

Estimates of Gene Action and Interrelationships Among Yield Characters in Diallel Crosses of Sesame (*Sesamum Indicum*, L.)

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Abstract:

The present investigation was carried out during 2011 and 2012 summer seasons at Shandaweel Research Station Sohag. Eight genetically diverse sesame genotypes were used for this study. All possible crosses among parents, without reciprocals, were done to make a diallel series of twenty eight hybrids. A randomized Complete Block Design with three replications was adopted. The major objectives of this work are to estimate the genetic components for seed yield, studying the interrelationships among traits, using path coefficient and factor analysis to determine the important traits which can be used as selection criteria.

The additive genetic component "D" was significant in all studied traits. The dominance genetic components (H_1 and H_2) were significant in all studied traits except h_2 for plant height and seed yield/plant were insignificant. Moreover, the dominance component (H_1) was higher in magnitude than (D) component for all studied traits except 1000-seed weight, resulting in the average degree of dominance ($H_1 \setminus D$)^{1/2} which was more than one indicating over dominance for all studied traits.

The magnitudes of H_1 were larger than H_2 , resulting in ($H_2 \setminus 4H_1$) which was less than 0.25 for all studied traits except 1000-seed weight, indicating that positive and negative alleles of loci for these traits are not equally distributed among the parents.

The (F) component coupled with (KD\KR), was found to be positive in all studied traits, indicating an excess of dominant alleles genetic constitution of parental genotypes for these traits, resulting KD\KR value which was more than one for all studied traits except 1000-seed weight and capsule length.

High broad sense heritability values were obtained for all studied traits, while narrow sense heritability values were moderate.

Path analysis indicated that, number of pods/plant, fruiting zone length, and weight of 1000 seeds and their interactions seemed as the main sources of seed yield variation. It could be recommended from the previous results that, the important traits overall the three statistical (Correlation analysis, Path analysis and Factor analysis) procedures of analysis were number of pods/plant and weight of 1000 seeds. The two traits will enable breeders to develop high yielding sesame genotypes. Number of pods/plant is more important to plant breeders.

Keywords: *Sesame, diallel, gene action, heritability, Correlation, Path analysis, Factor analysis.*

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Introduction:

Sesame (*Sesamum indicum* L.) is an important ancient oilseed crop cultivated for its superior quality oil and protein. The total cultivated area in the world was 66,288,276 ha produced 4,092,236 tons, while in Egypt the cultivated area was 33,768 ha produced 44,427 tons (FAO 2011). Sesame seed contains up to 58% oil (Yermanos, 1980). The oil is demanded in the food industry because of its excellent cooking quality, flavor and stability. Therefore, knowledge of gene action is useful to plant breeder in three principal ways, viz., 1) selection of parents for hybridization, 2) the choice of breeding procedures for the genetic improvement of various quantitative traits, and 3) the estimation of some other genetic parameters (Singh and Narayanan, 2000).

Bakheit and Mahdy (1987) found that epistasis was detected for plant height and number of branches. With regard to D and H_1 , the inheritance of number of branches was mainly additive, while the dominance variation was more important in plant height. The narrow sense heritability values were high (0.88) for number of branches, while it was low or intermediate for the other traits.

Mahdy and Bakheit (1987) estimated the genetic parameters (D, F, H_1 , H_2 and h^2) for seed yield /plant. They indicated that the graphical analysis of F_1 and F_2 generations, and a test for epistasis ;both revealed the presence of non-allelic interaction for seed yield. The dominance genetic component (H_1) exceeded the additive one (D) for seed yield in the two generations.

Biswas and Akbar (1995) demonstrated that heritability in the broad sense was high for days to flowering (

89.20 %). It was suggested that number of branches / plant, 1000-seed weight and days to flowering were the most important characters for improving yield. El-Ahmar *et al.* (1996) reported that partial dominance was detected for plant height and number of branches; while seed yield/plant seed oil content exhibited over dominance. In all studied characters the results showed the importance of both additive (D) and dominance (H_1) genetic components except for oil content. Seed yield showed the lowest narrow sense heritability (9.34 %). Kumar and Sivasmy (1996) indicated that seed yield is explained by an epistatic model in 15 of the crosses and by an additive-dominance model in the other three.

Backiyarani *et al.* (1997) employed a diallel analysis, involving six parents of sesame and using data on six yield components, indicated significant additive and non-additive genetic effects for all studied traits. However, additive genetic variance was predominant for days to first flowering, plant height, number of primary branches, seed oil percentage and single plant yield. Mishra *et al.* (1997) indicated that high heritability estimates along with moderate to high genetic advance were observed for branches / plant. Also, Shanmugavalli and Vanniarajan (1988) showed that single plant yield had high heritability with high genetic advance.

Das and Gupta (1999) stated that additive genetic variance was of greater importance for number of primary branches/plant, number of secondary branches/plant and seed yield/plant, whereas additive and non-additive genetic variances were equally important for days to flowering and oil content. Arriel *et al.* (1999) found that the largest values

for heritability were recorded for plant height (73.68) and seed production (70.92), while the smallest (30.23) was for fruit number. On the other hand, Kamala (1999) found that plant height, branches/plant and seed yield/plant showed moderate to low heritability with non-additive effects in the form of dominance.

HobAllah *et al.* (2001) obtained high estimates of narrow sense heritability for stem height to first capsule, fruiting zone and branches/plant in the F₂ generation. However, the predominant of non-additive gene effects and low estimates of narrow sense heritability for capsules/plant and seed yield/plant in the F₁ generation. Hamouda (2001) concluded that additive genetic component (D) was significant for F₁ in days to flowering, height to first capsule, number of branches/plant, plant height and seed yield/ plant.

Kar *et al.* (2002) reported non-additive gene action was important for days to 50% flowering, branches/plant and seed yield/ plant.

Saravanan *et al.* (2003) reported that additive genetic variance was of greater importance for days to 50% flowering, plant height, number of branches/plant and oil content, while non-additive genetic variance played a major role for single plant yield.

Also, In the review of several studies concerning estimates of the genetic parameters, of sesame diallel crosses for yield and its attributes, Saravanan *et al.*, (2000 a and b), HobAllah, 2000; Abdel-Gawad *et al.*, 2002; Samar El-Shakhess, 2003 , El-Bramawy and Shaban, 2007 and Yolle *et al.* (2010).

The information of association between characters are of prime importance to the breeder, where they broadens the prospective with which

he can manipulate indirect selection for the economic characters and the possibility of selection for two or more characters simultaneously. Path coefficient and factor analysis could be used effectively in this respect by Reddy and Priya (1991), Babu and Sivasubramanian (1993) ,Fathy (1995) , Yolle, *et al.*, (2010),Reddy *et al.*(1984), Backiyarani *et al.*(1999) , Arulmozhi *et al.*(2001), Pawar *et al.*(2002), Siddiqui *et al.*(2005), Gnanasekavan *et al.*(2008), Ibrahim and Khidir(2012) and Jadhav and Mohrir (2012).

Therefore, the major objectives of this work are:

- 1- Estimating type of gene action, genetic ratios and heritability values for earliness yield and yield components in sesame.
- 2- Studying the interrelationships among traits, using path coefficient and factor analysis to determine the important traits which can be used as selection criteria.
- 3- Estimate the genetic components for seed yield and some of its attributes in sesame.

Materials and Methods:

The experiments reported herein were conducted at Shandaweel Agricultural Research Station, Sohag, Egypt, during 2011 and 2012 summer seasons to study the inheritance of yield and its related characters in sesame. Eight genetically diverse sesame (*Sesamum indicum*, L.) genotypes Table (1) were crossed in all possible combinations without reciprocals to make a diallel series of twenty-eight crosses, using hand emasculation and pollination as described by Yermanos (1980).

In 2011 season the eight genetically diverse sesame genotypes were crossed in a diallel fashion, excluding

reciprocals to obtain 28 F₁s. In the summer season of 2012, the parents, F₁ populations were sown on 22th May. The Randomized Complete Block Design with three replications was used. Each genotype was grown in a plot of 3 rows, 4meter long and 60cm apart, plant spacing was 20cm within rows. Plants were thinned to two plants /hill; the plot area was (6m²). The recommended cultural practices were adopted throughout the growing season. The following traits were measured on ten random plants in each plot.

- 1- Days to flowering: expressed as the number of days from sowing to the first flower appearance on 50% of plants.
- 2-plant height (cm): was measured as the distance, in centimeters, from the soil surface to the apex of sesame plant.
- 3-Fruiting zone height: length of fruiting zone in cm. from basic capsule to plant apex.
- 4- Number of capsules\plant.
- 5-Capsul length (cm): ten random capsules on individual plant were harvested at different sites on the plant and measured in centimeters.
- 6- Seed weight/ plant (g): was determined as an average seed weight in (g) on plant.
- 7- Thousand Seed weight (g): was estimated as an average of two samples of 1000-seeds on plot.

Statistical Analysis:

Gene action and heritability:

The diallel analysis proposed by Hayman (1954 a and b) was used to estimate the relative magnitudes of the genetic components of the total variability and to provide adequate infor-

mation on the genetic mechanisms by which traits are inherited.

The interrelationships among seed weight/plant and its related traits were studied overall the parents and crosses using three statistical procedures which differ in their mathematical background, goals and final outputs. These used models are summarized as follows:

1- Correlation analysis:

Simple correlation coefficients were computed among seed weight/plant and days to flowering, plant height, fruiting zone height, number of capsules\plant, capsule length , seed weight/ plant and 1000-Seed weight as suggested by Snedecor and Cochran (1981).

2- Path analysis:

Path analysis methodology was primarily proposed by Wright (1921 and 1934), that was rediscovered and used by Dewey and Lu (1959) in the agricultural research.

3- Factor analysis:

This approach was applied according to Catell (1965) to reduce a large number of correlated variables to a much smaller number of independent clusters of variables called factors. After the extraction of factors and their corresponding loadings are happened, the matrix of factor loadings was submitted to a Varimax Orthogonal Rotation, as applied by Kaiser (1958). The purpose of rotation was to rebuilding the larger loadings in each factor and to suppress the minor loading coefficient so as to improve the opportunity of achieving meaningful biological interpretation of each factor.

Table (1) .Origin and description of the different genotypes included in the experiment.

No	Genotype	Origin	Main description				
			No. of capsules / leaf axel	Branching habit	Seed colour	Shattering	Tolerant for welting disease
1	Shandaweel3	Egypt	Three	Non branched	White	Dehiscent	Tolerant
2	RH6F6	Egypt	Three	Branched	Cream	Indehiscent	Tolerant
3	Giza32	Egypt	Single	Non branched	Cream	Indehiscent	Tolerant
4	H. 107 Family6	Egypt	Three	Branched	Brawn	Indehiscent	Susceptible
5	H. 129 Family1	Egypt	Single	Branched	White	Indehiscent	Tolerant
6	Intro.602	U.S.A.	Three	Branched	White	Indehiscent	Tolerant
7	Intro.542	Ethiopia	Single	Non branched	Yellow	Indehiscent	Tolerant
8	Intro.553	U.S.A.	Single	Branched	White	Indehiscent	Tolerant

Results and Discussion:

Types of gene action genetic ratios and heritability.

Data of the eight parents and 28 F_1 s crosses were subjected to the diallel analysis proposed by Hayman (1954a and b) for seven traits comprising earliness and yield attributes.

The components estimated by diallel analysis as shown in Table (2) indicated that the additive genetic component "D" was highly significant for most studied traits, except for days to flowering and fruiting zone length. The value of " H_1 " which represents variation due to dominance components was highly significant for all aimed traits, indicating that both additive and non-additive gene effects were existed. The component of variation due to dominance effects adjusted for gene distribution " H_2 " was highly significant for all traits except plant height and seed yield/plant. Moreover, " H_2 " values were smaller to " H_1 " values for all traits studied, which complies with theoretical assumption of Hayman (1954 a and b) and could be a further proof for the unequal proportions of positive and negative alleles in the parents at all loci for each of studied traits, indicating unequal allele frequency. Similar results were also reported by El-Ahmer *et al* (1996), Ramesh *et al* (1998), Bakheit *et al* (2000), Saravanan *et al* (2000 a and b), Hamouda (2001) and Abdel-Gawad *et al* (2002).

The value of "F" which represents covariance of additive and dominance effects and determines gene symmetry was positive and highly significant for length of capsule, 1000-seed weight and seed yield/plant, revealing that there was asymmetric gene distribution with an excess of dominant alleles as com-

pared to recessive ones in the parents for these traits. On the other hand, the value of "F" was insignificant for the remaining characters, revealing that no excess of either dominant or recessive alleles was verified.

The overall dominance effect of heterozygous loci " h^2 " were highly significant for all traits except one, indicating that the dominance effects were mainly attributed to heterozygous phase in all crosses and that dominance was unidirectional for these traits. On the other hand, the value of " h^2 " was insignificant for plant height revealing that dominance was not unidirectional for this trait.

The environmental effects indicated by "E" values did not reach the level of significance for all traits except length of capsule and 1000-seed weight which were less or more sensitivity of these traits to environmental changes.

The average degree of dominance of each locus measured by the ratio $(H_1/D)^{1/2}$ was more than unity for days to flowering, plant height, fruiting zone length, length of capsule, 1000-seed weight and seed yield/plant, indicating the presence of overdominance in the expression of these traits, while this ratio was close to unity for length of capsule, suggesting the presence of complete dominance for this trait.

The ratio $(H_2/4H_1)$ was used to estimate the average frequency of positive vs. negative alleles in the parental genotypes. This ratio theoretically equal 0.25 when the distribution of positive equal negative genes among the genetic makeup of parents. As shown in Table (3), this ratio was less than 0.25 for all traits revealing asymmetric distributions of positive and negative alleles among parents.

The ratio of (KD/KR) that rep-

resents the total number of dominant to recessive alleles in the parents was more than unity for all traits, except for length of capsule and 100-seed weight where the ratio was near to unity. This indicates that the proportion of dominant alleles was greater for these traits.

Similar results concerning components of variation and ratios derived from Hayman analysis were obtained for one or more of the studied traits in sesame El-Ahmar *et al.*, 1996, Bakheit *et al.* (2000), Saravanan *et al.* (2000b), HobAllah, (2000), HobAllah *et al.* (2001), Abdel-Gawad *et al.* (2002), Samar El-Shakhess (2003) and El-Bramawy and Shaban (2007). High estimates of heritability values in the narrow sense (H_s) exceeding 50% were detected for days to flowering, plant height, fruiting zone length and seed yield/plant. These heritability values ranged from 50.64% for plant height to 52.84 to days to flowering, indicating the importance of additive and additive x additive gene effects in the inheritance of these traits and consequently the effectiveness of selection for im-

proving such traits in early segregating generations. However, moderate values of heritability in the narrow sense were obtained for number of capsules/plant, capsule length and 1000-seed weight ranged from 44.67 for 1000-seed weight to 48.54% for number of capsules/plant.

High estimates of heritability values in the broad sense (H_b) exceeding 98% were detected for days to flowering, number of capsules/plant and fruiting zone length while the other characters exhibited consistent high estimates of broad sense heritabilities as compared to their respective narrow sense values ranging from 80.29% for plant height to 86.76 % for length of capsule, indicating that dominance effects had prominent role in the inheritance of these traits. Similar results were obtained by Biswas and Akbar (1995), Mishra *et al.* (1997), El-Ahmar *et al.* (1996), Patil and Sherif (1996), Mishra and Yadav (1997), Jawar *et al.* (1998), Saravanan *et al.* (2000b), HobAllah *et al.* (2001), Abdel-Gawad *et al.* (2002) and Khan *et al.* (2007).

Table (2): Estimates of genetic components and ratios derived from a half diallel cross of sesame.

Genetic parameter	Days to Flowering	Plant height (cm)	Fruiting zone length (cm)	No. of Capsules/plant	capsule length (cm)	1000-seed weight (gm)	Seed yield/plant (gm)
D	4.852*	1057.047**	425.919*	627.176**	-17.637**	-7.664**	37.021**
H ₁	32.063**	2336.479**	1395.21**	1975.399**	-19.387**	-19.857**	103.749**
H ₂	-186.700**	1034.182	557.04**	1277.439**	-30.469**	-20.651**	-28.594
F	11.806	1475.919	656.488	707.647	-11.335**	-11.600**	57.255**
h ²	5144.674**	247.862	40064.35**	43074.22**	29.368**	22.133**	5.788**
E	7.905	171.945	7.905	7.905	7.905**	7.905**	2.141
(H ₁ /D) ^{1/2}	1.46	1.49	1.46	1.33	1.04	1.61	1.35
H ₂ /4H ₁	0.14	0.11	0.14	0.16	0.24	0.26	0.09
KD/Kr	2.31	2.77	2.31	1.93	0.97	0.96	2.59
Hn.s.	52.84	50.64	52.83	48.54	48.02	44.67	50.84
Hb.s.	98.59	80.29	98.35	98.75	86.76	84.6	86.48

*and ** denote significance at 0.05 and 0.01 probability level, respectively.

Correlation coefficients:

The correlation coefficients among all pairs of studied characters of sesame overall parents and crosses are presented in Table (3). Results showed that there was a highly significant positive association between seed weight/plant and each of weight of 1000 seeds (0.78**), number of

pods/plant (0.73**) and length of fruit zone (0.48**). It is suggested that seed weight/plant of sesame may be raised through the selection for one or more of these characters. However, insignificant associations were observed between seed weight/plant and each one of the remaining characters.

Table (3): Simple correlation coefficients among studied characters in sesame (n=36).

Characters	PH	LFZ	NPP	SI	LC	DF	SW/P
plant height (PH)	-						
Length of fruit zone (LFZ)	0.53**	-					
Number of pods/plant (NPP)	0.09	0.34*	-				
Weight of 1000 seeds (SI)	0.08	0.24	0.72**	-			
Length of capsule (LC)	0.22	-0.13	-0.07	0.06	-		
Days to flowering (DF)	-0.15	-0.21	0.12	0.03	0.16	-	
Seed weight/plant (SW/P)	0.29	0.48**	0.73**	0.78**	0.07	-0.09	-

*and**: Significant and highly significant at 0.05 and 0.01 probability levels, respectively.

On the other hand, the yield components exhibited various trends of associations among themselves. The correlation between plant height and length of fruiting zone was positive and highly significant being (0.53**). Number of pods/plant had highly significant and positive correlation

with weight of 1000 seeds (0.72**) and only significant positive association with length of fruit zone (0.34*). The correlation coefficients among the other traits were negligible and insignificant. These results are in agreement with those obtained by Sharma and Chauhan (1984a), Bakheit and Mahdy

(1988), El-Hifny *et al.* (1988), Fathy (1995) and Yolle *et al.* (2010).

It is important to indicate that the significance of some small correlation coefficients ($r < 0.5$) may be attributed to the large sample size of data ($n=36$).

In fact, selection decisions based only on correlation coefficient may not always be effective because it measures the mutual association between a pairs of traits neglecting the complicated interrelationships among other traits (Kang, 1994). Therefore, the simple correlation procedure may not provide a deep imagine about the importance of each component in the structure of seed yield. The path analysis can efficiently play this vital job role.

Path Analysis:

The matrix of direct and joint effects for the six characters on seed weight/plant is shown in Table (4). The maximum direct effect was obtained by weight of 1000 seed (0.495) followed by number of pods/plant (0.321) and length of fruiting zone (0.201). The positive direct effects of the previous mentioned characters in addition to their highly significant positive associations with seed

weight/plant indicated that the indirect selection for seed weight/plant through these characters would be effective for sesame improvement. However, plant height, length of capsule and days to flowering recorded low direct effects on seed weight/plant.

Considering the components of indirect effect, the marked part of plant height on seed weight/plant was only through length of fruit zone (0.107). Also, length of fruiting zone recorded two considerable components of joint effects on seed weight/plant via their associations with each of number of pods/plant (0.108) and weight of 1000 seeds (0.118). The joint effect of number of pods/plant was more important through weight of 1000 seeds recording (0.354). The weight of 1000 seeds recorded only one great component of indirect effects through the number of pods/plant being (0.229). All other values of indirect effects were very small and negligible. From the current results, it is concluded that, among the studied traits, length of fruit zone, number of pods/plant and weight of 1000 seeds had the greatest influence directly or indirectly upon seed weight/plant in sesame.

Table (4): Path analysis (direct and joint effects) of seed weight/plant and its related characters in sesame

Traits		
plant height Direct effects	(PH)	0.078
PH via Indirect effects	LFZ	<u>0.107</u>
	NPP	0.030
	SI	0.042
	LC	0.018
	DF	0.015
Total		0.29
Length of fruit zone	(LFZ)	<u>0.201</u>
LFZ via Indirect effects	PH	0.041
	NPP	<u>0.108</u>
	SI	<u>0.118</u>
	LC	-0.010
	DF	0.021
Total		0.48**
Number of pods/plant	(NPP)	<u>0.321</u>
NPP via Indirect effects	PH	0.007
	LFZ	0.068
	SI	<u>0.354</u>
	LC	-0.005
	DF	-0.012
Total		0.73**
Weight of 1000 seeds	(SI)	<u>0.495</u>
SI via Indirect effects	PH	0.007
	LFZ	0.048
	NPP	<u>0.229</u>
	LC	0.005
	DF	-0.003
Total		0.78**
Length of capsule	(LC)	0.082
LC via Indirect effects	PH	0.017
	LFZ	-0.025
	NPP	-0.021
	SI	0.032
	DF	-0.015
Total		0.07
Days to flowering	(DF)	-0.099
DF via Indirect effects	PH	-0.012
	LFZ	-0.043
	NPP	0.038
	LC	0.016
	SI	0.013
Total		-0.09

Residual effect

= 0.495

The coefficients of determination (CD) and relative importance (RI %) for the seed yield components of sesame are listed in Table (5). The results revealed that the greatest parts of seed weight/plant variation were explained by the direct effect for weight of 1000 seeds (23.53 %) followed by number of pods/plant (9.88 %) and length of fruiting zone (3.89 %). The valuable contributions of these three traits on seed weight/plant prove their magnitude as selection criteria in sesame breeding program. However, the other characters recorded small or negligible direct effects upon seed yield.

Regarding the relative importance of joint effects, it is obvious that their effective parts were obtained by length of fruiting zone on seed weight/plant through its associations with each of number of pods/plant (4.19 %) and weight of 1000 seeds (4.57 %). The highest value of the indirect effects was recorded by number of pods/plant via weight of 1000 seeds (21.08 %). Small values of relative importance ranging from 0.23 to 1.59 % were obtained by the other direct and indirect effects.

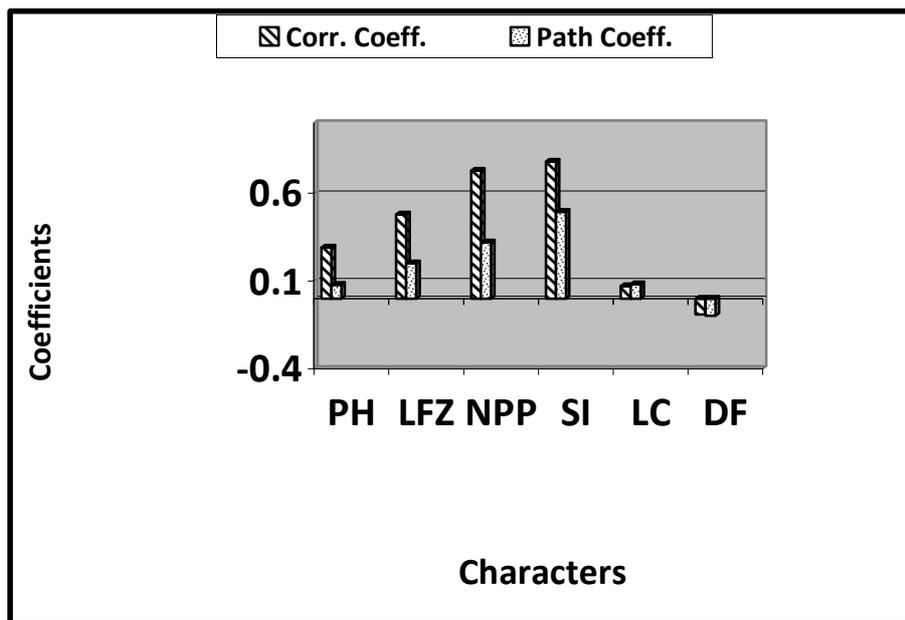
Table (5): The coefficient of determination (CD) and relative importance (RI %) according to path analysis of seed weight/plant and its components in sesame.

Charaters	seed weight/plant	
	CD	RI%
plant height (1)	0.006	0.579
Length of fruiting zone (2)	0.041	<u>3.889</u>
Number of pods/plant (3)	0.103	<u>9.877</u>
Weight of 1000 seeds (4)	0.245	<u>23.534</u>
Length of capsule (5)	0.007	0.641
Days to flowering (6)	0.010	0.938
1x2	0.017	1.590
1x3	0.005	0.445
1x4	0.006	0.620
1x5	0.003	0.269
1x6	0.002	0.227
2x3	0.044	<u>4.190</u>
2x4	0.048	<u>4.573</u>
2x5	-0.004	0.398
2x6	0.009	0.817
3x4	0.227	<u>21.802</u>
3x5	-0.003	0.327
3x6	-0.007	0.718
4x5	0.005	0.497
4x6	-0.003	0.310
5x6	-0.003	0.240
Residual Multiple determination	0.242	23.519

CD: Coefficient of determination
 RI: Relative importance

Totally, the studied characters accounted for 76.48 % of seed weight/plant variability. The residual content (23.52 %) may be returned to unknown factors (random error) and/or some other traits that were not included in the present study. The current results were in harmony with those obtained by Reddy and Priya

(1991), Babu and Sivasubramanian (1993) , Fathy (1995) Reddy *et al*(1984), Backiyarani *et al*(1999) , Arulmozhi *et al*(2001), Pawar *et al*(2002), Siddiqui *et al*(2005), Gnasekavan *et al*(2008), Yolle *et al*(2010), Ibrahim and Khidir (2012) and Jadhav and Mohrir (2012).



Factor analysis:

The factor analysis technique divided the six studied sesame yield components into three independent groups or factors which explained 77.4 % of the total variability in the dependence structure. The factors were constructed by applying the

principal component approach to establish the dependent relationship between seed yield attributes in sesame. Factor loadings that greater than 0.5 were considered important. Summary of the composition of variables of the three extracted factors with loadings are given in Table (6).

Table (6) : Summary of rotated factor loadings for six characters of sesame.

Characters	Loadings	% communality	Latent root	% Variance
Factor I				
Number of pods/plant	0.927	0.868	1.814	30.2
Weight of 1000 seeds	0.887	0.796		
Factor II				
Plant height	0.857	0.824	1.629	27.1
Length of fruit zone	0.782	0.752		
Factor III				
Length f capsule	-0.900	0.829	1.201	20.1
Days to flowering	-0.512	0.575		
Cumulative variance			4.64	77.4

Factor I included two variables which accounted for 30.2 % of the total variability. The two variables were number of pods/plant and weight of 1000 seeds that had high communality and large latent root exceeded 1 being 1.814. Factor II was made up of the plant height and length of fruit zone where they had high loading values. This factor accounted for 27.1 % of the total variability in the dependence structure and its eign value was grater than1 recording 1.63. Factor III was responsible for 20.1 % of the total variability where it included two characters namely: length of capsule and days to flowering. These results were in agreement with Engin Yolle, *et al* (2010).

Use of factor analysis by plant breeders has the potential of increasing the comprehension of the casual relationship of variables and can help to determine the nature and sequence of traits to be selected in a sesame breeding program.

Finally, it could be recommended from the previous results that, the important traits overall the three statistical procedures of analysis were number of pods/plant and weight of 1000 seeds. The two traits

will enable the breeders or agronomists to realize high yielding sesame genotypes. Number of pods/plant is more interest to plant breeder because it is relatively easy to visually be selected in the field.

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تقدير فعل الجين والعلاقة بين الصفات المحصولية في الهجن الدائرية للسمسم فنجري شحات صديق¹، وفاء وهبي محمد²

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أجريت هذه الدراسة في محطة البحوث الزراعيه بجزيرة شندويل - قسم بحوث المحاصيل الزيتية - مركز البحوث الزراعية خلال موسمي 2011 و 2012. وقد استخدم في هذه الدراسة ثمانية تراكيب وراثيه مختلفه من السمسم . تم التهجين بين الإباء بكل الطرق الممكنة وبدون الهجن العكسية لعمل 28 ونفذت تجربة التقييم التي اشتملت علي الإباء والجيل الأول. وقد استخدم تصميم القطاعات كاملة العشوائية في ثلاث مكررات. الهدف من الدراسه هو قياس المكونات الوراثية للمحصول والصفات المرتبطة به في السمسم.

كان المكون الوراثي المضيف D معنويا لجميع الصفات تحت الدراسة . اما المكون السيادي H_1 , H_2 كان معنويا لكل الصفات التي تم دراستها ما عدا H_2 في صفتي طول النبات ومحصول النبات الفردي، علاوة علي ذلك فان المكون السيادي H_1 اكبر من المكون الإضافي D لكل وكانت درجة السيادة (H_1/D) اكبر من الوحدة مشيرا الي سيادة فائقة لجميع الصفات ما عدا بعض الحالات .

كانت قيمة H_1 اكبر من H_2 وهذا نتيجة ($H_2/4H_1$) التي كانت اقل من 0.25 لجميع الصفات ما عدا صفة وزن الالف بذرة موضحة ان الاليات الموجبة والسالبة لتلك الصفات غير متساوية التوزيع بين الإباء .

أما المكون F فانه يتفق مع نسبة KD/KR فانه كان موجبا لكل الصفات تحت الدراسة مشيرا الي زيادة تكرار الاليات السائدة وهنا كانت نسبة KD/KR اكبر من الوحدة ما عدا بعض الحالات . تم الحصول علي درجة توريث عالية بالمعني العريض لجميع الصفات في حين كانت متوسطة بالمعني الضيق .

وقد اختلف توزيع الجينات السائدة والمتنحية بين التراكيب الوراثية للسمسم من صفة لأخري ومن أب لأخر .

أظهر تحليل المرور أن عدد الكبسولات للنبات ،طول المنطقه الثمريه و وزن الالف بذره والتفاعل بينهما هما المصدر الرئيسي للاختلافات في محصول البذور .

توصي النتائج السابقة بأهمية صفات عدد الكبسولات للنبات ووزن الألف بذره من خلال التحليلات الإحصائية الثلاث. هاتان الصفتان تمكن المربي من استنباط تراكيب وراثية عالية المحصول وأن صفة عدد الكبسولات للنبات مهمه جدا لمربي النبات.