



Gene effects for grain yield and related traits in sorghum [*Sorghum bicolor* (L.) Moench]

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Abstract

Generation mean analysis was carried out to estimate the nature and magnitude of gene effects in sorghum [*Sorghum bicolor* (L.) Moench]. Inadequacy of simple additive-dominance model reflected the presence of epistatic interaction. All the four traits in majority of crosses were under the influence of dominance gene effects. Higher magnitude of dominance and dominance \times dominance gene interactions could not be exploited in the crosses with duplicate epistasis as it minimizes the expression of heterosis. Reciprocal recurrent selection and/or biparental mating in early segregating generations can prove to be an effective approach for development of high yielding sorghum varieties.

Key words: Sorghum, gene effects, grain yield, scaling test, reciprocal recurrent selection

Introduction

Sorghum [*Sorghum bicolor* (L.) Moench], the third important cereal in India is grown on area of about 9.09 m ha with an annual production and productivity of 7.34 m tonnes and 8.07 q/ha, respectively [1]. Owing to its drought tolerance capacity, its cultivation in drought prone areas is effectively providing food and fodder security through risk aversion on sustainable basis. The demand of sorghum for food, fodder and feed purposes is increasing in India and other countries in Asia such as China. With the opening up of global cereal grain market, low priced sorghum grain import may hit hard the domestic production. To withstand this adverse impact, productivity of sorghum needs to be improved to make sorghum cultivation profitable in India. The knowledge on nature of gene action for yield and its component traits provides useful guidelines for genetic improvement. The present investigation was undertaken to estimate the gene effects for grain yield and its components in sorghum in order to formulate an efficient crop improvement programme.

Materials and methods

Five diverse genotypes of sorghum (Table 1) were selected to provide basic material in the study. Six generations viz., P₁, P₂, F₁, F₂, BC₁ and BC₂ of four inter-varietal crosses namely, KSE 33/DXE 2830 (C₁), IS 2205/ICSB 88005 (C₂), IS 2205/AKR 150 (C₃) and ICSB 88005/AKR 150 (C₄) were raised in a randomized block design with three replications at Crop Research Farm, Mauranipur (Jhansi) during *khari*, 2001. The parents and F₁s were planted in a single row of 4.2m length; BC₁ and BC₂ were planted in three rows of 4.2m length and F₂s were planted in six rows of 4.2m length. The inter and intra-row spacing was maintained at 45 \times 15 cm. Ten plants from each of parents and F₁s, 20 plants from BC₁ and BC₂ generations and 30 plants from F₂ populations were randomly selected for recording data on panicle length, panicle weight, 1000-grain weight and grain yield per plant. Mather's [2] scaling test was used to test the adequacy of additive - dominance model and gene effects were estimated following Hayman [3].

Results and discussion

Significance of scaling tests (A, B and C) reflected the presence of non-allelic interactions. In the present study, all the crosses exhibited non-allelic interactions for all the four traits (Table 2). Accordingly, the character wise findings on various genetic components are briefly described under following sub-heads:

Panicle length: Significant estimates and magnitude of dominance component (h) of generation mean in most of the crosses except C₄ suggested its major role in the inheritance of panicle length. Among the digenic effects, all the three non-allelic interactions (i) (j) and (l) were significant in cross C₃ whereas, in cross C₁ none were significant with complementary epistasis. Rest crosses exhibited duplicate type of epistasis having opposite signs of dominance and dominance \times dominance (l) interactions. The significance of additive \times additive (i) gene effects with positive sign

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Table 1. Salient features of the parental lines of sorghum

Sl.No.	Name	Features	Origin
1.	KSE 33	Early, medium tall, semi-erect resistant to leaf spot and tolerant to shoot fly/stem borer medium sized seed (25.3g/1000 seeds)	Sorghum Improvement Project, Mauranipur
2.	DXE 2830	Non-tan, dwarf, medium in maturity, semi-erect, tolerant to shoot fly and leaf spot diseases, medium seeded (19.7g/1000 seeds)	NRCS, Hyderabad
3.	IS 2205	Tan, tall, medium in maturity, semi-erect, resistant to stem borer and shoot fly, small seeded (11.7g/1000 seeds)	ICRISAT, Hyderabad
4.	ISCSB 88005	Tan, early, medium in height, semi-erect, small seeded (13.3g/1000 seeds)	ICRISAT, Hyderabad
5.	AKR 150	Tan, early, dwarf, semi-erect resistant to leaf spot and tolerant to shoot fly, medium seed size (26.7g/1000 seeds)	Sorghum Improvement Project, Akola

Table 2. Scaling tests and estimates of components of generation means for panicle length, panicle weight, 1000-grain weight and seed yield per plant in sorghum

Crosses	Scale			Genetic components						Type of epistasis
	A	B	C	m	d	h	i	j	l	
Panicle length										
C ₁	-8.83	0.00	-17.23**	23.33**	-4.07	11.65*	8.39	-4.42	0.43	C
C ₂	6.00*	3.23	-27.30**	16.67**	-5.60**	35.42**	36.53**	1.38	-45.77**	D
C ₃	7.73**	-1.47	-8.93	18.20**	3.73*	20.20**	15.20*	4.60*	-21.47*	D
C ₄	-4.13	8.53**	4.80	29.70**	-0.19	6.80	-0.39	-6.33**	-3.99	D
Panicle weight										
C ₁	-24.37	32.37*	-51.80*	59.40**	-19.23*	112.3**	59.8*	-28.37**	-67.8*	D
C ₂	33.30*	19.43	-81.20*	36.67**	-11.57	171.93**	133.93**	6.93	-186.67**	D
C ₃	74.10**	47.57**	48.67**	62.37**	-0.49	107.33**	72.99**	13.27	-194.67**	D
C ₄	-52.53**	11.87	-16.33	79.40**	-27.37**	39.37	-24.33	-32.20**	65.00	C
1000-grain weight										
C ₁	4.37**	2.67**	-9.57**	21.00**	3.23**	18.15**	16.60**	0.85*	-23.63**	D
C ₂	2.70**	7.17**	8.00**	18.03**	-3.00**	9.47**	1.87	-2.23**	-11.73**	D
C ₃	3.33**	-3.40**	-7.20**	17.57**	-3.77**	8.67**	7.13**	3.37**	-7.07**	D
C ₄	-2.87**	-11.13**	-9.53**	17.03**	-2.23**	-4.37**	-4.47**	4.13**	18.47**	D
Grain yield per plant										
C ₁	-21.33	23.83*	-45.57*	47.40**	-15.57**	96.02**	48.07*	-22.58**	-50.56	D
C ₂	28.23**	12.93	-64.97*	27.93**	-8.73	138.05**	106.13**	7.65	-147.30**	D
C ₃	58.00**	33.60**	39.73**	48.50**	-0.27	80.40**	51.87**	12.20*	-143.47**	D
C ₄	-43.83**	8.60	23.97	71.43**	-22.13**	-10.02	-59.19	-26.22**	94.43	D

in two crosses (C₂ and C₃) indicated presence of associated pair of genes and suggested that increased manifestation of this character can be achieved through single progeny selection. Significance of (i) component and its greater magnitude for panicle length was also reported earlier by several workers [4-7].

Panicle weight. All the components of generation mean were found to be significant in cross C₁ with duplicate epistasis. The positive dominance gene effects observed in all four crosses indicated presence of increaser alleles for panicle weights. For cross C₄, the digenic model revealed the significance of additive (d) and additive × dominance (j) type of gene effects along with complementary epistatic interaction and non-significant dominance component. Perusal of results suggested the importance of dominance gene effects in the inheritance of panicle weight as also reported earlier by several workers [4,6,7].

1000-grain weight. Estimates of (d) and (h) components were significant in all the four crosses suggesting the importance of both additive and dominance gene effects in the inheritance of 1000-grain weight [4]. However, negative value of dominance gene effects in the cross C₄ indicates the presence of decreaser alleles for this trait. Among the digenic interactions, all the three components *i.e.*, (i), (j) and (l) were significant in all the four crosses except C₂. Duplicate type of epistasis was observed in all the four crosses having opposite signs of dominance and dominance × dominance interactions.

Grain yield per plant. Simple additive-dominance model was found to be inadequate for grain yield per plant in all the four crosses. None of the cross showed significant value for all the components of generation mean. For cross C₁, both additive and dominance components as well as (i) and (j) interactions were

found to be significant. The positive sign of dominance and additive \times additive gene effects indicated presence of increaser alleles and associated pair of genes, respectively in the crosses C_1 , C_2 and C_3 . Significant additive \times additive component and non-significant dominance \times dominance gene interactions were also reported for grain yield in sorghum [8]. For cross C_4 , the digenic model revealed the significance of additive and additive \times dominance (j) type of gene effects. Opposite sign of dominance and dominance \times dominance gene effects revealed duplicate epistasis for this trait in all the four crosses under investigation. In addition to dispersion of partially or completely dominant genes and /or overdominance, the magnitude of heterosis is influenced also by non-allelic interactions. Non-allelic interactions are known to either reduce or enhance the extent of heterosis depending upon their direction and magnitude of action. Higher magnitude of dominance gene effects and dominance \times dominance interactions could not be exploited for heterosis breeding due to presence of duplicate epistasis in the present crosses as it minimizes the manifestation of heterosis [9].

The results obtained in the present set of materials revealed that the nature and magnitude of gene effects differ with different crosses character-wise. Hence, specific breeding strategy has to be adopted for a particular cross to get improvement in grain yield of sorghum. Reciprocal recurrent selection or biparental mating in early segregating generations for simultaneous exploitation of both additive and non-additive gene action can be recommended to develop high yielding sorghum genotypes.

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