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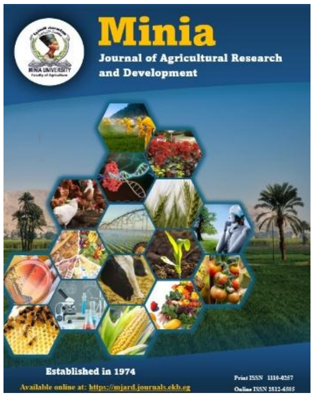

Combining ability for some genotypes and heterosis of F_1's crosses in sesame (*Sesamum indicum* L.)

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ABSTRACT

The present study was carried out during the two seasons 2022 and 2023 at the Educational Farm of Fac. Agric., Minia University, Egypt to assess of general combining abilities of 8 diverse parental lines of sesame in addition to heterotic effects and specific combining abilities of its 28 F's crosses. The results indicated that mean squares owing to genotypes, parents, crosses and parents vs crosses were highly significant for all tested traits. For seed yield/plant, all crosses except only one ($P_4 \times P_7$) exhibited highly significant positive mid-parent heterosis, confirming the superiority of these crosses over mid parents in seed yielding. All crosses exhibited substantiate positive better-parent heterosis for seed yield/plant, indicating the superiority of these crosses in seed yield/plant compared to their better-parents. Parent 8 considered to be a good general combiner for seed yield/plant, where it has a significant positive effect. From the obtained results, it could be concluded that three parents (P_3, P_5, and P_8) recorded significant effects in most of the studied traits indicating their rich source to improve yield. Concerning seed yield/plant, twenty two crosses achieved significant negative or positive specific combining ability SCA effects, seventeen of them recorded substantial positive SCA effects (14 highly significant positive SCA effects and 3 crosses possessed only significant positive SCA effects), indicating that most of tested crosses surpassed their parents with regard to this trait.

Keywords: sesame, general combining, crosses, heterosis

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INTRODUCTION

Sesame (*Sesamum indicum* L.) is oil summer crop belongs to Pedaliaceae family. Sesame seeds are widely involved in making healthy foods, which is increasingly in demand nowadays. Moreover, they have positive effects on human health because of their containment of antioxidants, minerals and vitamins. (**Mahmoud *et al*., 2024**).

Previously the crop didn't receive great attention by Egyptian plant breeders. Recently, the crop was getting more attention from the breeders due to the increase in demand in the local market to solving the issue of importing. The seed production per unit area was recently increased due to wide distribution of high yielding new released sesame varieties, namely Giza 32, Shandweel 3 and others. However, sesame breeders need to increase the genetic variability that help in the improvement such crops via crossing among diverse parents for the traits in question. In the context, diallel design crosses is considered as the most accurate mating design for 12 parents or less (**Singh and Chaudhary, 1985**).

Sesame is predominantly a self-pollinated crop, with natural cross-pollination occurring at an average rate of 4–5%. Achieving self-sufficiency in sesame production remains a primary goal for breeders. To lay a strong foundation for enhancing sesame yield, it is essential to thoroughly evaluate the heterotic effects, individual performance and both general and specific combining abilities of parental lines and their crosses concerning yield and its related traits. Heterotic effects play a critical role in helping breeders identify superior hybrids that demonstrate significantly enhanced yield and yield-contributing attributes, based on the genetic makeup of the parents. Given its self-pollinating nature, sesame is particularly well-suited for exploiting genetic variability through heterosis (**Andrade *et al*., 2014**).

Sesame has recently gained more attention in Egypt due to the increasing demand and attempts to cover the local demand (**Mahmoud *et al*., 2024**). Significant efforts have been made to exploit heterosis for yield improvement using various mating designs.

Diallel and line × tester analyses have proven effective in identifying superior hybrids. Studies revealed that several crosses such as TBS-10 × R-09, TBS-105 × R-09, and TBS-7 × R-20 exhibited significant positive heterosis for seed yield and its related traits (**Rathod *et al*., 2022**). Interspecific hybridization with *Sesamum malabaricum* also demonstrated improvement in vegetative traits; however, a trade-off with seed yield traits was observed, emphasizing the need for careful parent selection (**Kumari, 2023**).

Further investigations confirmed significant heterotic effects across genotypes, especially in hybrids such as TBS-10 × TBS-05 and TBS-07 × TBS-05, which outperformed both their parents and standard checks (**Gore *et al*., 2023**). In a multi-environment study, heterosis for seed yield reached over 150% in some hybrids, indicating the influence of genotype × environment interaction (**Rathod *et al*., 2022**). Crosses like AT-476 × Ingorala-5 and AT-332 × Ingorala-5 also recorded high standard heterosis (**Chaudhari *et al*., 2024**). Several studies confirmed that hybrid vigor remains a promising tool in sesame breeding (**Chaudhary *et al*, 2024; Ramana *et al*., 2024**).

In several studies, significant general combining ability (GCA) and specific combining ability (SCA) effects were reported. Parents like TKG-22, JLS-120, and RT–346 were identified as superior general combiners (**Sikarwar *et al*., 2021; Nehra *et al*., 2023**). Notably, crosses such as JTS-8 × JLS-120 and RT–346 × RT–351 showed high specific combining ability for yield traits, suggesting the potential for hybrid development (**Saleem *et al*., 2023**).

Combining ability studies have revealed genetic architecture controlling yield and its components in sesame. Full diallel and half-diallel analyses indicated that both additive and non-additive genetic variances influence key traits such as seed yield, number of branches and seed oil content (**Rathod *et al*., 2021**).

Recent studies have confirmed that non-additive gene action plays a more significant role in the inheritance of most yield-contributing traits, although some traits like capsule length and oil content may also benefit from additive effects (**Gore *et al*., 2024; Chaudhary *et al*., 2024).** Moreover**, (Serag *et al*., 2024**).

The current study aimed to assess heterotic effects, determine the magnitude of both general and specific combining abilities, estimate heritability to control the genetic expression of studied traits, to identify the most promising parents and hybrids that exhibit maintaining good yield potential.

MATERIALS AND METHODS

The present study was carried out during the two successive seasons of 2022 and 2023 at the Educational Farm of Fac. Agric., Minia University, Egypt . In this study, eight diverse Sesame (*Sesamum indicum* L.) genotypes were considered as parental lines. Names and Pedigree of studied parental genotypes are listed in Table 1.

Table 1. Names and Pedigree of studied parental genotypes.

S	Genotype	Origin	Pedigree
1	Shandaweel 3	Egypt 1987	A line selected from Giza 32 x N. A. 130
2	Giza 32	Egypt 1986	Local variety A line selected from Giza white x type 9
3	Sohag 1	Egypt	A line selected from Giza 32x N.A. 413
4	H.87 family3	Egypt	A line selected from Local 25xN.A. 129
5	H.104 family11	Egypt	Unknown
6	N. A. 194	USA	Unknown
7	H. 115 family4	Egypt	A line selected from B22 x N.A. 32
8	H. 38 family3	Egypt 1986	Unknown

The experimental materials were obtained from Agriculture Research Center, Research Crop Institute, Oil Research Crops Section, Shandaweel Research Station.

In the first season 2022, the eight parental genotypes grow at three different dates; 1st May, 15th May and 30th May, then crossing were made Crosse in all possible combinations using half diallel design except reciprocals to produce 28 F_1 crosses using hand emasculation and pollination as described by **Yermanos (1980).**

In second season 2023, the 36 genotypes included 28 F1 crosses and the 8 parental genotypes were grown in randomized complete blocks design (RCBD) with three replications. The experimental plot was one ridge, 4 m. long and 55 cm width. Sowing took place on 25th May in hills spaced 20 cm apart. Thinning was done twice to one plant/hill. The studied genotypes were evaluated under normal watering regime via irrigation every 12 days. All other cultural practices were done as recommended and followed for El-Minia province.

Data collected

Days to flowering (DF); number of days from sowing to appearance flowers of 50% plants. Days to maturity (DM); number of days from date of sowing to 85% maturity was taken as days to maturity. Number of primary branches per plant (NB/P); the total number of branches arising directly from the main stem at harvest time. Height to first capsule on the main stem cm (HFC); the height from soil surface to first capsule position. Fruiting zone Length cm (FZL); length from first to last capsule position on main stem in (cm). Number of capsules per branch (NC/B); total number of capsules per branch were counted at harvest time. Number of capsules per main stem (NC/MS); total number of capsules per main stem were counted at harvest time. Plant height (cm) (PH); the height from soil surface to plant tip. 1000-seed weight (g) (TSW); the weight of 1000 seeds were taken based on two samples of individual plants and recorded in grams. Seed yield per plant (g) (SY/P); the seed yield of taken plants was weighed in grams on digital balance after cleaning. Seed Oil % (O%); seed sample were taken randomly from the bulk product on a plot basis and oil percentage was determined by Soxhlet apparatus **(A.O.A.C., 2007).**

Biometrical procedures

Analyses of variance for all studied traits were performed according to **Gomez and Gomez (1984)**.

Heterosis

Mid-parent heterosis

Heterosis was determined as the percentage of deviation of the F1 mean from the mean of the mid-parent M.P. for all studied traits.

$$\mathbf{H\ (M.P)\ \%} = (\overline{F1} - \overline{M.P.}) / \overline{M.P.} \times 100$$

$$\mathbf{LSD\ (H\ M.P) = S.E.} \times t / \overline{M.P.}$$

Where; S.E. Standard Error = **t [3MSE/2r] $^{0.5}$**

t = t tabulated value at the error degree of freedom. **MSE** = mean square of error. r = the number of replications.

Better parent heterosis

Better parent heterosis was estimated based on better parent for all studied traits.

$$\mathbf{H\ (H.P)\ \%} = (\overline{F1} - \overline{H.P.}) / \overline{H.P.} \times 100$$

$$\mathbf{LSD\ (H\ BP) = SE \times t / BP}$$

Where; S.E. Standard Error = **t [2MSE/r] $^{0.5}$**

t = t tabulated value at the error degree of freedom. MSE = mean square of error.

r = the number of replications.

The least significant difference (LSD) value from zero can be determined to detect the importance of heterosis:

2 - Combining ability:

On the basis of the entry mean, statistical analysis was performed according to **Griffing (1956)**, method 2, model 1, (Fixed effects for the parents) in Table 2. The variance among parents and F_1 crosses was partitioned into general (GCA) and specific (SCA) combining ability.

Table 2: Form of analysis of variance for the six parents and their 15 F_1 crosses as well as expected mean (E.M.S) squares according to Griffing (1956) method II, model I.

S.O.V	d.f	M.S	E.M.S
Reps (R)	(r - 1)		
Genotypes	(g - 1)		
Parents (P)	(P - 1)		
Crosses (C)	{(P(P-1)/2} - 1		
P vs. C	1		
GCA	(P - 1)	Mg	$\sigma^2_e + (P+2)(1/P-1)\sum g_i^2$
SCA	{(P(P-1)/2}	Ms	$\sigma^2_e + [2/P(P-1)] \sum_i \sum_j s_{ij}^2$
Pooled error	(r - 1)(g - 1)	Me	σ^2_e

Where; d, r, g and p are number of dates, replications, genotypes and parents, respectively.

Estimates of genetic components are obtained as follows:

S.S. GCA = $1/(n+2)[\sum_i(Y_{i.}+Y_{ii})^2 - (4/n)Y_{..}^2]$

S.S. SCA = $\sum_i S_j Y_{ij}^2 - (1/n + 2) \sum_i (Y_{i.}+Y_{ii})^2 + [2/(n+1)(n + 2)]Y_{..}^2$

The general (g_i) and specific (s_{ij}) combining ability effects were computed for each parent and crosses as follows:

$g_i = 1/n+2\ [\ \sum(Y_{i.}+Y_{ii}) - (2/n)Y_{..}]$

$s_{ij} = Y_{ij} - 1/n+2\ [Y_i+Y_{ii}+Y_j+Y_{jj}] + [2/(n+1)(n+2)]Y_{..}$

Standard error of estimates of components and effects for F_1's were computed as follows:

S.E. (g_i) $= [(n-1)\ \sigma^2_e / n\ (n+2)]^{0.5}$

S.E. ($g_i - g_j$) $= [2\ \sigma^2_e / (n+2)]^{0.5}$

S.E. (s_{ij}) $= [(n^2+n+2)\ \sigma^2_e / (n+1)(n+2)]^{0.5}$

S.E. ($s_{ij} - s_{ik}$) $= [2(n+1)\ \sigma^2_e / (n+2)]^{0.5}$

S.E. ($s_{ij} - s_{kl}$) $= [2n\ \sigma^2_e / (n+2)]^{0.5}$

The estimates of phenotypic and genotypic correlations were calculated according to **Miller *et al.* (1958).** Genotypic correlation (r_g) = $\sigma g\ 1.2/(\sigma g_1 \times \sigma g_2)$ where; σg_1 is the genetic standard deviation of the first trait, σg_2 is the genetic standard deviation of the second trait and σg 1.2 is the genetic covariance between the two characters. Phenotypic correlation (r_p) = $\sigma p\ 1.2/(\sigma p_1, \times \sigma p_2)$ where σp_1, and σp_2 are phenotypic standard deviation for each trait and σp 1.2 is the phenotypic covariance between the two traits.

RESULTS AND DISCUSSION

Thirty-six sesame genotypes (8 parents and 28 F_1 crosses derived from 8×8 half diallel crossing) were evaluated to estimate heterosis and combining ability for seed yield and its attributing traits i.e., days to flowering (DF) and maturity (DM), plant height (PH), first capsule height (FCH), fruiting zone length (FZL), capsules no. per branches (CB) and main stem (CMS), 1000 seeds weight (TSW), seed oil content (O%).

Mean squares (variances)

Mean squares of tested traits for genotypes, parents, crosses and parents vs crosses in F_1 are shown in Table 3.

The results indicated that mean squares (variances) owing to genotypes, parents, crosses and parent vs crosses were highly significant ($P < 0.01$) for all tested traits. These results confirmed the genetic diversity among parental genotypes under study which caused highly significant differences in the tested traits. Similar results were obtained by **Rathod *et al*. (2022), (2021), Gore *et al.* (2023)** and **Kumari (2023).**

Table 3. Analysis of variance for the studied traits.

S.V.	d.f.	DF	DM	NB/P	FCH	FZL	NC/B	NC/MS	PH	TSW	O%	SY/P
Rep.	2	7.34	3.73	0.15	14.18	1400.68	121.45	428.68	2241.40	130.81	18.08	3.04
Genotypes	35	277.87**	51.57**	48.42**	3406.08**	1080.04**	3268.09**	12080.24**	3155.83**	481.61**	25.36**	504.95**
Parents P	7	453.12**	132.17**	85.60**	6422.66**	2045.12**	832.45**	4528.52**	5569.57**	131.50**	53.02**	128.62**
Crosses P	27	231.00**	31.61**	40.24**	2326.45**	789.59**	3691.03**	9803.69**	1798.58**	307.38**	16.74**	290.70**
P vs C	1	316.71**	26.46**	9.21**	11440.00**	2166.73**	8898.30**	126409.14**	22905.57**	7636.51**	64.38**	8924.03**
gca	7	153.54**	73.77**	143.15**	2329.09**	1529.69**	3248.88**	7762.97**	6298.40**	242.49**	23.10**	240.74**
sca	28	308.95**	46.02**	24.74**	3675.33**	967.63**	3272.89**	13159.56**	2370.19**	541.39**	25.92**	571.00**
Error	70	2.15	1.21	0.55	4.72	9.82	6.83	5.07	9.86	1.55	0.36	3.36
C.V.%	-	2.51	0.99	8.42	1.73	2.82	3.19	0.99	1.32	3.29	1.11	4.73
gca/sca	-	0.12	0.40	1.45	0.16	0.21	0.25	0.15	0.38	0.11	0.22	0.11

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

Mean performance

Mean performance of 8 parents and their 28 F’s crosses of sesame are presented in Table 4.

The Parental genotype Shandaweel3 (P$_1$) was the earliest flowering parent and had the greatest branches/plant but recorded the lowest values for the shortest fruiting zone length, capsules/main stem, 1000 seed weight and seed yield/plant. Among parental genotypes, Sohag 1 (P$_3$) recorded the higher plants and the first capsule position. However, H.87 family 3 (P$_4$) was the latest maturing parent and possessed the highest capsules/branches. H.104 family 1 parental genotype recorded the greatest capsules/main stem, 1000-seed weight, seed oil% and seed yield/plant. N.A. 196 (P$_6$) parental genotype was the earliest in maturity and possessed the lowest first capsule position. H.115 family 4 (P7) had the highest fruiting zone length.

Concerning F$_1$ ’s crosses, cross (P1 × P5) recorded the highest first capsule length (143.00 cm), number of capsules/branches (197.00), and main stem (422.33) and possessed the heaviest 1000 seed weight (63.67 g) and seed yield (63.67 g).Cross (P$_1$ × P$_4$) gave higher first capsule position and the lowest fruiting zone length. Cross (P1 × P6) was

the latest cross in flowering and maturity, while cross (P$_1$×P$_8$) was the earliest genotype in maturity and had the highest seed oil %.The cross (P$_2$×P$_6$) was earliest cross in flowering but possessed lower first capsule on the stem and the shortest plants. Among crosses, cross (P$_4$×P$_7$) resulted the lowest branches per plant, capsules/branches and stem, 1000 seed weight and seed yield/plant.

Table 4. Mean performance of the studied traits for 8 cultivar parents and their F_1s.

Genot.\Trait	**DF**	**DM**	**NB/P**	**FCH**	**FZL**	**NC/B**	**NC/MS**	**PH**	**TSW**	**O%**	**SY/P**
P1	41.67	105.67	16.00	52.00	70.00	76.33	102.67	122.33	11.33	54.67	11.33
P2	62.67	116.33	2.33	118.00	102.67	49.67	201.33	223.00	17.67	54.00	16.67
P3	69.00	116.00	10.67	175.67	75.67	80.33	152.33	252.00	21.00	60.33	20.67
P4	70.67	116.67	13.00	146.33	87.00	90.67	195.67	231.00	21.67	53.33	21.67
P5	50.33	107.33	10.00	86.33	133.33	60.33	215.33	220.00	33.00	63.33	32.67
P6	42.67	99.67	1.33	45.67	118.33	39.67	173.67	167.00	29.00	55.33	28.00
P7	42.67	106.33	3.33	86.67	141.00	62.67	131.67	230.67	20.33	53.33	19.67
P8	62.33	116.67	9.33	138.33	94.00	61.00	141.67	233.67	22.67	50.33	23.17
p1×p2	59.33	108.33	10.00	122.67	104.00	52.67	281.33	225.33	41.67	55.33	42.00
p1×p3	56.00	110.00	14.00	102.00	143.00	197.00	422.33	243.33	63.67	51.00	63.67
p1×p4	73.33	115.00	8.33	174.67	83.00	101.00	215.33	255.33	28.67	55.00	30.00
p1×p5	63.33	113.67	17.00	132.00	100.67	91.67	252.33	233.33	39.67	53.00	45.67
p1×p6	75.00	115.33	13.33	144.33	112.00	51.00	242.33	255.33	33.67	53.00	33.67
p1×p7	73.67	114.00	8.67	174.33	87.00	59.67	206.33	257.00	35.67	55.00	37.00
p1×p8	50.33	105.33	14.33	97.67	107.67	102.67	219.33	206.00	30.67	57.00	32.17
p2×p3	61.67	111.00	9.00	128.33	135.67	119.67	337.33	263.00	55.67	54.00	55.67
p2×p4	65.00	111.67	11.67	157.33	96.00	97.67	254.33	253.33	41.67	55.00	43.33
p2×p5	65.33	110.00	13.67	141.00	121.00	98.67	247.33	262.33	43.67	57.00	43.40
p2×p6	42.00	106.00	6.00	57.33	102.00	79.67	240.33	162.00	43.67	58.00	43.33
p2×p7	54.67	111.67	3.33	125.33	117.00	69.67	261.33	244.67	40.67	54.00	41.00
p2×p8	59.67	112.67	7.67	124.67	123.67	59.67	237.33	249.00	42.67	56.00	43.67
p3×p4	61.00	111.67	8.00	115.67	123.67	55.67	216.33	241.33	45.67	49.00	45.50
p3×p5	45.33	106.67	9.00	87.67	112.33	87.67	227.33	203.33	40.67	53.00	42.33
p3×p6	44.00	105.67	4.67	112.33	123.67	49.67	226.33	237.33	45.67	56.00	46.17
p3×p7	54.67	114.00	2.67	147.67	115.67	74.67	173.33	262.33	29.67	55.00	30.33
p3×p8	57.33	114.33	8.33	132.33	134.00	78.67	269.33	267.33	54.67	54.00	56.00
p4×p5	62.33	114.33	9.00	124.33	147.00	165.67	323.33	272.33	61.67	56.00	61.17
p4×p6	55.67	110.33	5.33	116.33	115.33	47.67	155.33	231.67	33.67	56.00	35.67
p4×p7	44.33	114.67	1.33	96.33	125.00	29.67	108.33	222.33	23.67	54.00	25.00
p4×p8	56.33	114.67	12.33	136.00	113.33	98.67	282.33	248.67	49.67	51.00	51.23
p5×p6	66.33	115.67	8.67	163.67	90.33	99.67	234.33	255.00	33.67	51.00	35.67
p5×p7	67.67	116.67	10.67	178.33	103.00	108.67	233.33	284.00	43.67	50.00	45.67
p5×p8	68.67	115.33	9.33	161.67	89.00	101.67	252.33	254.00	32.67	51.00	36.00
p6×p7	61.67	110.00	9.33	141.67	116.67	69.67	245.33	257.67	38.67	51.00	41.67
p6×p8	58.33	110.67	6.67	130.00	121.00	97.67	254.33	253.67	54.67	52.00	56.67
p7×p8	59.33	110.33	8.33	139.00	116.00	87.67	285.33	258.67	54.67	52.00	57.00
Average	58.45	111.51	8.80	125.38	111.13	82.06	228.30	237.20	37.81	54.14	38.74
RLSD 5%	2.10	1.57	1.06	3.10	4.48	3.74	3.22	4.49	1.78	0.86	2.62
RLSD 1%	2.74	2.05	1.38	4.06	5.86	4.89	4.21	5.87	2.33	1.12	3.43

P1: Shandaweel 3, P2: Giza 32, P3: Sohag 1, P4: H.87 Family 3, P5: H.104 Family 11, P6: N.A. 194, P7: H.115 Family 4, P8: H.38 Family 3

Heterosis estimates

It’s well-known plant breeders highly depend on available genetic variation raised from the different mating designs to improve any trait. The goal of the hybridization breeding program was to produce some crosses to have more desirable genes. So, some crosses contain new recombination's may be better than their parents to improve any trait of sesame breeding program.

Mid-parent heterosis.

Heterosis expressed as percentage deviation of F1 mean from the mid-parent are shown in Table 5.

Results of mid-parent heterosis for days to flowering were negatively substantial ($P < 0.05$ or 0.01) for seven crosses (P_2×P_3), (P_2×P_4), (P_2×P_6), (P_3×P_4), (P_3×P_5), (P_3×P_6), and (P_4×P_7) with −6.33, −3.62, −28.89, −12.65, −28.42, −24.36 and −14.05%, respectively, indicating these crosses were earlier in flowering than mid-parents For days to maturity, eight crosses (P_1×P_8), (P_2×P_3), (P_2×P_4), (P_2×P_5), (P_2×P_6), (P_3×P_4), (P_3×P_5) and (P_3×P_6) exhibited highly significant negative mid-parent heterosis, indicating that these crosses were earlier in maturity than mid-parents.

Concerning branches / plant, thirteen crosses: (P_1×P_5), (P_1×P_6), (P1× P_8), (P_2×P_3), (P_2×P_4), (P_2×P_5), (P_4×P_6), (P_5×P_6), (P_5×P_7), (P_5×P_8), (P_6×P_7), (P_6×P_8) and (P_7×P_8) showed substantial ($P < 0.01$) positive mid-parent heterosis, indicating that these crosses had potential in producing more branches than their parents.

For First capsule height, five crosses, (P_1×P_3), (P_2×P_3), (P_2×P_6), (P_3×P_4) and (P_3×P_5) had highly significant negative mid-parent heterosis. Therefore, these crosses had lower first capsule position.

With regard to fruiting zone length, it could be detected that among 28 crosses, 16 showed positive substantial ($P < 0.05$ or 0.01) mid-parent heterosis, (p_1×p_3), (p_1×p_4), (p_1×p_6), (p_1×p_8), (p_2×p_3), (p_2×p_4), (p_2×p_5), (p_2×p_7), (p_2×p_8), (p_3×p_4), (p_3×p_5), (p_3×p_6), (p_3×p_7), (p_3×p_8), (p_4×p_5) and (p_4×p_7), supporting that most of crosses resulted in taller fruiting zone than their parents.

For capsules Per branches and main stem, all crosses exhibited highly significant positive mid-parent heterosis except 8 crosses for capsules per branches [(P_1×P_2), (P_1×P_6), (P_1×P_7), (P_2×P_8), (P_3×P_4), (P_3×P_6), (P_4×P_6) and (P_4×P_7)] and 3 crosses for capsules per main stem [(P_3×P_7), (P_4×P_6) and (P_4×P_7)], confirming that most of the crosses were superior than their parents in capsule number. For plant height, all crosses except 3 crosses [(P_2×P_6), (P_3×P_4) and (P_5×P_6)] showed highly significant ($P < 0.01$) positive mid-parent heterosis, indicating that these crosses were tallest than their parents.with regard to thousand seed weight, all crosses except (P_4×P_7) and (P_2×P_8)exhibited substantial ($P < 0.01$) positive mid-parent heterosis, indicating the superiority of these crosses for this trait over than their parents. For seed oil%, only four crosses [(P_1×P_2), (P_1×P_4), (P_1×P_7), (P_4×P_6) and (P1×P8)] showed substantial ($P < 0.05$ or 0.01) positive mid-parent heterosis, indicating that these crosses surpassed their parents in seed oil%.

For seed yield/plant, all crosses except only one (P_4×P_7) exhibited highly significant ($P<0.01$) positive mid-parent heterosis, confirming the superiority of these crosses over their parents in seed yielding.

Table 5. Heterosis in percentage the mid parent for the studied traits.

Crosses \Trait	**DF**	**DM**	**NB/P**	**FCH**	**FZL**	**NC/B**	**NC/MS**	**PH**	**TSW**	**O%**	**SY/P**
p1×**p2**	13.74**	-2.4	9.09	44.31	20.46	-16.40**	85.09**	30.50**	187.36**	1.84*	200.00**
p1×**p3**	1.2	-0.75	5	-10.40**	96.34**	151.49**	231.24**	30.01**	293.81**	-11.30**	297.92**
p1×**p4**	30.56**	3.45**	-42.53**	76.13**	5.73*	20.96**	44.36**	44.53**	73.74**	1.85*	81.82**
p1×**p5**	37.68**	6.73**	30.77**	90.84**	-0.98	34.15**	58.70**	36.32**	78.95**	-10.17**	107.58**
p1×**p6**	77.87**	12.34**	53.85**	195.56**	18.94**	-12.07**	75.39**	76.50**	66.94**	-3.64**	71.19**
p1×**p7**	74.70**	7.55**	-10.34	151.44**	-17.54**	-14.15**	76.10**	45.61**	125.26**	1.85*	138.71**
p1×**p8**	-3.21	-5.25**	13.16**	2.63**	31.30**	49.51**	79.54**	15.73**	80.39**	8.57**	86.47**
p2×**p3**	-6.33**	-4.45**	38.46**	-12.60**	52.15**	84.10**	90.76**	10.74**	187.93**	-5.54*	198.21**
p2×**p4**	-3.62*	-4.01**	34.62**	7.27**	8.54**	32.78**	38.90**	7.65**	107.18**	-1.59**	120.34**
p2×**p5**	3.43*	-3.58**	51.85**	7.16**	21.40**	40.45**	29.38**	13.32**	87.14**	-1.3	89.38**
p2×**p6**	-28.89**	-4.68**	-19.64**	-49.88**	-1.35	24.22**	28.06**	-25.89**	78.47**	1.28	81.06**
p2×**p7**	-2.96	1.16	-50.82**	14.17**	6.69**	9.04**	46.54**	10.90**	71.03**	-4.61**	76.56**
p2×**p8**	4.33**	1.24	7.33	9.49**	15.12**	-6.00*	37.11**	11.92**	80.65**	0.51	88.10**
p3×**p4**	-12.65**	-4.01**	-32.39**	-28.16**	52.05**	-34.89**	24.33**	-0.07	114.06**	-13.78**	114.96**
p3×**p5**	-28.42**	-5.88**	-19.80**	-35.59**	13.85**	13.69**	21.07**	-13.23**	61.23**	-10.17**	69.33**
p3×**p6**	-24.36**	-3.87**	-46.67**	-1.03	19.39**	-26.69**	22.84**	9.12**	74.52**	-3.59**	79.29**
p3×**p7**	-0.73	4.40**	-65.22**	36.56**	4.14*	11.89**	-0.23	19.17**	18.67**	-3.73**	23.64**
p3×**p8**	1.88	3.52**	4.9	16.94**	23.82**	19.59**	59.95**	20.21**	122.12**	-3.57**	130.40**
p4×**p5**	3.03	2.08**	-21.74**	6.88**	33.43**	119.43**	57.34**	20.77**	125.61**	-4.00**	125.15**
p4×**p6**	2.04	2.27**	-34.25**	25.39**	2.17	-25.00**	-20.30**	12.46**	20.72**	-2.33**	29.96**
p4×**p7**	-14.05**	6.67**	-80.72**	5.57**	4.24*	-53.16**	-39.51**	4.79**	-8.97**	-4.14**	-1.96
p4×**p8**	4.84*	4.88**	66.67**	35.10**	-1.22	56.95**	64.53**	14.88**	96.05**	-7.50**	104.66**
p5×**p6**	42.65**	11.76**	52.94**	147.98**	-28.21**	99.33**	20.48**	31.78**	8.60**	-14.04**	17.58**
p5×**p7**	49.63**	11.70**	118.18**	144.66**	-21.31**	100.41**	34.44**	37.94**	59.11**	-12.79**	70.54**
p5×**p8**	38.72**	7.29**	55.56**	81.14**	-26.85**	81.82**	52.39**	19.34**	24.44**	-8.25**	39.13**
p6×**p7**	44.53**	6.80**	300.00**	114.11**	-10.03**	36.16**	60.70**	29.59**	56.76**	-6.13**	74.83**
p6×**p8**	18.51**	2.89**	42.86**	44.09**	2.74	79.39**	70.69**	20.54**	127.78**	-1.89*	140.00**
p7×**p8**	13.02**	-1.05	31.58**	2.35E+07	-1.28	41.78**	108.78**	1.14E+02	154.26**	0.32	166.15**
LSD 5%	2.07	1.55	1.04	3.06	4.42	3.69	3.17	4.43	1.75	0.85	2.59
LSD 1%	2.75	2.06	1.39	4.07	5.87	4.9	4.21	5.88	2.33	1.12	3.43

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

Better-parent heterosis*:*

Heterosis based on better parent for the studied crosses are presented in Table 6.

For days to flowering, five crosses: (P_2×P_8), (P_3×P_4), (P_3×P_5), (P_3×P_8) and (P_4×P_8) revealed substantial (P<0.05 or 0.01) negative better-parent heterosis, indicating these crosses were earlier than their better parent by -4.28, -11.59, -9.93, -8.02 and -9.63%, respectively. However, five crosses (P_2×P_3), (P_2×P_4), (P_2×P_8), (P_3×P_4) and (P_4×P_8) with respect to days to maturity had substantial (P<0.05 or 0.01) negative better-parent heterosis by -4.31, -4.01, -3.15, -3.74 and -1.71%, respectively. From these results, it could be noticed that crosses (P_2×P_8), (P_3×P_4) and (P_4×P_8) had negative and significant better-parent heterosis for flowering and maturity under watering normal Therefore, these crosses were earlier than their better parent and considered to be promising for further studies. For branches per plant, out of 28 crosses, only three cross (P_2×P_3), (P_2×P_6) and (P_6×P_7) exhibited highly significant (P<0.01) positive better parent heterosis.

However, only nine crosses with regard fruiting zone length had substantial (P ≤ 0.05 or 0.01) positive better-parent heterosis. These crosses were (P_1×P_2), (P_1×P_8), (P_2×P_3), (P_2×P_8), (P_3×P_4), (P_3×P_6), (P_3×P_8), (P_4×P_5), and (P_4×P_8).

For capsules number either per branch or per main stem, it could be detected that eighteen crosses for capsules per branch and all crosses, except (P_4×P_6) and (P_4×P_7) exhibited highly significant (P <0.01) positive better parent heterosis, indicating that most of studied crosses surpassed their better parent for number of capsules per plant. For plant height, nineteen crosses showed highly significant ($P < 0.01$) positive better-parent heterosis and also there were seven crosses: ($P_1 \times P_3$),($P_1 \times P_8$),($P_2 \times P_6$),($P_3 \times P_4$) ,($P_3 \times P_5$),($P_3 \times P_6$),($P_4 \times P_7$) had highly significant ($P < 0.01$) negative better-parent heterosis, indicating these crosses could be used for further studies to select for shortness varieties. All crosses except ($P_4 \times P_7$), ($P_5 \times P_6$), and ($P_5 \times P_8$) had highly significant ($P < 0.01$) positive better-parent heterosis, supporting the superiority of these crosses over their better-parent concern 1000 seed weight. Only five crosses ($P_1 \times P_3$), ($P_2 \times P_4$), ($P_2 \times P_6$), ($P_2 \times P_8$), and ($P_7 \times P_8$) showed substantial ($P < 0.05$ or 0.01) positive better-parent heterosis for oil seed %.

All crosses exhibited substantiated ($P<0.05$ or 0.01) positive better-parent heterosis for seed yield/plant, indicating the superiority of these crosses in seed yield/plant compared to their better-parents.

Table 6. Heterosis in percentage the batter parent for the studied traits.

Cross\ Trait	DF	DM	NB/P	FCH	FZL	NC/B	NC/MS	PH	TSW	O%	SY/P
p1×p2	42.40**	2.52**	-37.50**	3.95*	1.3	-31.00**	39.74**	1.05	135.85**	1.22	152.00**
p1×p3	34.40**	4.10**	-12.50**	-41.94**	88.99**	145.23**	177.24**	-3.44**	203.17**	-15.47**	208.06**
p1×p4	76.00**	8.83**	-47.92**	19.36**	-4.6	11.40**	10.05**	10.53**	32.31**	0.61	38.46**
p1×p5	52.00**	7.57**	6.25	52.90**	-24.50**	20.09**	17.18**	6.06**	20.20**	-16.32**	39.80**
p1×p6	80.00**	15.72**	-16.67**	177.56**	-5.35*	-33.19**	39.54**	52.89**	16.09**	-3.05**	20.24**
p1×p7	76.80**	7.89**	-45.83**	101.15**	-38.30**	-21.83**	56.71**	11.42**	75.41**	0.61	88.14**
p1×p8	20.80**	-0.32	-10.42**	-29.40**	14.54**	34.50**	54.82**	-11.84**	35.29**	4.27**	38.85**
p2×p3	-1.6	-4.31**	-15.63**	-26.94**	32.14**	48.96**	67.55**	4.37**	165.08**	-10.50**	169.35**
p2×p4	3.72	-4.01**	-10.26*	7.52**	-6.49*	7.72**	26.32**	9.67**	92.31**	1.85*	100.00**
p2×p5	29.80**	2.48**	36.67**	19.49**	-9.25**	63.54**	14.86**	17.64**	32.32**	-10.00**	32.86**
p2×p6	-1.56	6.35**	157.14**	-51.41**	-13.80**	100.84	19.37**	-27.35**	50.57**	7.41**	54.76**
p2×p7	28.13**	5.02**	0	6.21**	-17.02**	11.17**	29.80**	6.07**	100.00**	0	108.47**
p2×p8	-4.28*	-3.15**	-17.86**	-9.88**	20.45**	-2.19	17.88**	6.56**	88.24**	3.70**	88.49**
p3×p4	-11.59**	-3.74**	-38.46**	-34.16**	42.15**	-38.60**	10.56**	-4.23**	110.77**	-18.78**	110.00**
p3×p5	-9.93**	-0.62	-15.63**	-50.09**	-15.75**	9.13**	5.57**	-19.31**	23.23**	-16.32**	29.59**
p3×p6	3.13	6.02**	-56.25**	-36.05**	4.51*	-38.17**	30.33**	-5.82**	57.47**	-7.18**	64.88**
p3×p7	28.13**	7.21**	-75.00**	-15.94**	-17.97**	-7.05**	13.79**	4.10**	45.90**	-8.84**	46.77**
p3×p8	-8.02**	-1.44	-21.88**	-24.67**	42.55**	-2.07**	76.81**	6.08**	141.18**	-10.50**	141.73**
p4×p5	23.84**	6.52**	-30.77**	-15.03**	10.25**	82.72**	50.15**	17.89**	86.87**	-11.58**	87.24**
p4×p6	30.47**	10.70**	-58.97**	-20.50**	-2.54	-47.43**	-20.61**	0.29	16.09**	1.2	27.38**
p4×p7	3.91	7.84**	-89.74**	-34.17**	-11.35**	-67.28**	-44.63**	-3.75**	9.23	1.25	15.38**
p4×p8	-9.63**	-1.71*	-5.13	-7.06**	20.57**	8.82**	44.29**	6.42**	119.12**	1.32	121.15**
p5×p6	55.47**	16.05**	-13.33*	89.58**	-32.25**	65.19**	8.82**	15.91**	2.02	-19.47**	9.18*
p5×p7	58.59**	9.72**	6.67	105.77**	-26.95**	73.40**	8.36**	23.12**	32.32**	-21.05**	39.80**
p5×p8	36.42**	7.45**	-6.67	16.87**	-33.25**	66.67**	17.18**	8.70**	-1.01	-19.47**	10.20*
p6×p7	44.53**	10.37**	180.00**	63.46**	-17.26**	11.17**	41.27**	11.71**	33.33**	-7.83**	48.81**
p6×p8	36.72**	11.04**	-28.57**	-6.02**	2.25	60.11**	46.45**	8.56**	88.51**	-6.02**	102.38**
p7×p8	39.06**	3.76**	-10.71	0.48	-17.73**	39.89**	101.41**	10.70**	141.18**	3.31**	146.04**
LSD0.05	4.27	1.55	0.93	3.18	0.7	5.67	2.39	0.33	3.24	0.35	2.5
LSD0.01	5.66	2.05	1.23	4.22	0.93	7.53	3.18	0.44	4.3	0.46	3.32

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

Combining ability:

General combining ability.

Mean squares of general and specific combining ability under normal watering were highly significant for all studied traits (Table 3), indicating presence of differences among the eight parents for GCA and among the 28 F_1 crosses for SCA. GCA variance was greater in magnitude than SCA variance (GCA/SCA more than unity) for only one trait, NB/P, revealing that additive gene action plays a major role in inheritance of this trait. Meanwhile, SCA variances were higher than GCA variances (GCA/SCA less than unity) for the rest traits., indicating that non-additive gene actions (dominance) govern the inheritance of these traits.

General combining ability for each parent for the studied traits under normal watering are recorded in Table 7. General combining ability for P_1 (Shandaweel 3) was highly significant/positive for B/P and C/B, so it was a good general combiner for these traits, while it showed significant ($P < 0.05$) negative effect for DM, this may indicate the ability to use this parent as a source for earliness. Parent 2 (Giza 32) revealed a good general combining ability for NC/MS and O%. Parent 3 (Sohag 3) proved to be a good general combiner for all traits except DF, DM, NB/P and FZL. However, parent 4 (H.38 Family-1) was a good general combiner for five traits i.e., FCH, NC/B and PH, since it recorded highly significant positive effects for these traits. Parent 5 (H.38 Family-3) exhibited significant ($P < 0.05$ or 0.01) positive effects for all traits except DF, DM and FZL it proved to be a good general combiner for most of studied traits.

However, P_6 (N.A.194) possessed highly significant ($P < 0.05$) negative GCA effects for DF, DM and FZL indicating that this parent could be used as a source for earliness. Parent 7 (H.45 Family-1) showed highly significant ($P < 0.01$) negative effect for DF and highly significant ($P < 0.01$) positive effects for three traits; FCH and PH. Indicating that this parent was a good general combiner for these traits. Parent 8 (H.38 Family-3) considered to be a good general combiner for NB/P, FCH, NC/MS, PH, TSW, and SYP, where it recorded significant ($P < 0.05$ or 0.01) positive effects for these traits. From the obtained results, it could be concluded that three parents (P_3, P_5, and P_8) recorded significant ($P < 0.05$ or 0.01) effects in most of the studied traits indicating their rich source to improve yield and may be attributed to breeding programs. These results agree with those obtained by **Saleem *et al.* (2023), Sikarwar *et al.* (2021) , Rathod *et al.* (2021), Mahmoud *et al.* (2024) and Serag *et al.* (2024**

Table 7. General combining ability GCA effects of the eight parental genotypes for the studied traits.

Parent\Trait	DF	DM	NB/P	FCH	FZL	NC/B	NC/MS	PH	TSW	O%	SY/P
P1	0.83	-1.06*	3.85**	-7.52**	-10.82**	9.45**	-1	-33.28**	-4.40**	0.14	-4.18**
P2	0.69	0.04	-1.32	-22.25**	-5.62**	-6.98**	20.73**	-1.08	0.47	1.01**	-0.29
P3	-0.81	0.18	-0.22	12.78**	4.95**	7.68**	12.23**	5.78**	3.73**	0.54*	3.24**
P4	3.33**	2.21**	0.28	9.15**	-0.12	6.35**	-10.80**	5.78**	-1.23*	-0.46*	-1.34*
P5	1.36*	0.34	1.82**	10.58**	11.48**	12.75**	14.63**	3.15*	2.13**	1.04**	2.66**
P6	-3.78**	-3.06**	-2.25**	-16.25**	-5.62**	-17.25**	-10.90**	-3.35*	0.13	0.04	0.02
P7	-2.48**	0.04	-2.82**	5.32**	4.28**	-12.18**	-27.80**	13.52**	-3.30**	-0.96**	-3.16**
P8	0.86	1.31**	0.65*	8.18**	1.45	0.18	2.90**	9.48**	2.47**	-1.36**	3.05**
S.E. (gi)	0.43	0.33	0.22	0.64	0.93	0.77	0.67	0.93	0.37	0.18	0.54
S.E. (gi-gj)	0.66	0.49	0.33	0.97	1.4	1.17	1.01	1.4	0.56	0.27	0.82

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

P1: Shandaweel 3, P2: Giza 32, P3: Sohag 1, P4: H.87 Family 3, P5: H.104 Family 11, P6: N.A. 194, P7: H.115 Family 4, P8: H.38 Family 3

Specific combining ability effects for the crosses.

Out of 28 crosses, 17 crosses recorded significant ($P < 0.05$ or 0.01) negative or positive SCA effects for DF (Table 8). Seven of them ($P_1×P_8$), ($P_2×P_6$), ($P_2×P_7$), ($P_3×P_5$), ($P_3×P_6$), ($P_4×P_7$) and ($P_4×P_8$) exhibited negative highly significant negative SCA effects, indicating that these crosses were a good combination for flowering earliness. For DM, among the crosses. Eight crosses of ($P_1×P_2$), ($P_1×P_8$), ($P_2×P_4$), ($P_2×P_6$), ($P_3×P_4$), ($P_3×P_5$), ($P_3×P_6$) and ($P_7×P_8$) showed significant ($P < 0.05$) negative SCA effects, revealing these crosses were a good combination for maturity earliness. Among 28 crosses, 18 revealed significant ($P < 0.05$ or 0.01) negative or positive SCA effects for NB/P, ten of them recorded significant ($P < 0.05$ or 0.01) positive effects. Considering these combinations were a good to produce more branch :($P_1×P_3$), ($P_1×P_5$), ($P_1×P_6$), ($P_2×P_3$), ($P_2×P_4$), ($P_2×P_5$), ($P_4×P_8$), ($P_5×P_7$), ($P_6×P_7$) and ($P_7×P_8$).

All crosses except four crosses, $P_1×P_6$, $P_1×P_7$, $P_4×P_6$ and $P_5×P_8$ showed highly significant ($P < 0.01$) positive or negative SCA effects for FCH, nine of them exhibited highly significant negative SCA effects ($P_1×P_3$), ($P_1×P_8$), ($P_2×P_6$), ($P_3×P_4$), ($P_3×P_6$), ($P_3×P_8$), ($P_4×P_5$), ($P_4×P_7$) and ($P_4×P_8$), indicating that these crosses were better than their parents concerning this desirable trait. However, nine crosses ($P_1×P_2$),($P_1×P_5$), ($P_1×P_6$), ($P_1×P_7$), ($P_2×P_3$), ($P_2×P_6$), ($P_3×P_8$), ($P_4×P_6$) and ($P_4×P_8$) possessed substantial ($P < 0.05$ or 0.01) positive SCA effects for FZL, indicating that these crosses are distinguished for this trait. 16 crosses had substantial ($P < 0.05$ or 0.01) negative or positive SCA effects.

For NC/B ranged from 5.75 of ($P_5×P_8$) to 96.89 of ($P_1×P_3$) and ranged for 6.50 and 182.80 of NC/MS for some crosses , indicating that these crosses more capsules/plant are considered superior than their parents for capsules number per branch and main stem .

For plant height, for ten crosses exhibited significant ($P < 0.05$ or 0.01) positive SCA effects, indicating these crosses could be used as a material for selecting the tallest of plants.

Out of the 28 crosses studied, 18 crosses possessed highly significant positive SCA effects, indicating that most of the crosses are promising and good combinations for improvement of this trait.

For seed oil, ten crosses recorded significant ($P <0.05$ or 0.01) positive SCA effects, indicating the superiority of these crosses for this trait over their parents. Concerning seed yield/plant, seventeen of them recorded substantial ($P <0.05$ or 0.01) positive SCA effects (14 highly significant positive SCA effects and 3 crosses possessed only significant positive SCA effects), indicating that most of tested crosses surpassed their parents regarding this trait and considered to be good combinations for this trait.

Table 8. Specific combining ability effects for the crosses.

Cross\ Trait	DF	DM	NB/P	FCH	FZL	NC/B	NC/MS	PH	TSW	O%	SY/P
P1XP2	-0.64	-2.16*	-1.33	28.82**	7.97**	-32.78**	33.30**	20.16**	7.79**	0.04	7.73**
P1XP3	-2.47	-0.63	1.57*	-26.88**	-29.60**	96.89**	182.80**	42.30**	26.52**	-3.82**	25.87**
P1XP4	10.73**	2.34*	-4.60**	47.42**	-13.20**	35.22**	-1.16	21.30**	-3.51**	1.18*	-3.22
P1XP5	2.7	2.87**	2.54**	3.99	21.54**	-13.51**	10.40**	12.93**	4.12**	-2.32**	8.45**
P1XP6	19.50**	7.94**	2.94**	42.49**	23.64**	-24.18**	25.94**	-33.57**	0.12	-1.32*	-0.91
P1XP7	16.86**	3.51**	-1.16	47.59**	36.40**	-20.58**	6.84**	13.23**	5.55**	1.68**	5.60*
P1XP8	-9.80**	-6.43**	1.04	-26.94**	-7.76**	10.05**	-10.86**	20.26**	-5.21**	4.08**	-5.44*
P2XP3	3.33*	-0.73	1.74*	12.52**	32.54**	35.99**	76.07**	1.43	13.65**	-1.69**	13.98**
P2XP4	2.53	-2.09*	3.90**	45.49**	-22.40**	15.32**	16.10**	13.43**	4.62**	0.31	6.22*
P2XP5	4.83**	-1.89	4.37**	29.06**	-16.33**	9.92**	-16.33**	-5.94*	3.25**	0.81	2.29
P2XP6	-13.37**	-2.49*	0.77	-27.78**	12.10**	20.92**	2..20	22.56**	5.25**	2.81**	4.86**
P2XP7	-2. 00**	0.07	-1.33	18.66**	-22.80**	5.85**	40.10**	7.36*	5.69**	-0.19	5.71**
P2XP8	-0.34	-0.19	-0.46	14.79**	0.7	-16.51**	-14.60**	-39.60**	1.92	2.21**	2.17
P3XP4	0.03	-2.23*	-0.86	-31.21**	-19.96**	-41.35**	-13.40**	4.56	5.35**	-5.22**	4.86**
P3XP5	-13.67**	-5.36**	-1.40*	7.36**	-6.56*	-15.75**	-27.83**	16.20**	-3.01*	-2.72**	-2.3
P3XP6	-9.87**	-2.96**	-1.66*	-7.48**	-8.46**	-23.75**	-3.3	-77.64**	3.99**	1.28*	4.17*
P3XP7	-0.5	2.27*	-3.10**	3.96	-3.36	-3.81	-39.40**	-11.84**	-8.58**	1.28*	-8.48**
P3XP8	-1.17	1.34**	-0.9	-11.24**	6.14*	-12.18**	25.90**	-3.47	10.65**	0.68	10.98**
P4XP5	-0.8	0.27	-1.90**	-19.68**	-10.16**	63.59**	91.20**	-42.80**	22.95**	1.28*	21.11**
P4XP6	-2.34	-0.33	-1.50*	-1.18	18.27**	-24.41**	-51.26**	-2.3	-3.05*	2.28**	-1.75
P4XP7	-14.97**	0.91	-4.93**	-41.41**	0.37	-47.48**	-81.36**	5.83*	-9.61**	1.28*	-9.24**
P4XP8	-6.30**	-0.36	2.60**	-6.28**	21.54**	9.15**	61.94**	14.86**	10.62**	-1.32*	10.79**
P5XP6	10.30**	6.87**	0.3	44.39**	-1.66	21.19**	2.3	-5.34	-6.41**	-4.22**	-5.75**
P5XP7	10.33**	4.77**	2.87**	38.16**	-1.9	25.12**	18.20**	-31.54**	7.02**	-4.22**	7.43**
P5XP8	8.00**	2.17*	-1.93**	17.62**	-10.73**	5.75*	6.50**	-1.17	-9.75**	-2.82**	-8.44**
P6XP7	9.46**	1.51	5.60**	28.32**	-6.80*	16.12**	55.74**	36.63**	4.02**	-2.22**	6.07**
P6XP8	2.80*	0.91	-0.53	14.12**	-17.96**	31.75**	34.04**	10.66**	14.25**	-0.82	14.86**
P7XP8	2.5	-2.53*	1.70*	2.56	4.14	16.69**	81.94**	-6.54*	17.69**	0.18	18.38**
S.E.(sij)	1.33	1	0.67	1.97	2.84	2.37	2.04	2.85	1.13	0.54	1.66
S.E.(sij-sik)	1.97	1.47	0.99	2.91	4.2	3.51	3.02	4.21	1.67	0.8	2.46
S.E.(sij-skl)	1.86	1.39	0.94	2.75	3.96	3.31	2.85	3.97	1.57	0.76	2.32

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

Rank correlation coefficients for the studied traits between means of the eight parents, means of their GCA effects, and means of 28 crosses ($\bar{x}F_1$) and their SCA effects are shown in Table 9.

High positive significant (P <0.05 or 0.01) correlation between means ($\bar{x}P$) and their GCA effects was detected for DM (0.82), NB/P (0.88), PH and Oil% (0.745), as

Based on these results, the correlation between mean performance and GCA effects could be an indication for the performance of a parent, and it was possible to use the parent means to predict cross values. Other traits either did not show significant correlation between parents' means and GCA effects.

Correlation coefficients between ($\bar{x}F_1$) and SCA effects were highly significant and positive for all studied traits except for FZL and PH.

Genotypic and Phenotypic Correlation

Genotypic and phenotypic correlation coefficients are presented in Table 10.

Days to 50% flowering showed highly significant (P<0.05 or 0.01) genotypic and phenotypic correlations with each of days to maturity, number of branches per plant and height of first capsule. While **days to 50% flowering** showed negative genotypic and phenotypic correlation with fruiting zone. **Days to maturity** showed high significant positive genotypic and phenotypic correlation with height of first capsule. Negative genotypic and phenotypic correlation coefficients were found among days to flowering and maturity and oil percent. **Days to flowering** showed significant positive genotypic and phenotypic correlation with each of NCB, C/P, TSW and seed yield per plant. **Days to maturity** showed negative genotypic and phenotypic correlation with seed yield/plant, TSW and oil percent.

Table 9. Correlation coefficients between parents mean and their gca effects and F_1s crosses and their sca effects.

	$\bar{X}$ **P, gca**	$\bar{X}$ **F_1, sca**
DF	0.576	0.948**
DM	0.822*	0.845**
NB/P	0.878**	0.669**
FCH	0.535	0.777**
FZL	0.488	-0.172
NC/B	0.702	0.921**
NC/MS	0.418	0.937**
PH	0.903**	-0.340
TSW	0.555	0.937**
O%	0.745*	0.893**
SY/P	0.629	0.934**

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

Table 10. Genotypic and phenotypic correlation coefficients among the studied traits.

	r	**DF**	**DM**	**NB/P**	**HFC**	**LFZ**	**NC/B**	**NCMS**	**PH**	**TSW**	**OIL**
DM	**r g**	0.77**									
	r p	0.73**									
NB/P	**r g**	0.37*	0.13								
	r p	0.36**	0.12								
HFC	**r g**	0.88**	0.80**	0.21							
	r p	0.87**	0.77**	0.20							
LFZ	**r g**	0.23	0.35*	0.01	0.29						
	r p	0.22	0.33*	0.02	0.29						
NC/B	**r g**	0.23	0.15	0.48**	0.19	-0.14					
	r p	0.23	0.15	0.47**	0.19	-0.14					
NC/MS	**r g**	0.26	0.05	0.31	0.18	-0.05	0.71**				
	r p	0.26	0.05	0.31	0.18	-0.05	0.71**				
PH	**r g**	0.00	0.06	-0.28	0.10	0.26	0.04	0.11			
	r p	-0.01	0.06	-0.27	0.10	0.26	0.04	0.11			
TSW	**r g**	0.07	-0.04	0.13	0.11	0.02	0.56**	0.86**	0.14		
	r p	0.07	-0.04	0.13	0.11	0.02	0.56**	0.86**	0.14		
OIL	**r g**	-0.23	-0.33*	-0.06	-0.25	0.18	-0.18	-0.19	-0.06	-0.19	
	r p	-0.22	-0.32	-0.05	-0.25	0.18	-0.18	-0.20	-0.06	-0.20	
SY/P	**r g**	0.10	-0.01	0.16	0.15	0.03	0.56**	0.86**	0.15	1.00**	-0.23
	r p	0.10	-0.01	0.16	0.14	0.04	0.55**	0.85**	0.15	0.98**	-0.22

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

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الملخص العربي:

القدرة على التآلف لبعض التراكيب الوراثية وقوة الهجين لهجن الجيل الأول في السمسم

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أجرى هذا البحث في موسمي 2022 و2023 بالمزرعة التعليمية لكلية الزراعة، جامعة المنيا، لتقدير القدرة العامة على التآلف لثمانية آباء مختلفة وراثياً من السمسم بالإضافة إلي قوة الهجين والقدرة الخاصة على التآلف لهجنها الثمانية والعشرين، أظهرت النتائج وجود تباينات عالية المعنوية في كل الصفات تحت الدراسة بين التراكيب الوراثية ، الآباء ، الهجين ،الآباء مقابل الهجن وفيما عدا الهجين P_7xP_4 أظهرت كل الهجن قوة هجين عالية المعنوية لصفة محصول البذور/نبات مما يؤكد تفوق هذه الهجن على متوسط الأبوين في إنتاجية البذور، كما سجلت كل الهجن قوة هجين موجبة معنويه أو عالية المعنوية علي أساس الأب الأفضل ، وكان الأب رقم ٨ أفضل الآباء للقدرة العامة على التآلف لصفة محصول البذور/نبات، كما سجلت الآباء الثالث والخامس والثامن تأثيرات معنوية موجبة للقدرة العامة علي التآلف وهذا يؤشر على أنها مصدر لتحسين محصول البذور، وسجل ١٧ هجين من الهجن تأثيرات معنوية موجبة للقدرة الخاصة على التآلف لصفة محصول البذور/نبات مما يدل على أن معظم الهجن المختبرة تفوقت على آبائها وتعتبر توليفات جيدة لصفة محصول البذور.