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Molecular Characterization of some *Sesamum indicum* L. Genotypes under Drought Conditions

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ABSTRACT



To face the increasing global climate change in water level and to achieve sustainable development of seed yield and oil yield production in the sesame crop, five cultivars of sesame, H 102/58 (P1), M2 A6 (P2), M1 A38 (P3), shandaweel3 (P4), and H 11/9 (P5), were employed to implement a half-diallel mating design. Studied cultivars and their hybrids were grown for evaluation under two water regimes: normal irrigation and drought stress, to study the growth, yield performance, heritability, heterosis, and combining ability. Results under normal and stress conditions showed that all the studied parents and their crosses had different distinct traits, especially P3, which had the highest mean value for most growth and yield traits. P3, P4, and P5 had the highest mean values for the 1000 seed weight trait, while P2 recorded the highest mean values for oil content percent. The superiority of crosses was detected by positive and significant values of specific combining ability (SCA) effects and heterosis in P1 ×P3, P2 ×P4, and P4 ×P5. Start codon targeted (SCoT) polymorphism is an effective method for fingerprinting and genetic diversity analysis. 126 amplified fragments with a 52% polymorphism of 15 *Sesamum indicum* L. genotypes were obtained in the current study utilizing 10 SCoT primers. In this instance, there were 66 polymorphic bands and 60 monomorphic bands. Genetic similarity ranged from 75% to 92%, according to the SCoT data analysis. The 15 genotypes of sesame examined were divided into two main clusters and two main sub-clusters using a dendrogram.

Keywords: Sesamum indicum, drought, GCA and SCA effects, Genetic diversity, SCoT molecular marker.

INTRODUCTION

Sesame (*Sesamum indicum* L.) is one of the oldest cultivated oil seed crops (44–58% dry seed weight), protein (18–25%), and carbohydrate (13.5%). According to FAO (2019), the world production of sesame exceeded 6 million tons in 2019. Egypt has 81000 fed acres under cultivation, with a production of 39000 tons in 2020 (FAO, 2020). Sesame oil is a high-quality vegetable oil due to its high levels of antioxidants such as sesamin, sesamolin, and sesamol and unsaturated fatty acids such as oleic and linoleic acids (Li *et al.*, 2018; and Myint *et al.*, 2020), so it is used in food and widely in pharmaceutical products. Sesame is an annual plant in the family Pedaliaceae with diploid species 2n = 26 chromosomes. The most significant abiotic stress that affects plant growth and production is drought stress (Jaleel *et al.*, 2009).

Water stress caused significant effects at different stages of growth and reproduction organs, especially at the flowering stage of sesame (Nilanthi *et al.*, 2015). Progress in the improvement process of drought-tolerant genotypes of sesame is considered the main goal of sesame breeding programs in arid regions (Amani *et al.*, 2012).

Because there are decreasing in the organic matter content of the soils in Ismailia governorate, the soil cannot keep water for a long time, especially in summer. So, the summer crops, such as the sesame crop, need an increasing amount of water during the growth season. According to the results of Amira *et al.*, (2021) regarding the geomorphological, physiochemical, and classification properties of the soils in select regions of the governorate of Ismailia, situated between latitudes 30° 22' 30" and 30° 57' 00" N and longitudes 32° 06' 45" and 32° 22' 30" E. Warm winters with little rainfall and scorching, dry summers define the study region. These soils have less than 7% CaCO3 (w.p.m.), making them moderately calcareous. There is extremely little (<1%) gypsum content. Less than 1% of the total matter is organic (OM). Depending on the amount of organic matter and fine fractions, the cation exchange capacity (CEC) is likewise low. Approximately 80% or more of these soils (89.4% from the research region) have a sand to loamy sand texture.

Molecular, cellular, and whole plant physiological responses are all impacted by drought, a well-known environmental limitation. The drought-stricken plants were subjected to oxidative stress (Zhang *et al.*, 2015). Sesame yields are restricted during periods of dryness, primarily during their vegetative stages. The metabolic status of the source tissues is not the only element that affects sesame oil production; stress factors may also play a role (Sangwan *et al.*, 2001). In comparison to ideal watering conditions, severe drought stress decreased the oil yield by 62% (Gholinezhad *et al.*, 2012). Diallel mating design was utilized to offer gene activity and information on superior parents and crosses, and hybridization can boost sesame yield by producing desirable lines with desirable traits (Nehar *et al.*, 2023). In breeding programs, characteristics

linked to drought tolerance, such as physiological traits and yield components, are useful markers for choosing genotypes that are tolerant of drought and lessen the effect of water scarcity on crop productivity (Golestani and Pakniyat, 2015). Non-additive gene action plays a crucial role in the inheritance of some growth and yield traits, such as 1000-seed weight, plant yield, days to 50% flowering, branch number/plant, and capsule number/plant (Anyanga et al., 2016). Desirable genotypes for optimal recombination are identified using combining ability (Singh et al., 2022; Nehar et al., 2023). Through determining the degree and nature of genetic effects, directing the traits of yield, and selecting suitable parents to use in the making of genetic variability for crop improvement (Mahmoud et al., 2018; Sikarwar et al., 2021).

Molecular markers can accurately depict the genetic variation across genotypes and reflect genetic diversity (Cui et al., 2017). The genetic upgrading of sesame has advanced somewhat by means of gene transfer methods (Das and Parida, 2014; Leonetti et al., 2018). Collard and Mackill (2009) identified SCoT polymorphism based on the shortconserved plant gene areas encircling the start codon translation of ATG. In general, SCoT markers are reproducible and dominant. There are other factors besides primer length and annealing temperature that affect repeatability (Collard and Mackill, 2009). Furthermore, several co-dominant markers were generated throughout the amplification, indicating that they are dominant markers (Gorji et al., 2011). According to Cabo et al. (2014), Heikrujam et al. (2015), and Satya et al. (2015), the SCoT technique was utilized to map quantitative trait loci (QTL), evaluate structure and genetic diversity, and fingerprint the DNA of numerous agricultural cultivars.

This research aimed to produce a good resource of sesame genotypes with high growth and yield performance under drought conditions. To select better combiner parents, which could generate more desirable recombinants through the estimation of the combining ability. Determining the mode of gene action for twelve traits of studied sesame genotypes (parents and crosses) to identify the most efficient genotype under drought conditions. Characterize and assess genetic diversity among and within 15 genotypes of sesame via the application of 10 SCoT primers.

MATERIALS AND METHODS

An experiment was conducted at the experimental farm of the Faculty of Agriculture at Suez Canal University, Ismailia, Egypt, during summer 2022 and 2023. Five parents of the sesame cultivar, namely H 102 A 58, M2 A6, M1 A38, shandaweel3 and H 11 A 9, were taken from the Oil Seeds Crops Research Department, Agricultural Research Centre (A.R.C.), Giza, Egypt. Table (1) presents the names of the studied parents and their pedigree.

Designing of field experiment:

Seeds of the five parents (Table 1) were sown on summer (15th May) 2022 and crossed in a half diallel mating design to produce 10 F1 hybrids. Direct F1 crosses were generated using a half-diallel mating design after a crossing block was constructed. in summer 2023. In a randomized complete block design (RCBD) with three replications, a split-plot arrangement was employed. The area of plot was 2 x 4 m². Water treatment was the focus of the main plots.

Fifteen genotypes (ten crossings and five parents) each had a sub-plot. The recommended practices for all other agricultural operations were adhered to.

Table 1. The pedigree of s	studied genotypes
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Code	Genotypes	Pedigree
P1	H102/58	Imported217 * Giza25
P2	M2A6	Giza32 * Imported413
P3	M1A38	Imported130 * B21
P4	Shandaweel3	Giza32 * Imported130
P5	H11/9	Giza3 * Sharqia

Determination the Irrigation treatments:

During the summer 2023 season, evaporation (Eo), relative humidity (Rh), and the average values of temperature were employed to determine the evapotranspiration (ETo) of reference crops by the equation of Penman-Monteith (Allen et al., 1998). The surface irrigation method was used to provide the two water treatments: normal (100% from ETo) and stress (60% from ETo).

Measurements of crop:

Two samples were taken to record the mean data of ten individual plants. The first sample concerned growth traits (plant height (cm), number of leaves, number of branches, fresh and dry weight of the shoot, and root length) during the flowering stage, which were selected at random from each of the three replication plots. Four months after planting, the second sample of sesame plants was gathered. For yield traits: number of capsules / plants; seed yield /plant (g); 1000 seeds weighted (g).

Seed oil percentage: was determined by Soxhelt apparatus according to (A.O.A.C., 1990).

Statistical analysis

Analyses of variance (ANOVA) were done for the collected data based on Steel and Torrie (1980), who used the COSTAT system for Windows, version 6.311 (cohort software, Berkeley, CA, USA).

The Diallel 98 program software computer package was used to carry out the analysis (Ukai, 2002).

According to Griffing's (1956) model, method II, the general combining ability (GCA) and the specific combining ability (SCA) were estimated.

The formula for heritability in the narrow sense, h2 (n.s.), was derived using Mather and Jinks (1982).

Heterosis: Based on mid-parent, heterosis was estimated. % Heterosis (MP) = $\frac{F1-Mp}{Mp} X100$

In accordance with Bhatt (1971), a test of significance for the F1 hybrids mean from the mid-parent values was computed.

DNA extraction and purification

Total DNA was extracted from leaf samples of five parental cultivars and their hybrids by the DNeasy Plant Kit Germany). By using NanoDrop, (QIAGEN, the concentration and quality of the isolated DNA were assessed. **SCoT-PCR Reactions**

Ten SCoT primers were used for the detection of polymorphism and phylogenetic analysis for all the studied genotypes (Table 2), which was carried out at genetics and genetic engineering lab, faculty of agriculture, Benha University, EGYPT. As per Ibrahim et al., (2019), the amplification reaction was conducted in a 25 µl reaction container with 12.5 µl Master Mix (Sigma), 2.5 µl primer (10 pcmol), 3 µl DNA template (10ng), and 7 µl dH2O.

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Primer Name	Sequence
SCoT-1	5'-ACGACATGGCGACCACGC-3'
SCoT-2	5'-ACCATGGCTACCACCGGC-3'
SCoT-3	5'-ACGACATGGCGACCCACA-3'
SCoT-4	5'-ACCATGGCTACCACCGCA-3'
SCoT-5	5'-CAATGGCTACCACTAGCG-3'
SCoT-6	5'-CAATGGCTACCACTACAG-3'
SCoT-7	5'-ACAATGGCTACCACTGAC-3'
SCoT-8	5'-ACAATGGCTACCACTGCC-3'
SCoT-9	5'-ACAATGGCTACCACCAGC-3'
SCoT-10	5'-CAACAATGGCTACCACCG-3'

Table 2. List of SCoT primers used.

PCR Products detection and Thermocycling profile

PCR amplification was carried out using a Perkin-Elmer/GeneAmp® PCR System 9700 (PE Applied Biosystems), which was set up to complete 40 cycles following a 5-minute denaturation cycle at 94 °C. Every cycle included an annealing phase at 50 °C for 50 seconds, an elongation stage at 72 °C for one minute, and a denaturation step at 94 °C for 45 seconds. In the last cycle, the primer extension segment was increased to 7 minutes at 72 degrees Celsius.

Detection of the PCR Products:

Using electrophoresis on a 1.5% agarose gel with ethidium bromide (0.5 ug/ml) in 1X TBE buffer at 95 volts, the amplification products were visualized. Using a Gel Documentation System (BIO-RAD 2000), PCR products were seen under UV light and captured.

Data analysis

The SCoT analysis involved the visual scoring of only distinct and unambiguous bands for each sample, resulting in the final data sets containing both polymorphic and monomorphic bands. The bands were rated as present (1) or absent (0). The next step was creating a binary statistic matrix. We then used the unweighted pair-group technique with arithmetic averages (UPGMA) to obtain dice's similarity matrix coefficients between genotypes. With the PAST program, Version 1.91 (Hammer *et al.*, 2001), this matrix was utilized to create a phylogenetic tree (dendrogram) based on the Euclidean similarity index.

RESULTS AND DISCUSSION

Growth characters:

The mean performance values of the studied growth characters presented in Tables (3 and 4) showed a decrease in mean values for all genotypes under drought treatment (60% ETo.) compared with normal treatment (100% ETo.) due to the negative effect of drought on all metabolic processes in plant cells. Results in Table (2) showed that P3 (M1 A38) parent had the highest mean values for leaf number (40.67), shoot fresh weight (101.7 g), and shoot dry weight (23.33 g), followed by P2 (M2A6) under drought conditions for these traits. P1 and P2 had the highest mean values for the number of branches / plant (1.33) under drought conditions. For F1 crosses under drought conditions, the P1 X P3 cross recorded the highest mean values in leaf number/ plant (48). P1 X P2 and P1 X P5 crosses had the highest mean values for number of branches and plant trait (1.33) under drought conditions. P2 X P4 cross had the highest fresh weight shoot (88 g). The P3 X P5 cross had the highest dry weight of the shoot (28.33 g).

Table 3. Mean performance of studied sesame cultivars and their crosses for growth traits; number of leaves and branches / plant, fresh and dry weight of shoot (g) under normal (100%ETo) and drought (60%ETo) conditions.

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Characters	No. o	f leaves/ pl	ant	No. of b	oranches/ pl	ant	Fresh weig	ht of shoot/p	lant (g)	Dry wei	ight of shoo	t (g)
Genotypes	100% Eto	60% Eto	Mean	100% ETo	60%ETo	Mean	100% Eto	60%ETo	Mean	100% ETo	60%ETo	Mean
\mathbf{P}_1	41.33	15.00	28.2	1.67	1.33	1.5	138.33	45.00	91.7	33.33	11.67	22.5
P ₂	37.00	27.33	32.2	1.67	1.33	1.5	95.00	90.00	92.5	21.67	20.00	20.8
P ₃	51.00	40.67	45.8	3.00	1.00	2.0	110.00	101.7	105.9	26.67	23.33	25.0
\mathbf{P}_4	30.33	15.00	22.7	1.00	1.00	1.0	105.00	38.33	71.7	23.33	10.00	16.7
P5	38.33	13.00	25.7	1.00	1.00	1.0	173.33	33.33	103.3	41.67	20.00	30.8
$P_1 x P_2$	43.67	22.00	32.8	2.00	1.33	1.7	103.33	43.33	73.3	26.67	15.00	20.8
$P_1 x P_3$	87.67	48.00	67.8	1.33	1.00	1.2	161.67	73.33	117.5	36.67	23.33	30.0
$P_1 x P_4$	36.33	23.00	29.7	1.00	1.00	1.0	91.67	63.33	77.5	20.00	16.67	18.3
P1 x P5	51.67	21.00	36.3	1.33	1.33	1.3	128.33	50.00	89.2	33.33	15.00	24.2
$P_2 x P_3$	46.67	26.00	36.3	3.00	1.00	2.0	238.33	53.33	145.8	30.00	23.33	26.7
$P_2 x P_4$	30.33	26.00	28.2	1.00	1.00	1.0	100.00	88.33	94.2	27.00	23.33	25.2
P2x P5	25.00	19.33	22.2	1.00	1.00	1.0	101.67	78.33	90.0	27.00	24.00	25.5
P3x P4	41.67	28.00	34.8	2.33	1.00	1.7	185.00	78.33	131.7	43.33	23.33	33.3
P3x P5	25.00	22.67	23.8	1.00	1.00	1.0	211.67	68.33	140.0	46.67	28.33	37.5
P4x P5	25.00	20.67	22.8	1.00	1.00	1.0	83.33	76.67	80.0	16.67	16.67	16.7
Mean	40.7	24.5	32.6	1.6	1.1	1.3	135.1	65.4	100.3	30.3	19.6	24.9
LCD	Genot.	Water	G*W	Genot.	Water	G*W	Genot.	Water	G*W	Genot.	Water	G*W
LSD 0.05	0.41	0.25	0.59	0.47	0.44	0.68	0.41	0.44	0.59	0.43	0.48	0.61

Results in Table (4) reported that P1 (H102/58) had the highest mean value of fresh weight of root (10 g), followed by P3 (M1 A38) (8.33 g), and also for dry weight of root trait under drought conditions. P3 had the highest plants (118cm). For F1 crosses under drought conditions, the P1 X P3 crosses noticed the highest mean values for plant height (152 cm). P3 X P4 and P3 X P5 crosses had high mean values for plant height (118 cm) and (117.3 cm) respectively. P2 X P5, P3 X P4, P3 X P5, and P4 X P5

recorded high mean values for the root length trait under normal and drought conditions compared with other crosses. P2 X P4, P2 X P5, and P4 X P5 had the highest dry weight of root under drought conditions. These crosses might be tolerant to drought, according to Fazal *et al.*, (2022), who reported that the fresh and dry weight of seedling traits were used as a useful selection criterion in developing the drought tolerance genotypes in sesame.

Characters	Root fr	esh weight	t (g)	Root o	lry weight	(g)	Plant height (cm)		m)	Root length (cm)		
Genotypes	100% Eto	60% Eto	Mean	100% Eto	60% ETo	Mean	100% Eto	60% Eto	Mean	100% ETo	60% ETo	Mean
P1	18.33	10.0	14.2	6.67	1.67	4.2	124.67	86.3	105.5	9.00	8.00	8.5
P_2	16.67	5.00	10.8	5.50	1.00	3.3	115.00	104	109.5	11.00	10.00	10.5
P ₃	11.67	8.33	10.0	4.00	1.33	2.7	145.00	118	131.5	10.00	8.67	9.3
P_4	10.00	6.67	8.3	3.50	1.13	2.3	124.00	98	111.0	11.00	10.00	10.5
P5	20.00	5.00	12.5	6.67	1.67	4.2	146.67	83	114.8	7.67	7.00	7.3
$P_1 x P_2$	10.00	5.00	7.5	3.90	1.10	2.5	131.33	101	116.2	7.33	7.00	7.2
$P_1 x P_3$	18.33	11.7	15.0	5.00	3.33	4.2	161.67	152	156.8	11.00	10.00	10.5
$P_1 x P_4$	18.33	6.67	12.5	5.50	1.40	3.5	129.33	119	124.2	8.00	7.00	7.5
P1 x P5	13.33	6.67	10.0	5.00	3.33	4.2	132.33	105	118.7	8.00	7.00	7.5
$P_2 x P_3$	15.00	8.33	11.7	5.00	3.33	4.2	136.67	120	128.3	10.00	9.00	9.5
$P_2 x P_4$	16.67	16.7	16.7	6.67	5.00	5.8	119.67	103	111.3	8.00	7.00	7.5
P2 x P5	16.67	15.0	15.8	6.67	5.00	5.8	105.67	100	102.8	10.67	10.00	10.3
P3 x P4	25.00	8.33	16.7	8.33	3.33	5.8	121.00	115	118.0	11.00	10.00	10.5
P ₃ x P ₅	35.00	8.33	21.7	15.00	3.33	9.2	121.00	113.3	117.2	10.33	10.00	10.2
P4 x P5	15.00	15.0	15.0	5.00	5.00	5.0	114.00	107.7	110.9	11.00	10.00	10.5
Mean	17.3	9.1	13.2	5.8	3.4	4.6	128.5	108.4	118.4	9.6	8.7	9.2
100	Genot.	Water	G*W	Genot.	Water	G*W	Genot.	Water	G*W	Genot.	Water	G*W
LSD 0.05	0.39	0.1	0.57	0.45	0.53	0.64	0.46	0.53	0.66	0.27	0.1	0.40

Table 4. Mean performance of studied sesame cultivars and their crosses for growth traits; fresh and dry weight of root (g), plant height and root length (cm) under normal (100%ETo) and drought (60%ETo) conditions.

Yield and oil traits:

The mean performance values of seed weight / plant, capsule number / plant, 1000 seed weight, and oil percent were presented in Table (5). Results showed that P5 (H11/9) had the highest yield of seeds (4.2 g) under drought conditions. P3 (M1 A38) parent had the highest number of capsules / plants, with average values of 37 and 33.33 g under both normal and drought conditions, respectively. For the 1000 seed weight trait, P3 had the highest mean values, followed by P5 (H 11/9) and P4 (Shandaweel3) in response to both conditions. P2 (M2 A6) recorded the highest oil percents of 60.17 and 55.5 over all studied parents and their crosses under normal and stress conditions, respectively. P3 X P5 and P4 X P5 crosses had the highest seed yield/ plant (3.33 and 3.67 g, respectively) under drought conditions. For the number of capsules trait, P3 X P5 crosse had the highest mean value of 50, followed by P3 X P4 and P2 XP3 at 42.76 and 41.33, respectively, under normal conditions. While P1 X P3 and P3 X P4 crosses had the highest number

of capsules / plant (29 and 20), respectively, under drought conditions, For the 1000 seed weight trait, the highest mean values were found in P4 X P5 (8.20, 7.20 g) and P1 X P5 (6.48, 6.10 g) under normal and drought conditions, respectively. P2XP3, P1XP2, P1XP3, P3XP5, and P2XP4 crosses had high oil percents under both conditions. Harfi et al., (2021) found varied influences of drought on the growth and yield traits of sesame. Fazal et al., (2022), who consider the 1000 seed weight trait a useful indicator for selection for the drought tolerance genotype of sesame, The variations among each parent and crosses were explained by Boureima et al., (2012) and Myint et al., (2020), who illustrated that the yield decreasing as well as the oil content were due to the studied genotypes and the intensity of drought. Golestani and Pakniyat (2015) reported that physiological features and vield components can be used as useful indicators in breeding program to select genotypes that are tolerant of drought and lessen the effect of water scarcity on agricultural output.

Table 5. Mean performance of studied sesame cultivars and their crosses for yield traits; seed yield (g) and number of capsules/ plants, 1000 seeds weight (g) and percent of oil content under normal (100%ETo) and drought (60%ETo) conditions.

Characters	Seed y	ield/ plant	(g)	Number	of capsules/	/plants	1000-s	eed weigh	t (g)	Oil	content (%))
Genotypes	100% Eto	60% Eto	Mean	100% Eto	60% ETo	Mean	100% Eto	60% ETo	Mean	100% ETo	60% ETo	Mean
P1	5.61	2.00	3.8	29.67	18.00	23.8	2.38	2.00	2.2	50.07	44.07	47.1
P ₂	6.00	2.00	4.0	23.00	19.00	21.0	4.30	3.80	4.1	60.17	55.50	57.8
P ₃	2.00	2.00	2.0	37.00	33.33	35.2	6.17	5.00	5.6	51.50	45.20	48.4
P_4	4.20	1.33	2.8	25.00	10.00	17.5	5.17	4.67	4.9	46.30	39.00	42.7
P 5	5.00	4.20	4.6	35.67	11.00	23.3	5.50	5.00	5.3	51.80	47.00	49.4
$P_1 x P_2$	5.00	1.50	3.3	27.33	18.00	22.7	5.33	5.12	5.2	54.00	48.10	51.1
$P_1 x P_3$	3.00	3.00	3.0	39.00	29.00	34.0	6.10	4.03	5.1	54.40	48.00	51.2
$P_1 x P_4$	3.50	1.00	2.3	16.33	15.33	15.8	6.43	4.50	5.5	50.33	46.57	48.5
$P_1 x P_5$	3.00	3.00	3.0	37.67	14.00	25.8	6.48	6.10	6.3	51.70	46.40	49.1
$P_{2x}P_3$	5.00	2.80	3.9	41.33	14.00	27.7	6.13	5.08	5.6	54.67	49.07	51.9
$P_2 x P_4$	3.57	2.50	3.0	23.00	17.00	20.0	5.90	3.60	4.8	52.73	48.40	50.6
$P_2 x P_5$	6.00	2.50	4.3	24.00	18.00	21.0	6.99	5.01	6.0	52.73	42.63	47.7
P ₃ x P ₄	4.27	3.00	3.6	42.67	20.00	31.3	6.55	4.10	5.3	52.63	47.83	50.2
P ₃ x P ₅	6.70	3.33	5.0	50.00	18.00	34.0	4.50	4.00	4.3	50.77	49.00	49.9
P4xP5	4.17	3.67	3.9	21.00	17.33	19.2	8.20	7.20	7.7	52.30	45.50	48.9
Mean	4.5	2.5	3.5	31.5	18.1	24.8	5.7	4.6	5.2	52.4	46.8	49.6
ISDaar	Genot.	Water	G*W	Genot.	Water	G*W	Genot.	Water	G*W	Genot.	Water	G*W
LOD 0.05	0.14	0.12	0.19	0.50	0.69	0.71	0.045	0.02	0.06	1.1	0.93	1.52

General and specific combining ability variance:

Results revealed highly significant values of GCA and SCA mean squares for all studied characters except branch number /plant under drought condition and root length under normal condition (Table 6). GCA values were more than values of SCA. The proportion of $\sigma 2$ GCA/ $\sigma 2$ SCA were more unity for all characters except root fresh and dry weight under normal and drought conditions and 1000 seeds weight under normal condition. These results reported that the effects of GCA in the inheritance of these characteristics were more than SCA effects while for root weight traits and 1000 seeds weight; SCA was more effective in them. These results were matched with Disowja et al., (2021) who illustrate that for each character, the estimations of o2 SCA were higher than the matching o2 GCA of sesame because of the dominance and epistasis (non-additive) had great contribute among genes in the inheritance of it. These results were explained by Zabet et al., (2021) who found by using Griffith analysis that significant GCA for all traits in normal and drought stress. SCA held significance for every characteristic, except plant height, the height of first capsule and capsule number, in normal conditions and reported by using Hayman analysis that the significant additive genetic variance for all traits in normal and drought stress. and significant dominant genetic variance for all traits, except plant height and the height of first capsule, in normal conditions. Although there were significant variations of the contribution of each component according to water regime and measurement these results were in harmony with Bishnoi et al., (2018a) and Mahmoud et al., (2018) who reported that dominance and the

cumulative effects of genetic components drive the inheritance processes for the measurement features.

Heritability in narrow sense:

The values of heritability in a narrow sense percent for studied trait growth, yield, and oil percent ranged from 11.93 for the fresh weight of the root under drought conditions to 67.6 for the number of capsules / plant under normal conditions (Table 6). Zabet *et al.*, (2021) reported that the narrow sense heritability varied from 0.27 to 0.99 for harvest index and number of capsules, respectively, in both conditions.

Studied traits were divided into two classes. First class had narrow rang or nearly values of heritability percent $(h^2 (n.s.))$ between both conditions. Such values of $h^2 (n.s.)$ for leaves number/plant were 54.36 and 56.67, root dry weight 25.86 and 22.79, plant height 47.96 and 47.1, and root length 34.45 and 32.63 under normal and stress conditions, respectively. While the second class had a broad range or great variation in the values of h^2 (n.s.) between both conditions, such values of h² (n.s.) for seed yield/plant were 31.97 and 60.84, capsules number/plant 67.6 and 51, root fresh weight 28.09 and 11.93, branches number/plant 56.73 and 43.54, shoot fresh weight 46.56 and 32, shoot dry weight 42.43 and 65.1, and oil percent 60.71 and 31.82 under normal and stress, respectively. Mahmoud et al. (2018) explained that the variations between the results of the two classes might be due to the additive and additive x additive gene effects having a high effect on the traits of the first class. While dominance effects and environmental conditions had a high effect on the traits of the second class.

Table 6. Combining ability variance and narrow sense heritability (h² (n.s)) in sesame genotypes for growth, yield and oil characters under normal (100%ETo) and drought (60%ETo) conditions.

a	iu vii	characters	unuel nori	11AI (100 /0E I	0) anu urot	igiit (00 /0E 10) Co	nunnons.		
Source of	Jf	No. of leav	/es/ plant	No. of branc	hes/ plant	Fresh weight of sh	oot/plant (g)	Dry weight	of shoot (g)
Variation	ai	100% ETo	60% ETo	100% ETo	60% ETo	100% ETo	60% ETo	100% ETo	60% ETo
Genotypes	14	743.72**	260.7**	1.56**	0.07	6921.98**	1292.2**	233.39**	81.5**
GCA	4	1241.8**	563.4**	3.52**	0.16	7963.45**	1903.3**	321.08**	188.1**
SCA	10	544.50**	139.6**	0.77*	0.03	6505.40**	1047.8**	198.31**	38.8**
Error	28	0.60	0.75	0.26	0.09	0.38	0.28	0.30	0.3
$\sigma^2 GCA \! / \sigma^2$	SCA	2.28	4.04	4.59	4.50	1.22	1.82	1.62	4.84
h (n.s)		54.36	56.67	56.73	43.54	46.56	32	42.43	65.1
Source of	đ	Fresh weight	t of root (g)	Dry weight	of root (g)	Plant height	(cm)	Root len	gth (cm)
Variation	ui	100% ETo	60% Eto	100% ETo	60% ETo	100% ETo	60% ETo	100% ETo	60% ETo
Genotypes	14	117.62**	43.89**	22.93**	6.75**	628.23**	801.57**	6.15	5.76**
GCA	4	75.36**	5.60**	14.51**	3.07**	902.59**	1215.4**	6.56	5.30**
SCA	10	134.52**	59.21**	26.30**	8.21**	518.49**	636.03**	5.99	5.94**
Error	28	0.19	0.16	0.38	0.13	0.63	0.38	0.09	0.02
σ^2 GCA/ σ^2	SCA	0.56	0.09	0.55	0.37	1.74	1.91	1.09	0.89
h (n.s)		28.09	11.93	25.86	22.79	47.96	47.1	34.45	32.63
Source of	JL	Seed yield	/ plant (g)	Number of cap	osules/plants	1000-seed we	ight (g)	Oil cont	ent (%)
Variation	ai	100% ETo	60% Eto	100% ETo	60% ETo	100% ETo	60% ETo	100% ETo	60% ETo
Genotypes	14	5.18**	2.39**	280.61**	110.23**	5.42**	4.14**	26.48**	39.13**
GCA	4	6.04**	5.34**	612.77**	244.56**	5.19**	4.26**	66.41**	62.64**
SCA	10	4.84**	1.21**	147.75**	56.50**	5.50**	4.10**	10.50**	29.72**
Error	28	0.00	0.03	0.28	0.64	0.00	0.00	1.03	0.67
$\sigma^2 \overline{GCA}/\sigma^2$	SCA	1.25	4.43	4.15	4.33	0.94	1.04	6.32	2.11
h (n.s)		31.97	60.84	67.60	51.00	23.01	26.52	61.71	31.82

General combining ability (GCA) effects:

Selecting the optimal genotypes as parents for reproduction depends on the estimation of GCA effects. Values of GCA effects of studied parents (Table 7) revealed that P3 recorded positive and significant values for leaf number, fresh and dry weight of shoot, plant height, root length, and number of capsules under both conditions, while for number of branches, fresh and dry weight of root, seed yield, and oil percent under normal conditions. P5 (H 11/9) had positive and significant values of GCA in shoot dry weight, fresh and dry weight of root, seed yield / plant, and 1000 seed weight under both

conditions, and for shoot fresh weight and number of capsules under normal conditions only, while rest traits recorded negative significant values. P2 recorded positive and significant values for oil percent under both conditions, fresh and dry weight of the shoot, root length under drought conditions, and seed yield under normal conditions. P1 recorded positive and significant values for the leaf number, dry weight of the shoot, plant height traits under normal conditions, and the number of capsules trait under drought conditions. P4 found significant and positive values for root length and 1000 seed weight traits under both conditions. From these results, P3 and P5 parents were good combiners for most studied traits. P2 was considered a good combiner for oil content percent and some growth traits under drought conditions. These results were in harmony with Singh *et al.*, (2022) and Nehar *et al.*, (2023), who stated that the best recombination is produced by identifying genes with the most desired combining ability. Kouighat *et al.*, (2020) reported that combining ability analysis, which is thought to be a potent approach for identifying the best combiner in sesame, is dependent on the selection of parents and understanding the nature of gene action for economic qualities. Mukhtar *et al.*, (2022) mentioned that the high value of GCA of genotype is considered a sign of wide adaptation and additive effects; moreover, it has great potential for use as a parent in the construction of widely utilizing hybrids with high seed yield and flexibility to drought stress.

Table 7. General combining ability effects for genotypes for growth, yield and oil characters under normal (100%ETo) and drought (60% ETo) conditions.

Characters	No. of leav	ves/ plant	No. of brai	nches/ plant	Fresh weight of shoot/plant (g)		Dry weight	of shoot (g)
Genotypes	100% ETo	60% ETo	100% ETo	60% ETo	100% ETo	60% ETo	100% ETo	60% ETo
P ₁	8.23**	-0.44**	-0.05	0.11	-7.00**	-10.381**	0.25*	-3.47**
\mathbf{P}_2	-3.53**	0.13	0.14	0.07	-11.05**	7.238**	-3.94**	1.15**
P ₃	8.37**	8.42**	0.62**	-0.08	29.43**	12.000**	4.06**	3.91**
\mathbf{P}_4	-7.20**	-2.77**	-0.29**	-0.08	-20.10**	-1.333**	-3.99**	-2.51**
P 5	-5.87**	-5.34**	-0.43**	-0.03	8.71**	-7.524**	3.63**	0.91**
S.E. (gi-gj)	0.151	0.169	0.100	0.060	0.120	0.103	0.108	0.103
Characters	Fresh weight	t of root (g)	Dry weigh	t of root (g)	Plant heigh	t (cm)	Root len	gth (cm)
Genotypes	100% ETo	60% ETo	100% ETo	60% ETo	100% ETo	60% ETo	100% ETo	60% ETo
P ₁	-1.05**	-0.67**	-0.60**	-0.55**	4.69**	-0.09	-0.75**	-0.75**
\mathbf{P}_2	-1.76**	0.05	-0.53**	0.01	-6.84**	-2.61**	0.06	0.10**
P ₃	1.81**	-0.19*	0.62^{**}	-0.06	8.45**	12.39**	0.68**	0.58**
P_4	-1.29**	0.76**	-0.64**	0.09	-5.60**	-1.37**	0.34**	0.25**
P 5	2.29**	0.05	1.15^{**}	0.52^{**}	-0.70**	-8.32**	-0.32**	-0.18**
S.E. (gi-gj)	0.085	0.077	0.120	0.071	0.155	0.120	0.059	0.029
Characters	Seed yield	/ plant (g)	Number of ca	apsules/plants	1000-seed we	eight (g)	Oil cont	ent (%)
Genotypes	100% ETo	60% ETo	100% ETo	60% ETo	100% ETo	60% ETo	100% ETo	60% ETo
P ₁	-0.15**	-0.38**	-1.34**	0.50**	-0.77**	-0.56**	-0.55**	-0.53**
P_2	0.68**	-0.26**	-3.91**	-0.54**	-0.21**	-0.18**	2.86**	2.61**
P ₃	-0.55**	0.14**	8.28**	5.55**	0.17**	-0.07**	0.15	0.48**
P_4	-0.41**	-0.33**	-5.15**	-2.73**	0.42**	0.15**	-1.98**	-2.09**
P5	0.44**	0.82**	2.13**	-2.78**	0.39**	0.66**	-0.48*	-0.48**
S.E. (gi-gj)	0.005	0.032	0.103	0.156	0.009	0.006	0.198	0.160

Specific combining ability (SCA) effects:

Results of specific combining ability effects (Table 8) showed that P1 X P3 and P2 X P4 crosses had positive and significant SCA effects under drought conditions for most studied traits, and most studied crosses recorded positive and significant values for oil percent and 1000 seed weight traits under normal and drought conditions. P4 x P5 showed positive and significant values for most growth and yield traits under drought conditions. While under normal conditions, it recorded positive and significant values for oil percent, root length, and 1000 seed weight traits. P3 X P5 cross showed positive and significant results for shoot and root dry weight and root length under both conditions. Also, fresh weight of the shoot, fresh and dry weight of the root, seed yield, and capsule number under normal conditions, in addition to oil content under drought conditions, The P3 X P4 cross illustrated positive and significant values for fresh and dry weight of the shoot, dry weight of the root, root length, seed yield, and oil content percent under normal and drought conditions. Moreover; number of capsules, fresh weight of root and 1000 seeds weight under normal condition. P1 X P4 cross showed positive and significant values for leaf number, shoot fresh and dry weight, and oil percent under the drought condition, but for plant height and 1000 seed weight under both conditions. Baghery et al., (2022) Sikarwar et al., (2021) stated that SCA will supply appropriate standards. In subsequent generations, it is anticipated that a crosscombination displaying high SCA and high performance will produce attractive transgressive segregants if at least one parent serves as a good general combiner for that particular characteristic. In breeding populations, the effects of GCA and SCA are important in the process of selection (Viana and Matta 2003). Fazal et al., (2022) found that one of the main goals of sesame hybrid breeding continues to be the creation of inbred lines with high general combining ability (GCA) and specific combining ability (SCA) for significant yield attributes. P2 X P5 showed positive and significant values for fresh and dry weight of shoot and root, plant height, and number of capsules traits under drought conditions. And for root length under both conditions, while it had negative and significant values for oil content in both conditions. Heterosis:

Results of heterosis ratios relative to mid-parent (MP) of studied sesame crosses (Table 9) showed that the highest value of heterosis (73.7) was recorded by P2 X P4 for dry weight of root trait under drought conditions.

Table 8.	. Specific	combining	ability	effects	for	genotypes	for	growth,	yield	and	oil	characters	under	normal
	(100%E]	[o) and drou	ight (60	%ETo)	cond	ditions.								

Characters	No. of leav	es/ plant	No. of bran	ches/ plant	Shoot fresh w	eight/plant (g)	Shoot dry	weight (g)
Genotypes	100% ETo	60% Eto	100% ETo	60% ETo	100% ETo	60% Eto	100% ETo	60% ETo
$P_1 x P_2$	-1.76**	-2.21**	0.35	0.06	-13.73**	-18.97**	0.10	-2.29**
$P_1 x P_3$	30.33**	15.51**	-0.79**	-0.13	4.13**	6.27**	2.10**	3.29**
$P_1 x P_4$	-5.43**	1.70**	-0.22	-0.13	-16.35**	9.60**	-6.52**	3.05**
$P_1 x P_5$	8.57**	2.27**	0.25	0.16	-8.49**	2.46**	-0.81**	-2.05**
$P_2 x P_3$	1.10**	-7.06**	0.68**	-0.08	84.84**	-31.35**	-0.38	-1.33**
$P_2 x P_4$	0.33	4.13**	-0.41	-0.08	-3.97**	16.98**	4.67**	5.10**
P2 x P5	-6.33**	0.03	-0.27	-0.13	-31.11**	13.17**	-2.95**	2.33**
$P_3 x P_4$	-0.24	-2.16**	0.44	0.06	40.56**	2.22**	13.00**	2.33**
P ₃ x P ₅	-18.24**	-4.92**	-0.75**	0.02	38.41**	-1.59**	8.71**	3.90**
P4 x P5	-2.67**	4.27**	0.16	0.02	-40.40**	20.08**	-13.24**	-1.33**
S.E. (sij - sji)	0.583	0.655	0.386	0.231	0.466	0.400	0.417	0.401
Characters	Root fresh	weight (g)	Root dry v	weight (g)	Plant hei	ght (cm)	Root len	gth (cm)
Genotypes	100% ETo	60% ETo	100% ETo	60% ETo	100% ETo	60% Eto	100% ETo	60% ÉTo
$P_1 x P_2$	-4.52**	-3.49**	-1.12**	-1.08**	4.95**	-4.68**	-1.57**	-1.06**
$P_1 x P_3$	0.24	3.41**	-1.18**	1.21**	20.00**	31.32**	1.48**	1.46**
$P_1 x P_4$	3.33**	-2.54**	0.58	-0.86**	1.71**	12.08**	-1.19**	-1.21**
$P_1 x P_5$	-5.24**	-1.83**	-1.70**	0.64**	-0.19	5.03**	-0.52**	-0.78**
$P_2 x P_3$	-2.38**	-0.63**	-1.25**	0.65**	6.52**	1.84**	-0.33*	-0.40**
$P_2 x P_4$	2.38**	6.75**	1.68**	2.18**	3.57**	-1.40**	-2.00**	-2.06**
P2 x P5	-1.19**	5.79**	-0.11	1.75**	-15.33**	2.56**	1.33**	1.37**
P ₃ x P ₄	7.14**	-1.35**	2.19**	0.57**	-10.38**	-4.40**	0.38*	0.46**
$P_3 x P_5$	13.57**	-0.63**	7.07**	0.14	-15.29**	0.89**	0.38*	0.89**
P ₄ x P ₅	-3.33**	5.08**	-1.67**	1.67**	-8.24**	8.98**	1.38**	1.22**
S.E. (sij -sji)	0.330	0.298	0.464	0.276	0.599	0.466	0.227	0.113
Characters	Seed yield	/ plant (g)	Number of ca	psules/plants	1000-seed	weight (g)	Oil cont	ent (%)
Genotypes	100% ETo	60% ETo	100% ETo	60% ETo	100% ETo	60% Eto	100% ETo	60% ETo
$P_1 x P_2$	0.01	-0.38**	1.08**	-0.10	0.57**	1.25**	-0.71	-0.802
$P_1 x P_3$	-0.76**	0.71**	0.56*	4.81**	0.96**	0.05**	2.40**	1.227**
$P_1 x P_4$	-0.40**	-0.82**	-8.68**	-0.57	1.03**	0.30**	0.46	2.365**
$P_1 x P_5$	-1.75**	0.03	5.37**	-1.86**	1.11**	1.39**	0.32	0.594
$P_2 \times P_3$	0.40**	0.40**	5.46**	-9.14**	0.44 * *	0.71**	-0.75	-0.849*
P ₂ x P ₄	-1.17**	0.57**	0.56*	2.14**	-0.05*	-0.98**	-0.56	1.056*
P2 x P5	0.41**	-0.58**	-5.73**	3.19**	1.07**	-0.09**	-2.06**	-6.316**
P ₃ x P ₄	0.76**	0.66**	8.03**	-0.95*	0.22**	-0.60**	2.06**	2.617**
P ₃ x P ₅	2.34**	-0.16	8.08**	-2.90**	-1.80**	-1.21**	-1.31*	2.179**
P4 x P5	-0.32**	0.65**	-7.49**	4.71**	1.65**	1.78**	2.35**	1.251**
S.E.(sii -sii)	0.020	0.124	0.400	0.604	0.034	0.024	0.768	0.621

 Table 9. Heterosis percentages relative to mid-parent of sesame genotypes for growth, yield and oil characters under normal (100%ETo) and drought (60%ETo) conditions.

Characters	No. of lea	ves/ plant	No. of bran	ches/ plant	Fresh weight of s	hoot/plant (g)	Dry weight	of shoot (g)
Genotypes	100% Eto	60% Eto	100% Eto	60% ETo	100% ETo	60% ETo	100% ETo	60% ETo
$P_1 x P_2$	10.31**	3.79	16.67	0.00	-12.90**	-55.77**	-3.13*	-5.56**
$P_1 x P_3$	47.34**	42.01**	-75.00**	-16.67	23.20**	0.00	18.18**	25.00**
$P_1 x P_4$	1.38	34.78**	-33.33	-16.67	-32.73**	34.21**	-41.67**	35.00**
P1 x P5	22.90**	33.33**	0.00	12.50	-21.43**	21.67**	-12.50**	-5.56**
$P_2 x P_3$	5.71**	-30.77**	22.22*	-16.67	56.99**	-79.69**	19.44**	7.14**
$P_2 x P_4$	-10.99**	18.59**	-33.33	-16.67	0.00	27.36**	16.67**	35.71**
$P_2 x P_5$	-50.67**	-4.31	-33.33	-16.67	-31.97**	21.28**	-17.28**	16.67**
P3 x P4	2.40*	0.60	14.29	0.00	41.89**	10.64**	42.31**	28.57**
P ₃ x P ₅	-78.67**	-18.38**	-100**	0.00	33.07**	1.22**	26.79**	23.53**
P4 x P5	-37.33**	32.26**	0.00	0.00	-67.00**	53.26**	-95.00**	10.00**
Characters	Fresh weigh	nt of root (g)	Dry weight	of root (g)	Plant heigh	nt (cm)	Root leng	gth (cm)
Genotypes	100% Eto	60% Eto	100% Eto	60% ĒTo	100% ETo	60% ETo	100% ETo	60% ETo
$P_1 x P_2$	-75.00**	-50.00**	-55.98**	-21.21	8.76**	5.78**	-36.36**	-28.57**
$P_1 x P_3$	18.18**	21.43**	-6.67	55.05**	16.60**	32.68**	13.64**	16.67**
$P_1 x P_4$	22.73**	-25.00**	7.58	0.12	3.87**	22.55**	-25.00**	-28.57*
$P_1 x P_5$	-43.75**	-12.50**	-33.33**	50.00**	-2.52**	19.37**	-4.17	-7.14**
$P_2 x P_3$	5.56**	20.00**	5.00	65.05^{**}	4.88**	7.36**	-5.00**	-3.70**
$P_2 x P_4$	20.00**	65.00**	32.50**	78.70**	0.14	1.94**	-37.50**	-42.86**
$P_2 x P_5$	-10.00**	66.67**	8.75	73.33**	-23.82**	6.50**	12.50**	15.00**
P ₃ x P ₄	56.67**	10.00**	55.00**	63.10**	-11.16**	5.94**	4.55**	6.67**
P ₃ x P ₅	54.76**	20.00	64.44**	55.05**	-20.52**	11.18**	14.52**	21.67**
P ₄ x P ₅	0.00	61.11	-1.67	72.03**	-18.71**	15.94**	15.15**	15.00**
Characters	Seed yield	l/ plant (g)	Number of ca	psules/plants	1000-seed w	eight (g)	Oil conte	ent (%)
Genotypes	100% Eto	60% Eto	100% Eto	60% ETo	100% ETo	60% ETo	100% ETo	60% ETo
$P_1 x P_2$	-16.10**	-33.33**	3.66**	-2.78	37.37**	43.36**	-2.07	-3.50**
$P_1 x P_3$	-26.83**	33.33**	14.53**	11.49**	30.01**	13.22**	6.65**	7.01**
$P_1 x P_4$	-40.14**	-66.67**	-67.35**	8.70**	41.34**	25.93**	4.27**	10.81**
$P_1 x P_5$	-76.83**	-3.33	13.27**	-3.57	39.22**	42.62**	1.48	1.87
$P_2 x P_3$	20.00**	28.57**	27.42**	-86.90**	14.67**	13.33**	-2.13	-2.62*
$P_2 x P_4$	-42.99**	33.33**	-4.35**	14.71**	19.82**	-17.59**	-0.95	2.38*
$P_2 x P_5$	8.33**	-24.00**	-22.22**	16.67**	29.90**	12.12**	-6.16**	-20.21**
P ₃ x P ₄	27.34**	44.44**	27.34**	-8.33**	13.53**	-17.89**	7.09**	11.99**
P ₃ x P ₅	47.76**	7.00*	27.33**	-23.15**	-29.63**	-25.00**	-1.74	5.92**
P ₄ x P ₅	-10.40**	24.55**	-44.44**	39.42**	34.96**	32.87**	6.21**	5.49**

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In addition, this cross had significant positive values of heterosis for most growth traits except root length. P4 X P5 cross had superiority for all studied traits under drought conditions, but under normal conditions, it had a different response and noted both significant positive and significant negative values for studied traits. The P1 X P3 cross had superiority in most studied growth and yield traits under both conditions. P2 X P5 cross had superiority under drought conditions for all studied traits except leaf number, branch number, and seed yield. In normal conditions, it showed positive and significant values for root dry weight, root length, seed yield/ plant, and 1000 seed weight. P3 X P4 and P3 X P5 crosses had a significant positive value of heterosis for most studied traits under both conditions, except number of capsules and 1000 seeds weight under drought conditions and plant height under normal

conditions. P3 X P4 had the highest values of heterosis for seed yield (44.44) and oil content percent (11.99) traits under drought conditions. Zabet *et al.*, (2021) found the highest heterosis relative to mid-parent (29.2%) for grain yield under normal conditions. These results were consistent with those of Nehar *et al.*, (2023), who mentioned that the hybridization process can increase the productivity of sesame by creating desirable lines with desirable features.

SCoT molecular marker

A total of 10 SCoT primers designed for sites around the start codon were examined for selective amplification of DNA fragments of five parental cultivars and their 10 hybrids of *Sesamum indicum* L. Table 10 lists the polymorphism levels. Reliable PCR products were obtained by the 10 SCoT primers (Figure 1).



Figure 1. M: marker; (1): H 102/58 (P1), (2): M2 A6 (P2), (3): M1 A38 (P3), (4): shandaweel3 (P4), (5): H 11/9 (P5), (6): P₁x P₂, (7): P₁x P₃, (8): P₁x P₄, (9): P₁x P₅, (10): P₂ x P₃, (11): P₂ x P₄, (12): P₂ x P₅, (13): P₃ x P₄, (14): P₃ x P₅ and (15): P₄ x P₅.

Using 10 SCoT primers, data analysis revealed 126 amplified fragments with a polymorphism of 52%. The primer SCoT-8 amplified a maximum of 17 fragments, whereas the primer SCoT-2 amplified a minimum of nine fragments. There were 66 polymorphic bands and 60 monomorphic bands.

 Table 10. Sesame polymorphic SCoT primers statistics used.

Code	Total number	Monomorp	Polymorph	Polymorph
Code	of bands	hic Bands	ic bands	ism % (%)
SCoT -1	11	8	3	27
SCoT -2	9	7	2	22
SCoT -3	11	7	4	36
SCoT-4	13	7	6	46
SCoT -5	14	4	10	71
SCoT-6	15	5	10	67
SCoT-7	12	7	5	42
SCoT -8	17	6	11	64
SCoT -9	12	4	8	67
SCoT-10	12	5	7	58
Total	126	60	66	52

These results are consistent with those of Mesfer *et al.*, (2022), who assessed utilizing physiological and cyto/molecular analysis with ISSR and SCoT primers, the genetic diversity and connections between sesame cultivars. 233 and 275 alleles were amplified in the genotypes under investigation, and the average polymorphism percentage for all the genotypes under study was 65.32% (ISSR) and 77.8% (SCoT), respectively. BHATTACHARJEE and

DASGUPTA (2020) used thirty sesame genotypes for genetic diversity, which was determined using SCoT and expressed sequence tag (EST)-SSR markers. Elayaraja *et al.*, (2019) used SCoT markers to reveal the regenerated frequency of *Sesamum indicum* L.

Genetic similarity and dendrogram analysis

Amplified bands generated using SCoT molecular markers were visually evaluated for the presence (1) and absence (0) of bands for all genotypes. Based on Jaccard's coefficient, the genetic similarity estimations for the primers employed in sesame varied from 75 to 92%. The relationships with 92% similarity between (P2 x P3) and (P2 x P4) were the closest (Table 11). H 11/9 (P5) and (P3 x P4) had the lowest percentage (75%) of all.

The genotypes were divided into two main clusters by the dendrogram. The first included two genotypes (P4, P4 x P5). The second cluster could be divided into two subclusters, one containing P1. Sub-cluster two contained two main sub-clusters, as shown in Figure 2.

These results are consistent with those of Talebi *et al.*, (2023), who examined the genetic diversity of *Sesamum indicum* L. using 10 SCoT molecular primers. Mesfer *et al.*, (2022) studied the phylogenetic relationship as revealed by cluster analysis using SCoT data from sesame plants. Singh *et al.*, (2016) investigated phylogenetic linkages, genetic diversity assessment, and various gene pools of sesame genetic resources.

 Table 11. Genetic similarity between the fifteen sesame genotypes, as determined using the studied SCoT primers data.

	P1	P2	P3	P4	P5	P ₁ x P ₂	P ₁ x P ₃	P1 x P4	P ₁ x P ₅	P ₂ x P ₃	P2 x P4	P2 x P5	P ₃ x P ₄	P3 x P5	P ₄ x P ₅
P1	100														
P2	84	100													
P3	83	85	100												
P4	82	85	82	100											
P5	83	85	85	86	100										
$P_1 x P_2$	80	82	85	83	89	100									
P1 x P3	82	86	87	82	81	89	100								
$P_1 x P_4$	80	84	85	81	82	86	90	100							
P1 x P5	82	83	83	84	84	84	84	89	100						
P ₂ x P ₃	84	83	83	86	88	84	82	85	91	100					
$P_2 x P_4$	85	84	85	85	86	81	85	87	88	92	100				
P2 x P5	83	84	83	78	80	82	86	86	85	85	89	100			
$P_3 x P_4$	82	79	82	78	75	77	84	82	81	80	84	84	100		
P3 x P5	82	84	81	81	80	79	85	84	86	86	90	87	89	100	
P ₄ x P ₅	78	85	84	85	81	78	81	81	80	82	82	80	85	82	100



Figure 2. Dendrogram generated among the fifteen sesame genotypes by SCoT analysis based on UPGMA clustering method and Jacquared's coefficient

CONCLUSION

Our breeding material had a high amount of genetic variability that could be used in developing high-yield drought-tolerant genotypes of sesame. GCA and SCA effects reported that P3 (M1 A38) and P5 (H 11/9) parents were good combiners. P4 X P5, P1 X P3, P3 X P5, and P3 X P4 crosses showed superior heterosis values for most studied traits under normal and drought conditions. The phylogenetic relationship between all the genotypes under study was successfully established by the current SCoT analysis.

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التوصيف الجزيئي لبعض الطرز الوراثيه من نبات السمسم (.Sesamum indicum L) تحت ظروف الجفاف

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الملخص

لمواجهة التغير المناخي العلمي المتزايد في مستوي المياه وتحقق التنمية المستدامة لإنتاج البنرر وابتاج الزيت في محصول السمسم، تمت در اسه خمسة أصناف من السمسم وهي؛ H ملتين؛ الري الطبيعي والري تحت ظروف الاجهد النتج من تأثير الجفف لدراسة النمو وأداء المحصول والتوريث وقوه الهجين والقدرة على التألف. أظهرت الناتج في الظروف الطبيعية وظروف الاجهد أن جميع الأباء والهجن تحت ظروف الاجهد النتج من تأثير الجفف لدراسة النمو وأداء المحصول والتوريث وقوه الهجين والقدرة على التألف. أظهرت الناتج في الظروف الطبيعية وظروف الاجهد أن جميع الأباء والهجن تحت ظروف الاجهد النتج من تأثير الجفف لدراسة النمو وأداء المحصول والتوريث وقوه الهجين والقدرة على التألف. أظهرت الناتة في الفلروف الطبيعية وظروف الاجهد أن جميع الأباء والهجن تحت الدراسه لديهم سمات مميزة مختلفة؛ كان لـ 73 أعلى متوسط أداء لمعظم صفات النمو والإنتاج. كان لـ 79 و10 و57 أعلى القير المتوسطة لصفة وزن 1000 بنرة. ورجع لذي جميع الأباء والهجن تحت الدراسه لديهم سمات مميزة مختلفة؛ كان لـ 73 أعلى متوسط أداء لمعظم صفات النمو والإنتاج. كان لـ 79 و40 و 15 أعلى القير الموسطة لصفة وزن 1000 بنرة. وعلم الحبيك 12 على القير المهجن تحتر نقيبة تعدي الذي له عن تقوق الهجن من القير الموجية والمعوبية التأثير الخلص على التألف (SCA) وقوه الهجين في 29 X P4 و20 عن 29 معلى التوسمة الورث وح2 X P4 في معظم الصفات. تعتبر تقنية تعدد الأشكل لمستجدفة (SCOT - marker) واليصمه الور الي بني الحسم على التراسة الحرائي الحد الإجملي الحرم المتحصل عليها و54 X P4 في معظم الصفات. تعتبر تقنية تعدد الأشكل المستجد (Scot - marker) واليصمه الور الثيه في الذر المتحمل عليه من الخمسه عشر طراز ور لثي محل الدر السه من نبك السمسر الى Scot - Scot المتر الموالي بيتر والي من المائية المواقع متعدد الأشكل 20٪. بلغ عد الحزم متحدة الأشكل 60، بينما بلغ عد الحرم الدر المي نبكان 60 أظهر تحليل بيتر اوح ما بين 75 إلى 29. مراسه درج القرابي الور أل طور معد الأشكل 60، بينما بلغ عد الحزم الحديه الشكل 60 أظهر تعلي بيتو الع الي يتر اوح ما بين 75 إلى 29. تم در المعرم وه المرالي المروف. الإشكل 60 من بينه المع مومو عنين رئيلي بين 61 أطهر توزيع من عنين مرعين مر عيني معتبات حمي علي الربي الموية الموليو