J. Plant Production, Mansoura Univ., Vol. 9 (8): 695 - 702, 2018

Gene Action and Combining Ability for Seed Yield and its Components in Eight Sesame Genotyps Diallel Crosses

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ABSTRACT

In order to study the combining ability, type of gene action and partition the components of the genetic variance to its constituents of additive and dominance gene effects using half diallel cross for eight genotypes to produce twenty eight sesame crosses. Two field experiments were carried out during two summer growing seasons 2016 and 2017 at Arab El-Awammer Research Station, Assuit, Agricultural Research Center. Results showed that mean squares due to both general (GCA) and specific (SCA) combining ability were highly significant for all characters, indicating the importance of both additive and non-additive gene effects in the inheritance of studied traits. The ratio of GCA/SCA indicated that the largest part of the total genetic variability due to the additive and additive x additive was very important than the non-additive gene effects in the genetic variability for all studied traits. Estimates of GCA for eight parents revealed that P_8 was good combiner for plant height, length of fruiting zone, seed yield/plot and number of days to 50% flowering, while P_1, P_2 was good combiner for number of capsules/plant, seed yield/plant and 1000-seed weight. Significant SCA effects were observed for some crosses, cross (P1xP5), (P1xP7) and (P2xP3) were the best ones for seed yield/plant. Additive "D" and dominance (H_1 and H_2) genetic variation were significant for plant height and seed yield/plot. The "D" parameter estimating the additive effect was highly significant and was larger in magnitude than the dominance parameters (H_1 and H_2) in the all studied traits indicating that the type of gene action is partial dominance. The positive and negative alleles were unequally distributed among the parents. All studied traits had a high values for the broad sense than the narrow sense heritability. Graphical analysis revealed that the regression lines cuts Wr axis above origin point, indicating partial dominance for all the studied characters.

Keywords: *Sesamum indicum* L., *GCA, SCA, Hybrid vigor, Diallel and Combining ability.*

INTRODUCTION

In the world, sesame is one of the most important oil seed crops. It is cultivated in tropical and subtropical environments. In Egypt, sesame is careful as a food crop rather than on oil crop because most of its seeds expended straight, without oil extraction, in different confectionery purposes, bakery products, paste and other food industries. Therefore, the main problem of sesame in Egypt is the unstable production of the cultivated varieties. The total cultivated area was 32 thousand hectares of sesame were harvested worldwide and producing about 14 thousand tons of seeds in the world. In Egypt the cultivated area about 10 million hectares (23.8 million fed.) produced about 5 thousand tons of seeds (FAO, 2016).

In spite of doubling the yielding ability the past five decades increasing productivity remains one of the principal objectives of sesame improvements. The use of desirable parents with high yielding ability and quality characters in hybridization may affect the performance of their hybrids. The plant breeder is interested in estimating the gene effects in order to apply the most effective breeding procedure for improvement of the attributes in question. Moreover, the choice of the most efficient breeding methodology mainly depends upon the type of gene action controlling the genetic variation. Hence, information on the mode of inheritance of economic sesame characters, their genetic behavior and general and specific combining ability are highly important for sesame improvement.

Combining ability is frequently employed to identify the desirable genotypes for producing better recombination. If general combining ability having clear significant, the genetic variance should be due to additive gene effect. While, specific combining ability is due to genes with non-additive gene effects. If additive gene action was major importance, the most effective breeding procedures will be the inter-population selection (Griffing, 1956), while the hybrid program may be the better choice, if non-additive gene action playing the major rule in controlling such quantitative traits (Cockerhan, 1961).

In this respect, Hayman's analysis of diallel crosses was used to determine the genetic nature of yield and yield components in sesame. The genetic components were studied by many authors using this method and different conclusion was obtained. Mahdy and Bakheit (1988) found that additive x additive effect were small as compared to dominance and dominance x dominance effects for the most sesame traits. Chatchaval (1989) reported that dominance gene effect was more important than the additive effect for yield/plant. The results of Narkheda and Kumar (1991) revealed that the number of capsules/plant and yield/plant were generally controlled by dominance gene action. Reddy *et al*. (1992) found that the inheritance of seed yield was predominantly under the control of non-additive gene action. The results of Ramesh *et al*. (1995) and Ammar (1999) indicated that both additive and non-additive effects were important for capsules/plant and 1000-seed weight. Bakheit *et al*. (2000), HobAllah *et al*. (2001) and Saravanan *et al*. (2001) reported that over-dominance was found to be involved in the expression of 1000-seed weight, capsules/ plant and seed yield/plant. Ghada (2004) mentioned that additive gene action was the most important for all traits. Moreover, Ammar (2004) reported that variances for general combining ability was greater than specific combining ability for all studied characters except hight of the first capsule, indicating that additive gene action involved in controlling all studied traits, except hight of the first capsule.

The present investigation was designed to study the nature of gene action and to determine general and specific combining ability of yield and its components for eight diverse parents and their crosses in sesame and consequently identify the most efficient breeding procedure leading to maximum genetic improvement.

MATERIALS AND METHODS

In both two summer growing seasons of 2016 and 2017, this investigation was supported at Arab El-Awammer Research Station Farm, Agricultural Research

Center, Egypt. Eight parental sesame genotypes were used as plant materials for this study. Pedigree and origin of these genotypes are given in Table (1). In 2016 season, the eight parental genotypes were grown and they were crossed in all possible combinations except reciprocals to produce 28 F_1 hybrids using hand emasculation and pollination as described by Yermanos (1980).

Table 1. Name and Pedigree of the eight genotypes used in the experiment.

Item	Name	Origin	Pedigree
P1	H59i3-5	Egypt1968	S14*Mahally30
P2	H36i1	Egypt1965	Giza24*Shrtih95
P3	H88i8	Egypt1974	Local25*Intr.126
P4	Intr.554	FAO 1983	Unknown
P5	Intr.376	USA	Unknown
P6	Intr.263	USA	Unknown
P7	H102i36-2	Egypt1976	Giza25*Intr.217
P8	Shandweel3	Egypt	Giza32*Intr.314

In 2017 summer season, thirty-six entries (eight parents and twenty-eight hybrids) were sown in three replications at Randomized Complete Block Design (RCBD) with. Each genotype was established in a three rows, 4 meters length, and 60 cm apart with hills spaced 20 cm apart. After 19 days from the sowing date, plants were thinned, leaving two plants per hill. At harvest time, sampling of ten guarded plants at random were taken and dimensions were recorded for the following characters:

-No. of days to 50% flowering: Number of days from sowing to 50% flowering.

-Mean of plant height (cm): From the ground surface to the apex of the plant.

-The length of fruiting zone (cm): From the first capsule in the base to the last one on the top of the main stem.

-Mean number of capsules plant^{-1}.

-Seed yield plant^{-1} (g).

-Weight of 1000-seed weight (g).

-Seed yield plot^{-1} (g).

Before proceeding with the biometrical analysis, differences among genotypes were tested by running regular analysis of variance reported by Steel and Torrie (1980). The difference between parents and F_1 crosses was partitioned into general and specific combining ability as demonstrated by Griffing (1956) Method (2), fixed Model (1). Also statistical analysis were performed according to Hayman (1954a,b, 1957 and 1958). GCA: SCA ratio was estimated according to (Baker 1978) as follows:

$$\mathbf{GCA/SCA = 2MS_{gca} / (2MS_{gca} + MS_{sca})}$$

Broad and narrow sense heritability was estimated according to the formula suggested by Mather and Jinks (1971). The validity of diallel analysis assumptions made by Hayman (1954) was tested by the analysis of variance covariance for Wr, Vr following the formula proposed by Singh and Chaudhary (1979).

RESULTS AND DISCUSSION

Analysis of variance:

The analysis of variance (Table 2) indicated that highly significant differences among sesame genotypes including parents and their F_1 crosses for all the studied traits. It could recommended that parents selected were quite variable and adequate amount of variability existed among the hybrids for all of the studied traits. This indicated that both additive and non-additive gene action played a role in determining various traits. Thus, the importance of these two components of genetic variance cannot be underestimated for the improvement of sesame. These results provided evidence for presence of fair amount of genetic variability considered adequate for further biometrical assessment.

Table 2. Analysis of variance of eight sesame parents and their F_1 crosses for earliness, yield and its attributes traits in 2017 season.

S.O.V.	df	No. of days to 50% flowering	Plant height (cm)	Length of fruiting zone (cm)	Capsules No. plant^{-1}	Weight of 1000-seed (g)	Seed yield plant^{-1}(g)	Seed yield plot^{-1} (g)
Replication	2	5.778	38.4	65.9	44.59	0.102	1.702	977.5
Genotypes	35	33.46^{**}	3021.4^{**}	1522.6^{**}	2839.5^{**}	0.364^{**}	44.29^{**}	25360.8^{**}
Crosses	27	31.68^{**}	2743.4^{**}	1379.6^{**}	2298.9^{**}	0.299^{**}	37.91^{**}	22489.0^{**}
Parents	7	42.85^{**}	3782.0^{**}	1466.5^{**}	5251.1^{**}	0.641^{**}	70.04^{**}	38672.8^{**}
P vs C	1	15.79^{**}	5203.2^{**}	5776.3^{**}	554.5^{**}	0.18^{**}	36.3^{**}	9715.4^{**}
Error	70	3.34	119.3	196.6	162.2	0.038	4.062	277.9

***and **: Significant at 0.05 and 0.01 level of probability, respectively.**

Performance of the studied genotypes:

The performance of sesame parents for all calculated x characters were presented in (Table 3). A wide range of variation among the parental genotypes was observed. These results are in harmony with those obtained by Sharaan and Ghallab (1998), Aly (1999), Bayoumi (2003) and Ghada (2004).

The results showed that parent P2 had the lowest mean of days to 50% flowering (37.33 days), while Parent P8 possessed the highest values of plant height (223.33 cm) and fruiting zone length on the main stem (148.33 cm). However, parent P1 possessed highest number of capsule per plant (185.00 capsules), 1000-seed weight (4.47 g) and seed yield plant^{-1} (22.15 g) and also parent P5 was the best one for seed yield/plot. Then genotype P1 had the highest value for capsules number/plant, seed yield/plant and weight of 1000-seed.

Crosses data showed that, the earliest cross combinations were (P2 x P5) for days to 50% flowering, which possessed the lowest mean performance (35.67 day) depending on a minor gene complex. The best cross combinations were (P5 x P8) for plant height, (P3x P8) for the fruiting zone length, (P1 x P4) for number of capsules plant^{-1}, (P1 x P2) for thousand seed weight, (P1 x P3) for seed yield plant^{-1} and also the best cross (P5 x P8) for seed yield plot^{-1}, which recorded (230.00 cm, 161.67 cm, 196.33 capsules, 4.56 g, 23.73 g and 464.50 g, respectively). These crosses revealed the superior values over all their respective parents. The average number of the crosses revealed that the cross (P1xP4) for number of capsules plant^{-1} exceeded the average of the parents and the crosses indicating a positive heterotic effects. Regarding crosses included the parent P1 as a common parent showed the highest capsules number/plant, while the cross having P8 showed the lowest one. In general, the crosses (P1 x P2) and (P1 x P5) were considered as the best promising hybrids for yield and its traits. Also the crosses included the parent P1 showed the highest seed yield plant^{-1}. The present results confirm the findings of Ghada (1999), Babu *et al*. (2004), Kumar *et al*. (2004) and Mansouri (2016). Consequently, it should own the genetic factors for high yield potential, revealing their importance in sesame improving programs. These conclusions were in arrangement with who's reported by (Abd El-Kader *et al.,* 2017).

General and specific combining ability:

The analysis of combining ability has been utilized to know the nature and extent of gene action controlling expression of different characters including seed yield and its attributes would help in proper planning of a successful breeding programme, these results agreement with Saravanan *et al.* (2000). Results in Table (4) represented mean squares for general (GCA) and specific combining ability (SCA) as well as GCA/SCA ratio.

Mean squares due to GCA and SCA were highly significant for all studied characters, suggesting that both additive and non-additive gene actions were importance in the inheritance of all studied characters. The GCA variance was more than SCA variance, indicating the role of additive gene action for the inheritance of all studied traits. The present results confirm the findings of (Abd El-Kader *et al.,* 2017).

The GCA/SCA ratio indicated that the largest part of the total genetic variability due to the additive and additive x additive was very important than the non-additive gene effects in the genetic variability of all studied traits. Comparable consequences were gotten by Bakheit and Mahdy (1987), Fathy (1995), Backiyarani *et al.* (1997), Devi *et al.* (2002), Pushpa *et al.* (2002), Ammar (2004), Ghada (2004) and Abd El-Kader *et al.* (2017).

Table 3. Mean presentation of the studied eight parental genotypes and its crosses for studied traits in sesame.

Genotype code	No. of days to 50% flowering	Plant height(cm)	Length of fruiting zone (cm)	Capsules No. plant^{-1}	Weight of 1000-seed (g)	Seed yield plant^{-1}(g)	Seed yield plot^{-1} (g)
P1	47.33	146.67	98.33	185.00	4.47	22.15	314.60
P2	37.33	150.00	106.67	121.33	4.21	20.23	235.90
P3	40.33	108.33	71.67	67.33	4.09	9.14	92.00
P4	45.67	146.67	110.00	160.00	3.41	15.53	342.00
P5	47.00	193.33	111.67	88.33	3.54	14.12	418.60
P6	45.33	140.00	95.00	90.67	3.95	8.53	133.50
P7	45.00	143.33	90.00	106.67	3.48	12.07	228.70
P8	39.67	223.33	148.33	73.33	3.13	13.65	359.10
P1xP2	44.33	166.67	135.00	166.33	3.81	23.73	284.40
P1xP3	42.00	133.33	86.67	157.00	4.56	17.18	212.60
P1xP4	45.33	160.00	130.00	196.33	4.21	19.15	357.10
P1xP5	44.33	181.67	116.67	134.33	3.88	22.26	387.10
P1xP6	46.00	158.33	120.00	141.00	4.55	16.29	260.40
P1xP7	46.67	151.67	103.33	123.67	3.71	21.88	279.70
P1xP8	43.00	206.67	145.00	103.33	3.96	16.66	392.60
P2xP3	37.33	131.67	103.33	102.00	4.38	18.07	196.70
P2xP4	39.33	171.67	135.00	146.33	3.64	20.45	309.10
P2xP5	35.67	195.00	131.67	106.67	3.45	17.85	379.80
P2xP6	41.33	148.33	108.33	125.33	4.32	14.05	200.20
P2xP7	40.33	161.67	105.00	128.00	4.16	17.19	229.90
P2xP8	37.33	221.67	158.33	96.00	3.70	14.50	337.20
P3xP4	42.67	140.00	110.00	101.67	3.92	15.81	252.90
P3xP5	45.00	198.33	135.00	95.67	3.73	12.10	307.20
P3xP6	39.67	136.70	90.00	90.67	4.15	10.25	123.90
P3xP7	44.67	145.00	100.00	108.33	3.76	11.99	137.20
P3xP8	37.00	225.00	161.67	84.67	3.60	11.59	193.70
P4xP5	44.67	191.67	128.33	143.33	3.83	15.83	390.80
P4xP6	44.33	145.00	105.00	110.00	3.93	13.22	277.70
P4xP7	43.33	155.00	113.33	135.33	3.75	16.86	297.70
P4xP8	39.67	206.67	143.33	98.33	3.31	17.12	357.80
P5xP6	44.67	153.33	90.00	96.67	4.01	10.17	265.50
P5xP7	47.67	213.33	150.00	123.67	3.75	15.69	418.50
P5xP8	44.33	230.00	150.00	91.00	3.42	14.43	464.50
P6xP7	46.67	148.33	98.33	102.00	3.91	11.65	178.90
P6xP8	40.33	200.00	135.00	79.67	3.75	13.22	250.40
P7xP8	43.67	171.67	115.00	89.67	3.69	13.77	330.40
Grand mean	42.75	169.45	117.64	115.82	3.86	15.51	283.29
L.S.D 5%	2.95	17.70	22.70	20.60	0.31	3.26	26.95

Table 4. The mean squares for general (GCA) and specific (SCA) combining ability for considered characters in sesame.

S.O.V.	df	No. of days to 50% flowering	Plant height(cm)	Length of fruiting zone (cm)	Capsules No. plant^{-1}	Weight of 1000-seed (g)	Seed yield plant^{-1}(g)	Seed yield plot^{-1} (g)
GCA	7	128.20^{**}	11970.70^{**}	4611.80^{**}	12100.70^{**}	1.28^{**}	191.10^{**}	117640.90^{**}
SCA	28	9.76^{*}	784.10^{**}	750.20^{**}	524.20^{**}	0.14^{**}	27.58^{**}	2290.70^{**}
Error	70	3.34	119.33	196.60	162.20	0.038	4.06	277.90
GCA/SCA		0.96	0.97	0.92	0.98	0.95	0.93	0.99

***and **: Significant at 0.05 and 0.01 level of probability, respectively.**

General combining ability effects:

Estimates of general combining ability effects for parental genotypes for studied characters are presented in Table (5). Parents P2 and P8 had highly significant negative (GCA) effects for days to 50% flowering, indicating the parent possessed more decreasing alleles towards earliness. By contrast, plant height and fruiting zone revealed that parents P5 and P8 had highly significant positive (GCA) effects, P1and P2 for number of capsules plant^{-1} and P1and P6 had the for 1000-seed weight. However, the considerable highly significant positive GCA effects were achieved by P1 and P2 for seed yield plant^{-1}. P5 and P8 had the highest values for seed yield/plot.

These results revealed that P_8 was good combiner for height of plant, fruiting zone length, seed yield/plot and days number of to 50% flowering, while P_1 was good combiner for capsules number/plant, seed yield/plant and weight of 1000-seed. Therefore, it could be careful as promising foundation for improving those characters. This genetic diversity or allelic divergence among the parents is very important in selection parents for hybridization programme to recognizing heterotic crosses and procurement desirable recombinants in the segregating generation.

Table 5. Estimates of general combining ability effects of eight sesame parents for the studied characters in 2017.

Genotypes	No. of days to 50% flowering	Plant height	Length of fruiting zone	No. of capsules/ plant	weight of 1000-seed	Seed yield/ plant	Seed yield/ plot
P1	2.16	-7.33	-2.54^{**}	34.96^{**}	0.29^{**}	4.18^{**}	25.35^{**}
P2	-3.44^{**}	-2.83^{**}	3.13^{*}	7.09^{**}	0.11^{*}	2.67^{**}	-14.04^{**}
P3	-1.57^{*}	-19.83^{**}	-12.88^{**}	-16.78	0.15^{*}	-2.43	-94.15^{**}
P4	0.59	-6.17	2.63	20.89^{**}	-0.14^{*}	0.99	37.74^{**}
P5	1.56^{**}	22.50^{**}	6.63^{**}	-7.44	-0.16^{*}	-0.30	90.11^{**}
P6	0.89	-15.50^{*}	-12.21	-11.58^{*}	0.17^{*}	-3.68	-72.56^{**}
P7	1.82^{*}	-9.17^{**}	-9.37^{*}	-1.84	-0.11^{*}	-0.64	-21.97^{**}
P8	-2.01^{*}	38.33^{**}	24.63^{**}	-25.31	-0.31	-1.10	49.53^{**}
S.E(gi)	0.31	0.66	2.39	2.17	0.03	0.34	2.85
LSD (5%)	0.61	1.29	4.69	4.26	0.06	0.67	5.58

***and **: Significant at 0.05 and 0.01 level of probability, respectively.**

Effects of specific Combining Ability (SCA):

Effects of specific combining ability (SCA) for studied characters are presented in Table (6). With regard to number of days to 50% flowering, the maximum negative significant SCA value was obtained by cross P2xP5 as the earliest cross. The tallest crosses were (P3 x P8) for height of plant with other five crosses. However, cross (P5 x P7) SCA estimate affects for length of fruiting zone revealed highly significant positive effects among five crosses, indicating the possibility for breeding a long length of fruiting zone which could led directly to increase number of capsules plant^{-1}. Moreover, with respect to number of capsules plant^{-1}, (P1xP4) among five crosses showed highly significant and positive SCA effect. Concerning with seed yield plant^{-1}, cross (P1xP5) from four crosses had highly significant and positive SCA effect. Moreover, seed yield/plot eleven crosses exhibited highly significant and positive SCA effects. Similar conclusion are in contract with those reported by Devi *et al*. (2002), Ammar (2004) and Okello-Anyanga *et al*. (2014). Consequently, it suggested that SCA performance might be considered as criterion for selecting the best crosses. A perusal of F_1's hybrids revealed that (P1 x P5), (P1 x P7) and (P2 x P3) for seed yield plant^{-1} and (P5 x P7) and (P5 x P8) for seed yield plot^{-1} were identified as the best crosses since they possessed desirable SCA effects.

Genetic components of variance:

Separating the total genetic variance to its components additive and dominance gene effects for the studied traits are given in Table (7). The estimated value of the additive (D) and dominance (H_1 and H_2) genetic variance were significant for plant height and seed yield plot^{-1} only, while the D parameter estimating the additive effect was highly significant and was larger in magnitude than the dominance parameter H1 and H2 in all the studied traits, indicating that the type of gene action is partial dominance.

The obtained results are in contract with those gotten by Hamouda (2001) and Ahmed and Adam (2014).The F parameter was negative and highly significant for plant height, seed yield plot^{-1} and number of days to 50% flowering, indicating more negative alleles exhibiting dominance effects. Bakheit *et al*. (2001) reported similar results. The relative size of "D" and "H" estimated as $(H1/D)^{½}$ could be used as weighted measure of the average degree of dominance. This average value in all the studied traits, which was less than one indicating, partial-dominance except length of fruiting zone, this average, was more than one, indicating over-dominance. These results are in harmony with those obtained by Saravanan *et al*. (2000) and Shekhat *et al*. (2011). The average frequency of negative versus positive alleles in the parents was detected by the ratio ($H_2/4H_1$) and the ratio is expected theoretically to be 0.25. The values of ($H_2/4H_1$) were less than one quarter, indicating that positive and negative alleles were not equally distributed among the parents.

Table 6. Estimates of specific combining ability (SCA) effects in 8x8 diallel set of sesame in 2017.

Crosses	No. of days to 50% flowering	Plant height(cm)	Length of fruiting zone (cm)	Capsules No. plant^{-1}	Weight of 1000-seed (g)	Seed yield plant^{-1}(g)	Seed yield plot^{-1} (g)
P1xP2	2.87*	7.39	-14.22	8.459	-0.45**	1.36	-10.20
P1xP3	-1.33	-8.94	16.78*	22.99**	0.26**	-0.08	-1.91
P1xP4	-0.17	4.06	-15.56*	24.66**	0.20*	-1.54	10.69
P1xP5	-2.13	-2.94	12.28	-9.01	-0.10	2.87**	-11.67
P1xP6	0.20	11.72*	-5.06	1.79	0.22**	-0.04	24.36**
P1xP7	-0.07	-1.28	17.11**	-25.27**	-0.33**	2.83**	-6.96
P1xP8	0.10	6.22	-2.39	-22.14**	0.12	-1.93	34.42**
P2xP3	-0.40	-15.11**	5.28	-4.14	0.26**	2.32**	21.57**
P2xP4	-0.57	11.22*	11.61	2.53	-0.20*	1.28	2.123
P2xP5	-5.20**	5.89	4.28	-8.81	-0.36**	-0.03	20.49**
P2xP6	1.13	-2.78	-0.22	13.99*	0.17	-0.76	3.48
P2xP7	-0.80	4.22	-6.39	6.93	0.29**	-0.35	-17.36**
P2xP8	0.03	16.72**	12.94	-1.61	0.03	-2.58**	18.42**
P3xP4	0.90	-3.44	2.61	-18.27**	0.04	1.74	26.00**
P3xP5	2.27	26.22**	23.61**	4.06	-0.12	-0.67	27.95**
P3xP6	-2.40	2.56	-2.56	3.19	-0.04	0.54	7.34
P3xP7	1.67	4.56	4.61	11.13	-0.14	-0.45	-29.92**
P3xP8	-2.17	37.06**	32.28**	10.93	-0.10	-0.38	-45.00**
P4xP5	-0.23	5.89	1.44	14.06*	0.26**	-0.37	-20.31**
P4xP6	0.10	-2.78	-3.06	-15.14**	0.03	0.08	29.20**
P4xP7	-1.83	0.89	2.44	0.46	0.13	1.00	-1.313
P4xP8	-1.67	5.06	-1.56	-13.07*	-0.11	1.72	-12.76
P5xP6	-0.53	-23.11**	-22.06**	-0.14	0.13	-1.67	-35.36**
P5xP7	1.53	30.56**	35.11**	17.13**	0.16	1.13	67.14**
P5xP8	2.03	-0.28	1.11	7.93	0.03	0.32	41.59**
P6xP7	1.20	3.56	2.28	-0.41	-0.01	0.15	-9.81
P6xP8	-1.30	7.72	4.94	0.73	0.02	2.18*	-9.82
P7xP8	1.10	-26.94**	-17.89**	0.99	0.24*	0.01	19.57*
S.E(sij)	1.41	5.72	7.34	6.67	0.10	1.05	8.73
LSD (5%)	11.21	14.39	13.06	2.07	17.11	0.20	2.77

***and **: Significant at 0.05 and 0.01 level of probability, respectively.**

Heritability estimates in the narrow sense as well as in the broad sense for all the studied traits also presented in Table (7). It was obvious that all the studied traits had a high value for the broad sense heritability than the narrow sense. Broad and narrow sense heritability values were ranged between (0.67 to 0.97) and (0.49 to 0.91), respectively. The highest heritability values were suggested for days to seed yield plot^{-1}, Plant height and number of capsule per plant (0.97-0.91, 0.89-0.75 and 0.84-0.76) for broad and narrow sense, respectively, indicating that, these characters are controlled mainly by genetic factors. Meanwhile, length of fruiting zone recorded the lowest values for broad and narrow sense, respectively, indicating that, this character is controlled additive and non-additive genes with preponderance of by non-additive genes. These results confirm that additive gene effects are the main source of genetic variation for all the studied traits and that selection applied in the early segregating generations could be very effective. Similar results were obtained by Shabana *et al.* (1996) and Abd El-Kader *et al.* (2017) who found that additive gene action was predominant.

Table 7. Additive (D), dominance (H) genetic variance and their derived parameters for the studied characters.

	D	H_1	H_2	F	$(H_1/D)^{1/2}$	$H_2/4H_1$	h^2 B	h^2 N
Days to 50% flowering	11.10** ±1.20	4.82 ±2.75	5.85** ±2.39	-7.13** ±2.83	0.66	0.30	0.76	0.65
Plant height	1141.80** ± 87.65	677.70** ±201.50	658.20** ±175.30	-507.70** ±207.10	0.77	0.24	0.89	0.75
Fruiting zone length	285.70** ± 92.28	371.30 ±209.80	446.80** ±182.60	-395.70 ±215.70	1.14	0.30	0.67	0.49
No. of capsules plant^{-1}	1591.80** ±90.49	307.60 ±208.00	337.70 ± 180.90	8.34 ± 213.80	0.44	0.27	0.84	0.76
1000-seed weight	0.18** ±0.02	0.08 ±0.05	0.09** ±0.04	0.02 ±0.05	0.69	0.27	0.72	0.56
Seed yield plant^{-1}	19.71** ±2.41	0.10 ±5.55	1.70 ±4.83	-7.13 ±5.71	0.07	4.37	0.78	0.76
Seed yield plot^{-1}	12613.90** ±228.60	2252.5** ±525.50	2198.40** ±457.20	-692.30** ±540.20	0.42	0.24	0.97	0.91

***and **: Significant at 0.05 and 0.01 level of probability, respectively.**

Graphical analysis of F_1 hybrids:

More insight into genetic control of the intentional characters may be obtained from the relationship of Vr with Wr. (Figs. 1-7). The slope of the regression line was significantly different from zero and not from unity (b= 0.700±0.222) indicating that plant height is controlled by both additive and dominance gene action (additive-dominance model is adequate). The regression line cuts the Wr axis in the origin indicating that this trait is mainly controlled by complete dominance. According to the distribution of the parents along the regression line, parents 4 and 8 seem to contain the largest number of dominant alleles, while parent 3 has the largest number of recessive alleles (Fig. 1).

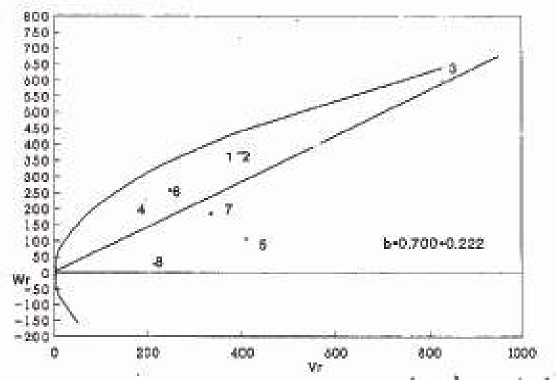

Fig. 1. Relationship between Wr/Vr for plant height.

The slope of the regression line was significantly dissimilar from zero and unity (b=0.629±0.062) indicating that the simple-additive-dominance model is not adequate. The distribution of the parents indicating that parent 8 contains the largest number of dominance alleles while parent number 3 has the largest number of recessive alleles (Fig. 2).

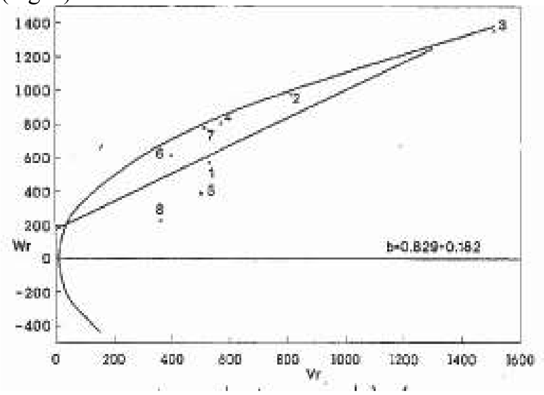

Fig. 2. Relationship between Wr/Vr for length of fruiting zone

The slope of the regression line was significantly dissimilar from zero, but not from unity (b= 0.946±0.113) indicating that the simple additive-dominance model is adequate. The regression line cuts the Wr axis in a positive point (a= 4) indicating that capsules/plant is controlled by partial dominance gene action. Parent 8 contains most of the dominant alleles while parent 6 contains most of the recessive alleles (Fig. 3).

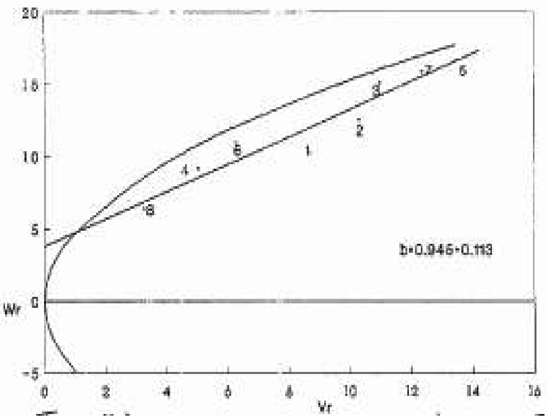

Fig. 3. Relationship between Wr/Vr for capsules/plant.

The slope of the regression line was significantly different from zero and one (b=0.642±0.111) indicating that one or more of the assumption of diallel analysis were not fulfilled. The order of the points along the regression line indicating that parent 6 and 7 have the most dominant genes. Parents 2 and 4 were the furthest points from the origin indicating that they have the most recessive genes of seed yield plant^{-1} (Fig. 4).

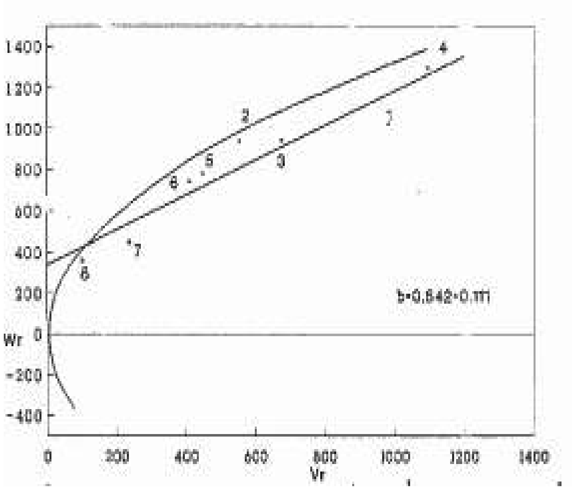

Fig. 4. Relationship between Wr/Vr for seed yield/plant.

The joint linear regression coefficient was not differ significantly from unity and zero (b= 0.504±0.397) indicating that the simple additive-dominance model does not adequate for seed yield/plot. According to the order of the parent's points, parents 7 and 5 have the most of dominant genes controlling this trait. Parents 1 and 2 have the most recessive genes controlling the inheritance of this trait (Fig. 5).

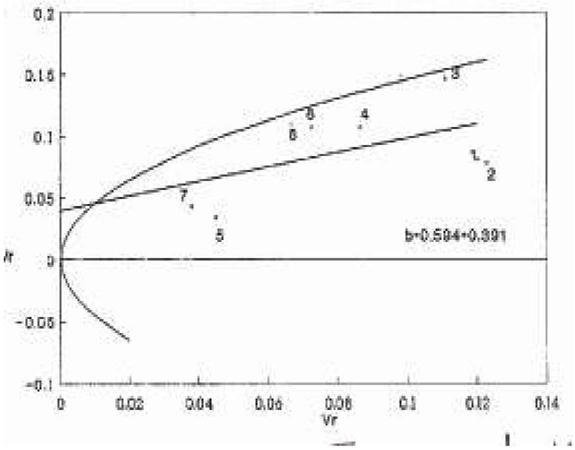

Fig. 5. Relationship between Wr/Vr for seed yield/plot.

The linear regression coefficient was significantly differ from unity and zero (b= 0.605±0.0788) indicating that simple-additive-dominance model was not adequate for the inheritance of 1000-seed weight. Parent 4 was the genotype which contain most of the dominant genes, whereas, parent 7 contain most of the recessive ones controlling this trait (Fig. 6).

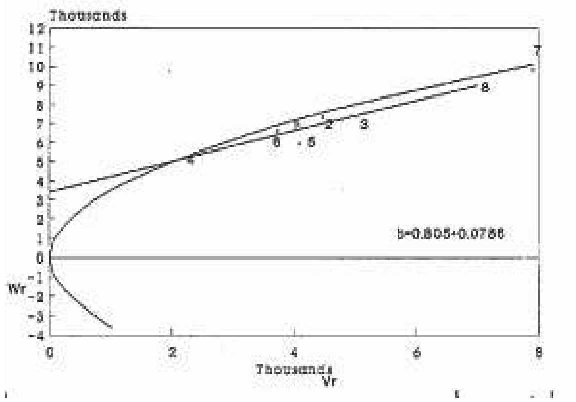

Fig. 6. Relationship between Wr/Vr for 1000-seed weight

The slope of the regression line was significantly differ from unity and zero (b= 0.406±0.184) indicating that of the diallel assumption was net fulfilled. The order of the parents based on number of dominant genes which they are containing was 1, 4, 6, 8, 2, 3, and 5 (Fig. 7).

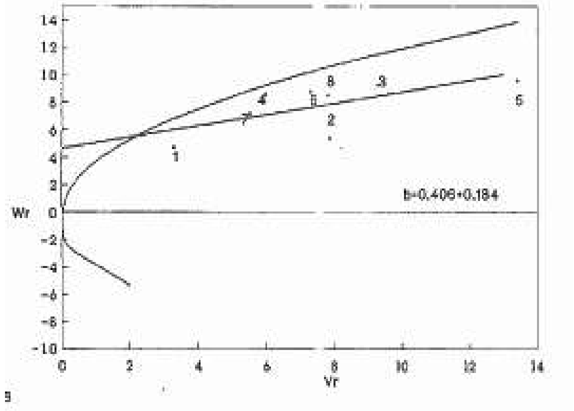

Fig. 7. Relationship between Wr/Vr for number of days to 50% flowering.

Similar outcomes are in agreement with those gotten by Kuselan and Thirugnanakumar (2009), Reddy *et al*. (2015) and Abd El-Kader *et al.* (2017).

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القدرة على الائتلاف وفعل الجين للمحصول ومكوناته في الهجن الدائرية لثمانية تراكيب وراثية من السمسم

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أجريت تجربتان حقليتان خلال موسمين 2016 و2017 في مزرعة محطة البحوث الزراعية بعرب العوامر باسيوط التابعة لمركز البحوث الزراعية. وذلك باستخدام ثمانية آباء بغرض دراسة فعل الجين وفصل مكونات التباين الوراثي (الفعل الجيني المضيف والسيادي) في السمسم وذلك باستخدام طريقة الهجن النصف دائرية لثمانية أباء و28 هجيناً من السمسم. وقد تم تحليل البيانات إحصائياً ووراثياً طبقاً لطريقة جريفنج الثانية الموديل الأول (1956) وهايمان (1954). وفيما يلي ملخص لأهم النتائج: 1-أظهرت نتائج القدرة العامة والخاصة على الائتلاف قيما معنوية عالية مشيرة إلى أهمية كل من التأثير الإضافي والغير إضافي للجينات على توارث الصفات المدروسة. 2-أشارت النسبة بين القدرة العامة والخاصة على الائتلاف أشارت إلى أن الجزء الأكبر من التباين الوراثي والراجع للتأثير الإضافي أهم من الجزء الراجع للتأثير السيادي لكل الصفات المدروسة. أوضح تقدير القدرة العامة على الائتلاف للآباء الثمانية أن الأب رقم (8) كانت له قدرة ائتلافية عامة عالية بالنسبة لصفات طول النبات، طول المنطقة التمرية، وزن محصول القطعة والتزهير، بينما الأبوان رقم (1 و 2) كانت لهما قدرة ائتلافية عامة عالية بالنسبة لصفات عدد الكبسولات/ النبات، وزن محصول النبات، وزن الألف بذرة. 3-أظهرت بعض الهجن قدرة ائتلافية خاصة معنوية. الهجين (1×5) و(1×7) (2×3) هي أفضل التوليفات بالنسبة للمحصول البذري للنبات. أظهرت نتائج تحليل الدياليل أن تأثير الفعل الجيني الإضافي والسيادي عالي المعنوية لصفتي طول النبات ووزن محصول القطعة بينما كان المكون الوراثي المضيف (D) عالي المعنوية وأكبر من المكون الوراثي الغير مضيف (H_1 وH_2) لكل الصفات المدروسة مشيراً لسيادة جزئية. اختلف توزيع الجينات السائدة والمتنحية بين التراكيب الوراثية من صفة لأخري ومن أب لآخر. درجة التوريث بمعناها العريض كانت أكبر من درجة التوريث بمعناها الضيق لكل الصفات المدروسة. 4-أوضحت نتائج التحليل البياني أن خط الانحدار قطع محور الـ Wr فوق نقطة الأصل مشيراً إلى سيادة جزئية في كل الصفات المدروسة.