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Role of epistatic gene action in inheritance of quantitative traits in sesame (*Sesamum indicum* L.)

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Abstract
Finding means to improve productivity of sesame crop is crucial to harness the nutritional and medicinal properties of the crop. It can be best done with genetic improvement of the crop. Seven lines and two testers were evaluated using generation mean analysis to know the nature of gene actions and identify epistasis for yield and its components in sesame. Results showed that two crosses namely, ES-3 x TC-289 and GT-1 x JLT-8 exhibited both additive (d) and additive x additive (i) interactions for seed yield. Characters like plant height, length of capsule, number of seeds per capsule and seed weight also showed d and i effects coupled with heterobeltiosis. F_2 generation of these two crosses showed high seed yield, length of capsule, number of seeds per capsule and seed weight. It was concluded that ES-3 x TC-289 and GT-1 x JLT-8 can be exploited for isolation of promising recombinant lines having higher seed yield.

Keywords: Sesame, epistasis, gene action, generation mean analysis

Introduction
Sesame (*Sesamum indicum* L.) is nature's wonderful gift to mankind because of high oil content (44-52%) richness in protein (26-52%) coupled with innumerable bio medicinal and pharmaceutical qualities. But productivity of sesame is very low (372 kilograms per hectare) in India, practically stagnant as compared to other sesame growing countries of the world. This is primarily due to its susceptibility to various biotic (phyllody, leaf roller etc.) and abiotic (waterlogging and drought) stresses coupled with lack of productive genotypes. Thus genetic improvement of this crop is the need of the hour. Genetic studies on the sesame crop are limited involving only limited location specific genotypes and that too with inconclusive inferences. The present study was undertaken using two testers and seven lines of diverse origin to detect the possible role of additive and non-additive gene action including epistasis in control of yield and certain yield traits using generation mean analysis.

Materials and Methods
The experimental materials consisted of two females (ES-3 and GT-1) and seven males (JLT-8, Shekhar, TC-289, MT-29, T-12, Uma and T-4) along with their fourteen F_1s. In *Kharif* 2007, six generations (P_1, P_2, F_1, F_2, B_1 and B_2) of each of the fourteen crosses were grown in Randomised Block Design in three replications at Dryland Agriculture Research Farm, Banaras Hindu University, Varanasi. Parents and F_1s were grown in two-row plots, F_2 in five-row plots and backcrosses (B_1 and B_2) in three-row plots of 5 metre length with row to row distance of 45 cm and plant to plant distance of 10-15 cm. Five plants from each of the parents and F_1s, twenty plants from each B_1 and B_2 and fifty plants from F_2 were selected randomly from each replication for recording data on plant height, length of capsule, number of seeds per capsule, seed yield per plant and 1000-seed weight. Data were subjected to generation mean analysis following Hayman (1958) [4], Jinks and Jones (1958) [6] and Hayman and Mather (1955) [5].

Results and Discussion
The breeding procedure that was adopted depends mainly on the nature and magnitude of genetic make-up of the parents in relation to the yield and yield traits. Combining ability analysis fails to analyze the nature of gene action; internal cancellation of components of gene effects, therefore, remains undetected. However, generation mean analysis appears to be efficient in resolving the epistasis in terms of its nature and magnitude. The present study on fourteen crosses (2 x 7; L x T crosses) showed the presence of epistasis in almost all the crosses in different traits, indicating a possible role of epistasis in the control of different traits

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(Table 1). The magnitude and nature of additive, dominance and epistasis type of gene effects varied cross-wise as well as character-wise. Among the main effects, dominance [h] effect was distinct in most of the characters, especially in length of capsule, while both 'd' and 'h' effects were prominent for plant height, number of seeds per capsule, seed yield per plant and seed weight. Similar results were also found by Deenamani and Dorairaj (1994) [2] and Sharmila *et al.* (2007) [8]. Among the interaction effects, dominance x dominance [1] followed by additive x additive (i) types of interaction were predominant in inheritance of most of the characters under study. In most of the crosses dominance [h] and dominance x dominance [1] were in opposite direction suggesting the presence of duplicate (D) type of epistasis in most of the characters. The finding was in agreement with Bakheit *et al.* (1996) [1] and Pathak and Dixit (1988) [7].

Although dominance gene effect was predominant (h>d) in most of the crosses and characters, it could not be utilized due to presence of duplicate type of epistasis (D) leading to internal cancellation of dominant effect. Moreover, in self-pollinated crop like sesame, the exploitation of additive (d) and additive x additive (i) interaction effects, which are fixable, need to be examined. In two crosses, namely, ES-3 x TC-289 and GT-1 x JLT-8, both additive (d) and additive x additive (i) interactions were prominent (Table 1) and might be exploited. These two crosses may be subjected to breeding for component traits. The component traits, such as plant height, length of capsule, number of seeds per capsule and seed weight also showed adequate amount of fixable gene effect (d and i) coupled with good amount of heterobeltiosis (Dasgupta, 2008) [3]. The recombinants in F_2 generation of the above two crosses having high seed yield coupled with enhanced level of length of capsule, number of seeds per capsule and seed weight are likely to result in the isolation of promising lines.

Table 1: Estimates of gene effects from analysis of generation means for yield, yield traits and heterobeltiosis.

Cross/Gene effects heterobeltiosis		Plant height	Length of capsule	No. of seeds/capsule	Seed yield/ plant	Seed weight
ES-3 × JLT -8	m	140.65**	3.14**	79.02**	4.67**	2.83**
	d	-11.18*	-0.21**	-5.91**	-2.15*	0.21**
	h	-28.08*	-1.15**	-35.07**	6.89*	0.15**
	i	-53.64**	-2.18**	-52.41**	4.93	-0.02**
	j	-7.78	-0.13	-4.58**	-3.31**	-0.08**
	l	13.94	0.41**	83.75**	0.62	0.15**
Epistasis		-	D	D	-	C
Heterobeltiosis		27.29*	36.95**	23.51**	10.84**	-3.92**
ES-3 × Shekhar	m	127.67**	2.70**	76.00**	14.79**	3.54**
	d	4.60	0.13	3.90**	1.51*	0.21**
	h	6.75	0.31	-6.57*	1.65	-0.19**
	i	63.07**	0.15	-12.04**	-0.02	-0.41**
	j	18.31**	0.26*	7.53**	3.21**	0.34**
	l	-270.93**	-1.03*	0.51	-19.14**	-0.12
Epistasis		-	-	-	-	-
Heterobeltiosis		-3.76	1.96	2.58	-0.28	2.40**
ES-3 × TC-289	m	134.99**	2.67**	70.18**	13.18**	3.26**
	d	11.12**	0.14**	6.63**	4.09**	-0.16**
	h	61.31**	0.80**	20.34**	1.29	0.92**
	i	46.73**	0.62**	18.08**	-0.27	0.73**
	j	27.77**	0.18**	7.83**	6.55**	-0.15**
	l	-129.08**	-2.13	-52.62**	-9.32**	-1.80**
Epistasis		D	-	D	-	D
Heterobeltiosis		1.48	5.42**	1.62	-7.18	5.83**
ES-3 × MT-29	m	104.47**	2.77**	66.33**	9.76**	3.43**
	d	-0.28	-0.06	-1.24*	0.07	-0.02
	h	5.87	0.07	11.03**	7.67*	0.53**
	i	14.83**	-0.27	9.63**	4.50	0.06
	j	7.04	0.06	-0.04	-0.81	-0.12**
	l	-11.74	-0.14	-22.07**	-15.34*	-1.06**
Epistasis		-	-	D	D	D
Heterobeltiosis		-2.17	3.92*	-5.53*	22.22	1.46**
ES-3 × T-12	m	122.73**	2.58**	66.67**	8.04**	3.57**
	d	3.89	-0.05	1.96	0.92	-060**
	h	26.51	0.85**	13.37*	16.82**	-0.28**
	i	32.86*	0.85**	15.61*	19.13**	-0.54**
	j	18.84*	0.13*	7.20*	2.16**	-0.36**
	l	-85.01**	-2.07**	-26.48*	-40.23**	0.52**
Epistasis		-	D	D	D	D
Heterobeltiosis		-15.66	-5.26	-10.07**	-35.78**	-20.56**
ES-3 × Uma	m	133.67**	2.60**	71.99**	11.00**	3.13**
	d	-4.20	-0.02	0.11	0.97	-0.13**
	h	14.63	0.25	8.52	4.48	0.14**
	i	5.38	+0.05	-	-	0.04
	j	6.99	0.04	-	-	-0.14**
	l	-57.67*	-0.64	-	-	-0.21**

Epistasis		-	-	-	-	D
Heterobeltiosis		-1.50	1.59	11.67*	18.37	2.94**
ES-3 × T-4	m	145.33**	2.72**	72.87**	10.79**	2.61**
	d	-0.43	0.15	-0.25	-0.55	-0.01
	h	21.62*	1.84**	18.14	6.55	0.62**
	i	18.25*	1.57**	12.71	-	0.83**
	j	12.40**	0.27	5.79	-	-0.11**
	l	-135.25**	-3.76**	-26.95	-	-0.73**
Epistasis		D	-	-	-	D
Heterobeltiosis		-7.19	-1.46	-0.79	16.15	-10.46**
GT-1 × JLT-8	m	121.57**	2.59**	66.67**	8.04**	2.92**
	d	10.66	0.08	4.26	3.78**	0.58**
	h	56.74**	0.68**	11.64	15.11**	1.78**
	i	49.83**	0.60**	9.94	11.82**	1.25**
	j	11.56	0.09	4.42	4.40**	0.75**
	l	-116.80**	-1.49**	-16.88	-26.14**	-2.56**
Epistasis		D	D	-	D	D
Heterobeltiosis		5.24	2.81	2.29	41.78*	12.41**
GT-1 × Shekhar	m	131.75**	2.74**	73.98**	9.47**	2.73**
	d	-1.86	0.01	0.22	1.00	0.21**
	h	47.18**	0.17	-12.61	21.56**	2.75**
	i	36.99**	0.11	-12.80	17.90**	2.75**
	j	8.24	0.06	2.52	3.86*	0.63**
	l	-88.47**	-1.01**	4.85	-34.30**	-4.79**
Epistasis		D	-	-	D	D
Heterobeltiosis		0.07	0.78	-2.97	7.37	-12.91**
GT-1 × TC-289	m	131.33**	2.63**	69.82**	13.47**	3.13**
	d	-13.40*	-0.19**	-2.58	-2.90**	-0.18**
	h	5.05	0.42*	-0.04	-10.74**	-0.90**
	i	-2.55	0.31	-1.75	-13.35**	-1.29**
	j	-4.15	-0.22**	-2.71	0.72	0.13**
	l	-16.28	-1.15**	-7.27	13.10**	1.96**
Epistasis		-	D	-	D	D
Heterobeltiosis		-1.26	4.07*	2.38	-8.15	2.60**
GT-1 × MT-29	m	132.45**	2.53**	66.22**	8.32**	2.91**
	d	-4.54	-0.08*	-0.55	-3.96*	0.22
	h	2.32	0.47*	17.47*	11.08*	-0.32
	i	-12.26	0.41	16.66*	5.95	-0.69
	j	-064	-0.03	-0.68	-3.68*	0.41
	l	-8.78	-0.80**	-31.50**	-13.22	1.17
Epistasis		-	D	D	-	-
Heterobeltiosis		8.85	0.78	1.02	84.76**	6.30**
GT-1 × T-12	m	121.94**	2.65**	70.00**	9.77**	3.16**
	d	6.48	0.01	-11.51**	3.71**	-0.62**
	h	50.87	0.05	4.26	6.60*	0.25*
	i	54.38**	-0.48	10.56	4.76*	-0.09
	j	18.03	0.11*	-7.61**	-1.31	-0.08**
	l	-105.63**	-0.28	-32.53**	-14.69**	0.25*
Epistasis		D	-	-	D	C
Heterobeltiosis		-11.07	-1.88	-13.76**	-5.53	-5.63**
GT-1 × Uma	m	135.37**	2.73**	73.86**	8.65**	2.91**
	d	-5.88*	-0.31**	-2.88**	-1.88*	-0.49**
	h	5.22	1.12*	-8.11	4.10	0.79**
	i	-	0.37	-16.38	-	0.28**
	j	-	-0.33**	-2.88*	-	-0.21**
	l	-	-0.39	19.47	-	-0.12
Epistasis		-	-	-	-	-
Heterobeltiosis		5.94	26.59**	12.45**	-27.31	7.57**
GT-1 × T-4	m	132.40**	2.74**	75.20**	9.46**	2.69**
	d	-12.90**	-0.12**	-5.44**	-4.16**	-0.16
	h	27.08**	0.28**	14.91**	14.87**	0.63**
	i	27.11**	0.09	10.81**	10.60**	0.56**
	j	-3.47	-0.07	-0.74	-1.57**	0.03
	l	-94.43**	-072**	-29.83**	-19.52**	-1.09**
Epistasis		D	D	D	D	D
Heterobeltiosis		-7.18	-11.16	-0.79	16.15	-3.86**

*Significant at p = 0.05; **Significant at p = 0.01; M=mean effect; d=additive effect; h=dominance effect; i=additive×additive; j=additive×dominance and; l=dominance×dominance type of gene interaction; D is Duplicate type of epistasis and C is Complementary type of epistasis.

Summary and Conclusion

Generation mean analysis was performed on fourteen crosses constituting nine parents to study the nature and magnitude of gene effects for yield and its components in sesame. Scaling tests were successfully adopted to test the adequacy of the scales (A, B, C and D) and generation mean analysis was performed. Dominant (h) and dominance x dominance (l) gene effects were predominantly coupled with duplicate type of epistasis in most of the characters/crosses. Two crosses that is, ES-3 x TC-289 and GT-1 x JLT-8 showed appreciable amount of additive (d) and additive x additive (i) gene effects. These two crosses may be exploited in the isolation of recombinants with enhanced level of seed yield. While selection of promising lines/recombinants, component traits may also be considered in addition to seed yield.

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