** (0.37)	3.89** (1.62)	Duplicate
	RSV1006 x RSV458	8.50** (0.22)	-0.90** (0.30)	-1.89** (1.11)	-0.33** (1.06)	0.75** (0.37)	2.57** (1.65)	Duplicate
	RSV1098 x RSV1003	9.02** (0.25)	-1.49** (0.30)	-2.37** (1.21)	-1.64** (1.15)	0.31** (0.37)	3.73** (1.71)	Duplicate
	RSV1006 x RSV1093	8.14** (0.19)	-0.54** (0.31)	-1.73** (1.07)	-0.29** (0.99)	1.60** (0.38)	4.33** (1.67)	Duplicate
Leaf surface wetness	BJV74 x RSV1093	2.83** (0.03)	-0.54** (0.04)	-0.57** (0.15)	-0.38** (0.14)	0.09** (0.05)	0.49** (0.22)	Duplicate
	RSV1006 x RSV458	3.00** (0.03)	-0.45** (0.09)	-0.49** (0.28)	-0.32** (0.26)	0.05** (0.11)	0.30** (0.44)	Duplicate
	RSV1098 x RSV1003	2.67** (0.05)	-0.49** (0.08)	-0.53** (0.28)	-0.36** (0.26)	0.17** (0.10)	1.05** (0.43)	Duplicate
	RSV1006 x RSV1093	3.00** (0.05)	-0.46** (0.07)	-0.49** (0.26)	-0.32** (0.23)	0.06** (0.00)	0.30** (0.41)	Duplicate

Seedling vigor	BJV74 x RSV1093	2.50** (0.05)	0.67** (0.09)	0.75** (0.27)	0.66** (0.26)	0.26** (0.10)	-0.81** (0.43)	Duplicate
	RSV1006 x RSV458	2.67** (0.05)	0.40** (0.09)	0.50** (0.28)	0.32** (0.26)	0.08** (0.11)	-0.16** (0.44)	Duplicate
	RSV1098 x RSV1003	3.17** (0.05)	0.71** (0.08)	0.79** (0.28)	0.66** (0.26)	0.42** (0.10)	-0.84** (0.43)	Duplicate
	RSV1006 x RSV1093	2.50** (0.05)	0.17** (0.07)	1.66** (0.26)	1.69** (0.23)	-0.33** (0.00)	-2.64** (0.41)	Duplicate

Gene action for days to 50 per cent flowering

Significance of 'B' and 'C' scaling test in all the four crosses, indicated inadequacy of additive-dominance model and non-allelic interactions are present. The magnitude of dominance x dominance (l) and additive x additive (i) gene interaction effects were greater and highly significant in both direction. However, the effect of mean (m) were found highly significant in all the four crosses indicating the presence of epistasis. For the character days to 50 per cent flowering the additive (d) as well as dominance (h) components were negatively significant indicating the magnitude of additive (d) component was observed lower but desirable direction than dominant (h) component in the crosses BJV74 x RSV1093, RSV1098 x RSV1003 and RSV1006 x RSV1093 except for the cross RSV1006 x RSV458. The role of additive gene action in the inheritance of this trait and parent RSV1098 (P_1) and RSV458 (P_2) were superior in contributing this trait. However, the magnitude of dominance x dominance (l) interaction effects was greater than additive x additive (i) and additive x dominance (j) interaction effects, indicated the importance of additive (d) and dominance x dominance (l) gene effects in both the crosses BJV74 x RSV1093 and RSV1006 x RSV458 for governing this trait, while in the cross RSV1098 x RSV1003 and RSV1006 x RSV1093 the magnitude of additive x additive (i) interaction effects was greater than additive x dominance (j) and dominance x dominance (l) interaction effects indicated the importance of additive (d) and additive x additive (i) gene effects. Whereas, the opposite sign of dominance (h) and dominance x dominance (l) gene effects indicated that duplicate gene action played an important role in the inheritance of days to 50 per cent flowering for all the crosses. The magnitude of additive gene effect was higher in desirable direction than the dominance gene effect which suggested that additive gene action played an important role in the expression of this character, indicated predominance of additive gene action in the inheritance of days to 50 per cent flowering in the cross BJV74 x RSV1093, RSV1006 x RSV458, RSV1098 x RSV1003 and RSV1006 x RSV1093 suggested that simple selection would be more effective for improvement, which is in accordance with the earlier findings of Premlatha *et al.* (2006), Kulkarni *et al.* (2006) [4], Thul (2007) [13], Patil (2008) [7].

Gene action for trichome density (mm^2)

Trichome density contributed mainly toward genetic divergence in shootfly resistance, followed by glossiness and trichome on abaxial surface of leaves are associated with shootfly tolerance. The scaling test 'A', 'B' and 'C' in all the four crosses were highly significant in negative direction and scaling test 'D' was 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 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.

The estimate of additive (d) and dominance (h) gene effects were negatively significant and greater magnitude of parameter 'h' in desirable direction over the parameter 'd' indicated the importance of dominance (h) gene effects for expression of trait trichome density in all four crosses *viz.*, BJV74 x RSV1093, RSV1006 x RSV458, RSV1098 x RSV1003 and RSV1006 x RSV1093. From the negative estimates of additive (d) gene effect, it was revealed that the parent RSV1098 (P_1) and RSV1093 (P_2) showed superior performance in this trait. However, the dominance x dominance (l) component was magnitudinaly higher, followed by additive x dominance (j) in positive direction and additive x additive (i) component was relatively lower in magnitude in negative direction indicated the preponderance of dominance (h) component and dominance x dominance (l) for the expression of this trait in all the four crosses, indicating the presence of all three non-allelic interaction effects. While considering the predominance of dominance (h) and dominance x dominance (l) gene effect in the expression of trichome density, indicated the opposite sign, suggesting duplicate type of epitasis suggested that the breeding progress shall be through exploitation of heterosis. These findings are in accordance with the earlier report of Thul (2007) [13], Patil (2008) [7] and Lad (2009) [5].

Gene action for leaf surface wetness (LSW)

Sorghum cultivars with high transpiration rate were preferred for oviposition. The susceptibility of sorghum to the shoot fly *Atherigona soccata* Rondaniis affected by leaf surface wetness and seedling age and is highest when seedlings are 8–12 days old. Significance of scaling test 'A', 'B' and 'C' in the cross BJV74 x RSV1093, RSV1006 x RSV458, RSV1098 x RSV1003 and RSV1006 x RSV1093 indicated inadequacy of additive-dominance model. Consequently significance of scaling test 'C' in negative direction exhibited presence of dominance x dominance (l) and additive x additive (i) gene interaction effects were greater and highly significant in negative direction for 'l' and 'i'. However, the joint scaling tests were found significant in all crosses, exhibited the presence of epistasis. The significantly negative additive (d) and dominance (h) components, with near to equal magnitude of additive (d) and dominance (h) components indicated the equal importance of additive (d) and dominance (h) gene effects. This projects the role of additive and non additive gene action in the inheritance of this trait. It has been reported earlier by Kulkarni *et al.* (2006) [4] and Solanki *et al.* (2007) [11].

Parent RSV1098 (P_1) and RSV1003 (P_2) were superior in contributing this trait. The interaction effects for the crosses BJV74 x RSV1093, RSV1006 x RSV458, RSV1098 x RSV1003 and RSV1006 x RSV1093 significantly positive additive x dominance (j), dominance x dominance (l) and significantly negative additive x additive (i) gene effects indicated the presence of all these non-allelic interaction. Both dominance ‘h’ and dominance x dominance ‘l’ component had opposite sign, suggesting the duplicate gene action in inheritance of this trait. The estimates of genetic parameter, revealed that in the presence of both additive (d) as well as dominance (h) gene effects and all three types of non-allelic interaction, which is fixable and could be utilized in reciprocal recurrent selection programme would be effective in improvement of these traits. This finding confirms the earlier report of Patil (2000).

Gene action for seedling vigor

Seedling vigor in sorghum [*Sorghum bicolor* (L.) Moench] is important for improving stand establishment of the crop, particularly in arid regions and in areas where low soil temperatures prevail at planting time. Significance of scaling test ‘A’, ‘B’ and ‘C’ in the crosses BJV74 x RSV1093, RSV1006 x RSV458, RSV1098 x RSV1003 and RSV1006 x RSV1093, indicated inadequacy of additive-dominance model. Consequently significance of scales test ‘C’ in negative direction exhibited presence of dominance x dominance (l) and additive x additive (i) gene interaction effects as expected were greater and highly significant in negative direction for ‘l’ and ‘i’. However, the joint scaling tests were found significant in all crosses exhibited the presence of epistasis. The significantly positive dominance (h) and significantly negative additive (d) components with higher magnitude of dominance (h) over the additive (d) components, indicated the preponderance of dominance (h) gene effects for governing this trait. The role of additive gene action in the inheritance of this trait seedling vigor, as has been reported earlier by Prakash *et al.* (2010) [9], Tariq *et al.* (2012) [12] and Prabhakar *et al.* (2013) [8]. Among these predominance of additive x additive (i) gene effects followed by additive x dominance (j) played an important role in the expression of the character seedling vigor. As dominance (h) as well as dominance x dominance (l) gene effect were predominant and both had opposite sign, suggesting the duplicate gene action in inheritance of this trait. Above indicated gene effects which is non-fixable and could be utilized in heterosis breeding programme would be effective in improvement of the trait seedling vigor.

Conclusions

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. The importance of additive gene effects in trait days to 50 per cent flowering 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.*, trichome density and seedling vigor of 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. The estimates of leaf surface wetness, revealed that in the presence of both additive (d) as well as dominance (h) gene effects and all three types of non-allelic interaction, which is fixable and could be utilized in reciprocal recurrent selection.

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