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RESEARCH ARTICLE

Breeding sesame for resistance to charcoal rot caused by *Macrophomina phaseolina*

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Abstract

To assess the combining ability, heterosis, and heritability of growth traits, yield and its attributes, seeds oil content (%), and disease infection percentage in sesame, a half diallel set comprising five diverse parental genotypes was studied at the Experimental Farm of the Agriculture Faculty, Suez Canal University, Ismailia, Egypt. The experiment was laid out using a Randomized Complete Block Design with three replications. Highly significant mean squares were found for both general combining ability (GCA) and specific combining ability (SCA) for all studied traits. The narrow sense heritability ranged from low to high, with values ranging from 3.3 to 76.43% across the studied traits. In addition, these findings suggest that both dominance effects and environmental factors have a major impact on the traits under study. Shandaweel 3 (P_4) exhibited positive and highly significant general combining ability (GCA) effects for all studied traits. This suggests that this parent could be a valuable source of genes for improving yield potential. It showed a highly significant negative effect on disease infection percentage, indicating its potential to contribute genes for disease resistance. Based on its performance as the best general combiner and possessing desirable genes for decreasing charcoal rot infection while increasing resistance to charcoal rot. Furthermore, the parent M1A38 (P_3) demonstrated positive and highly significant effects for most of the studied traits, along with a highly significant negative effect on disease infection percentage. The crosses (P_1 x P_4), (P_3 x P_5), (P_2 x P_4), and (P_4 x P_5) exhibited desirable specific combining ability (SCA) effects and significant heterosis values for most of the studied traits. The cross (P_3 x P_4) displayed significant heterosis values for most of the studied traits as well. These crosses might be used in sesame breeding programs to produce high-yielding ability and highly resistant pure lines.

Keywords: Sesamum indicum, Half diallel analysis, Heterosis, Combining ability, Heritability, Charcoal rot, *Macrophomina phaseolina*

1. Introduction

Sesame (*Sesamum indicum* L., Pedaliaceae) is a highly significant oilseed crop known for its high oil content (40-60%), good keeping quality, and rich nutritional value. It is a diploid (2n=26) dicotyledonous plant and one of the earliest cultivated oilseed crops, cultivated extensively in tropical and subtropical regions for its edible oil, vitamins, amino acids, and proteins (20-40%). Sesame is primarily a self-pollinated crop, with cross-pollination occurring at a mean rate of around 4 to 5 percent. Achieving self-sufficiency in sesame production is a key objective for sesame breeders. Therefore, to establish a robust foundation for achieving high yields of sesame, it is crucial to meticulously gather information on heterotic effects, individual performance, general and specific combining abilities of parent plants regarding yield and related traits. Heterotic effects assist breeders in identifying desirable hybrids that exhibit significantly positive traits for yield and yield attributing characteristics, based on the genetic potential of the parent plants.

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Sesame, being a self-pollinated crop, is well-suited for harnessing variability through heterosis (Andrade *et al.,* 2014). The utilization of heterosis has proven successful in enhancing both seed and oil yields in sesame. Reports on heterosis in sesame date back to as early as 1945, as documented by Pal. Subsequent studies have further confirmed the significance of heterosis as a valuable tool for improving crops, including sesame. In any breeding program, it is essential to identify superior parents for hybridization and crosses to expand genetic variability, thereby enabling the selection of superior genotypes. The success of a heterotic hybrid combination depends on the combining abilities of its parents. Identifying the optimal parental combination is the most crucial challenge for breeders because both general combining ability and specific combining ability have a significant influence, as noted by Bajaj *et al.* (1997). General combining ability (GCA) is an invaluable tool for parent selection in breeding programs. It indicates that even if one parent performs poorly in a combination, it can still contribute positively when paired with the right partner. On the other hand, specific combining ability (SCA) helps determine the type of gene action involved in hybrid combinations. A higher specific combining ability (SCA) indicates that the best general combiners can result from additive-by-additive gene action (Reddy *et al.,* 1984; Krishnadoss *et al.*, 1986, 1987; Ramakrishnan and Soundarapandian, 1990). The combining ability analysis developed by Griffing (1956) is a widely used biometrical tool in diallel analysis. It helps identify the best combiners that can be used either to exploit heterosis or to introduce and fix promising genes in breeding programs. Developing inbred lines with high specific combining ability (SCA) and general combining ability (GCA) for crucial yield traits remains a primary objective in sesame hybrid breeding programs. Combining ability analysis plays a crucial role in the selection of parents and understanding the extent and nature of gene action for economically significant traits in sesame. It is considered a powerful tool for identifying the best combiners in sesame breeding programs, as highlighted by Rajaravindran *et al.* (2000), Kouighat *et al.* (2020), and Fazal *et al.* (2022). Higher specific combining ability (SCA) effects are indicative of dominant gene effects, while higher general combining ability (GCA) effects suggest additive gene effects. Epistatic effects are also possible due to the small magnitude of both general combining ability (GCA) and specific combining ability (SCA) effects, as noted by Fehr (1993). Performing combining ability analysis can provide insights into gene effects for specific traits under selection. With this information, breeders can determine the best strategy for selecting parents or conducting breeding programs to enhance desirable trait performance in sesame, as highlighted by Praveenkumar (2009). Numerous studies have shown that both general combining ability (GCA) and specific combining ability (SCA) play a crucial role in influencing multiple traits in sesame, as documented by Banerjee and Kole (2009), Joshi *et al.* (2015) and Dissanayake *et al.* (2020). The use of analyses such as diallel is instrumental in determining combining abilities in breeding programs. However, there are certain restrictions associated with this method. These include the need for genetic assumptions in diallel analysis and the necessity for extended mating patterns, which can sometimes be challenging to implement. (Kempthorne, 1957; Baghery *et al.*, 2022).

Improving sesame productivity involves a combination of selection and hybridization strategies. Furthermore, understanding genetic parameters such as heritability is crucial for choosing an appropriate crop improvement strategy in sesame, high heritability has been recorded for traits such as plant height, number of branches, number of capsules per plant, and seed yield, as indicated by studies conducted by Saxena and Bisen (2017), Divya *et al.* (2018), and

Gedifew *et al.* (2023). Additionally, high heritability has been observed in traits such as the number of seeds per capsule, 1000 seed weight, and seed oil content in sesame, as reported by Saxena and Bisen (2017) and Gedifew *et al.* (2023). Heritability quantifies the strength of the relationship between genotype and phenotype, as noted by Shukla *et al.* (2004). Conditions with high heritability are considered optimal for selection processes, as emphasized by Larik *et al.* (2000).

Charcoal stem rot disease is a significant soil-borne disease in sesame, causing substantial losses in seed yield. Charcoal stem rot disease in sesame is attributed to the fungus *Macrophomina phaseolina* (Tassi.) Goid. Charcoal stem rot disease caused by Macrophomina phaseolina (MP) is a widespread problem globally, as documented by Mihail and Taylor (1995), Rajput *et al*. (1998), and El-Bramawy and Wahid (2006). Charcoal stem rot disease can indeed affect sesame plants at all stages of their life cycle, with incidence rates ranging from 10 to 25%, resulting in significant yield losses, as reported by Wang *et al.* (2017). Common symptoms of this disease include sudden wilting, spot blight on the plant stem, browning and blackening of stems, and a gradual upward spread of the syndrome. This can lead to the eventual death of the plant as the blackened and infected stem extends. The peak stage of the disease typically occurs during the final flowering stage. When infected by the Macrophomina phaseolina (MP) pathogen, the roots of sesame plants become brittle and turn black. Infected plants may also exhibit blackened and prematurely cracked capsules, along with shriveled seeds of low yield and quality. Charcoal stem rot disease has a wide host range and geographic distribution, as highlighted by Jana *et al.* (2005), Babu *et al.* (2010) and Saleh *et al.* (2010).

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

2. Materials and methods

2.1. Isolation and identification

Samples of diseased sesame plants displaying symptoms of Charcoal rot were collected from sesame fields. The infected roots and stems of each plant sample were carefully washed with tap water, cut into small segments, and then surface sterilized by immersing them in a 1% sodium hypochlorite solution for two minutes. They were subsequently rinsed three times with sterile water and dried between sterilized filter papers. The segments were then placed onto Petri dishes containing potato dextrose agar (PDA) medium supplemented with streptomycin sulfate. The plates were incubated at a temperature of 25±5ºC for five days, following the protocol outlined by Bedawy and Moharm (2019). The fungal growth obtained was purified using the hyphal tip technique and identified based on cultural and morphological characteristics as described by Domsch *et al.* (1980) and Sutton (1980). The identification was further confirmed by the Mycological Research and Disease Survey Department at the Plant Pathology Research Institute, Agricultural Research Center (ARC) in Giza, Egypt.

2.2. Greenhouse experiment

The study involved testing 15 sesame entries, including five parental genotypes and their resulting crosses (10 F1 hybrids), to assess their reaction to infection with *Macrophomina phaseolina* (*M. phaseolina*). The inoculation of *M. phaseolina* was prepared using a sorghum-coarse sand-water medium in a 2:1:2 v/v ratio. This medium was mixed, bottled, and autoclaved for two hours at 1.5 air pressure. Then, it was inoculated separately using agar discs obtained from the periphery of a 7-day-old colony of *M. phaseolina* and incubated at 25±5ºC for 20 days.

Soil infestation with fungal inoculum was added to potted soil at a rate of 2% (v/v) and irrigated for a week, following the protocol outlined by Shabana *et al.* (2014). Seeds used in the experiment were disinfected by dipping them in a 2% sodium hypochlorite solution for three minutes, rinsed three times in sterile water for five minutes each, and then sown at a rate of ten seeds per pot. The experiment was set up with three pots as replicates for each genotype, arranged in a completely randomized design. Disease assessment was conducted by measuring percentages of pre- and post-emergence damping-off after 15 and 45 days from sowing, respectively. Survival plants and disease infection percentages of charcoal rot (CR) were estimated and recorded after 90 days from sowing. Charcoal rot infection was characterized by root discoloration, black stem rot, and a significant reduction in the root system of infected plants. The resistance levels of tested genotypes were scored based on disease severity ratings as described by Thiyagu *et al*. (2007) and presented in Table 1. The percentage of the CR disease severity index (DSI%) was calculated using a formula suggested by Chiang *et al.* (2017).

Table 1. The disease scale used for evaluation of disease resistance in sesame lines.

Disease scale	Infection %	Category
1	1 – 10	Resistant (R)
3	11 – 20	Moderately Resistant (MR)
5	21– 30	Moderately Susceptible (MS)
7	31 – 50	Susceptible (S)
9	51 - 100	Highly Susceptible (HS)

2.3. Field experiment

The study was conducted over two summer growing seasons in 2022 and 2023, using natural soil infested with *Macrophomina phaseolina* at the Experimental Farm of the Agriculture Faculty, Suez Canal University in Ismailia, Egypt. Five different sesame genotypes were selected for the study: H102/58 (P1), M2A6 (P2), M1A38 (P3), Shandaweel 3 (P4), and H11/9 (P5). These genotypes were chosen to represent a wide range of variability in their agronomic traits. During the summer season of 2022, seeds of all parent genotypes were sown on the 15th of May and crossed in a half diallel mating design to produce 10 F1 hybrids. In the subsequent 2023 season, the five parental genotypes and their crosses (10 F1 hybrids) were sown until harvest. Standard agricultural practices were followed as recommended for sesame cultivation. A randomized complete block design (RCBD) with three replications was used for the experiment. Each experimental plot consisted of three ridges measuring five meters in length and 60 centimeters in width. Hills were spaced at 20 centimeters with two plants per hill, arranged on one side of the ridges.

At harvest, ten guarded plants were randomly sampled from each plot to measure the following traits: Number of leaves per plant, number of branches per plant, shoot fresh weight/plant (g), Shoot dry weight (g), Root fresh weight (g), Root dry weight (g), Plant height (cm), Root length (cm), Seed yield/ plant (g), Number of capsules/plants, 1000-seed weight (g), Seeds oil content (%) and disease severity index (%)

2.4. Oil extraction

The dried sesame seeds were ground, and oil extraction was carried out using light petroleum ether (40-60°C) through the Soxhlet method, following the procedure outlined by de Peña and Arredondo (1992).

Table 2. The pedigree of the used sesame genotypes.

Code No.	Genotypes	Pedigree
1	H102/58	Imported217 * Giza25
2	M2A6	Giza32 * Imported413
3	M1A38	Imported130 * B21
4	Shandaweel 3	Giza32 * Imported130
5	H11/9	Giza3 * Sharkia

2.5. Statistical analysis

The collected data were first subjected to analysis of variance (ANOVA) following the guidelines outlined by Steel and Torrie (1980) using the COSTAT system for Windows, version 6.311 developed by Cohort Software in Berkeley. Differences between means were compared by least significant difference (LSD) at 5% level of significant (Gomez and Gomez, 1984). CA, USA. To estimate GCA and SCA, the Griffing (1956) model method II analysis was employed. This analysis was conducted using the Diallel program software package developed by Ukai (2002). Furthermore, heritability in the narrow sense (h^2) was calculated according to the method described by Mather and Jinks (1982).

2.6. Heterosis

The estimate of heterosis relative to mid – parent (MP).

% Heterosis $\overline{(MP)}$ = $\frac{\overline{F_1} - \overline{m.P}}{\overline{m.p}} x100$

The test was used to compute a test of significance for the F1 crossings mean from the mid-parent values by Bhatt (1971), where:

$$t = (\overline{F_1 ij} - \overline{MP.ij}) / \sqrt{3/8MSe}$$

$\overline{F_1 ij}$ = the mean of the ij th F_1.

$\overline{M.P.ij}$ = the mean of the mid parent of ij $^{\underline{th}}$ cross.

3. Results and discussion

3.1. Effect of M. phaseolina on different tested sesame parents and their crosses under greenhouse conditions

Based on the data presented in Table 3, it is evident that the tested sesame parents and their crosses exhibited varied and statistically significant reactions throughout different stages of disease development, including pre- and post-emergence damping off, survival rates of plants, and percentages of the disease severity index of charcoal rot. The percentages observed for pre-emergence damping off ranged from 0.00 to 16.33%, while post-emergence damping off ranged from 0.00 to 18.70%. Survival rates of plants ranged from 64.84 to 95.81%, indicating differences in resistance or susceptibility to the disease among the genotypes. Additionally, the disease severity index ranged from 6.69 to 55.23%, highlighting the varying degrees of susceptibility of the genotypes to charcoal rot infection. These findings underscore the importance of genetic variability in disease resistance/susceptibility among sesame genotypes and hybrids, emphasizing the potential for selecting resistant cultivars through breeding programs. Based on the data provided in Table 3, it is evident that crosses P3 x P4, P1 x P4, P2 x P4, P4 x P5, P2 x P3 as well as parent P4, exhibited higher resistance to the disease compared to other crosses and parental genotypes. These genotypes showed the lowest percentages of pre-emergence damping off, post-emergence damping off, and charcoal rotted, along with the highest percentages of survival plants. This information highlights the potential for utilizing these resistant genotypes, including specific crosses and parent P4, in breeding programs aimed at developing sesame cultivars with improved resistance to charcoal rot disease. Based on the data presented in Table 3, crosses P1 x P5, P2 x P5, P1 x P2, and parent P5 exhibited higher susceptibility to the disease compared to other crosses and parental genotypes. These genotypes showed the highest percentages of pre-emergence damping off, post-emergence damping off, and charcoal rotted, along with the lowest percentages of survival plants. This information highlights the susceptibility of these genotypes to charcoal rot disease and emphasizes the need to avoid or minimize their use in breeding programs aimed at developing resistant sesame cultivars. Instead, focus should be placed on utilizing more resistant genotypes for improving disease resistance in sesame varieties. It seems that the parental genotype P4 was the sole parent that possessed genes for resistance (Table 3). Besides, parents P_3 and P_2 showed medium resistance for charcoal rot of *M. phaseolina.*

This result is in contrast with the results of Shabana *et al.* (2014) who found that the tested material comprised 24 elite sesame lines in F6, their parents and a check local cultivar. They were reacted differently and significantly throughout the different stages of disease development (Pre-, post-emergence damping off, charcoal rotted, and healthy mature plants) in an artificially infested soil with *M. phaseolina* as the causal pathogens of charcoal rot under greenhouse conditions and classified as highly susceptible; susceptible; moderate susceptible; moderate resistant; resistant and highly resistant for charcoal rot of sesame plant.

Table 3. Reaction of different sesame parents and their crosses against infection with *M. phaseolina*

Characters / Genotypes	Pre emergence Damping off (%)	Post emergence Damping off (%)	Survival plants %	Disease severity index %	Reaction
P_1	14.07	8.17	77.76	28.69	MS
P_2	10.03	10.00	79.97	16.27	MR
P_3	7.43	6.66	85.83	12.50	MR
P_4	6.40	0.00	93.40	9.53	R
P_5	12.43	15.37	71.84	40.20	S
P_1 x P_2	13.17	16.80	70.13	33.17	S
P_1 x P_3	10.56	7.90	81.53	23.69	MS
P_1 x P_4	3.33	2.33	94.34	8.60	R
P_1 x P_5	16.33	18.70	64.84	55.23	HS
P_2 x P_3	3.73	5.20	91.10	9.33	R
P_2 x P_4	3.47	6.93	89.55	9.77	R
P_2 x P_5	14.16	16.91	68.92	52.09	HS
P_3 x P_4	0.00	4.19	95.81	6.69	R
P_3 x P_5	7.03	7.54	84.77	12.98	MR
P_4 x P_5	3.63	4.88	91.49	10.00	R
LSD $_{0.05}$	1.83	1.39	2.11	1.35	

3.2. Analysis of variances

The illustrated data in Tables 4 and 5 clearly show that the mean squares attributed to genotypes and their partitioning into parents, crosses, and parents × crosses (P × C) were highly significant for all studied traits, except for root dry weight (g). This indicates the presence of substantial genetic variability among genotypes, parents, and crosses, which provides opportunities for improving these traits. Furthermore, the significant mean squares suggest the presence of sufficient heterosis among hybrids. These findings align with the results reported by Fahmy *et al.* (2015), Abdel-Moneam *et al.* (2022) and

Parameshwarappa *et al.* (2023), which also highlighted significant genetic variability and heterosis effects in sesame traits. These results collectively underscore the potential for genetic improvement and trait enhancement in sesame through breeding programs and hybridization.

Table 4. Mean squares of various sources of variation for parents, crosses and parents as opposed to crosses for growth characters.

Source of Variation	d.f	Plant height (cm)	Root length (cm)	No. of leaves / plant	No. of branches / plant	Shoot fresh weight /plant (g)	Shoot dry weight (g)	Root fresh weight (g)	Root dry weight (g)
Replicates	2	3.8	0.02	0.16	0.16	0.07	0.00	0.07	0.60
Genotypes	14	611.8**	10.23**	321.3**	6.04**	1819.2**	141.3**	7.63**	0.80
Parents	4	173.1**	14.07**	336.9**	3.60**	2561.1**	218.4**	9.60**	0.90
Crosses	9	768**	9.66**	314.4**	7.48**	1613.2**	122.7**	7.50**	0.83
P. *vs*. C.	1	960.4**	0.01	321.1**	2.84**	705.6**	0.10	0.90	0.10
Error	28	0.80	0.07	0.94	0.18	1.07	0.57	0.50	0.46

***, * Significant at 0.01 and 0.05 probability levels, respectively.*
*Where ** means signficat at 1 % level of probability*

Table 5. Mean squares of various sources of variation for parents, crosses and parents versus crosses for capsules/plant, seed yield, 1000-seed weight, oil content (%) and Disease severity index %.

S.O.V	d.f	Number of capsules/plants	Seed yield/ plant (g)	1000 seed weight (g)	Oil content (%)	Disease severity index %
Replicates	2	8.07	6.05	0.00	0.93	1.07
Genotypes	14	89.94**	4.74**	4.47**	28.29**	410.26**
Parents	4	129.90**	5.21**	6.43**	77.68**	138.76**
Crosses	9	72.83**	4.63**	3.61**	8.12**	554.97**
P. *vs*. C.	1	84.10**	3.84**	4.41**	12.24**	193.86**
Error	28	0.50	0.43	0.01	0.96	0.92

**, ** Significant at 0.05 and 0.01 probability levels, respectively.*
*Where ** means significant at 1 % level of probability*

3.3. Mean performance

The mean performance of parents and their crosses for the studied traits is summarized in Tables 6 and 7. The results indicate that the parent Shandaweel 3 (P4) exhibited high values for most of the studied characters. Additionally, the parent M1A38 (P3) displayed high values for plant height (101.00 cm), root length (10.00 cm), and number of leaves per plant (48.00). Moreover, the parent M2A6 (P2) showed the highest mean value for seeds oil content (58.17%). In terms of disease severity index, the parent Shandaweel 3 (P4) demonstrated the lowest average value (9%). These findings highlight the superior performance of specific parents for different traits, such as Shandaweel 3 (P4) for disease resistance and overall performance, M1A38 (P3) for plant height, root length, and leaf number, and M2A6 (P2) for oil content. These insights can be valuable for selecting parental genotypes in breeding programs aimed at improving these traits in sesame cultivars.

Comparison of the performance of F_1 hybrids to the corresponding highest parents revealed that F_1

cross (P_3 x P_4) significantly surpassed the highest parental genotype for root length (10.00 cm), number of capsules/plants (27.00), seed yield/ plant (6.50 g), 1000-seed weight (7.50 g).

Table 6. Mean performance of sesame genotypes for growth characters

Characters Genotypes	Plant height (cm)	Root length (cm)	No. of leaves/ plant	No. of branches/ plant	Shoot fresh weight/plant (g)	Shoot dry weight (g)	Root fresh weight (g)	Root dry weight (g)
P_1	94.00	5.00	36.00	3.00	64.00	17.00	7.00	5.00
P_2	90.00	5.00	25.00	1.00	35.00	15.00	5.00	4.00
P_3	101.00	10.00	48.00	1.00	74.00	27.00	5.00	4.00
P_4	99.00	6.33	44.00	3.00	107.00	34.00	9.00	5.00
P_5	82.00	5.00	25.00	1.00	39.00	15.00	5.00	5.00
P_1 x P_2	99.00	5.00	34.00	1.67	67.00	20.00	5.00	4.00
P_1 x P_3	116.00	6.67	37.00	1.00	60.00	17.00	7.00	5.00
P_1 x P_4	104.00	8.00	39.00	5.67	92.00	27.00	7.00	5.00
P_1 x P_5	93.00	5.00	27.33	3.00	74.00	24.00	5.00	4.00
P_2 x P_3	107.00	5.00	23.00	1.00	57.00	17.00	7.00	5.00
P_2 x P_4	131.00	5.33	25.00	2.00	62.00	20.00	5.00	4.00
P_2 x P_5	86.00	5.00	20.00	1.00	74.00	20.00	7.00	5.00
P_3 x P_4	76.00	10.00	12.00	1.00	37.00	15.00	5.00	4.00
P_3 x P_5	117.00	8.00	46.00	4.00	124.00	37.00	10.00	5.00
P_4 x P_5	101.00	5.00	36.00	3.00	75.00	20.00	7.00	4.00
LSD $_{0.05}$	*1.50*	0.44	1.63	0.71	1.73	1.27	1.18	1.14

Table 7. Mean performance of sesame genotypes for several capsules/plant, seed yield, 1000-seed weight, seeds oil content (%), and disease severity index(%).

Characters Genotypes	Number of capsules/plants	Seed yield/ plant (g)	1000-seed weight (g)	seeds oil content (%)	Disease severity index %	Reaction
P_1	11.00	2.20	2.38	48.00	17.10	MR
P_2	12.00	2.60	4.30	58.17	15.60	MR
P_3	24.00	4.80	5.17	49.50	10.00	R
P_4	25.00	5.20	6.17	44.30	9.00	R
P_5	16.00	3.50	5.50	49.57	26.00	MS
P_1 x P_2	15.00	2.80	4.33	52.00	26.70	MS
P_1 x P_3	16.00	2.90	4.03	52.40	24.70	MS
P_1 x P_4	24.00	3.80	5.40	48.33	9.13	R
P_1 x P_5	18.00	5.40	6.50	49.70	49.40	S
P_2 x P_3	23.00	4.40	5.08	52.63	18.00	MR
P_2 x P_4	26.00	5.50	6.30	50.73	8.00	R
P_2 x P_5	13.00	3.00	5.01	53.73	32.70	S
P_3 x P_4	27.00	6.50	7.50	50.63	7.30	R
P_3 x P_5	19.00	3.90	4.34	49.77	13.30	MR
P_4 x P_5	24.00	4.50	5.20	50.30	10.00	R
LSD $_{0.05}$	1.18	1.10	0.20	1.65	1.61	

Meanwhile, the F_1 cross (P_3 x P_5) significantly surpassed the highest parental genotype for no. of leaves/ plant (46.00), shoot fresh weight/plant (124.00 g), shoot dry weight (37.00 g), root fresh weight (10.00 g) and root dry weight (5.00 g).

The F_1 cross (P_2 x P_4) had the tallest plants (131.00 cm). Meanwhile, the F_1 cross (P_1 x P_4) gave the highest value for no. of branches/ plant (5.67). For oil content, the F_1 cross (P_2 x P_5) exhibited the highest value (53.73%). The F_1 cross (P_3 x P_4) recorded the lowest value for the disease severity index (7.3%). These results may suggest that the above-mentioned parents and F_1 crosses may be of value for improving the seed yield of sesame through the improvement of yield components, and it could be concluded that the previous superior genotypes can be utilized in sesame-improving programs. These results are in agreement with those obtained by Anjay *et al.* (2013), Narendra *et al.* (2013), Fahmy *et al.* (2015), Abdel-Moneam *et al.* (2022) and Parameshwarappa *et al.* (2023).

3.4. Combining ability and heritability

The analysis of variance for combining ability is shown in Tables 8 and 9. The mean squares for both general combining ability (GCA) and specific combining ability (SCA) were significantly high for all traits examined, except for root dry weight (g), indicating the presence of both additive and non-additive genes (dominance and epistasis) in the genetic system governing these traits. Furthermore, the variances attributed to general combining ability (GCA) were greater than those for specific combining ability (SCA). The ratio of σ^2 GCA/σ^2 SCA surpassed unity for root length (cm), number of branches per plant, number of capsules per plant, seed yield per plant (g), 1000-seed weight (g), seeds oil content (%), and disease severity index %. The findings indicated that the variance attributed to general combining ability (GCA) was more significant than that of specific combining ability (SCA) concerning the genetics of the studied traits. This suggests a predominant role of additive gene action in shaping these traits' genetic composition. These results highlight the potential for developing and enhancing these traits through phenotypic selection. This conclusion aligns with previous studies by Ahmed *et al.* (2019), Abdelsatar *et al.* (2020), Abdelsatar and Hassan (2020), Ibrahim *et al.* (2021), Abdel-Moneam *et al.* (2022), and Parameshwarappa *et al.* (2023), which also observed a higher magnitude of GCA variance compared to SCA variance for yield and its associated components. The obtained results revealed that the ratios of GCA/SCA were below unity for plant height (cm), number of leaves per plant, shoot fresh weight per plant (g), shoot dry weight (g), root fresh weight (g), and root dry weight (g). These findings suggest that these traits are primarily governed by non-additive gene actions such as dominance and epistasis, as indicated in Table 6. Consequently, it can be inferred that selection processes would be effective in enhancing these traits, particularly in later segregating generations. This conclusion is consistent with the findings of Fahmy *et al.* (2015), Abd El-Satar (2017), Ahmed *et al.* (2019), Abdelsatar and Hassan (2020), Abdelsatar *et al.* (2020), Ibrahim *et al.* (2021) and Abdel-Moneam *et al.* (2022).

The heritability in a narrow sense varied from low to high, ranging from 3.3 to 76.43% as shown in Tables 6 and 7. These findings suggest that these traits are significantly influenced by dominance and environmental factors. Traits with higher heritability can serve as valuable selection criteria for future breeding programs. Notably, high heritability was observed for traits such as the number of capsules per plant, seeds oil content (%), root length (cm), and disease severity index %. Similar conclusions were drawn by Uzun *et al.* (2013), Hika *et al.* (2015) and Kadvani *et al.* (2020) in their respective studies.

Table 8. Combining ability variance and narrow sense heritability in sesame genotypes to growth characters.

Source of Variation	df	Plant height (cm)	Root length (cm)	No. of leaves/ plant	No. of branches/ plant	Shoot fresh weight/plant (g)	Shoot dry weight (g)	Root fresh weight (g)	Root dry weight (g)
Genotypes	14	611.8**	10.23**	321.3**	6.04**	1819.2**	141.3**	7.6**	0.80
GCA	4	207.9**	25.68**	278.9**	9.10**	1253.3**	117.2**	3.6**	0.30
SCA	10	773.3**	4.05**	338.2**	4.82**	2045.6**	150.9**	9.3**	1.0*
Error	28	0.80	0.07	0.94	0.18	1.07	0.57	0.50	0.46
σ^2 GCA/ σ^2 SCA		*0.27*	6.33	0.82	1.89	0.61	0.78	0.38	0.30
h(n.s)		7.04	67.85	20.14	41.6	14.56	16.21	12.4	3.33

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

Table 9. Narrow sense heritability and combining ability variance in sesame genotypes for number of capsules/plant, seed yield, 1000 seed weight , oil content (%) and disease severity index %

Source of variation	df	Number of capsules/plant	Seed yield/ plant (g)	1000-seed weight (g)	Oil content (%)	Disease severity index %
Genotypes	14	89.94**	4.74**	4.47**	28.29**	410.26**
GCA	4	243.51**	9.15**	7.80**	78.17**	799.94**
SCA	10	28.51**	2.98**	3.14**	8.34**	254.39**
Error	28	0.50	0.43	0.01	0.96	0.92
σ^2 GCA/ σ^2 SCA		8.54	3.07	2.49	9.38	3.14
h(n.s)		76.43	46.65	41.78	71.69	61.33

*Where ** means significant at 1% level of probability*

The comparison of general combining ability (GCA) effects associated with each parent, as shown in Tables 10 and 11, revealed that Shandaweel 3 (P4) exhibited positive and highly significant effects for all the studied traits, except for root dry weight (g) and oil content (%). This suggests that P4 could serve as a valuable source of genes for high seed yield and its components. Furthermore, P4 demonstrated a significantly negative effect on disease infection %. This indicates that P4 is the best general combiner and possesses desirable genes for reducing charcoal rot severity and enhancing resistance to charcoal rot in the study. Therefore, including P4 in a hybrid breeding program may be beneficial for developing highly resistant pure lines.

Similar negative and significant GCA effects for charcoal rot resistance were reported by El-Bramawy and Shaban (2007) and Shabana *et al.* (2014), further supporting the potential of P4 in improving resistance to charcoal rot in breeding programs. The parent M1A38 (P_3) revealed positive and highly significant effects for plant height (cm), root length (cm), no. of leaves/ plant, shoot fresh weight/plant (g), shoot dry weight (g), number of capsules/plant and seed yield/ plant (g), additionally, it showed highly significant negative for disease severity index %. Therefore parent (P_3) was the best general combiner and owned more desired genes for these traits.

The parent M2A6 (P2) demonstrated positive and highly significant effects for oil content (%), indicating that it is the best general combiner and possesses desirable genes for this trait.

Table10. General combining ability (GCA) effects for growth characters.

Characters / Genotypes	Plant height (cm)	Root length (cm)	No. of leaves/ plant	No. of branches/ plant	Shoot fresh weight/plant (g)	Shoot dry weight (g)	Root fresh weight (g)	Root dry weight (g)
P_1	0.23	-0.4**	2.63**	0.63**	0.66**	-1.14**	-0.06	0.11
P_2	0.66**	-1.1**	-5.6**	-0.75**	-12.34**	-3.29**	-0.63**	-0.17
P_3	2.80**	1.70**	3.30**	-0.56**	1.37**	1.43**	0.09	-0.03
P_4	1.66**	0.47**	1.30**	0.68**	9.09**	2.86**	0.51**	-0.03
P_5	-5.34**	-0.7**	-1.7**	0.01	1.23**	0.14	0.09	0.11
S.E.(gi-gj)	0.175	0.052	0.189	0.083	0.202	0.148	0.137	0.132

*Where ** means significant at 1% level of probability.*

Table 11. General combining ability effects for several capsules/plant, seed yield/ plant (g), 1000-seed weight (g), oil content (%), and disease infection %.

Characters / Genotypes	Number of capsules/plant	Seed yield/ plant (g)	1000-seed weight (g)	Oil content (%)	Disease severity index %
P_1	-3.17**	-0.72**	-0.84**	-0.78**	4.74**
P_2	-2.31**	-0.50**	-0.22**	3.08**	0.84**
P_3	2.26**	0.41**	0.06*	0.07	-3.92**
P_4	4.83**	0.89**	0.84**	-2.18**	-8.33**
P_5	-1.60**	-0.08	0.17**	-0.19	6.67**
S.E.(gi-gj)	0.137	0.127	0.023	0.192	0.188

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

This finding aligns with previous studies by Abd ElSatar *et al*. (2015), Abd El-Satar (2017), Ahmed *et al.* (2019), Abdelsatar *et al.* (2020), Abdelsatar and Hassan (2020), Ibrahim *et al.* (2021), Abdel Moneam *et al.* (2022) and Parameshwarappa *et al.* (2023), which reported positive and significant GCA effects for seed yield and many of its components. This suggests that P2 could be a valuable genetic resource for enhancing oil content and other related traits in breeding programs.

The specific combining ability (SCA) effects of F1-cross combinations were calculated for each cross for the studied traits, as shown in Tables 12 and 13. The cross (P3 x P5) exhibited highly significant positive SCA effects for growth-related traits, except for root dry weight (g), and showed highly significant negative effects for disease infection %. The cross (P1 x P4) demonstrated highly significant and positive specific combining ability (SCA) effects for growth-related traits, except for root fresh and dry weight (g). Additionally, it showed highly significant positive SCA effects for the number of capsules per plant and 1000-seed weight (g). Moreover, this cross exhibited highly significant negative effects for disease infection %. The cross (P2 x P4) displayed highly significant and positive specific combining ability (SCA) effects for plant height (cm), number of capsules per plant, seed yield per plant (g), and 1000-seed weight (g). Additionally, it exhibited highly significant negative effects for disease infection %. The cross (P4 x P5) yielded highly significant and positive specific combining ability (SCA) effects for plant height (cm), number of leaves per plant, number of capsules per plant, and oil content (%). Furthermore, it exhibited highly significant negative effects for disease severity index %. General combining ability (GCA) effects serve as a suitable criterion for assessing the merit of a genotype in hybrid combinations, whereas specific combining ability (SCA) effects may be associated with heterosis. This conclusion is consistent with the findings of Abd El-Satar *et al.* (2015), Abd El-Satar (2017), Ahmed *et al.* (2019), Abd-elsatar *et al.* (2020), Abd-elsatar and Hassan (2020), Ibrahim *et al.* (2021), Abdel Moneam *et al.* (2022) and Parameshwarappa *et al.* (2023).

Table 12. Specific combining ability (SCA) effects for growth characters

Characters / Genotypes	Plant height (cm)	Root length (cm)	No. of leaves/ plant	No. of branches/ plant	Shoot fresh weight/plant (g)	Shoot dry weight (g)	Root fresh weight (g)	Root dry weight (g)
P_1 x P_2	-1.62**	0.21	5.11**	-0.37	9.3**	2.76**	-0.7*	-0.48
P_1 x P_3	13.24**	-0.9**	-0.75	-1.22**	-11.4**	-4.9**	0.57	0.38
P_1 x P_4	2.38**	1.7**	3.3**	2.21**	12.86**	3.6**	0.14	0.38
P_1 x P_5	-1.62	-0.17	-5.5**	0.21	2.71**	3.33**	-1.4**	-0.76*
P_2 x P_3	3.81**	-1.94*	-6.6**	0.16	-1.43**	-2.8**	1.14**	0.67*
P_2 x P_4	28.95**	-0.4**	-2.6**	-0.08	-4.14**	-1.2**	-1.3**	-0.33
P_2 x P_5	-9.05**	0.44**	-4.6**	-0.41	15.71**	1.48**	1.14**	0.52
P_3 x P_4	-28.2**	1.54**	-24**	-1.27**	-42.86**	-11**	-2.0**	-0.48
P_3 x P_5	19.8**	0.68**	12.54**	2.40**	52.00**	13.8**	3.43**	0.38
P_4 x P_5	4.95**	-1.1**	4.54**	0.16	-4.71**	-4.7**	0.00	-0.62
S.E.(sij - sji)	0.676	0.200	0.733	0.320	0.781	0.571	0.532	0.511

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

Table 13. Specific combining ability effects for several capsules/plant, seed yield/ plant (g), 1000-seed weight (g), oil content (%), and Disease severity index %.

Characters / Genotypes	Number of capsules/plant	Seed yield/ plant (g)	1000-seed weight (g)	Oil content (%)	Disease severity index %
P_1 x P_2	0.95**	-0.02	0.25**	-0.95	2.66**
P_1 x P_3	-2.62**	-0.86**	-0.33**	2.46**	5.42**
P_1 x P_4	2.81**	-0.45	0.26**	0.65	-5.74**
P_1 x P_5	3.24**	2.20**	2.01**	0.02	19.54**
P_2 x P_3	3.52**	0.42	0.10	-1.16*	2.63**
P_2 x P_4	3.95**	1.03**	0.54**	-0.81	-2.96**
P_2 x P_5	-2.62**	-0.49	-0.08	0.20	6.74**
P_3 x P_4	0.38	1.12**	1.46**	2.10**	1.09*
P_3 x P_5	-1.19**	-0.50	-1.03**	-0.85	-7.90**
P_4 x P_5	1.24**	-0.39	-0.95**	2.03**	-6.79**
S.E.(sij - sji)	0.532	0.494	0.090	0.742	0.727

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

3.5. Heterosis

The resolution to the original sin of inbreeding depression is its counterpart, "hybrid vigor" or heterosis. When inbred lines are crossed, their offspring exhibit an increase in those traits that previously experienced a decline due to inbreeding. In essence, the fitness lost due to inbreeding depression can be restored through crossing, as highlighted by Abdel-Moneam *et al.* (2022). The heterosis percentages relative to mid-parents (MP) are provided in Tables 14 and 15. The cross P3 x P5 exhibited highly significant and positive heterosis for growth-related traits, except for root dry weight (g). It showed highly significant negative heterosis for disease severity index %. The cross (P1 x P4) displayed highly significant and positive heterosis for growth-related traits, except for root fresh and dry weight (g) and the number of leaves per plant. Furthermore, it showed highly significant positive heterosis for the number of capsules per plant, 1000-seed weight (g), and oil content (%). It exhibited highly significant negative heterosis for disease infection %. The cross (P2 x P4) demonstrated highly significant and positive heterosis for plant height (cm), number of capsules per plant, seed yield per plant (g), and 1000-seed weight (g). It exhibited highly significant negative heterosis for disease infection %. The cross (P4 x P5) exhibited highly significant and positive heterosis for plant height (cm), number of leaves per plant, number of branches per plant, shoot fresh weight per plant (g), number of capsules per plant, and oil content (%). It showed highly significant negative heterosis for disease infection %. The cross P3 x P4 exhibited highly significant and positive heterotic effects for root length (cm), number of capsules per plant, seed yield per plant (g), 1000-seed weight (g), and oil content (%). It showed highly significant negative heterosis for disease severity index %.

Table 14. Heterosis % relative to the mid parent of sesame for growth characters.

Characters Genotypes	Plant height (cm)	Root length (cm)	No. of leaves/ plant	No. of branches/ plant	Shoot fresh weight/plant (g)	Shoot dry weight (g)	Root fresh weight (g)	Root dry weight (g)
P_1 x P_2	7.1**	0.00	10.3**	-20	26.12**	20.0**	-20.0*	-12.50
P_1 x P_3	15.95**	-12.5**	-13.5**	-100**	-15.0**	-29.4**	14.3*	10.00
P_1 x P_4	7.21**	29.2**	-2.56	47.06**	7.07**	5.56**	-14.3*	0.00
P_1 x P_5	5.38**	0.00	-11.6**	33.33**	30.41**	33.33**	-20.0*	-25.0*
P_2 x P_3	10.75**	-50.0**	-58.7**	0.00	4.39**	-23.5**	28.6**	20.0*
P_2 x P_4	27.86**	-6.25*	-38**	0.00	-14.5**	-22.5**	-40**	-12.50
P_2 x P_5	0.00	0.00	-25**	0.00	50.0**	25.0**	28.6**	10.00
P_3 x P_4	-31.6**	18.3**	-283**	-100**	-144.6**	-103**	-40**	-12.50
P_3 x P_5	21.79**	6.25**	20.6**	75**	54.44**	43.24**	50.0**	10.00
P_4 x P_5	10.4**	-13.3**	4.17*	33.33**	2.67**	-22.5**	0.00	-25.0*

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

Table 15. Heterosis percentages relative to mid (MP) parent of sesame for number of capsules/plant, seed yield/ plant (g), 1000-seed weight (g), oil content (%) and disease severity index %

Characters Genotypes	Number of capsules/plant	Seed yield/ plant (g)	1000-seed weight (g)	Oil content (%)	Disease severity index %
P_1 x P_2	23.33**	15.29	22.90**	-2.08	38.95**
P_1 x P_3	-9.38**	-20.69	6.41**	6.97**	45.34**
P_1 x P_4	25.00**	2.63	20.90**	4.52**	-42.39**
P_1 x P_5	25.00**	47.87**	39.22**	1.84	56.48**
P_2 x P_3	21.74**	15.91	6.76**	-2.28*	28.89**
P_2 x P_4	28.85**	29.09**	16.93**	-0.99	-53.75**
P_2 x P_5	-7.69*	-1.67	2.13	-0.25	36.39**
P_3 x P_4	9.26**	23.08**	24.44**	7.37**	-30.14**
P_3 x P_5	-5.26*	-6.41	-22.89**	0.27	-35.34**
P_4 x P_5	14.58**	3.33	-12.18**	6.69**	-75.00**

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

The varying values of heterosis can be attributed to the genetic diversity among the parents, leading to non-allelic interactions that either decrease or increase heterosis expression, as noted by Hayman (1958). Alghamdi (2009) also highlighted that heterosis estimates for different traits suggest sufficient genetic divergence among the parent lines, creating favorable conditions for breeding. The degree of F1 superiority in specific traits can vary among different cross combinations due to the combination of genes from the parents, directly or indirectly influencing those traits. Many researchers, including Abdel-Moneam *et al.* (2022), Kumar *et al.* (2022), Tavadare *et al.* (2022), Kumari (2023), Thouseem *et al.* (2023), Saleem *et al.* (2023) and Yogameenakshi *et al.* (2023), have found that favorable heterosis varies depending on the specific cross combinations and traits under consideration.

4. Conclusion and Recommendations

It was concluded from the results of this study that sesame genotypes and their components (parents, hybrids, and comparisons between parents and hybrids) respond differentially to resistance to charcoal rot. Shandaweel 3 (P4) exhibited positive and highly significant general combining ability (GCA) effects for all studied traits, except for root dry weight (g) and seeds oil content (%). This suggests that this parent could be a valuable source of genes for improving yield potential. It showed a highly significant negative effect on disease infection percentage, indicating its potential to contribute genes for disease resistance. Based on its performance as the best general combiner and possessing desirable genes for decreasing charcoal rot infection while increasing resistance to charcoal rot, Shandaweel 3 (P4) emerges as a valuable candidate for hybrid breeding programs aimed at developing high-resistant pure lines. Utilizing this parent in such breeding programs may lead to the creation of new varieties with enhanced resistance to charcoal rot, contributing positively to agricultural sustainability and productivity. Furthermor, the parent M1A38 (P3) demonstrated positive and highly significant effects for most of the studied traits, along with a highly significant negative effect on disease infection percentage. This indicates that P3 is the best general combiner and possesses desirable genes for these traits. As such, incorporating P3 into hybrid breeding programs could be beneficial for developing new varieties with improved traits, including enhanced disease resistance and other desired agricultural characteristics. The crosses (P1 x P4), (P3 x P5), (P2 x P4), and (P4 x P5) exhibited desirable specific combining ability (SCA) effects and significant heterosis values for most of the studied traits. The cross (P3 x P4) displayed significant heterosis values for most of the studied traits as well. These findings indicate the potential for these crosses to produce offspring with improved traits, highlighting their suitability for further evaluation and potential incorporation into breeding programs aimed at enhancing trait performance in sesame crops. These crosses might be used in sesame breeding programs to produce high-yielding ability and highly resistant pure lines.

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All authors are contributed in this research

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Not applicable

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Conflicts of Interest

The authors disclosed no conflict of interest.

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