



## Generation Mean Analysis for Seed Yield and Yield Traits in Sesame (*Sesamum indicum*)

J V Ramana, V Satyanarayana Rao, M Lal Ahamed, Y Ashoka Rani and P Anil Kumar

Department of Genetic & Pland Breeding, Agricultural College, Bapatla 522 101, Andhra Pradesh

### ABSTRACT

Six parents, five  $F_1$ s, five  $F_2$ s and five  $F_3$ s of sesame were evaluated for nine characters viz., days to 50% flowering, days to maturity, plant height, number of primary branches/plant, number of capsules per plant, number of seeds per capsule, 1000 seed weight, oil content and seed yield per plant to study the gene action during *rabi* 2012-13 at Agricultural Research Station, Yallamanchili, Andhra Pradesh. The results of generation mean analysis of various seed yield and yield components of ten crosses showed very less variability in the material for most of the characters in terms of mean values. The results of C and / or D scaling tests were significant for all the crosses indicating the presence of epistatic interactions in all the crosses for all the traits. Complementary epistasis for yield and oil content was observed in the crosses YLM 89 x YLM 92 and YLM 95 x YLM 92 while, duplicate type of epistasis was noticed in the cross YLM 93 x YLM 92.

Key words: *Epistasis, Generation mean analysis, Sesame.*

Sesame or gingelly, the Queen of oil seeds, is the oldest oil seed crop which is under cultivation in Asia from ancient times. It belongs to the order *Tubiflorae* and family *Pedaliaceae*. The sesame oil has 50-53% of oil and 20-26% of protein with antioxidants, vitamin E and amino acid methionine. Sesame is cultivated in an area of about 1.94 million hectares in India with a production of about 0.58 million tones (Ministry of Agriculture, 2013-14). In Andhra Pradesh, the area under sesame is 0.09 million hectares with a production of 0.2 million tonnes. The average productivity of sesame in Andhra Pradesh (222.2 kg/ha) is far less as compared to the Indian average of 303 kg/ha (Ministry of Agriculture, 2013-14) indicating the importance of high yielding varieties for yield improvement.

In India, oil and yield productivity of sesame are low and the slow progress in improvement programmes is due to the arbitrary choice of parents and inadequate information about the nature of gene action in governing the traits. A thorough knowledge on gene action will provide the basis for selection of suitable breeding programme for the improvement of oil/ yield. Keeping this in view, the experiment was planned with the objective to identify the gene action in the selected crosses for desirable traits for their further exploitation.

### MATERIAL AND METHODS

The present investigation was carried out with six parents (Five females and one male), five  $F_1$ s, five  $F_2$ s and five  $F_3$ s for knowing the type of gene action involved in the expression of the traits viz., days to 50% flowering, days to maturity, plant height, primary branches/plant, capsules per plant, number of seeds per capsule, 1000 seed weight, oil content and seed yield per plant during *rabi* 2012-13 in randomized block design with three replications at Agricultural Research Station, Yelamanchili, Andhra Pradesh. The parents and  $F_1$ s were grown in single rows of 2 m length while, the  $F_2$ s and  $F_3$ s were grown in 5 rows of 2 m length. The intra and inter row spacing was 10 cm x 20 cm. Recommended package of practices were followed to raise a good crop. The mean values were used for the statistical analysis. The data was analysed statistically to compute the scaling tests (Mather, 1949) and generation mean analysis using five parameter model (Hayman, 1958).

### RESULTS AND DISCUSSION

Mean performance observed for nine characters of five generations of five crosses generated by crossing five female lines (YLM 89, YLM 90, YLM 93, YLM 95 and YLM 96) with one male genotype (YLM 92) are presented in Table 1. The mean performance of the basic generations

*viz.*, P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, F<sub>3</sub> of the crosses showed very less variability in the material for most of the characters. The results of C and D scaling tests and gene effects in five parameter model for all the traits studied for five generations in five crosses are presented character wise in Table 2. The results of generation mean analysis of various seed yield and yield components of five crosses are discussed here under.

### Days to 50% flowering

Mean values of days to 50% flowering for five generations of five crosses are furnished in Table 1. The F<sub>1</sub> generation mean values were lower than the both parents for all the crosses barring YLM 96 x YLM 92 in which mean value was lower than the mid parental value. The cross, YLM 89 x YLM 92 recorded lowest mean (35.66) in F<sub>1</sub> generation. The mean values of segregating generations were gradually increased when compared to their corresponding F<sub>1</sub> means for all the crosses. Significant increase in mean values in segregating generations indicated the presence of dominance and epistatic interactions in the expression of this trait.

The crosses, YLM 90 x YLM 92 and YLM 93 x YLM 92, recorded F<sub>2</sub> and F<sub>3</sub> mean values very near to F<sub>1</sub> mean values which might be due to linkage or complementary factors or both. Intermediate performance of F<sub>1</sub> of YLM 96 x YLM 92 over parents indicates the partial dominance for this character in this cross.

The differences among five generations means were significant. The estimates of scaling tests and gene effects in five parameter model for days to 50% flowering along with type of epistasis are presented in Table 2.

The scaling tests C and / or D were found to be significant for all the crosses indicating the presence of epistatic interactions. All the gene effects in five parameter model were significant in the cross YLM 93 x YLM 92 while, the cross YLM 96 x YLM 92 recorded significant gene effects for all five parameters except for additive x additive component (*i*). The crosses YLM 89 x YLM 92 and YLM 95 x YLM 92 showed significant gene effects except for additive component (*d*). The cross YLM 90 x YLM 92 recorded non significant values for additive x additive (*i*) and dominant x

dominant (*l*) components. Higher magnitude of dominant effects (*h*) were recorded in the expression of the trait while, in epistatic interactions, dominant x dominant (*l*) component is greater in magnitude than additive x additive (*i*) component except in the crosses YLM 89 x YLM 92 and YLM 93 x YLM 92 indicating the possible use of selection procedures which can break gene constellations for improvement of this trait.

In general, interaction (*i + l*) is higher than the main effects (*d + h*) in all the crosses except YLM 89 x YLM 92 and YLM 90 x YLM 92 indicating the importance of epistatic component in the inheritance of days to 50% flowering. The positive sign of additive x additive component (*i*) indicated that there would be increased expression of the character in the successive generations in the crosses YLM 90 x YLM 92 and YLM 93 x YLM 92. The similar signs of *h* (dominant) and *i* (dominance x dominance) indicates the complementary type of epistasis in the crosses YLM 89 x YLM 92 and YLM 93 x YLM 92. However, contradictory results were reported by Gaikwad *et al.* (2009) indicating duplicate type of epistasis for this character.

### Days to maturity

Mean values of days to maturity over generations of ten crosses were presented in Table 1. The mean values of F<sub>1</sub>s were lower than the both parents for the crosses YLM 89 x YLM 92, YLM 90 x YLM 92, YLM 93 x YLM 92 and YLM 95 x YLM 92. The cross YLM 96 x YLM 92 recorded higher F<sub>1</sub> mean values than both the parents indicating the involvement of dominant genes of both the parents. The mean values of segregating generations (F<sub>2</sub>, F<sub>3</sub>) were higher when compared to their corresponding F<sub>1</sub> means for all the crosses except YLM 96 x YLM 92 indicating the role of dominance epistatic interactions in the expression of this trait. The cross YLM 90 x YLM 92 recorded similar mean values to F<sub>1</sub> in segregating generations indicating the presence of linkage or complementary factors or both.

The estimates of scaling tests and gene effects in five parameter model are presented in Table 2. The significance of C and D scaling tests revealed the inadequacy of simple additive-dominance model to explain the total genetic

Table 1. Mean values of seed yield and yield contributing traits for five generations in five crosses of Sesame (*Sesamum indicum* L.).

S.No.	Crosses	GENERATIONS					GENERATIONS				
		P <sub>1</sub>	P <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>	F <sub>3</sub>	P <sub>1</sub>	P <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>	F <sub>3</sub>
		<b>Days to 50% flowering</b>									
1.	YLM 89 x YLM 92	36.83	36.50	35.66	36.74	37.25	76.66	76.66	75.83	77.70	77.37
2.	YLM 90 x YLM 92	37.50	36.50	36.00	36.60	37.10	78.33	76.66	76.33	76.38	76.72
3.	YLM 93 x YLM 92	37.75	36.50	36.00	36.73	36.94	76.00	76.66	75.33	76.82	77.12
4.	YLM 95 x YLM 92	37.00	36.50	36.00	36.60	37.26	78.33	76.66	75.66	76.32	77.13
5.	YLM 96 x YLM 92	37.58	36.50	36.66	36.91	37.51	78.50	76.66	79.33	77.93	78.24
		<b>Plant height</b>									
1.	YLM 89 x YLM 92	97.73	99.83	94.27	95.36	97.09	6.06	6.03	6.500	6.46	6.30
2.	YLM 90 x YLM 92	100.80	99.83	92.57	93.61	95.15	6.10	6.03	6.417	6.36	6.30
3.	YLM 93 x YLM 92	101.10	99.83	98.32	98.55	98.60	6.10	6.03	6.300	6.23	6.43
4.	YLM 95 x YLM 92	94.80	99.83	92.76	94.82	97.26	6.06	6.03	7.367	7.20	7.16
5.	YLM 96 x YLM 92	101.13	99.83	99.36	99.13	98.24	6.06	6.03	7.400	7.36	7.26
		<b>Seeds per capsule</b>									
1.	YLM 89 x YLM 92	57.86	61.43	65.83	65.33	65.06	84.53	83.00	80.79	80.29	78.86
2.	YLM 90 x YLM 92	58.66	61.43	64.50	62.20	68.13	83.70	83.00	79.52	79.47	77.88
3.	YLM 93 x YLM 92	59.56	61.43	63.93	63.63	69.33	83.66	83.00	78.68	78.31	76.20
4.	YLM 95 x YLM 92	62.33	61.43	66.46	63.30	62.16	83.56	83.00	83.04	81.70	81.44
5.	YLM 96 x YLM 92	61.40	61.43	71.06	68.16	64.90	81.80	83.00	80.76	82.93	81.14
		<b>1000 Seed Weight (g)</b>									
1.	YLM 89 x YLM 92	2.36	2.82	2.41	2.38	2.37	51.36	48.80	47.50	45.46	44.79
2.	YLM 90 x YLM 92	2.45	2.82	2.40	2.36	2.35	49.90	48.80	48.14	46.50	45.68
3.	YLM 93 x YLM 92	2.47	2.82	2.48	2.43	2.42	51.40	48.80	47.50	47.56	44.84
4.	YLM 95 x YLM 92	2.43	2.82	2.50	2.44	2.43	49.93	48.80	46.01	43.39	43.58
5.	YLM 96 x YLM 92	2.46	2.82	2.52	2.43	2.43	50.60	48.80	46.50	44.06	42.87
		<b>Seed yield per plant (g)</b>									
1.	YLM 89 x YLM 92	11.18	12.36	12.55	11.84	11.76					
2.	YLM 90 x YLM 92	11.48	12.36	11.56	10.82	12.07					
3.	YLM 93 x YLM 92	11.86	12.36	11.73	11.57	11.75					
4.	YLM 95 x YLM 92	12.53	12.36	12.77	12.09	11.81					
5.	YLM 96 x YLM 92	12.03	12.36	13.71	13.12	12.83					

variability indicating the presence of epistasis in the expression of this trait in all crosses. The fitting of five parameter model showed the involvement of all three kinds of gene effects (additive, dominance and epistatic) in the inheritance of days to maturity in all the crosses except YLM 89 x YLM 92 and YLM 96 x YLM 92. The cross YLM 89 x YLM 92 showed non significant *i* component of gene effects while the cross YLM 96 x YLM 92 showed non significant *h* and *i* components. The additive component was significant in all the crosses except in the cross YLM 89 x YLM 92. The magnitude of main effects (*d* + *h*) was lower over the interaction component (*i* + *l*) in the crosses indicating higher magnitude of interaction component over main effects i.e., major role of epistatic component in the inheritance of days to maturity. The negative sign of *i* component in the cross YLM 93 x YLM 92 indicated that there would be decrease in the expression of character in successive generations. The *h* and *l* components were having opposite signs revealing the presence of duplicate epistasis in the expression of the trait in the crosses YLM 90 x YLM 92 and YLM 95 x YLM 92. Gaikwad *et al.* (2009) and Sharmila *et al.* (2007) was observed complementary type of interaction which is in tune with the results of the present study.

### Plant height

Plant height recorded lowest mean value (92.57) in the cross YLM 90 x YLM 92 while highest (100.18) in YLM 90 x YLM 92 F<sub>1</sub> generation (Table 1). The F<sub>1</sub> mean values were lower than both the parents. The segregating generations recorded higher mean values than the F<sub>1</sub> generation except for the cross YLM 96 x YLM 92 (98.24) indicating the role of dominant epistatic interactions in the expression of this trait. The mean values of F<sub>1</sub>, F<sub>2</sub> and F<sub>3</sub> generations were very closer in the crosses YLM 93 x YLM 92 and YLM 96 x YLM 92 indicating the presence of linkage or complementary factors or both in the expression of this trait. The cross combination YLM 90 x YLM 92 recorded the lowest mean value for all the generations indicating its usefulness in developing medium height genotypes.

Scaling tests and gene effects in five parameter model estimates are presented in Table 2. The C and D scaling tests were significant for

all the crosses revealing the inadequacy of simple additive-dominance model to explain the total genetic variability in all the crosses. Gene effects in five parameter model showed the presence of three kinds of gene effects *d*, *h* and epistasis in the expression of this trait in all the crosses. The additive component was significant in all the crosses except in the cross YLM 90 x YLM 92. The cross YLM 93 x YLM 92 showed non significant *h* and *l* components. The main effects (*d* and *h*) were lower in magnitudes over the interaction component *i* and *l* for all the crosses indicating high proportion of interaction component i.e., the role of epistatic components in the inheritance of this trait and the possibility of obtaining the desirable segregants through intermating in early generations by breaking the undesirable linkage for handling the above crosses for rapid improvement. The negative sign of the *i* component indicates decrease in plant height in successive generations. The *h* and *l* components were opposite in direction revealing the presence of duplicate type of interaction in all the crosses except YLM 93 x YLM 92. Results of the current finding are in accordance with Senthilkumar and Ganesan (2004), Sharmila *et al.* (2007) and Sundari *et al.* (2012).

### Number of primary branches per plant

The mean performance for primary branches per plant in five crosses is presented in Table 1. The cross YLM 96 x YLM 92 recorded the highest number of primary branches per plant in all the generations, while YLM 93 x YLM 92 recorded the lowest F<sub>1</sub> mean value; YLM 93 x YLM 92 recorded the lowest F<sub>2</sub> mean value; YLM 89 x YLM 92 and YLM 90 x YLM 92 showed lowest values in F<sub>3</sub> generation. The F<sub>1</sub> mean values were higher over both the parents in all the crosses indicating the role of dominant genes of the two parents in the expression of the trait. The segregating generations showed lesser mean values compared to F<sub>1</sub> mean values indicating the presence of dominant epistatic interactions in the expression of the trait. The mean values of segregating generations were very closer to the F<sub>1</sub> mean revealing the role of linkage or complementary factors or both.

The estimates of scaling tests and gene effects in five parameter model are given in Table

Table 2. Estimates of scaling tests and gene effects in 5 parameter model for the five crosses in Sesame.

S.No.	Crosses	Scaling Tests		Gene Effects in 5 Parameter Model Scaling test					Type of Epistasis
		C	D	m (Hayman)	d (Hayman)	h (Hayman)	i(Add x Add)	l(Dom x Dom)	
1.	YLM 89 x YLM 92	2.29 **	2.21 **	36.740 **	0.16	-2.09 **	-0.76 **	-0.10	C
2.	YLM 90 x YLM 92	0.41	1.19 **	36.603 **	0.50 **	-1.72 **	0.27	1.04	D
3.	YLM 93 x YLM 92	0.69 *	0.06	36.737 **	0.62 **	-1.05 **	1.32 **	-0.84 *	C
4.	YLM 95 x YLM 92	0.90 **	2.35 **	36.600 **	0.25	-2.16 **	-0.91 **	1.93 **	D
5.	YLM 96 x YLM 92	0.25	2.13 **	36.917 **	0.54 **	-1.75 **	-0.29	2.51 **	D
<b>Days to 50% flowering</b>									
1	YLM 89 x YLM 92	5.81 **	0.75 *	77.70 **		-0.36 **	0.46	-6.74 **	C
2	YLM 90 x YLM 92	-2.14 **	-0.88 **	76.38 **	0.83 **	-0.93 **	1.89 **	1.68 **	D
3	YLM 93 x YLM 92	3.94 **	2.20 **	76.82 **	-0.33 **	-1.80 **	-1.47 **	-2.32 **	C
4	YLM 95 x YLM 92	-1.02 **	0.88 **	76.32 **	0.83 **	-2.59 **	0.90 **	2.54 **	D
5	YLM 96 x YLM 92	-2.10 **	1.95 **	77.93 **	0.91 **	0.09	0.18	5.40 **	C
<b>Plant height</b>									
1	YLM 89 x YLM 92	-4.68 **	0.10	95.36 **	-1.05 **	-5.35 **	-2.94 **	6.37 **	D
2	YLM 90 x YLM 92	-11.33 **	-7.23 **	93.61 **	0.48	-4.80 **	3.90 **	5.46 **	D
3	YLM 93 x YLM 92	-3.36 **	-3.61 **	98.55 **	0.63 *	-0.29 **	3.11 **	-0.33	C
4	YLM 95 x YLM 92	-0.87	4.78 **	94.82 **	-2.51 **	-7.88 **	-8.36 **	7.53 **	D
5	YLM 96 x YLM 92	-3.16 **	-6.26 **	99.13 **	0.65 *	2.52 **	4.94 **	-4.12 **	D
<b>Primary branches per plant</b>									
1	YLM 89 x YLM 92	-5.23 **	-1.83 **	3.46 **	0.017	-2.20 **	0.38 **	4.53 **	D
2	YLM 90 x YLM 92	-5.50 **	-1.66 **	3.36 **	0.03	-2.45 **	0.26 **	5.11 **	D
3	YLM 93 x YLM 92	-5.80 **	-0.86 **	3.23 **	0.03	-3.15 **	-0.32 **	6.57 **	D
4	YLM 95 x YLM 92	-4.03 **	-3.83 **	4.20 **	0.01	0.20 **	1.91 **	0.26 *	C
5	YLM 96 x YLM 92	-3.43 **	-3.76 **	4.36 **	0.01	0.28 **	1.97 **	-0.44 **	D
<b>Capsules per plant</b>									
1	YLM 89 x YLM 92	10.36 **	10.30 **	65.33 **	-1.78 **	1.04 *	-8.70 **	-0.08	D
2	YLM 90 x YLM 92	-0.30	28.03 **	62.20 **	-1.38 **	-14.28 **	-21.50 **	37.77 **	D
3	YLM 93 x YLM 92	5.66 **	29.06 **	63.63 **	-0.93 **	-15.00 **	-20.30 **	31.20 **	D
4	YLM 95 x YLM 92	-3.50 *	-1.70 **	63.30 **	0.45 **	5.13 **	1.45 *	2.40	C
5	YLM 96 x YLM 92	7.70 **	0.43	68.16 **	-0.01	10.64 **	0.96 *	-9.68 **	D

\* and \*\* represents 5% and 1% level of significance, respectively. Type of epistasis C = Complementary and D = Duplicate

2. The scaling tests were significant for all the crosses indicating the inadequacy of simple additive-dominance model and the importance of five parameter model to partition the gene effects. All the crosses recorded significant *m*, *h*, *i* and *l* components. The *d* component was non significant for all the crosses indicating the importance of additive component over dominant component. In the interaction components *l* component was higher in magnitude over *h* and *i* components except in the crosses YLM 95 x YLM 92 and YLM 96 x YLM 92. The interaction component was higher in magnitude over main effects (*d + h*) indicating the possibility of obtaining the desirable segregants through intermating in early generations by breaking the undesirable linkage for handling the above crosses for rapid improvement. The negative sign of *i* component in the cross YLM 93 x YLM 92 indicated that there would be decrease in the number of primary branches in the successive generation. The *h* and *l* components were opposite in direction indicating presence of duplicate type of interaction. Similar results were also reported by Sundari *et al.* (2012).

### Number of capsules per plant

The mean values of ten crosses over generations for capsules per plant are presented in Table 1. The range of  $F_1$  mean values varied from 63.93 (YLM 93 x YLM 92) to 71.06 (YLM 96 x YLM 92). Overall the crosses showed higher mean values in  $F_1$  over both the parents indicating the involvement of dominant genes of the parents. The mean values of  $F_2$  and  $F_3$  generations were lower over  $F_1$  generation (except the crosses YLM 90 x YLM 92 and YLM 93 x YLM 92 in  $F_3$  generation) indicating the role of dominant epistasis in controlling this trait. The  $F_3$  mean values of YLM 90 x YLM 92 and YLM 93 x YLM 92 indicate the presence of transgressive segregation for number of capsules per plant which may be exploited for developing high yielding genotypes. The mean values of segregating generations were very closer to the  $F_1$  mean values in the cross YLM 89 x YLM 92.

C and D components of scaling tests were significant (Table 2) indicating the importance of five parameter model in partitioning the gene effects. The *m*, *d*, *h*, *i* and *l* components were significant in all the crosses except YLM 96 x YLM

92 for additive component. Dominant component was higher in magnitude over additive component in all the crosses while *l* component was higher in magnitude over *i* component except in the cross YLM 89 x YLM 92. Interaction components (*i + l*) were higher in magnitude over main effects (*d + h*) in the crosses YLM 89 x YLM 92, YLM 90 x YLM 92 and YLM 93 x YLM 92 indicating the preponderance of epistatic interactions. Hence, desirable segregants may be isolated through intermating in early generation individuals by breaking the undesirable linkage for handling the above crosses for rapid improvement. The crosses YLM 95 x YLM 92 and YLM 96 x YLM 92 recorded positive *i* values indicating increase in number of capsules per plant in successive generations. The *h* and *l* components are in similar direction in the cross YLM 95 x YLM 92 indicating the existence of complimentary type of interaction, while other crosses recorded duplicate type of epistasis. These results for duplicate type of interaction are in concurrence with those of Senthilkumar and Ganesan (2004), Sharmila *et al.* (2007), Gaikwad *et al.* (2009) and Sundari *et al.* (2012).

### Number of seeds per capsule

The mean values of five crosses for number of seeds per capsule are given in Table 1. The  $F_1$  mean values ranged from 78.68 (YLM 93 x YLM 92) to 83.04 (YLM 95 x YLM 92). The  $F_1$  mean values of all the crosses were lower over the parents indicating preponderance of non allelic interactions in the expression of the trait. The segregating generations showed lesser mean values than the  $F_1$  mean values indicating the presence of dominant and epistatic interactions in the expression of this trait. The mean values of  $F_1$ ,  $F_2$  and  $F_3$  were very closer in the cross YLM 89 x YLM 92 revealing the existence of linkage or complementary factors or both in the expression of this trait.

The estimates of scaling tests and gene effects in five parameter model are presented in Table 2. The scaling tests were significant for all the crosses revealing the utilization of five parameter model in deciphering the gene effects into different components. The crosses YLM 90 x YLM 92 and YLM 93 x YLM 92 recorded non significant additive component while YLM 95 x

YLM 92 recorded non significant additive and dominant x dominant components. In general, the dominant component was higher in magnitude over additive component in all the crosses while additive x additive component was higher in magnitude over dominant x dominant component in all the crosses except in the cross YLM 96 x YLM 92. The main effects ( $d + h$ ) were lower in magnitude over interaction effects ( $i + l$ ) in the crosses indicating presence of dominance interactions in the expression of this trait. The  $i$  component was positive in all the crosses revealing increased number of seeds per capsule in successive generations. The type of epistasis was duplicate in all the crosses except YLM 95 x YLM 92 as  $h$  and  $l$  components showed opposite signs. Similar results were also reported by Senthilkumar and Ganesan (2004), Gaikwad *et al.* (2009) and Sundari *et al.* (2012).

### 1000 seed weight

The mean values of all the generations for this trait are given in Table 1. The  $F_1$  mean values of 1000 seed weight varied from 2.40 (YLM 90 x YLM 92) to 2.52 (YLM 96 x YLM 92). All the cross combinations of  $F_1$  generation showed lesser mean values compared to the parent ( $P_2$ ) indicating the role of non allelic interactions in the expression of this trait. The segregating generation ( $F_2$  and  $F_3$ ) recorded lower mean values over the  $F_1$  and the differences between the generations was minimum indicating the existence of linkage or complementary factors or both in the expression of this trait.

1000 seed weight estimates pertaining to scaling tests and gene effects in five parameter model are presented in Table 2. The scaling tests recorded significant values for C and / or D indicating inadequacy of simple additive-dominance model for partitioning the gene effects. The five parameter model for all the crosses recorded significant  $m$ ,  $d$ ,  $h$  and  $i$  components. The  $l$  component was significant only in the crosses YLM 93 x YLM 92 and YLM 96 x YLM 92. The additive component was higher in magnitude over dominant component for all the crosses while  $i$  component was higher in magnitude over  $l$  component in all the crosses except YLM 96 x YLM 92. The main effects ( $d + h$ ) were higher in magnitude over the

interaction components ( $i + l$ ) in all the crosses except YLM 96 x YLM 92 indicating the important role of main effects in the inheritance of this trait. The  $i$  component was in negative direction in all the crosses revealing decrease in weight with successive generations.  $h$  and  $l$  components had similar signs indicating complementary type of epistasis in all the crosses. These results for complementary type of epistasis are in agreement with Senthilkumar and Ganesan (2004) and Sundari *et al.* (2012).

### Oil content

The mean values for oil content over generations are presented in Table 1. The  $F_1$  mean values ranged from 46.01 (YLM 95 x YLM 92) to 48.14 (YLM 90 x YLM 92) and the  $F_1$  mean values were lower than the parents in all the crosses indicating the existence of non allelic interactions. The segregating generations ( $F_2$  &  $F_3$ ) showed decrease in mean values from  $F_1$  mean values.

The estimates of scaling tests and gene effects in five parameter model are given in Table 2. The scaling tests were significant in all the crosses indicating the importance of five parameter model for partitioning the gene effects. The gene effects were significant for all the crosses except YLM 90 x YLM 92 and YLM 96 x YLM 92 for  $l$  component. Dominant component was higher in magnitude over additive component in all the crosses while additive x additive was higher in magnitude over dominant x dominant component. The interaction component ( $i + l$ ) was higher in magnitude over the main effects ( $d + h$ ) indicating the role of epistatic interactions in the inheritance of the trait. Hence, desirable segregants may be isolated through intermating in early generation individuals by breaking the undesirable linkages for handling the above crosses for rapid improvement. The positive sign of  $i$  component in all the crosses indicates increase in oil content in successful generations. All the crosses showed opposite signs for  $h$  and  $l$  components indicating the existence of duplicate type of epistasis except the crosses YLM 89 x YLM 92, YLM 95 x YLM 92 and YLM 96 x YLM 92. These results are in agreement with the findings of Gadekar and Jambhale (2002) in case of safflower.

Table 2. contd.....

S.No.	Crosses	Gene Effects in 5 Parameter Model Scaling test					Type of Epistasis		
		Scaling Tests		Gene Effects in 5 Parameter Model Scaling test					
		C	D	m (Hayman)	d (Hayman)	h (Hayman)	i(Add x Add)	l(Dom x Dom)	
<b>Seeds per capsule</b>									
1.	YLM 89 x YLM 92	-7.95**	-12.68**	80.29**	0.76*	4.15**	8.66**	-6.30**	D
2.	YLM 90 x YLM 92	-7.86**	-14.12**	79.47**	0.35	4.27**	8.80**	-8.34**	D
3.	YLM 93 x YLM 92	-10.80**	-18.48**	78.31**	0.33	5.87**	11.19**	-10.24**	D
4.	YLM 95 x YLM 92	-5.84**	-4.200**	81.70**	0.28	1.58**	2.39**	2.19	C
5.	YLM 96 x YLM 92	5.40**	-6.08**	82.93**	-0.60*	3.31**	3.75**	-15.31**	D
<b>1000 Seed Weight (g)</b>									
1	YLM 89 x YLM 92	-0.45**	-0.45**	2.38**	-0.22**	0.04**	-0.23**	0.00	C
2	YLM 90 x YLM 92	-0.61**	-0.59**	2.36**	-0.18**	0.06**	-0.07**	0.02	C
3	YLM 93 x YLM 92	-0.53**	-0.47**	2.43**	-0.17**	0.06**	-0.12**	0.08	C
4	YLM 95 x YLM 92	-0.46**	-0.42**	2.44**	-0.19**	0.08**	-0.18**	0.05*	C
5	YLM 96 x YLM 92	-0.57**	-0.42**	2.43**	-0.17**	0.06**	-0.17**	0.20	C
<b>Oil content (%)</b>									
1	YLM 89 x YLM 92	-13.32**	-11.92**	45.46**	1.28**	3.14**	8.29**	1.86*	C
2	YLM 90 x YLM 92	-8.96**	-8.96**	46.50**	0.55**	3.28**	5.58**		
3	YLM 93 x YLM 92	-4.96**	-15.94**	47.56**	1.30**	7.20**	12.40**	-14.64**	D
4	YLM 95 x YLM 92	-17.20**	-11.19**	43.39**	0.56**	1.24**	5.72**	8.01**	C
5	YLM 96 x YLM 92	-16.16**	-16.02**	44.06**	0.90**	4.79**	9.78**	0.18	C
<b>Seed yield per plant (g)</b>									
1	YLM 89 x YLM 92	-1.29**	-0.16**	11.84**	-0.59**	0.67**	-1.29**	1.51**	C
2	YLM 90 x YLM 92	-3.69**	2.81	10.82**	-0.44**	-2.85**	-3.37**	8.67**	D
3	YLM 93 x YLM 92	-1.42**	-0.36**	11.57**	-0.25**	-0.37	-0.49**	1.42V	D
4	YLM 95 x YLM 92	-2.06**	-1.83**	12.09**	0.08	1.19**	1.04**	0.31	C
5	YLM 96 x YLM 92	0.68**	0.68**	13.12**	-0.16*	1.17**	-0.67**	0.00	C

\* and \*\* represents 5% and 1% level of significance, respectively. Type of epistasis C = Complementary and D = Duplicate



### Seed yield per plant

The five generations mean data was presented in Table 1. The range for seed yield per plant in  $F_1$  was 11.56 (YLM 90 x YLM 92) to 13.71 (YLM 96 x YLM 92). The  $F_1$  mean values were higher over both the parents in the crosses YLM 89 x YLM 92, YLM 95 x YLM 92 and YLM 96 x YLM 92 while the cross YLM 90 x YLM 92 showed  $F_1$  mean values more than the parent ( $P_1$ ) indicating the role of dominant gene effects of these parents in the expression of the trait. The segregating generations recorded lower values over the  $F_1$  indicating the operation of dominant epistasis in the expression of this trait and the values of segregating generations was very closer to the  $F_1$  mean values indicating the operation of linkage or complementary factors or both in the expression of this trait.

The estimates of scaling tests and gene effects in five parameter model are presented in Table 2. The scaling tests C and / or D are significant in all the crosses indicating the inadequacy of these tests and importance of five parameter model for partitioning the gene effects. All the crosses showed significant gene effects in five parameter model except YLM 93 x YLM 92 for dominance YLM 95 x YLM 92 for additive and dominance x dominance, YLM 96 x YLM 92 for dominance x dominance components.

The additive component was higher in magnitude over dominance component. The  $i$  component was higher in magnitude over  $l$  component in the crosses YLM 95 x YLM 92 and YLM 96 x YLM 92. The magnitude of interaction component ( $i + l$ ) was higher over main effects ( $d + h$ ) except YLM 96 x YLM 92 indicating preponderance of epistatic interactions in the expression of the trait. Hence, desirable segregants may be isolated through intermating in early generation individuals by breaking the undesirable linkages for handling the above crosses for rapid improvement. All the crosses recorded negative signs for  $i$  component except YLM 95 x YLM 92 revealing the decreased level of seed yield in successive generations. The  $h$  and  $l$  components were opposite in direction in the crosses YLM 90 x YLM 92 and YLM 93 x YLM 92 indicating the presence of duplicate type of epistasis in these crosses and complementary type of epistasis in

other crosses. Similar results for duplicate type of epistasis were also reported by Senthilkumar and Ganesan (2004), Sharmila *et al.* (2007), Gaikwad *et al.* (2009) and Sundari *et al.* (2012).

The generation mean analysis clearly indicated that five parameter model is highly useful for partitioning the gene effects as the scaling tests were significant for all the traits in all the crosses. The cross YLM 89 x YLM 92 showed significance for all the traits for all the components of five parameter model, except  $d$  component for days to 50% flowering and primary branches per plant,  $l$  component for days to 50% flowering, capsules per plant and 1000 seed weight. The traits days to 50% flowering, days to maturity, 1000 seed weight, oil content and seed yield per plant showed complementary epistasis which increases the heterosis for these traits in this cross.

The gene effects of five parameter model were significant for all the traits in the cross YLM 90 x YLM 92 except plant height, primary branches per plant and seeds per capsule for  $d$  component,  $i$  component for days to 50% flowering and  $l$  component for days to 50% flowering and 1000 seed weight. Complementary epistasis was recorded only for the trait 1000 seed weight while other trait showed duplicate type of gene interaction which tends to reduce the heterosis effect and as such is not desirable.

The cross YLM 95 x YLM 92 significant  $m$  and  $i$  for all the traits. The  $d$  component was significant except for primary branches per plant and seeds per capsule while  $h$  component was non significant for plant height and seed yield per plant. All the traits recorded significant  $l$  component except for plant height. The complementary type of interaction was noticed for the traits days to 50% flowering, days to maturity, plant height and 1000 seed weight indicating their usefulness in heterosis breeding for these traits improvement for this cross.

The  $m$ ,  $h$  and  $i$  components of five parameter model were significant for all the traits in the cross YLM 95 x YLM 92. The  $d$  component was significant for all the traits except for days to 50% flowering, number of primary branches per plant, number of seeds per capsule and seed yield per plant while number of capsules per plant, number of seeds per capsule, 1000 seed weight and seed yield per plant showed non significant  $l$

component. The traits days to 50% flowering, days to maturity and plant height had duplicate type of gene interaction for the expression these traits while other traits recorded complementary type of interaction.

The cross YLM 96 x YLM 92 recorded significant gene effects of five parameter model for all the traits except number of primary branches per plant and number of capsules per plant for additive component, days to maturity for dominant component, days to 50% flowering and days to maturity for additive x additive component and oil content and seed yield per plant for dominance x dominance component. Complementary type of interaction was observed for the traits days to maturity, 1000 seed weight, number of seeds per capsule revealing the use of heterosis breeding for these traits improvement in this cross.

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