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RESEARCH ARTICLE

GENE EFFECTS FOR YIELD AND FATTY ACIDS IN Sesamum

***Rajput, S. D. and Kute, N. S.**

Department of Agriculture Botany, MPKV, Rahuri (Maharashtra)

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ABSTRACT

Generation mean analysis was carried out to study nature and magnitude of gene effects for yield, its component and fatty acid compositions in a cross of sesame (*Sesamumindicum* L.) The parents with their F_1, F_2, B_1 and B_2 were evaluated in replicated trail for ten quantitative and four qualitative traits. The analysis showed that scales A, B and C were highly significant for all the traits, indicating the predominance of non-allelic interactions or epistasis of Additive x Additive (i) and Dominance x Dominance (l) for almost all the characters in the cross. Predominance of non-additive (dominance) gene action was prevailed in the expression of seed yield/ plant, its components and fatty acid compositions with duplicate type of epistasis in the cross investigated. Hence, selection should be delayed until virtual homozygosity is attained to achieve the improvement in these traits.

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INTRODUCTION

Among the five vegetable oilseeds sesame (*Sesamumindicum* L.) ranking second after groundnut is preferred for its oil and protein in seed. Though India ranks first in area under sesame cultivation in the world. The productivity is very poor (304 Kg/ha) due to lack of stable high quality seeds with desirable attributes. Sesame is valued not only for its nutritive value but also for its quality and quantity of its oil (44-52%), which is rich in Vit. E and also contains significant levels of Linoleic acid which controls blood cholesterol levels. The protein content is about 26.5% (Mosjidis, 1982). Production of sesame seeds can be accomplished either through cytoplasmic male sterility or by emasculation and crossing. The emasculation and crossing is the preferred method in sesame seed production. For genetic improvement of the crop the breeding methods to be employed depends mainly on the nature of the gene action involved in the expression of quantitative trait. Line x Tester analysis is used to select parents based on their combining ability but cannot detect epistasis. The presence or absence of epistasis can be detected by generation mean analysis using the scaletest. For this purpose there is a need to augment its productivity through the development of high yielding varieties. The present study was undertaken to understand the gene effects involved in inheritance of various quantitative traits in sesame to provide a basis for an evaluation of selection methods for the improvement of sesame population.

****Corresponding author: Rajput, S. D.,***
Department of Agriculture Botany, MPKV, Rahuri (Maharashtra)

MATERIALS AND METHODS

The experimental material for this study consists of a cross*viz*JLS-120 x VRI $(sv)_2$was effected using the parentsJLS-120and VRI $(sv)_2$ by hand emasculation and pollination to study the genetics of traits imparting seed yield, its components and fatty acids compositions, for raising F_1 generation during kharif 2011. The selfing of F_1 generation and back crosses were effected to obtain enough self seed and back cross generations during summer 2012. The parents with their F_1, F_2, B_1 and B_2 were evaluated in replicated trail during *Kharif* 2012.The segregating and non-segregating parental populations were cultivated in a Randomized block design with two replications at Post Graduate Research Farm of Department of Botany, Mahatma Phule Agricultural University, Rahuri during *kharif* 2012. The observation recorded on ten randomly selected plants in P_1, P_2 and F_1, 20 plants were randomly selected in F_2, B_1 and B_2.The traits assessed were days to 50 per cent flowering, days to maturity, Plant height (cm), Number of branches per plant, number of capsules per plant, length of capsule (cm), number of seeds per capsule, seed yield per plant (g), 1000 seed weight (g) ,oil content (%), oleic acid content (%), lenoleic acid content (%), palmatic acid content (%) and steric acid content (%). The mean values, standard errors and variances of the different

generations were subjected to weighed least-squares analysis using the scaling test (Mather 1949) and the joint scaling test to estimate gene effects. The genetic effects were estimated using the models suggested by Mather and Jinks (1971) and Jinks and Jones (1958). The significance of the scales and gene effects were tested byusing the t-test (Singh and Chaudhary, 1985). The A, B and C scaling tests were carried out for fourteen traits indicated the presence of non-allelic interactions in almost all cases. The A and B scaling tests provided the evidence for the presence of additive x additive (*i*), additivex dominance (*j*) and dominance x dominance (*l*) type gene interactions. The C scaling test provided a test for typel epistasis. The type of epistasis was determined only when dominance (*h*) and dominance x dominance (*l*) effects were significant, when these effects had the same sign the effects were complementary while different signs indicated duplicate epistasis (Kearsey and Pooni, 1996). Indicators d / a, heterosis and inheritance of the trait in the broad and narrow sense were made by formulas of Mather (1949). The presence or absence of reproach action is calculated by the average of six generations (P_1, P_2, F_1, F_2, BCP_1, BCP_2) and verified by the formulas:

A = 2 * Δ VSR1 - Δ P1 - Δ F1
B = 2 * Δ BCP2-Δ P2-Δ F1
C = 4 * Δ F2 - 2 * Δ F1 - Δ P1 - Δ P2

RESULTS AND DISCUSSION

The mean and standard error of the six generations for fourteen traits are presented in Table 1, with the means values for the scaling joint scaling tests and their interaction effects being presented in Table 2,3. The hybrids performed better than their respective parents in the cross except days to 50% flowering, days to maturity, oil content, oleic acid (%),and lenoleic acid content cross showing inferior performance than their respective P_1parent while parentP_2 showed superior performance in regard to length of capsule, oil content and steric acid content, cross showing inferior performance than their respective parent $P_1$and parent P_2 showed superior performance in regard to 1000 seed weight. The expected mean (*m*) of the three possible homozygotes was positive and significant in the crosses for all the traits. A simple additive/dominance model was adequate as inferred from the non-significance of all the scales for number of capsules per plant in the cross. While for all other characters in the cross, an epistaticdigenic interaction was found to be a suitable fit, since the scaling and/or joint scaling tests were significant. The additive, dominance and epistatic types of gene interaction in the cross for different trait were found to be different from each other. The dominance x dominance (*l*) interaction was larger than the additive x additive (*i*) and additive x dominance (*j*) effects put together, while for the main effects the dominance component (*h*) was greater than the additive (*d*) component. The dominance (*h*) and dominance x dominance (*l*) effects were in the opposite direction, suggesting that duplicate-type epistasis occurred in most cases and indicating predominantly dispersed alleles at the interacting loci (Jinks and Jones 1958). Dominance gene effects were found to be relatively more important, as indicated by the fact that in all cases the *dominance* (*h*) values were higher than the additive (*d*) values. The 'days to 50% flowering' trait for the cross showed a pronounced additive, dominance and non-allelic interaction additive x additive (*i*) type gene interaction. For this trait the dominance (*h*) and additive x additive (*i*)gene interaction were found to play a major role. The components (h, l) are opposite and highly significant in the crosssuggesting the duplicate epistatic interaction**.** Importance of non additive component was also reported by earlier worker Sumathi and Muralidharan (2008). The 'days to maturity' trait for the cross showed a pronounced additive, dominance and non-allelic interaction additive x additive (*i*) type gene interaction. Additive (d) and additive x additive (*i*) gene interaction were found to play a major role for this trait. Duplicate epistas is and the predominance of additive gene action was appeared for this trait which confirms the earlier findings Ramesh *et al*. (1995), Kumar and Vivekanandan (2009), Parameshwrappa *et al.* (2009), Yamanura *et al.* (2009) and Kumar *et al.* (2012). In case of plant height trait the additive x dominance (*j*) and dominance x dominance (l) gene effects were significant in the JLS-120 x VRI $(sv)_2$ cross, and this trait showed complementary type epistasis. Although additive x additive (*i*), additive x dominance (*j*) and dominance x dominance (l) gene effects were significant for the 'plant height' trait non-additive gene effects appear to have been more important, this predominance of dominant gene action is in accordance with the earlier reports of Kumar and Vivekanandan (2009), Parameshwrappa *et al.* (2009), Yamanura *et al.* (2009) and Kumar *et al.* (2012). Duplicate epistasis were reported by Kumar and Ganesan (2004) for this trait. For the 'number of branches per plant' trait the dominance gene component (h) and additive x dominance (j) effect were found to be the most important in the JLS-120 x VRI $(sv)_2$ cross. Duplicate type epistasis was predominance in the cross. Duplicate type of epistasis was also reported for this trait by Kumar and Vivekanandan (2009) Parameshwrappa *et al.* (2009), Yamanura *et al.* (2009) and Kumar *et al.* (2012).

In regard to the 'number of capsules per plant' trait dominance gene effects were found to be relatively more important because of the dominance (*h*) values were higher than the additive (*d*) in the cross. A simple additive-dominance model being adequate for this trait in the cross. Duplicate epistasis were also reported for this trait by Kumar and Ganesan (2004), Vijayarajan *et al*. (2007) and Gaikwad *et al*. (2009). The dominance effects and gene interaction dominance x dominance (*l*) were observed for length of capsule in the JLS-120 x VRI $(vs)_2$ cross with complementary epistasis. The preponderance of dominance (h) and dominance x dominance (l) gene actions revealed their potential in controlling this character, which supports the findings of Bakheit *et al.* (2001), Kumar and Ganesan (2004), Kumar and Vivekanandan (2009) and Sundari *et al.* (2012). The dominance effects and gene interaction dominance x dominance (*l*) were observed for number of seeds per capsules in the JLS-120 x VRI $(sv)_2$ cross with complementary epistasis. Non-additive gene action was appeared to be predominant in the expression of this character as has been reported by earlier workers Ramesh *et al*. (1995), Kumar and Ganesan (2004) and Kumar *et al.* (2012). Duplicate kind of epistatic interaction was prevailed in both crosses. Similar finding were also reported by Sumathi and Muralidharan (2008) and Gaikwad *et al*. (2009). For the 'seed yield per plant' trait dominance gene effects were found to be relatively more important because of the dominance (*h*) values were higher than the additive (*d*) in the cross. Non-allelic additive x additive (i) interactions and duplicate epistasis were observed for this trait in this cross. The dominance (*h*) and dominance x dominance (*l*) gene effects showed opposite signs, indicating the presence of duplicate dominant epistasis in the expression of this traitsimilar results also reported for

Table 1. Mean performance of different generations in JLS-120 X VRI(sv)$_2$ cross of Sesamum

Generations	No. of days to 50 % flowering	Days to maturity	Plant height (cm)	No. of branches per plant	No. of capsules per plant	Length of capsule (cm)	No. of seeds per capsule	Seed yield per plant (g)	1000 seed weight (g)	Oil content (%)	Oleic acid (%)	Lenoleicacid (%)	Palmatic acid (%)	Steric acid (%)
P_1	32.50	79.25	113.30	3.75	89.10	3.11	64.70	12.33	3.05	46.70	46.46	48.04	10.04	4.58
	±0.38	±0.23	±0.74	±0.10	±3.12	±0.01	±0.56	±0.48	±0.01	±0.28	±0.07	±0.13	±0.01	±0.01
P_2	47.80	93.60	135.65	4.60	83.50	2.44	56.25	12.63	2.40	41.02	38.42	42.66	7.62	3.56
	±0.17	±0.15	±0.88	±0.21	±2.24	±0.01	±0.46	±0.41	±0.04	±0.29	±0.03	±0.04	±0.08	±0.01
F_1	33.95	80.00	125.40	5.20	127.65	3.13	71.85	18.30	3.10	45.41	36.46	46.66	10.46	4.84
	±0.23	±0.24	±2.17	±0.21	±4.65	±0.01	±0.53	±0.32	±0.01	±0.07	±0.04	±0.09	±0.03	±0.03
F_2	37.38	84.15	116.40	4.55	109.20	2.63	62.70	20.36	3.03	44.04	40.25	44.33	10.52	4.23
	±0.77	±0.83	±2.15	±0.16	±4.03	±0.04	±0.65	±0.63	±0.02	±0.34	±0.40	±0.60	±0.12	±0.07
B_1	38.50	85.25	117.50	5.10	104.82	2.66	62.72	19.41	2.69	43.87	38.60	47.35	11.58	4.54
	±0.12	±0.23	±0.93	±0.17	±2.61	±0.02	±0.30	±0.42	±0.01	±0.02	±0.04	±0.16	±0.01	±0.02
B_2	42.13	88.10	118.25	4.40	111.95	2.78	61.62	20.38	3.02	41.89	41.10	47.20	11.28	4.14
	±0.16	±0.14	±1.07	±0.13	±1.99	±0.02	±0.27	±0.47	±0.02	±0.08	±0.07	±0.01	±0.01	±0.01

Table 2. Scaling tests of generation means of sesamum cross JLS-120 X VRI (sv)$_2$ for yield, its components and fatty acid compositions

Characters	Scales			
	A	B	C	χ^2
1.Days to 50% flowering	10.55**	2.50**	1.30**	443.697**
2. Days to maturity	11.25**	2.60**	3.75**	405.874**
3. Plant height (cm)	-3.70**	-24.55**	-34.15**	72.196**
4. No. of branches per plant	1.25**	-1.00**	-0.550**	24.253**
5. No. of capsules per plant	-7.10	12.75	8.90	7.762
6. Length of capsule (cm)	-0.919**	-0.009	-1.304**	540.034**
7. No. of seeds per capsule	-11.10**	-4.850**	-13.85**	133.995**
8. Seed yield per plant (g)	8.189**	9.825**	19.889**	163.293**
9. 1000 seed weight (g)	-0.763**	0.542**	0.483**	1445.793**
10. Oil content (%)	-4.376**	-2.643**	-2.369**	277.725**
11. Oleic acid (%)	-5.730**	7.299**	3.209	5358.615**
12. Lenoleicacid (%)	0.002	5.087**	-6.692**	2455.907**
13. Palmatic acid (%)	2.659**	4.496**	3.510**	5301.172**
14.Steric acid (%)	-0.334**	-0.109**	-0.867**	59.689**

*, ** significant at 5% and 1% level, respectively

Table 3. Estimates of gene effects for yield and its components inJLS-120 X VRI $(sv)_2$ cross ofsesamum

Character		Component						Type of epistasis
		m	d	h	i	j	l	
1.	Days to 50% flowering	37.37**	-3.62**	5.55**	11.75**	4.02**	-24.80**	Duplicate
		(0.77)	(0.20)	(3.11)	(3.10)	(0.29)	(3.23)	
2.	Days to maturity	84.15**	-2.85**	3.67	10.10**	4.32**	-23.95**	Duplicate
		(0.83)	(0.27)	(3.36)	(3.35)	(0.30)	(3.52)	
3.	Plant height (cm)	116.40**	-0.75	6.82	5.90	10.42**	22.35**	Complementary
		(2.15)	(1.42)	(9.33)	(9.05)	(1.53)	(11.24)	
4.	No. of branchs per plant	4.55**	0.700**	1.82**	0.800	1.125**	-1.05	Duplicate
		(0.16)	(0.22)	(0.80)	(0.76)	(0.25)	(1.17)	
5.	No. of capsules per plant	89.55**	2.80**	40.50**	A	A	A	-
		(17.50)	(1.92)	(38.48)				
6	Length of capsule (cm)	2.62**	-0.11**	0.727**	0.375**	-0.455**	0.554**	Complementary
		(0.03)	(0.03)	(0.17)	(0.17)	(0.03)	(0.19)	
7	No. of seeds per capsule	62.70**	1.10**	9.27**	-2.10	-3.12**	18.05**	Complementary
		(0.65)	(0.41)	(2.81)	(2.74)	(0.54)	(3.33)	
8	Seed yield per plant (g)	20.36**	-0.97	3.93	-1.87	-0.81	-16.13**	Duplicate
		(0.63)	(0.63)	(2.87)	(2.83)	(0.70)	(3.69)	
9	1000 seed weight (g)	3.03**	-0.32**	-0.323**	-0.704**	-0.653**	0.925**	Duplicate
		(0.02)	(0.02)	(0.10)	(0.10)	(0.03)	(0.13)	
10	Oil content (%)	44.04**	1.97**	-3.09**	-4.65**	-0.86**	11.66**	Duplicate
		(0.34)	(0.09)	(1.41)	(1.39)	(0.22)	(1.49)	
11	Oleic acid (%)	40.251**	-2.498**	-7.626**	-1.641	-6.515**	0.072	Duplicate
		(0.41)	(0.08)	(1.65)	(1.65)	(0.09)	(1.68)	
12	Lenoleicacid (%)	44.330**	0.151	13.084**	11.78**	-2.54**	-16.86**	Duplicate
		(0.60)	(0.16)	(2.42)	(2.42)	(0.18)	(2.49)	
13	PalmaticAcid (%)	10.52**	0.296**	5.27**	3.64**	-0.918**	-10.80**	Duplicate
		(0.12)	(0.02)	(0.50)	(0.50)	(0.05)	(0.51)	
14	Steric acid (%)	4.23**	0.399**	1.194**	0.424	-0.112**	0.020	Duplicate
		(0.07)	(0.02)	(0.27)	(0.27)	(0.02)	(0.28)	

*, ** significant at 5% and 1% level, respectively

this trait by Kumar and Vivekanandan (2009) Parameshwrappa *et al.* (2009), Yamanura *et al.* (2009) and Kumar *et al.* (2012). The 'weight per 1000 seeds' trait was additive (d) and duplicate epistasis were important in the cross while additive (*d*), dominance x dominance (*l*) and additive x dominance (*j*) effects and duplicate epistasis were important in the cross. Earlier workers Kumar and Vivekanandan (2009) and Kumar *et al.* (2012) also revealed the importance of additive component for this trait. The oil content trait was under the influence of additive (*d*) and dominance x dominance (*l*) effects with duplicate epistasis in the cross. Earlier workers Kumar and Vivekanandan (2009) and Kumar *et al.* (2012) also revealed the importance of additive component for this trait. For oleic acid (%) content Dominance (h) component was high as compared to additive (d) component and additive x dominance (j) gene interactions predominated in theJLS-120 x VRI $(sv)_2$ cross. While, among digenic interactions dominance x dominance (l) gene interactions was predominated.

The dominance (h) and dominance x dominance (l) interaction *i.e.* non-additive gene action was appeared to be predominant in the expression of this character as has been reported by earlier workers Das and Samanta (1998), Das and Chaudhury (1999) and additive gene action was predominant in the expression of this character as has been reported by Mosjidis (1982). Forlenoleic acid (%) content Dominance (h) component was high as compared to additive (d) component in thecross studied. While among digenic interactions additive x additive (i) gene interactions were predominated in the cross studied for fatty acid compositions. Duplicate type of epistasis was detected for this trait in the cross. The dominance (h) and additive x additive (i) interaction was appeared to be predominant in the expression of this character. Similar finding have been reported by earlier workers, Das and Samanta (1998) and Das and Chaudhury (1999). Forpalmatic acid (%) content Dominance (h) component was high as compared to additive (d) component in the cross studied for this trait. While among digenic interactions additive x additive (i) gene interactions was predominated incross and detected Duplicate type of epistasis for this trait. The dominance (h) gene effects was appeared to be predominant in the expression of this character as has been reported by earlier workers, Das and Samanta (1998) and Das and Chaudhury (1999). For steric acid (%) content Dominance (h) component was high as compared to additive (d) component in the cross studied. While among digenic interactions additive x dominance (j) gene interactions predominated inJLS-120 x VRI $(vs)_2$ cross of fatty acid composition. Complementary type of epistasis was detected for this trait in the cross studied. The dominance (h) and additive x dominance (j) interaction *i.e.* non-additive gene action was appeared to be predominant in the expression of this character. Such results have been reported by earlier workers Mosjidis (1982), Das and Samanta (1998) and Das and Chaudhury (1999). Presence of non-additive gene for days to 50% flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, number of seed per capsule,1000 seed weight, seed yield per plant, oleic acid (%) content and steric acid (%) content indicating that conventional selection procedure may not be effective enough for improvement of yield.

Therefore postponement of selection in later generations or intermating among the selected segregants followed by one or two generations of selfing could be suggested to break the undesirable linkage and allow the accumulation of favour able alleles for the improvement of these traits. The different types of gene effects estimated provided a test for gene action and are useful for analyzing the genetic architecture of a crop so as to further improve desirable traits. The estimates obtained from a cross may be unique to that cross and may not be applicable to the parental population. Additive genetic variance formed the major part of the genetic variance for the important yield component trait except length of capsules, number of seeds per capsules and oil content. Therefore genetic improvement in the

'seed yield per plant' trait would be easier through indirect selection for a component traits such as the plant height, number of branches per plant, number of capsules per plant and1000 seed weight than through direct selection for seed yield itself.

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