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COMBINING ABILITY, HETEROSIS AND GENE ACTION FOR SESAME YIELD AND ITS COMPONENTS

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ABSTRACT

The current work was done during the two successive summer seasons of 2022 and 2023 at El-Giza Agricultural Research Station, Agricultural Research Center, Giza Governorate, Egypt, to study the inheritance of yield and its components in sesame. Six parents were crossed in a half diallel mating design to produce 15 crosses. The analysis of variance showed highly significant mean squares for all the studied traits, indicating wide diversity among the parents in this study. The highest results were obtained for the traits of seed yield per plant (g), 1000 seeds weight (g) and oil percentage from P1 and P5, respectively. The cross (P2×P5) gave the highest value for seed yield per plant (g), 1000 seeds weight (g) and oil percentage. Mean squares due to both GCA and SCA combining abilities for crosses were highly significant for all studied traits. The GCA/SCA ratio large exceed the unity for all studied traits, suggesting that the largest part of total genetic variability associated with those measurements which were result of additive gene action. The P5 is good combiner for several traits. The crosses (P2XP5) and (P5XP6) gave SCA significant and positive effects for seed yield/plant (g) and oil percentage. The maximum and highly significant heterosis estimates for mid and better parents, for 1000 seed weight (g), seed yield/plant (g) and seed oil percentage were obtained by cross (P2XP5). Additive (D) was highly significant for Fruiting zone length (cm), number of branches/plant and capsules length (cm), indicating that the additive gene action was important in controlling the inheritance of these traits. Similarly dominance, (H1 and H2) components values were significantly positive for all studied traits. (H1) was greater than (H2) in all studied traits. All estimates of the environmental variance (E) were insignificant for all studied traits. The over- all dominant effect (h^2) was positive and significant for all traits except fruiting zone length (cm). $(H1/D)^{½}$ values were more than unity for all traits. The proportion ($H_2/4H_1$) was lower than 0.25. The ratio of KD/KR was greater than unity for all traits except number of capsules/plant, 1000 seed weight and seed yield/plant. Narrow-sense heritability ($h^{n.s}$) estimates was low for all traits.

Key Words: Sesame, combining ability, heterosis, GCA, SCA, gene action.

INTRODUCTION

Sesame (*Sesamum indicum* L.) is an important oilseed crop, that belongs to the family Pedaliaceae, a self-pollinated crop and a diploid (2n=26) chromosomes. Thought to have originated in Africa, most probably in Ethiopia (**Weiss, 2000**). It is called as “The queen of oilseeds” due to the high resistance to rancidity and oxidation of sesame oil and for the same reason. The oil percentage in sesame rang is from 50 to 60 % (**Suganthi 2018**). Sesame has high levels of morphological genetic diversity. But this has not been fully harnessed for genetic improvement of the existing cultivars through heterosis breeding (**Arriel *et al.,* 2007**). In Egypt, sesame is considered as a food crop rather than an oil seed crop because most of its seeds are used for some food industrial purposes, without oil extraction. The total cultivated area in Egypt was 37,000 ha produced 50,000 tons (**FAO 2023**). Therefore, the main goal of sesame breeding programs is to increase seed productivity. The Hybridization considered one of the most important tools that are used. Therefore, he resorts to identifying parental groups that have the ability to produce the highest level of hybrid effects in the first generation so that they have a high value in the commercial exploitation of hybrids. Also, the plant breeder is interested in estimating the gene effects to apply the most effective breeding procedure for the improvement of the attributes in question. Moreover, it depends mainly on the type of genetic action that controls genetic variation in choosing the most efficient breeding methodology. Hence, information on the mode of inheritance of sesame yield and its components, their genetic behavior, and general and specific combining abilities are highly important for sesame improvement.

The present work was carried out to provide some information with the hope that, this information might help full to fill the gap in genetical studies on sesame to clarify certain aspects of the inheritance of some quantitative traits of sesame. Therefore, five genotypes were selected for this study with sesame domestic product Shandaweel 3.

MATERIALS AND METHODS

The present investigation was conducted at El-Giza Agricultural Research Station, Agricultural Research Center, Egypt, during 2022 and 2023 summer seasons to study the inheritance of sesame yield and its components in sesame. Six diverse parents were chosen that represented a wide range of variation. The origin of parental lines used in this study is presented in Table (1).

Table 1: The origin of sesame genotypes for used in this experiment.

No.	Genotyp	Origin
P1	Shandaweel 3	Commercial Varity Selected line from Giza32 X N.A.130
P2	N.A. 463	USA 1976
P3	N.A. 648	Japan 1987
P4	N.A. 200	Tanzania 1975
P5	N.A. 527	India 1982
P6	N.A. 604	Greece 1986

In the 2022 season, the six parents were crossed in all possible combinations excluding reciprocals to obtain hybrid seeds from a total of 15 F1 crosses using a half diallel mating design. In the summer season of 2023. The six parents along with their 15 F1 hybrids (21 genotypes) were sown on June 6 in a Randomized Complete Blocks Design (RCBD) with three replications. Each experiment unit consisted of three rows. 4 meter long distance between rows was 60 cm and distance between plants within row was 20 cm, with one plant left per hill after thinning. The cultural practices were done according to the recommended method. At maturity, The following traits were measured on ten random gradual plants in each plot; plant height, height to first capsule on the main stem, fruiting zone length, number of branches/plant, capsule length, number of capsules/plant, 1000-seed weight, seed yield/plant and seed oil content the methods were according to official methods outlined by **Horwitz *et al.*, (1965)** using Soxhelt apparatus.

Analysis of variance:

The accrued information had been subjected to the normal evaluation of variance of RCBD consistent with **Snedecore and Cochran (1994)**.The degrees of freedom and sum of squares due to genotypes were further partitioned into parents, crosses and parents vs. crosses sum of squares and tested for significance. For separate out the components of genetic variance and their ratios, the data were subjected to the diallel analysis proposed by **Hayman (1954 a & b).** Narrow sense heritability was estimated according to the formulas suggested by **Mather and Jinks (1982).** The data were further subjected to the diallel analysis proposed by **Griffing (1956)**, method 2 model1, for estimating the General (GCA) and specific (SCA) combining ability. Heterosis of all possible 21 F1's was estimated for both mid-parent and better-parent using the following formulas:

- Heterosis for mid parent = ((F1 – M.P.)/M.P.) x 100
- Heterosis for better parent = ((F1 – B.P.)/B.P.) x 100

RESULTS AND DISCUSSION

Analysis of variance

Results in Table (2) indicated that the analysis of variance showed highly significant mean squares due to genotypes, parents, crosses and parents vs. crosses for all the studied traits this indicated that experimental material used in present study had sufficient variability for different traits. Similar results were obtained by **Meenakumara *et al.* (2015); Abd El-Kader *et a.l* (2017); Myint *et al.* (2018); Anter (2020);Ghule *et al.* (2022), Thouseem *et al.* (2023), and Gore *et al.* (2024).**

Table (2): Mean squares from ordinary analysis of variance for all the studied traits of sesame genotypes.

S.O.V.	DF	Plant Height (cm)	height first capsule	Fruiting zone length (cm)	Branches Number	No. of Capsules plant^{-1}	Capsules Length (cm)	1000 Seed weight (g)	Seed yield /plant	Oil (%)
Replication	2	22.90	14.11	13.78	0.28	12.34	0.017	0.01	2.12	1.31
Genotypes	20	173.04**	311.68**	247.01**	7.70**	94.94**	0.037**	0.36**	19.01**	3.76**
Parents	5	65.42**	181.69**	348.40**	14.68**	28.01**	0.040**	0.07**	9.18**	1.95*
Crosses	14	156.26**	324.50**	227.89**	4.41**	93.34**	0.022**	0.39**	17.35**	3.66**
P vs. C	1	946.01**	782.23**	7.78	18.89**	452.12**	0.223**	1.42**	91.53**	14.3**
Error	40	15.32	10.61	19.84	0.34	5.96	0.007	0.01	2.31	0.71

* and ** Significant at 0.05 and 0.01 levels of probability, respectively.

Mean performance

The results for mean performance of the six parents and its fifteen crosses showed in (Table 3). The P4 gave higher value for plant height (cm).The P2 gave higher value for height first capsule (cm) while P5 expressed the lowest height for first capsule and achieving the highest value for fruiting zone length (cm), branches number/plant and capsules number/plant. The highest results were obtained for the traits of capsule length, 1000 seeds weight (g), seed yield per plant and oil percentage from P1 and P5 respectively. The results indicated that the cross (P3×P5) gave the highest value in plant height (cm). The cross (P2×P4) gave the highest value for the height first capsule and capsule length. The cross (P3×P4) gave the highest value in the traits of the number of capsules/plant. While the cross (P2×P5) gave the highest number of branches/plant, 1000 seeds weight, seed yield per plant (g) and oil percentage. Many researchers found similar results, **Hassan and Sedeck (2015); Abd El-Kader *et al.*, (2017); Abd-Elsaber (2019 a&b); Anter (2020); Jeeva *et al.*, (2020); Rathod *et al.*, (2021) and Meenakumara (2023).**

Combining ability

Results in Table (4) indicated the analysis of variance for combining ability in sesame yield traits. Mean squares due to general (GCA) and specific (SCA) combining abilities for crosses were highly significant for all traits. The GCA variance contains additive effect, while SCA variance contains non-additive as outlined by **Griffing (1956).** Hence, the significant estimates of both GCA and SCA variances suggested that both additive and non-additive gene action were important in controlling the inheritance of the traits under study for all sesame genotypes. **Ahmed and Adam (2014); Anter (2020) and Jeeva *et al.*, (2020)**, reported that the mean squares value due to GCA and SCA were highly significant for all studied traits and the ratio of GCA/SCA was a higher magnitude for GCA variance in all traits, this suggesting the preponderance of an additive gene action. Several investigations revealed the importance of both additive and dominance gene effects in the genetic control of seed yield and its contributing traits in sesame: **MeenaKumara *et al.*, (2015); Abd El-Kader *et al.*, (2017); Abd-Elsaber *et al.*, (2019a, b); Kumar *et al.*, (2021); Anju *et al.*, (2023), and Gore *et al.*, (2024).**

Table (3): Mean performance of the parents and their F_1 crosses for all the studied treats of sesame.

Genotypes	Plant height (cm)	height first capsule	Fruiting zone length (cm)	Branches Number	No. of Capsules plant^{-1}	Capsules Length (cm)	1000 seed weight (g)	Seed yield /plant	Oil (%)
P1	180.00	88.33	91.67	1.00	133.53	3.41	3.54	33.32	45.43
P2	172.67	91.00	81.67	6.43	139.20	3.32	3.45	31.40	43.79
P3	182.67	75.33	107.33	5.93	138.70	3.14	3.32	33.27	44.17
P4	185.00	79.67	105.33	6.23	140.93	3.18	3.15	32.69	43.57
P5	177.33	71.00	106.33	7.13	141.53	3.40	3.48	35.64	45.41
P6	175.00	85.33	89.67	5.63	135.93	3.22	3.21	30.61	44.80
1x2	175.00	80.67	94.33	4.33	134.40	3.42	4.20	34.81	44.80
1x3	177.00	78.00	99.00	5.50	142.67	3.40	3.52	33.53	46.00
1x4	186.33	102.33	84.00	7.07	149.00	3.51	3.38	34.14	46.88
1x5	185.33	82.33	103.00	7.73	143.40	3.42	4.28	39.16	43.43
1x6	183.00	84.33	98.67	5.60	137.20	3.38	3.78	33.80	45.46
2x3	188.33	102.33	86.00	6.97	151.20	3.44	3.77	37.46	46.18
2x4	194.33	112.33	82.00	5.10	145.60	3.54	3.83	34.86	44.86
2x5	195.00	91.67	103.33	8.67	151.00	3.50	4.32	40.32	47.50
2x6	184.00	82.67	101.33	6.87	137.30	3.36	3.42	33.10	44.71
3x4	192.00	87.67	104.33	6.10	151.47	3.35	3.34	35.20	44.87
3x5	200.33	92.00	108.33	7.87	145.40	3.37	3.46	35.82	46.46
3x6	180.33	90.33	90.00	6.00	140.80	3.24	3.30	31.85	45.31
4x5	196.33	98.67	97.67	7.60	150.00	3.47	3.92	36.50	45.53
4x6	188.00	82.00	106.00	7.77	139.70	3.27	3.29	33.63	44.62
5x6	185.00	76.33	108.67	5.93	144.40	3.48	3.51	38.17	47.11
Mean of parents	178.78	81.78	97	5.39	138.31	3.28	3.36	32.82	44.53
Mean of Crosses	187.36	89.58	97.78	6.61	144.24	3.41	3.69	35.49	45.58
Mean of genotypes	184.90	87.35	97.56	6.26	142.54	3.37	3.59	34.73	45.28
L.S.D. 5 %	6.46	5.38	7.46	0.98	4.03	0.13	0.12	2.51	1.39
L.S.D. 1 %	8.64	7.19	9.84	1.29	5.39	0.18	0.16	3.35	1.86

Table (4): Mean squares of genotypes, general combining ability (G.C.A) and specific combining ability (S.C.A) for all the studied treats of sesame.

S.O.V	d.f.	Plant height (cm)	height first capsule	Fruiting zone length (cm)	Branches Number	No. of Capsules plant^{-1}	Capsules Length (cm)	1000 seed weight (g)	Seed yield Plant^{-1}	Oil (%)
G.C.A	5	78.51**	104.28**	153.64**	5.22**	54.49**	0.021**	0.23**	11.94**	0.66*
S.C.A	15	50.74**	103.77**	58.57**	1.68**	24.04**	0.009**	0.09**	4.47**	1.45**
Error	40	5.11	3.54	6.61	0.11	1.99	0.002	0.002	0.77	0.24
GCA/SCA		1.55	1.00	2.62	3.10	2.27	2.36	2.65	2.67	0.46

* and ** Significant at 0.05 and 0.01 levels of probability, respectively.

The GCA/SCA ratio large exceed the unity for all studied traits, suggesting that the largest part of total genetic variability associated with those measurements which were result of additive gene action. In this respect, **Ahmed and Adam (2014)** the ratio GCA/SCA was large exceed the unity for studied traits in both seasons, except seed yield per plant. **Anyanga *et al.*, (2016)**, reported that additive gene action controlled plant height, branches per plant, capsules on main stem, capsules on branches, and capsule length. **Abd-Elsaber *et al*., (2019)** showed that the ratio of GCA/SCA is largely exceed the unity for all studied except number of capsules/plant and number of branches/plant, Also, **Abd-Elsaber (2019b)**, in another research, made it clearer reported the GCA/SCA ratio was lower than 1, meaning that non-additive component was more important than additive for all the traits studied including plant height and oil percentage. However, **MeenaKumara *et al.*, (2015)** found, the ratio GCA/SCA variance was less than one, which indicated the preponderance of non-additive gene action for the quantitative traits studied. **Kumar *et al.*, (2021)** observing the σ^2GCA/σ^2SCA ratio was lower than unity for oil percentage content. These observations are in conformity with the finding of **Hassan and Sedeck (2015); Abd El-Kader *et al.*, (2017); Myint *et al.*, (2018);Anter (2020) and Gadhiya *et al.*, (2023),**

General combining ability effects

Estimates of GCA influences of all studied genotypes for each trait are listed in Table (5). The GCA was found to be significantly differed for most traits. The P4 recorded highly significant positive GCA influences for plant height and found to be a good general combiner for increasing plant height. In contrast, the P1 showed highly significant negative GCA effects for this trait and could be considered as a good general combiner for reducing plant height. Regard height first capsule the P2 recording highly significant positive GCA in this trait. For length of fruit zone and number of branches/plant, the P5 was found to be a good general combiners, where they recorded highly significant positive GCA Influences. With respect to number of capsules/plant trait, the P4 and P5 were good combiners as exhibited highly significant positive GCA effects. For capsule length, the P5 had highly significant positive GCA influences while, significant positive GCA influences were recorded by the P1, and so these two parents were good general combiners. For seed yield/plant, the P5 had highly significant positive estimates of GCA effects, indicating that this parent appeared to be the best general combiners for this trait. The P5 had highly significant positive GCA effect for 1000-seed weight, it could be considered as good donor for this trait. For seed oil content, the P5 had highly significant positive GCA influences. In that context, this P5 is good combiner for most of traits and several traits and sizable genetic gain could be expected from their crosses in sesame breeding programs in Egypt. Results on general combining ability for these traits were reported previously by **Dhillon (1975)** who reported that combining ability of parents gave useful information on the choice of parents. **Priya *et al*., (2016)** reported Knowledge on general combining ability coupled with per se performance would result in the identification of parents with good reservoir of superior genes. **Deshmukh *et al.*, (2019)** indicated that clearly there appeared to be close relationship between GCA and per se performance of most of the traits expressed by the parents. In turns it will help as criteria to select the parents for breeding programs. **Jawahar Lal *et al.*, (2020)** indicated that presence of at least one parent with high GCA effects indicating that a high general combiner in the cross combination might result in good specific combination. Also, these results are in agreement with **Abd El-Kader *et al.*, (2017), Myint *et al.*, (2018), Anter (2020); Jeeva *et al.*, (2020); Anju *et al*., (2023), and Gore *et al.*, (2024).** They created GCA effects in the desired direction for seed yield and yield components.

Table (5): Estimation of general combining ability (GCA) effects of the six sesame parents for all the studied traits.

Genotypes	**Plant height (cm)**	**height first capsule**	**Fruiting zone length (cm)**	**Branches Number**	**No. of Capsules plant^{-1}**	**Capsules Length (cm)**	**1000 seed weight (g)**	**Seed yield /plant**	**Oil (%)**
P1	-3.46**	-0.89	-2.57**	-1.45**	-3.01**	0.043**	0.135**	-0.13	0.06
P2	-1.54*	5.03**	-6.57**	0.12	0.01	0.036*	0.160**	0.03	-0.17
P3	1.13	-1.31*	2.43**	0.06	1.39**	-0.065**	-0.141**	-0.34	0.02
P4	4.08**	3.86**	0.22	0.28**	2.48**	-0.014	-0.136**	-0.42	-0.38*
P5	2.79**	-3.56**	6.35**	1.03**	2.43**	0.054**	0.162**	2.27**	0.49**
P6	-3.00**	-3.14**	0.14	-0.05	-3.32**	-0.054**	-0.180**	-1.42**	-0.02
LSD gi 5%	1.47	1.23	1.68	0.22	0.92	0.031	0.027	0.57	0.32
LSD gi 1%	1.97	1.64	2.24	0.29	1.23	0.041	0.036	0.77	0.43
LSD gi-gj 5%	2.28	1.90	2.60	0.34	1.42	0.047	0.041	0.89	0.49
LSD gi-gj 1%	3.06	2.54	3.48	0.45	1.91	0.063	0.055	1.19	0.66

* and ** Significant at 0.05 and 0.01 levels of probability, respectively.

Specific combining ability effects

The effects of specific combining ability (SCA) of all sesame parents' combinations for all traits are listed in Table (6). Regarding the plant height trait the magnitude of SCA effects in hybrids varied from -

5.57 (P1 x P3) to 11.51 (P3XP5). Out of 15 crosses, 5 hybrids exhibited significant and desirable (positive) SCA effects. The cross P3XP5 (11.51) ranked first, followed by P2XP5 (8.85). For height to first capsule, the spectrum of variation for SCA effects in hybrids was from -11.81 (P4 x P6) to 24.27 (P4 x P5), out of 15 crosses, 5 crosses showed significant and negative SCA effects in desirable direction. The cross P1xP2 (-10.82) ranked first trailed by P1xP3 (-7.15). With regard to length of fruit zone, two parental combinations; P2XP6 (10.21) and P4XP6 (8.08) expressed highly significant positive (SCA). For number of branches/plant, two parental combinations; P1XP4 (1.97) and P1XP5 (1.89) expressed highly significant positive (SCA). With respect to number of capsules/plant, highly significant and positive SCA effects were observed by cross P2X P3 (7.25) and P1XP4 (6.99) expressed highly significant positive (SCA). For capsule length, 4 hybrids showed significant SCA effects these, hybrids depicted positive and significant SCA estimates in desirable direction, thus they were good specific combinations. Some of the good specific combinations were P2 x P4 (0.15), P1 x P4 (0.11), P5 x P6 (0.11) and P2 x P3 (0.10). For 1000-seed weight, 6 hybrids were identified as good specific combinations by exhibiting significant and positive SCA effects. Hybrids (P2xP5) (0.40) and (P1xP5) (0.39). They were good specific combinations. For seed yield/plant, estimates of SCA effects were highly significant and positive for the crosses (P2XP5), (P2XP3), (P5XP6) and (P1XP5), indicating the superiority of these crosses. Three hybrids gave SCA significant and positive effects for oil percentage (%), the high SCA significant was obtained (P1xP4), (P2xP5) and (P5xP6), respectively. Suggesting that parents with high or low values of GCA effects may not always provide highly valuable crosses with high value of SCA effects. The highest positive value of SCA effect do not commonly participate in sesame crop (self-pollinated) improvement **(Pandey *et al.*, 2018). Gadhiya *et al.*, (2023)**, revealed that In the case of specific combining ability effects, none of the hybrids collectively exhibited a favorable SCA effect for all the traits. the trend of SCA effect for seed yield and its components were, more or less, in agreement with the results reported by **Hassan and Sedeck (2015); MeenaKumara *et al.*, (2015); Abd El-Kader *et al.*, (2017); Myint *et al.*, (2018); Abd-Elsaber *et al.* (2019a); Deshmukh *et al*,. (2019); Anter (2020); Jeeva *et al.*, (2020); Anju *et al.*, (2023) and Gore *et al.*, (2024). They** found that the genetic divergence among the parental genotypes had the largest effect on generated cross combinations, especially in estimation of SCA effects for seed yield and yield components.

Table (6): Estimates of specific combining ability effects for all the studied traits of sesame.

Cross	Plant height (cm)	height first capsule	Fruiting zone length (cm)	Branches Number	No. of Capsules plant^{-1}	apsules Length (cm)	1000 seed weight (g)	Seed yield /plant	Oil (%)
1x2	-4.90*	-10.82**	5.92*	-0.60*	-5.15**	-0.03	0.32**	0.18	-0.37
1x3	-5.57**	-7.15**	1.58	0.63*	1.74	0.05	-0.07	-0.73	0.64
1x4	0.80	12.01**	-11.21**	1.97**	6.99**	0.11*	-0.21**	-0.04	1.92**
1x5	1.10	-0.57	1.67	1.89**	1.43	-0.05	0.39**	2.29**	-2.40**
1x6	4.55*	1.01	3.54	0.84**	0.98	0.02	0.23**	0.62	0.14
2x3	3.85	11.26**	-7.42**	0.52	7.25**	0.10*	0.15**	3.04**	1.04*
2x4	6.89**	16.10**	-9.21**	-1.57**	0.56	0.15**	0.21**	0.52	0.13
2x5	8.85**	2.85	6.00*	1.25**	6.01**	0.04	0.40**	3.29**	1.90**
2x6	3.64	-6.57**	10.21**	0.53	-1.94	0.00	-0.15**	-0.25	-0.39
3x4	1.89	-2.24	4.12	-0.50	5.05**	0.06	0.03	1.23	-0.05
3x5	11.51**	9.51**	2.00	0.52	-0.97	0.01	-0.16**	-0.84	0.67
3x6	-2.70	7.43**	-10.13**	-0.27	0.18	-0.02	0.03	-1.13	0.02
4x5	4.55*	11.01**	-6.46**	0.02	2.54*	0.05	0.30**	-0.07	0.15
4x6	2.01	-6.07**	8.08**	1.27**	-2.01	-0.04	0.01	0.74	-0.26
5x6	0.30	-4.32*	4.63*	-1.31**	2.74*	0.11*	-0.07	2.59**	1.37**
SD Sij 5%	4.05	3.37	4.61	0.60	2.52	0.08	0.07	1.57	0.87
SD Sij 1%	5.42	4.51	6.16	0.81	3.38	0.11	0.10	2.10	1.17
SD sij-sik 5%	6.04	5.03	6.88	0.90	3.77	0.13	0.11	2.34	1.30
SD sij-sik 1%	8.08	6.73	9.20	1.20	5.04	0.17	0.15	3.14	1.74
SD sij-skl 5%	5.59	4.66	6.37	0.83	3.49	0.12	0.10	2.17	1.21

* and ** Significant at 0.05 and 0.01 levels of probability, respectively.

Estimation of heterosis

Table (7) indicated the estimates heterosis of grosses over mid and better parent for all studied traits. For plant height trait, two crosses, (P2XP5) and (P3XP5) gave the maximum and highly significant heterosis estimates. However, the maximum and highly significant heterosis estimates were observed for height first capsule in the crosses (P4XP5) and (P3XP5), length of fruit zone in the cross (P2XP6), number of branches/plant in the cross (P1XP4) and (P1XP5), number of capsules/plant in the cross (P2XP3), capsule length in the cross (P2XP4), 1000 seeds weight (g) in the cross (P2XP5), seed yield/plant in crosses (P2XP5) and seed oil content in crosses (P2XP5) over mid and better parents, respectively. These results are in the line with results reported by **Hassan and Sedeck (2015); Abd El-Kader *et al.*, (2017); Abd-Elsaber**

***et al.*, (2019 a&b); Jeeva *et al.*, (2020); Rathod *et al.*, (2021); Gadhiya *et al.*, (2023); Meenakumara (2023) and Naresh *et al.*, (2024).**

Table (7): Heterosis relative to Mid parent (MP) and Better parent (BP) for all the studied treats of sesame.

Treats	Plant height (cm)		height first capsule		Fruiting zone length (cm)		Branches Number	
Gen.	**MP**	**BP**	**MP**	**BP**	**MP**	**BP**	**MP**	**BP**
1x2	-0.76	-2.78	-10.04**	-11.36**	8.85*	2.91	16.59	-32.64**
1x3	-2.39	-3.10	-4.68	-11.70**	-0.50	-7.76*	58.65**	-7.30
1x4	2.10	0.72	21.83**	15.85**	-14.72**	-20.25**	95.39**	13.37
1x5	3.73*	2.96	3.35	-6.79*	4.04	-3.13	90.16**	8.41
1x6	3.10	1.67	-2.88	-4.53	8.82*	7.64	68.84**	-0.59
2x3	6.00**	3.10	23.05**	12.45**	-8.99*	-19.88**	12.67	8.29
2x4	8.67**	5.05**	31.64**	23.44**	-12.30**	-22.15**	-19.47*	-20.73**
2x5	11.43**	9.96**	13.17**	0.73	9.93*	-2.82	27.76**	21.50**
2x6	5.85**	5.14**	-6.24*	-9.16**	18.29**	13.01**	13.81	6.74
3x4	4.44*	3.78*	13.12**	10.04**	-1.88	-2.80	0.27	-2.14
3x5	11.30**	9.67**	25.74**	22.12**	1.40	0.93	20.41**	10.28
3x6	0.84	-1.28	12.45**	5.86	-8.63*	-16.15**	3.75	1.12
4x5	8.37**	6.13**	30.97**	23.85**	-7.72*	-8.15*	13.72	6.54
4x6	4.44*	1.62	-0.61	-3.91	8.72*	0.63	30.90**	24.60**
5x6	5.01**	4.32*	-2.35	-10.55**	10.88**	2.19	-7.05	-16.82*

Table 7: (continued)

Tr.	No. of Capsules plant^{-1}		Capsules Length (cm)		1000 seed weight (g)		Seed yield plant^{-1}		Seed Oil (%)	
Gen.	**M.P**	**B.P**	**M.P**	**B. P**	**M.P**	**B.P**	**M.P**	**B.P**	**M.P**	**B.P**
1x2	-1.44	-3.45*	1.68	0.29	20.38**	18.85**	7.57*	4.47	0.44	-1.37
1x3	4.81**	2.86*	3.97*	-0.20	2.58	-0.57	0.72	0.65	2.68*	1.26
1x4	8.57**	5.72**	6.42**	2.83	1.20	-4.34**	3.44	2.46	5.34**	3.19*
1x5	4.27**	1.32	0.34	0.20	22.00**	21.02**	13.58**	9.89**	-4.38**	-4.40**
1x6	1.83	0.93	2.01	-0.78	12.01**	6.79**	5.75	1.45	0.78	0.08
2x3	8.82**	8.62**	6.71**	3.82	11.33**	9.28**	15.84**	12.58**	5.00**	4.55**
2x4	3.95**	3.31*	8.98**	6.73**	16.12**	11.12**	8.78*	6.64	2.71	2.45
2x5	7.58**	6.69**	4.12*	2.84	24.74**	24.14**	20.29**	13.14**	6.51**	4.62**
2x6	-0.19	-1.36	2.65	1.21	2.81	-0.77	6.75	5.40	0.93	-0.21
3x4	8.33**	7.47**	6.17**	5.45*	3.35*	0.70	6.72*	5.78	2.29	1.59
3x5	3.77**	2.73	3.11	-0.88	1.76	-0.57	3.96	0.51	3.73**	2.32
3x6	2.54*	1.51	1.78	0.41	1.23	-0.50	-0.30	-4.29	1.85	1.13
4x5	6.21**	5.98**	5.37**	1.96	18.35**	12.74**	6.84*	2.41	2.34	0.27
4x6	0.92	-0.88	2.03	1.34	3.51*	2.60	6.25	2.88	0.98	-0.40
5x6	4.08**	2.03	5.18**	2.45	4.99**	0.86	15.25**	7.12*	4.46**	3.76*

* and ** Significant at 0.05 and 0.01 levels of probability, respectively.

Genetic Components analysis:

Results were further subjected to the diallel analysis proposed by **Hayman (1954 a&b)** to obtain more information about the genetic behavior for the traits under study. Additive (D), Dominance (H1 and

H2), (F) value, h², Environmental variances (E) and derived parameters for the studied traits are presented in Table (8).

Table (8): Estimates of genetic components and ratios derived from a 6×6 diallel cross analysis for all studied traits in sesame.

Genetic components	Plant height (cm)	height first capsule	Fruiting zone length (cm)	Branches Number	No. of Capsules plant^{-1}	Capsules Length (cm)	1000 seed weight (g)	Seed yield /plant	Oil (%)
D	16.58	56.97	109.61**	4.78**	7.25	0.012**	0.023	2.30	0.40
F	6.09	84.22	88.06	3.78**	-17.52	0.003	-0.064	-2.80	0.38
H_1	178.18**	428.36**	246.17**	6.33**	79.93**	0.024**	0.321**	13.85**	4.81**
H_2	133.24**	327.05**	191.40**	5.22**	69.13**	0.021**	0.247**	11.55**	4.59**
h^2	201.48**	167.00**	-1.94	4.02**	96.52**	0.047**	0.305**	19.35**	2.95**
E	5.23	3.59	6.52	0.11	2.09	0.002	0.002	0.77	0.25
$(H1/D)^{½}$	3.28	2.74	1.50	1.15	3.32	1.47	3.76	2.46	3.46
$(H_2/4H_1)$	0.19	0.19	0.19	0.21	0.22	0.22	0.19	0.21	0.24
KD/Kr	1.12	1.74	1.73	2.05	0.47	1.22	0.45	0.60	1.32
$h_{(n.s)}$	0.42	0.30	0.41	0.43	0.48	0.40	0.56	0.50	0.08

Additive (D) was highly significant for Fruiting zone length (cm), number of branches plant^{-1} and Capsules Length (cm), indicating that the additive gene action was important in controlling the inheritance of these traits and can be easily fixed in early generation **(Rathod *et al.*, 2021)**. Similarly, (H2) component value was significantly positive for all traits. Theoretically, (H2) should be equal to or less than (H1) **(Hayman1954a&b)**. (H1) was greater than (H2) in all traits indicating that the positive and negative alleles at the loci for these traits were not equal in proportion in the parents. Values of (H1) were greater than the respective D values for all traits indicating the important role of dominant genetic variance. The over-all dominant effects, as algebraic sum over all the loci in heterozygous phase in all crosses (h^2), was found to be positive and significant for all traits except fruiting zone length, stressing that dominance genes effects were mainly attributed to heterozygosity and dominance seeming to be acting in positive direction (unidirectional) for these traits. The fruiting zone length showed insignificant values of h^2, indicating that dominance gene effect was bi- directional in nature (both dominant and recessive alleles were involved at various loci) and did not indicate any direction of dominance. The distribution of relation frequencies of dominant versus recessive genes (F) were positive and significant for number of branches plant^{-1}, suggested greater frequencies of dominant alleles in the parents for this trait. All estimates of the environmental variance (E) were insignificant for all studied traits, indicating that all traits have not been greatly affected by environmental factors. The mean degree of dominance across as estimated by the ratio $(H/D)^{0.5}$ was found to be more than unity for all traits, indicating, the role over-dominance gene effects in the inheritance of the studied traits. The positive and negative alleles were not equally distributed between the parents as the ratio (H2/4H1) was less than 0.25. The ratio of KD/KR (dominance and recessive genes) in the parents was greater than unity for all traits except No. of capsules plant^{-1}, 1000 seed weight and seed yield plant^{-1} suggesting an excess of dominant genes in the parents for these traits. Meanwhile, the less than unity values for No. of capsules plant^{-1}, 1000 seed weight and seed yield plant^{-1}, revealing the recessive alleles compared to dominant ones. Narrow-sense heritability (h^2ns) recorded estimates for all traits with values ranging from 0.08 to 0.56 for oil percentage and 1000 seed weight respectively, confirming that the additive gene effects were more prevalent. Many investigators are in agreement with those results reported by **Hassan and Sedeck (2015); Anyanga *et al.*, (2016) ; Suganthi (2018) ; Sapara *et al.*, (2019) ; Gami *et al.*, (2020); Ramya *et al.*, (2021); Kabi *et al.*, (2022) and Gedifew *et al.*, (2023).**

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القدرة على الائتلاف و قوه الهجين و الفعل الجيني لمحصول السمسم ومكوناته

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2- **المعمل المركزي لبحوث التصميم والتحليل الاحصائي ، مركز البحوث الزراعية جمهورية مصر العربية**

اجري التهجين النصف دائري بين ستة أباء من السمسم وتم الحصول على خمسة عشر هجيناً خلال موسم الصيف 2022 وفى الموسم التالي 2023 تم تقييم الاباء و الهجن الخمسة عشر فى تجربة حقلية في قطاعات كاملة العشوائيه في ثلاث مكررات بمحطة البحوث الزراعية بالجيزة – مركز البحوث الزراعية بهدف دراسة توريث المحصول ومكوناته في السمسم. أظهر تحليل التباين وجود فروق معنوية عالية لجميع الصفات المدروسة، مما يدل على تنوع واسع بين الآباء المستخدمين في هذه الدراسة. تم تسجيل أعلى النتائج لصفات وزن 1000 بذرة (جم) ومحصول البذور للنبات (جم) ونسبة الزيت من الاباء P1 و P5 على التوالي بينما أعطى الهجين (P2×P5) أعلى قيمة لوزن 1000 بذرة (جم) ومحصول البذرة للنبات (جم) ونسبة الزيت (%). كان متوسط التباين الناتج عن كل من القدره العامة والخاصة للأئتلاف عالي المعنوية لجميع الصفات تحت الدراسة. كانت النسبة بين GCA/SCA اعلى من الواحد لجميع الصفات المدروسة مما يشير إلى الدور الاكبر للفعل المضيف في تباين هذه الصفات. أظهرت نتائج القدرة العامة على الائتلاف أن الاب P5 ذا قدره عامة على التألف موجبة و معنوية للعديد من الصفات. أظهرت الهجن (P2XP5) و (P5XP6) أفضل قدرة خاصة على

التألف ذات تأثيرات معنوية وموجبة في محصول البذور/نبات (جم) ونسبة الزيت (٪). كان الهجين (P2XP5) هوافضل الهجن و ذو معنوية عالية لمتوسط الابوين و الاب الافضل لصفات وزن ال 1000 بذرة (جم) ومحصول البذور/ نبات (جم) والنسبة المئوية للزيت بالبذور. اوضحت النتائج ان الفعل الجينى المضيف (D) كان عالى المعنوية في طول المنطقة الثمرية (سم) وعدد الأفرع/ النبات وطول الكبسوله (سم) مما يشير إلى أن الفعل الجيني المضيف كان مهماً في التحكم في توريث هذه الصفات. ايضاً كانت قيم مكونات (H1,H2) موجبة معنوياً لجميع الصفات. وكان التأثير السيادى (H1) أكبر من الفعل الجينى الغير مضيف (H2) في جميع الصفات. و كان تأثير السياده الفائقة (h2) موجباً ومعنوياً لجميع الصفات باستثناء طول المنطقة الثمرية (سم). وكانت جميع تقديرات التباين البيئي (E) غير معنوية لجميع الصفات المدروسة. و كانت قيم متوسط درجة السياده $(H1/D)^{½}$ أكبر من الوحدة لجميع الصفات. توزعت الجينات الموجبة و السالبة توزيعا غير متساوى بين الاباء حيث كانت قيمة (H2/4H1) أقل من اعلى قيمة لها (0.25) لجميع الصفات تحت الدراسة. سجلت كفاءة التوريث بالمعنى الضيق ($h^{n.s}$) قيما متوسطة (0.30 – 0.56) لجميع الصفات ما عدا النسبة المئوية للزيت كانت (0.08) مما يوضح امكانية تحسين بعض صفات محصول السمسم بالانتخاب.