Nature of Gene Action for Yield and Yield Related Traits in Sesame (*Sesamum indicum* L.) Genotypes

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Abstract

*An understanding of the nature of gene action is a prerequisite for any successful breeding program. The aim of this study was to determine the genetic system governing yield and yield related traits in sesame (***Sesamum indicum*** L.) genotypes. Ten sesame lines viz., EW002, BG006, EW023-2, EW006, EW003-1, EW019, Obsa, Dicho, Wama and EW010-1 were crossed in year 2011 in a complete diallel fashion. Seeds of all* F_1 *and their parents were planted at Wama research sub sites in Randomized Complete Block Design with three replications. Data for days to flowering, branches per plant, plant height, capsules per plant and seed yield per plant were recorded. The result of this study showed that additive and dominant gene effects were important for all the traits studied. Both maternal (c) and reciprocal (d) effects were significant for days to flowering and grain yields per plant. Medium narrow sense heritability was observed for plant height and branches per plant. In this study, the predominance of over dominance gene action was involved in all traits. This showed that there is high scope of heterosis breeding. On the other hand, recurrent selection is likely lead to overall population improvement of this crop for grain yield and yield related traits.*

Keywords: *Additive, Dominance, Gene effects, Genetic analysis, Inheritance*

Introduction

The choice of an efficient breeding procedure depends on the knowledge of the genetic system controlling the trait to be selected (Eshghi and Akhundova, 2009). An understanding of the nature of gene action is a prerequisite for any successful breeding program (Anyanga *et al.*, 2016). The main effort of sesame breeder is the detection of favorable genes and to assemble them into a particular genotype using the most suitable combination. So it is necessary to introduce different genes which are known to be yield contributor. The study of inheritance pattern and analysis of gene action is very important to make decision about selection of suitable parents.

The diallel analysis techniques developed by Hayman (1954 a, b) and

Jinks (1954, 1956) provide a reliable mechanism to properly understand the genetic system and gene action involved in the expression of important plant attributes. The diallel cross procedures provides statistical approach of genetic study which is widely used by breeders for analyzing metric traits in different species. It furnishes logical information about the genetic architecture of the plant and heredity behavior of the parameters under study in early generation like F_1 and F_2. It also describes how to measure additive and dominance variation and the relative dominance properties of the parental lines.

The study on the genetic analysis of sesame would help the breeder to formulate appropriate selection procedure for screening of these inbred lines and the evaluation of their progenies for various purposes (Swain *et al.*, 2001). It provides heritability estimates of the character, which helps to predict progress through selection. The character showing high heritability could be improved through direct selection. On the other hand, in the case of progenies involving a greater non-additive genetic variance including dominance, over dominance, epitasis and linkage; selection for desirable genotypes is not straightforward. There are number of biometrical approaches available to estimate genetic component of variations (Mather and Jinks, 1971) but there have been very few attempts to apply them to the phenomenon of genetic analysis of sesame. In Ethiopia, information on the inheritance of yield and yield related traits in sesame is lacking. Therefore, this experiment was designed to assess the nature and magnitude of gene actions controlling the inheritance of seed yield and yield related traits in sesame genotypes.

Materials and Methods

The experimental material comprised of ten morphologically and genetically diverse sesame genotypes viz., EW002, BG006, EW023-2, EW006, EW003-1, EW019, Obsa, Dicho, Wama and EW010-1. Varieties such as Obsa and Dicho are released cultivars while genotypes such as EW002, BG006, EW023-2, EW006, EW003-1, EW019 and Wama are elite breeding lines. These genotypes were primarily collected from Western part of Ethiopia. A single plant from each genotype was selected and multiplied in 2010 off-season to get pure lines. These ten genotypes were crossed in 10 x 10 diallel mating design including reciprocal crosses in 2011main cropping season. Seeds of all the F_1s and their parents were planted on 14th June 2012 at Wama testing sites of the Bako Agricultural Research Center (BARC) in a Randomized Complete Block Design (RCBD) with 3 replications. Wama has an altitude of 1436 meter above sea level (masl). Each plot consisted of a single row of 5 m length with 50 cm and 25 cm inter and intra row spacing, respectively. The seeds were drilled in each row at seeding rate of 5 kg ha^{-1}. Twenty days after planting, the plants were thinned out to adjust for required population per hectare. Nitrogen fertilizer in the form of Urea was applied as side dressing four weeks after emergence at the rate of 50 kg ha^{-1}. Hand weeding was carried out four times at two weeks interval starting twenty days after planting. Data for days to flowering was recorded on a plot basis while the remaining data were recorded on plant basis. Observations were made on ten randomly selected plants for branches per plant, plant height, capsules per plant, and seed yield per plant.

Analysis of variance (ANOVA) was performed as per the suggestions of Hayman (1954 a, b) and Jinks (1954,1956). In the first phase, formal analysis of variance of the diallel table divided the family mean effects into additive (a) and dominance (b) components. It also detects maternal (c) and reciprocal (d) effects. The dominance (b) component was further separated into directional dominance effects (b1, the mean deviation of the crosses from the mid parent values); effect due to unequal contribution of the dominance alleles by parents (b2) and the specific gene interaction (b3) which is termed as specific combining ability (Griffing, 1956a) and refers to those cases in which certain parental combinations perform relatively superior or inferior than expectation based on the average potential of the genotype involved. Each main effect was tested against its own interaction over blocks. If ‘c’ maternal difference was significant ‘a’ (additive effects) was retested against ‘c’. If ‘d’ reciprocal effects was significant ‘b’(dominant effects) and its components were retested against ‘d’.

The second step of analysis was the computation of the variance of each array (V_r), the covariance of all the offspring included in each parental array with the non-recurrent parents (W_r) and the variance of the parental means (V_0L_0). In addition, the means of the array variance (V_1L_1), the variance of the mean of array (V_0L_1) and the mean of the array covariance (W_0L_0) were also computed. The validity of the assumption regarding adequacy of additive dominance model was tested before undertaking any numerical analysis.

The genetic parameters such as E (environmental variance from analysis of variance), D (estimate of additive and some portions of additive x additive genetic variance), F (estimate of relative frequency of dominant and recessive alleles in the parent), H_1 and H_2 (estimate of dominance and dominance x dominance interactions, respectively), h^2 (dominant effect as algebraic sum over all loci in heterozygous phase in all crosses provides the direction of dominance i.e. positive sign shows that direction of dominance being towards parents and the negative sign shows towards off springs), $H^2/4H_1$ and $[(4DH_1)^{1/2} + F]/ [(4DH_1)^{1/2} - F]$ (KD/KR) provides the proportion of dominant and recessive genes in the parents, $(H_1/D)^{1/2}$, (as mean degree of dominance), and heritability in narrow sense were computed according to Mather and Jinks (1982). The correlation between parental order of dominance (Wr+Vr) and parental measurement (Yr) (r (Yr, Wr +Vr (the prediction for measurement of completely dominant and recessive parents) were also estimated as suggested by Mather and Jinks (1982). The minimum number of gene which exhibited some degrees of dominance and effective factor (k) were also computed as suggested by Hayman (1954a) , Jinks (1956) and Mather's (1949).

Results and Discussion

For all traits considered in the preset study, mean squares were highly significant, indicating that there is a considerable genetic variability among the parents and the crosses. In addition, these genotypes seem to have different genes controlling the investigated traits (Table 1). These results are also confirmed by earlier reports (El-Bramawy, 2010; Pham *et al.*, 2010). The Wr-Vr mean square was non-significant when tested against error mean square for five traits, indicating the validity of additive dominance model (Table 2).

Table 1.Mean squares values for five traits considered in the current study

Source of Variation	df	Mean squares				
		DF	PH	BP	CP	YP
Rep	2	130.04**	668.84**	71.61**	25632.67**	261.34**
Genotype	99	9.84**	324.18**	5.23**	3299.79**	42.231**
Error	198	4.2	199.30	2.08	1299.26	15.27

** Significant at p<0.01 level; df=degree of freedom, DF=days to 50% flowering; PH=plant height; BP=branches per plant; CP=capsules per plant and YP=yield per plant

Table 2. Results of analysis of variance for (Wr-Vr) in sesame genotypes

	df	Mean squares				
Source		DF	PH	BP	CP	YP
Rep	2	2.05	9779.42	5.87	36715554.9	93.3
Wr-Vr	9	2.29ns	5657.11ns	1.39ns	37003221.8ns	109.4ns
Error	18	3.00	4673.82	1.51	39604250.0	64.9

** Significant at p<0.01 level; DF=days to 50% flowering; PH=plant height; BP=branches per plant; CP=capsules per plant and YP=yield per plant

Hayman's ANOVA for studied traits were presented in Table 3. Item 'a' was significant for all traits except for days to 50% flowering, demonstrating that the additive genetic variance was important for these traits. Praveenkumar *et al.* (2012) were also reported additive gene effect for plant height, and seed yield per plant in sesame. Contrary to the present result, Sakhiya (2013) reported significant additive gene effect in sesame for days to 50 % flowering. Mather & Jinks (1982) observed maternal effects due to the significance of item 'c', which suggested that re-testing of 'a' against mean square of 'c'. After re-testing of 'a' against that of 'c', the significance level of 'a' item remained unchanged for branches per plant and yield per plant, demonstrating that maternal effects has not masked the effects of genes which were acting additively. Item 'b_1' was non-significant for all traits, indicating that dominance was ambi-directional for these traits. Among parents, asymmetrical gene distribution was evident due to significant of 'b_2' for days to flowering, plant height and branches per plant. This unequal distribution of dominant and recessive alleles genes clearly suggests that some parents have considerably more dominant alleles than others for these traits. On the other hand, the parents contained uniform distribution of dominant genes for capsule per plant and yield per plant as item 'b_2' was non-significant for these traits. For all traits, significance of 'b_3' items suggested that the genes with specific dominant gene effects were present. Item 'b' was highly significance for all traits, indicating the presence of dominant genes effects. Aladji Abatchoua *et al.* (2014)) also reported dominant gene action for these traits. For days to flowering, the reciprocal effects had masked the dominant genes as implied by the reduction to non-significant after retesting of b_2, b_3 and b items against item'd'. Maternal effects were exhibited due to significance of items 'c' for days to flowering, branches per plant and yield per plant. The presence of reciprocal effect was revealed by significance of 'd' for days to flowering, capsules per plant and yield per plant. The choice of female parent is critical in a breeding program (Arunga *et al.*, 2010). In the present study, both additive and dominant genes were involved in controlling the traits. Anyanga *et al.* (2016) also observed that both additive and non-additive gene actions were important for these traits.

Table 4 shows the estimates of genetic parameters for yield and yield related trait. The additive variance (D) was significant for plant height, branches per plant and yield per plant showing that successful selection could be practiced for these traits. The dominance variance component (H_1) was significant for all traits except for days to flowering, suggesting that, the non-additive type of gene actions were involved in the inheritance of these characters. Days to flowering, branches per plant, capsules per plant and yield per plant are under the influence of dominant gene effects as shown by the significant value of non-additive genetic effects (H_2). The higher value of H_1 than D revealed that, non-additive effects were more pronounced as compared to additive gene effects.

Table 3. Hayman's ANOVA table in 10x10 diallel cross of sesame genotypes considered in this study

Item		Days to 50% flowering			Plant height		Branches per plant		
	Df	MS	F- ratio	Retested against d	MS	F- ratio	MS	F- ratio	Retested against c
a	9	11.12	1.90ns		812.20	3.84**	16.48	16.55**	3.82*
b_1	1	9.60	2.09ns		98.61	1.40ns	7.89	13.94ns	
b_2	9	13.19	3.06*	1.37ns	728.35	4.79**	9.02	4.85**	
b_3	35	7.96	2.07**	0.83ns	282.50	1.86*	4.48	1.65**	
b	45	9.04	2.29**	0.94ns	367.59	2.49**	5.46	2.19**	
c	9	13.50	4.01**		232.00	0.61ns	4.32	3.02*	
d	36	9.60	2.22**		170.95	0.78ns	2.37	1.18ns	
Total	99	9.84			324.18		5.23		
a x B	18	5.85			211.61		1.0		
b_1 x B	2	4.58			70.58		0.66		
b_2 x B	18	4.28			152.72		1.86		
b_3 x B	70	3.85			151.69		2.72		
b x B	90	3.96			150.09		2.50		
c x B	18	3.37			356.64		1.43		
d x B	72	4.32			218.39		2.00		
B x interaction	198	4.2					2.08		

*, ** = significant at $P < 0.05$ and $P < 0.01$, respectively, B= block, df: Degree of freedom a = additive effects of genes; b =dominant effects of genes; b_1 = mean dominance effects; b_2 = additional dominance deviation due to the parents, b_3 = residual dominance effects; c=maternal effect; d=reciprocal difference

Item	Df	Capsules per plant			Yield per plant			
		MS	F- ratio	Retested against d	MS	F-ratio	Tested against c	Tested against d
a	9	4398.84	0.231ns		48.3	3.11**	16.1*	
b_1	1	2066.31	1.09ns		18.6	0.85ns		
b_2	9	2870.53	2.06ns		37.2	2.29ns		
b_3	35	3889.94	3.04**	3.59**	51.0	3.20**		2.9479**
b	45	3645.54	2.77**	3.36**	47.5	2.95**		2.7456**
c	9	2490.54	1.36ns		37.0	12.33**		
d	36	2795.15	2.58**		35.4	2.04**		
Total	99	3299.79			42.23			
a x B	18	18794.38			15.5			
b_1 x B	2	1880.64			21.8			
b_2 x B	18	1390.00			16.2			
b_3 x **B**	70	1277.74			15.9			
b x B	90	1313.60			16.1			
c x B	18	1818.63			3.0			
d x B	72	1083.27			17.3			
B x interaction	198	610.85			159.16			

*, ** = significant at $P < 0.05$ and $P < 0.01$, respectively, B= block, df: Degree of freedom a = additive effects of genes; b =dominant effects of genes; b_1 = mean dominance effects; b_2 = additional dominance deviation due to the parents, b_3 = residual dominance effects; c=maternal effect; d=reciprocal difference

The dominant effect (h^2) was significant and positive for yield per plant. The results indicated that the mean direction of dominance was positive for this trait. Sakhiya (2013) has also reported similar results in sesame. For days to flowering, branches per plant and capsules per plant, dominant gene effect was positive but not significant. The values of F were found be non-significant for capsule per plant and yield per plant, which indicated an equal distribution of dominant and recessive genes in the parents. Similar results have been also reported by Mothilal and Manoharan (2005) for seed yield per plant, and by Sakhiya (2013) for number of capsules per plant. The value of 'F' was negative for days to 50% flowering ,suggesting the this trait was under influence of recessive genes. The involvement of the environmental effects in the expression of all traits was revealed by the highly significant of environmental variance (E) for all traits except days to flowering. However, environmental variance was less than additive and dominant variances.The proportional value of $(H_1/D)^{1/2}$ indicated the control of over dominance gene action for all studied traits. This value suggested that the dominance component is relatively more important, so delayed selection in segregating generations should be preferred for the traits. Furthermore, this result showed plenty of possibilities for heterosis breeding in sesame. Significant over dominance for plant height, days to 50% flowering, number of capsules per plant, number of seeds per capsule and seed yield per plant were earlier reported by Praveenkumar *et al.* (2012). Biparental mating or recurrent selection in segregating materials followed by conventional selection scheme is likely to lead to improvement in the characters of the studied sesame genotypes. The proportions of dominant genes with positive or negative effects in parents $(H_2/4H_1)$ were different from 0.25 for all traits; hence, dominant genes having increasing and decreasing effects in these traits are irregularly distributed in parents.

The inferences drawn from the F value was also confirmed by the proportion of dominance to recessive alleles in the parents as measured by the value of KD/KR, which was more than unit for plant height, branches per plant, and capsules per plant and yield per plant. Symmetry of dominant and recessive allele's distribution in parents is further established by relative sizes of H_1 and H_2.The value of H_1 and H_2 were not equal for all traits, indicating the asymmetric distribution of dominant and recessive genes. The value of K (h^2/H_2) was greater than one for yield per plant, suggesting that more than one group of genes exhibiting dominance governed that character. For the other traits, value of K was less than one. Thus, the value of K did not provide any valid interpretation for all the traits about the group of genes exhibiting dominance. The ratio could be under estimated when the dominance effects of all the genes concerned are not equal in size and distribution, when the distribution of genes is correlated (Jinks, 1954), or when the complementary gene interactions occur (Mather and Jinks, 1971). Parents possess mostly negative genes in dominant form for branches per plant, capsule per plant and yield per plant as indicated by the positive correlation between parental value (Yr) and recessive factor (Wr + Vr) . These results are in harmony with the findings of El-Bramawy (2010).The association of these yield components with recessive genes might present some difficulties for selection during the early generations. On the other hand, the increasing genes were dominant for days to flowering and yield per plant as revealed by negative correlation between parental value (Yr) and recessive factor (Wr+Vr).

Narrow sense heritability ranging from 6.3 to 25% was observed for all traits, which suggested the need for population improvement or a good scope for the development of hybrids. Low narrow sense heritability was detected for seed yield per pant and days to flowering. Medium heritability was noticed for plant height and branches per plant. On the contrary, Vekaria *et al.* (2015) had reported high narrow sense heritability for plant height and branches per plant in sesame. In the present study, since non-additive genetic effects played major role along with low to medium heritability for the traits, little response to selection is expected in the early generations.

Table 4. Estimates of genetic parameters for yield and yield related traits in sesame genotypes

Genetic parameters	DF	PH	BP	CP	YP
D	2.207±3.96	64.95 ± 31.13**	1.44±0.36**	562.6±520.12	7.86±3.9**
H_1	10.68±8.43	239±66.25**	3.453±0.77**	2417±1107**	25.054±8.3**
H_2	14.57±7.16**	107.84±56.31	1.792±0.66**	2794' 92 ±940.94**	19.87 ± 7.02**
h^2	1.5±4.79ns	-12.60±37.68	0.61±0.44	126.08±629.64	33.87±4.7**
F	-2.42±9.13	149.98±71.82**	2.194±0.84**	0.36±12.00	11.008±9.0
E	1.82±1.19	58±9.38**	0.926±0.11**	514.19±156.82 **	5.91 ±1.2**
Proportional Values					
$(H_1/D)1/2$	2.19	1.92	2.232	2.072	1.785
$H_2/4H_1$	0.341	0.112	0.129	0.289	0.198
KD/KR	0.63	4.008	2.931	1.003	2.290
K (h^2/H_2)	0.1029	-0.116	0.340	0.45	1.704
r(Yr,Wr +Vr)	0.16	-0.74*	0.20	0.20	-0.33
Heredity coefficients:					
h^2ns (%)	6.3	21.4	25.0	7.1	9.0

ns, ** , non-significant and significant at 0.01 levels, respectively; DF=days to 50% flowering ,PH= plant height , BP=branches per plant, CP=capsules per plant, YP= yield per plant ;D=estimate of additive variance H_1 and H_2= (estimate of dominance and dominance x dominance interactions, respectively), h^2 =dominant effect as algebraic sum over all loci in heterozygous phase in all crosses provides the direction of dominance i.e. positive sign shows that direction of dominance being towards parents and the negative sign shows towards offsprings),E= environmental variance from ANOVA), F= estimate of relative frequency of dominant and recessive alleles in the parent).

Conclusion

For all traits, the result of the current study showed that both additive and dominant gene effects were important in sesame genotypes considered. Days to flowering, branches per plant and yield per plant were significantly controlled by maternal and reciprocal effects. Reciprocal effects were important for traits viz., days to flowering, capsules per plant, and yield per plant. For plant height and branches per plant, medium narrow sense heritability was observed. Over dominance was predominant in all traits and hence recurrent selection scheme is likely to lead to improvement of the crop for yield and yield related traits. Generally, the present study indicated that, there is high scope of heterosis breeding for grain yield in sesame genotypes.

Acknowledgements

The author acknowledges the financial support provided by Rural Capacity Building Project and also Bako Agricultural Research Center for all supports provided during the time of executing of this experiment.

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