

# Generation mean analysis for grain yield and its components in sorghum [*Sorghum bicolor* (L.) Moench] grown under two different environments

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## SUMMARY

The nature of gene effects for harvest index and its components in sorghum [*Sorghum bicolor* (L.) Moench] was analyzed in three crosses involving four diverse parents through generation mean analysis. Grain yield per plant, harvest index and biological yield per plant appeared to be influenced by additive and non-additive gene actions. Additive as well as dominance gene action were prevalent in expression of harvest index, biological yield per plant and grain yield per plant except in both the environments. For SPV 1329 x ICSV 272 where by dominance was prevalent in expression of biological yield per plant. Epistatic components were found to be important for all most all the characters. Duplicate type of interaction was predominantly involved in inheritance of most of the characters. For genetic improvement of harvest index utilizing non-additive components three crosses can be exploded through hybrid breeding after incorporating suitable male sterile system. The non-allelic interactions particularly at three gene level were predominant for this trait. Thus, a breeding method that can top up. The gene to form superior gene constellations interacting in a favourable manner would be more suitable to accelerate the pace of its genetic improvements. Negative 'I' suggest that heterosis may further be improved by providing better transgressive segregants if selection is practiced for positive dominant genes.

**Key Words :** Sorghum, Generation mean analysis, Scaling test, Gene effects, Harvest index, Grain yield, Biological yield, Coarser test Chi-square

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**I**nformation on nature and magnitude of genetic components of variations of a character is essential for doing an effective breeding programme for its genetic

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improvements (Panse and Sukhatme, 1978). Such knowledge would be helpful in the selection of effective and efficient breeding methods to accelerate the pace of its genetic improvement. Sorghum (*Sorghum bicolor*) commonly known as Jowar serves as an important source of food, feed, fodder and industrial raw material and suited for cultivation in arid and semi arid tropics region to augment the grain yield and fodder demand. However, the information on gene reactions for its yield as well as its component is very meager. Mather (1943) reported that the study revealed that inter allelic interactions at digenic and trigenic level played a greater role in controlling the inheritance of grain yield. Thus, breeder should follow such which can mop-up genes to form superior gene constellations interacting in a favourable manner. Further more, in the crosses where duplicate type of epistasis was observed. The selection

**Table 1: Scaling test and gene effects for harvest index and its components in sorghum grown under two different environment i.e. Kharif, 2000 (E<sub>1</sub>) and Kharif, 2001 (E<sub>2</sub>)**

Crosses	Environment t	Scale				m	Coarse r test	χ <sup>2</sup>	Gene effects							Non-allelic interaction
		A	B	C	D				d	h	i	j	l			
<b>Harvest index</b>																
SPV 1329 x ICSV 272	E <sub>1</sub>	14.25*	1.57	12.20*	-1.81	55.16*	+	0.00	-5.77*	28.06*	2.21	12.68*	-17.67*	D		
	E <sub>2</sub>	10.70*	2.15*	21.02*	2.08*	65.14*	+	0.03	-6.30*	3.36*	-10.49	12.55	-4.74*			
SU 248 x ICSV 272	E <sub>1</sub>	19.36*	-1.42	14.94*	-1.50	57.95*	+	0.05	-8.97*	18.38*	-4.91*	20.78*	-10.99*	D		
	E <sub>2</sub>	31.30*	2.14*	38.22*	2.39*	57.32*	+	0.01	-6.27*	27.14*	7.96*	29.16*	-24.65*	D		
SU 248 x ICSV 298	E <sub>1</sub>	18.13*	4.99*	22.33*	-0.40	59.71*	+	0.05	-8.48*	18.16*	-7.17*	13.13*	-13.89*	D		
	E <sub>2</sub>	21.31*	5.07*	24.68*	-0.85	58.33*	+	0.04	-8.62*	25.98*	-5.77*	16.24*	-18.69*	D		
<b>Grain yield per plant</b>																
SPV 1329 x ICSV 272	E <sub>1</sub>	27.42*	45.38*	108.77*	17.85*	72.16*	+	0.25	-5.10*	121.92*	-12.52*	-17.96*	-66.32			
	E <sub>2</sub>	17.05*	29.84*	88.59*	20.85*	76.39*	+	0.27	-6.10*	85.44*	-17.87*	-12.79*	-35.13*	D		
SU 248 x ICSV 272	E <sub>1</sub>	4.38*	22.36*	-24.00*	-25.37*	62.87*	+	1.45	-4.13*	72.39*	-0.77	-17.98	-12.69			
	E <sub>2</sub>	26.31*	5.98*	48.70*	8.21*	76.88*	+	0.00	-3.18*	52.57*	-17.80*	20.33*	-14.12*	D		
SU 248 x ICSV -298	E <sub>1</sub>	0.22*	19.12*	97.52*	39.09*	122.41*	+	0.28	-13.28*	-20.65*	-52.67*	-18.90*	27.76*	D		
	E <sub>2</sub>	-3.17*	29.07*	101.80*	37.95*	132.07*	+	0.09	-13.86*	-37.20*	-51.38*	-32.23*	31.74*	D		
<b>Number of primaries per panicle</b>																
SPV 1329 x ICSV 272	E <sub>1</sub>	-7.33*	16.00*	19.33*	5.33*	63.20*	+	0.00	8.33*	4.96	-9.23*	-23.33*	0.19			
	E <sub>2</sub>	-12.33*	6.67*	15.00*	10.33*	69.70*	+	0.03	8.50*	-16.87*	-13.97*	-19.00*	17.91*	D		
SU 248 x ICSV -272	E <sub>1</sub>	7.33	20.67*	32.00*	2.00	51.91*	+	0.00	2.00*	26.20*	-3.91	-13.33*	-24.11*	D		
	E <sub>2</sub>	-1.00	17.00*	10.00*	-3.00*	48.40*	+	0.03	4.00*	25.44*	0.36	-18.00*	-14.90*	D		
SU 248 x ICSV -298	E <sub>1</sub>	-9.67*	9.33*	16.33*	8.33*	52.78*	+	0.09	1.17	4.45	-6.76*	-19.00	4.54			
	E <sub>2</sub>	13.33*	12.67*	18.00*	9.33*	58.30*	+	0.05	1.00	-6.34	-11.08*	-26.00*	9.79			
<b>Plant height</b>																
SPV 1329 x ICSV 272	E <sub>1</sub>	-92.71*	-41.05*	27.77*	80.77*	161.29*	B	10.21*	8.31*	7.23	28.13*	-51.67*	56.73*			
	E <sub>2</sub>	-76.31*	-30.98*	25.30*	66.30*	179.76*	B	5.34*	7.39*	-0.55	6.11*	-45.32*	52.84*			
SU 248 x ICSV -272	E <sub>1</sub>	37.45*	-35.05*	-17.83*	-10.11*	193.50*	+	0.70	-17.33*	-50.34*	-29.37*	72.50*	39.76*	D		
	E <sub>2</sub>	-27.33*	-62.05*	-46.75*	-6.01*	194.81*	+	0.31	-21.07*	-62.24*	-21.42*	89.37*	64.77*	D		
SU 248 x ICSV -298	E <sub>1</sub>	-60.03*	-42.41*	-57.13*	22.65*	199.66*	B	0.05	-20.09*	-145.52*	-33.22*	-17.61*	32.55			
	E <sub>2</sub>	-65.67*	-61.35*	-55.21*	30.91*	203.69*	B	0.29	-22.99*	-148.15*	-30.68*	-4.32	149.67*	D		
<b>Biological yield per plant</b>																
SPV 1329 x ICSV 272	E <sub>1</sub>	18.48*	67.80*	151.49*	32.61*	117.27*	+	0.79	1.63	164.15*	-13.16*	-49.32*	-86.42*	D		
	E <sub>2</sub>	2.48	44.00*	100.21*	26.85*	114.55*	+	0.67	1.46	135.29*	-7.16*	45.51*	-51.33*	D		
SU 248 x ICSV -272	E <sub>1</sub>	-31.31*	41.10*	-53.99*	-36.89*	109.90*	+	1.45	12.13*	79.67*	9.00*	-72.41*	-2.08			
	E <sub>2</sub>	27.83*	7.25*	-7.76*	6.41*	133.41*	+	0.00	8.75*	26.50*	-12.35*	-35.08*	32.81*	C		
SU 248 x ICSV -298	E <sub>1</sub>	-35.69*	17.99*	107.75*	62.72*	200.27*	+	0.93	-3.81*	-69.43*	-57.98*	-53.67*	70.87*	D		
	E <sub>2</sub>	-47.00*	33.21*	107.07*	60.43*	218.10*	+	0.38	-4.32*	-113.17*	-84.17*	-80.22*	88.89*	D		

+ Unidirectional, B, Bidirectional, C, Complimentary and D, Duplicate

\* indicate significance of value at F=0.05,

intensity should be mild in the earlier and intense in the later generation under favourable environment. In view of this, the present investigation was carried out the objective of assessing the nature and magnitude of gene action for harvest index, grain yield and its components in sorghum through generation mean analysis.

## MATERIAL AND METHODS

The experimental material comprised of seven generation *i.e.* P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, F<sub>3</sub>, BC<sub>1</sub> and BC<sub>2</sub> of three crosses *viz.*, SPV 1329 x ICSV 272, SU248 x ICSV 272 and SU 248 x ICSV 298. These crossed along with seven generations were raised during *Kharif*, 2000 (E<sub>1</sub>) and 2001 (E<sub>2</sub>) in a Complete Randomized Block Design with three replications at Instructional Research Farm, Rajasthan College of Agriculture, Udaipur (Rajasthan). Each net plots had single row of non-segregating generation (P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>), four rows for F<sub>2</sub>, F<sub>3</sub> and back crosses segregation generations. Each row was of three meter length with maintained the plant geometry of 45 cm x 15 cm.

Observation of five quantitative traits relating to grain yielding per plant, harvest index, number of primaries per plant, plant height, biological yield per plant were recorded in each replication in both the environments on 10 randomly selected plants from parental and F<sub>1</sub> generation, 20 plants from F<sub>2</sub>, F<sub>3</sub> and back crosses generation. The data were first subjected to analysis of variance separately of each crossing in both the environments were done according to Panse and Sukhatme (1978). After that the data were subjected for individual scaling test was performed to test the adequacy of these parameters *i.e.* additive, dominance and epistatic by Mather (1943) and Mather (1949), when the additive dominance model was inadequate, the estimates of gene effects both allelic and non-allelic were obtained using the digenic epistatic model Cavalli (1952) and in absence of non-allelic interaction, mean, coarser test and chisquare ( $\chi^2$ ) were estimated. The Chi-square test for goodness of fit for 3:1 ratio was done using the formulae, if the calculated Chi-square value for 3:1 ratio is non-significant at 1 d.f. it suggested monogenic inheritance.

## RESULTS AND DISCUSSION

In view of A, B, C and D scaling test, at least two scales were significantly different from zero for all the characters in the three crosses in both the environments (Table 1). This suggests the influence of non-allelic interaction in inheritance for all components. In crosses SPV 1329 x ICSV 272, SU 248 x ICSV 272 and SU 248 x ICSV 298 all the gene effects were found to be significant for harvest index, grain yield per plant and biological yield per plant. Therefore, additive, dominance and all three epistatic interactions were prevalent for its inheritance for these crosses.

In cross SU 248 x ICSV 298 additive, dominance, additive x additive, additive x dominance and dominance x dominance components predominantly controlled directly by harvest index, grain yield per plant and biological yield per plant. The dominant component (h) was significant and greater in magnitude than additive (d) components for most of the traits in all three crosses over both the environments. This indicated the predominance role of dominant gene action in controlling all the traits. Simultaneously, the presence of non-additive gene action is a significant factor to exercise selection for evolving hybrids. In such a situation maximum gain could be achieved by providing better transgressive segregants if selection is practised for positive dominant genes only.

The same sign of 'h' and 'l' estimates in cross SU 248 x ICSV 272 in E<sub>2</sub> for biological yield per plant indicated the presence of complementary gene action suggesting the possibility of considerable amount of heterosis in this cross for biological yield per plant.

The 'j' type of components was positive and significant indicating greater role of additive x dominance for harvest index in all the three crosses except cross SPV 1329 x ICSV 272 in E<sub>2</sub>. The estimates of mean (m) was highly significant for all the characters in all the crosses (Table 1). Among the digenic interaction effects additive x additive (i) and dominance x dominance (l) were significant for most of the traits in all the crosses over both the environments.

In general, all the allelic as well as non-allelic interactions were prevalent in inheritance of harvest index and its component traits. The magnitude of dominance (h) and dominance x dominance (l) were found to be high for all most all the three crosses for harvest index in both the environments except SPV 1329 x ICSV 272 in E<sub>1</sub>. The signs of 'h' and 'l' components were screened for these traits where 'h' and 'l' components were significant thus, suggests the duplicate type of gene actions were observed for all the traits as mentioned by D in Table 1, except SU 248 x ICSV 272 for biological yield per plant in E<sub>2</sub> where, complementary gene action was observed. This indicated hinderance of selection improvement thus, selection is likely to be useful for effective utilization of both type of additive and non-additive type of gene action simultaneously Conostock *et al.* (1949). In this situation, heterosis may be further be improved on account of 'h' but negative 'l' suggested that it may provide better transgressive sergregants, if selection is practiced for positive dominate genes only.

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