

Genetic Analyses of Yield Components and Diseases Resistance in Sesame (*Sesamum indicum* L.) Using Two Progenies of Diallel Crosses

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Abstract: Improvement of seed yield components and resistance to diseases in sesame crop is the prime objective of a breeding programs. However, little genetic information is available for these approaches listen. Hence, the main objective of this study was to approximate the genetic parameters of seed yield components and resistance degree of Fusarium wilt and charcoal root-rot diseases. Therefore, six promising sesame lines as a hybrids and segregates line (H_1 , H_6 , H_9 , S_2 , S_3 and S_5) and Taka 2, a new variety were crossed in all combination using a diallel mating scheme without their reciprocals. Crosses were selfed to obtain seeds of F_2 generation. Progenies of F_1 's and F_2 's along with their parents were evaluated in two separate set of experiments at private farm in Abou Soltan village, Ismailia, Egypt during 2010 crop season. The results exhibited that the GCA mean squares were significant for all characters through both analyses (F_1 's and F_2 's). Positive and significant GCA effects for seed yield (g plant^{-1}) and seed yield (kg ha^{-1}) were found for sesame parental lines. S_2 (P_2) indicates that progeny with those genotypes as parents showed a seed yields with the genotype that was greater than the average of all crosses. Parental line S_4 (P_4) was the best combiner for developing genotypes with high oil seed content as well as resistance to *F. oxysporum* (FOS) and *M. Phaseolina* (MPH). For achieving genotypes with short time to flowering and plant height, fruiting branches number (plant^{-1}), capsules number (plant^{-1}), 1000 seed weight (g) and seed yield (kg ha^{-1}), S_6 (P_6) and Taka 2 (P_7) were the best parents. GCA/SCA ratio indicated additive effects for all the characters except seed yield (g plant^{-1}) in F_1 's and F_2 's and seed yield (kg ha^{-1}) only in F_2 's. Narrow sense heritability varied from 89.14% for plant height to 8.79% for seed yield (kg plant^{-1}). However, most of characters studied scored highest values of broad sense heritability (>75%) except seed yield (g plant^{-1}) (69.10, 73.21%) seed yield (kg ha^{-1}) (74.69, 63.28%), infection (%) by FOS (74.99, 64.95%) and infection (%) by MPH (67.32, 71.69%) in F_1 's and F_2 's, respectively. Positive with highly significant association coefficients between GCA effects and mean characters in all cases implied that parental sesame lines with high values of the characters have superior combining ability. The phenotypic (r_{ph}) and genotypic (r_g) coefficient between all studied characters shows negative to positive values with significant or non-significant correlation between each of both characters through F_1 's and F_2 's. It was noticed that the high resistance characters give the lowest seed yield. Therefore, a great care should be taken during selection for seed yield and its components as well as the resistance to infection (%) by each of FOS and MPH.

Key words: Charcoal root rot, combining ability, combining ability, diallel, diseases resistance, Fusarium wilt, heritability, sesame

INTRODUCTION

Sesame, *Sesamum indicum* L. is an ancient oil seed and is one of the oldest cultivated crops in the world according to some archaeological record (Bedigian, 2006). The first recorded as an oil crop was in Babylon and Assyria over 4,000 years ago while in Egypt history, it returned back to 1300 BC (Burkill, 1953). Sesame contains edible oil with antioxidative constituents, i.e., sesamol, sesamin and sesamol and protein content, quality vitamins and amino acids (Brar and Ahuja, 1979). According to world renowned organization, the Food and

Agriculture Organization (FAO) of the United Nations, sesame ranked 6th as an edible oil seed (2,995.624 million ton) and 12th in vegetable oil (854.148 million ton) through the world. In Egypt, the area of production is currently believed to be 79263 feddans (2.4 fedden = hectare) with a total production of 147985.29 ardab per feddan (1233.21Kg ha^{-1}). In Egypt, it is imperative to cultivate sesame for high yield and disease resistance as compared to other oil producing crops. Due to nutritional, historic and cultural value sesame enjoyed full previllage but lack of resistance against biotic and a biotic stresses Egypt sesame faced complex of

problems. Hence, application of some genetic improvement of diseases resistance in current genotypes has been proved a best option to formulate effective strategies to solve the diseases problems in sesame (Zagre *et al.*, 1999; Ziedan, 1993; Xiurong *et al.*, 2001; Ragab *et al.*, 2002; El-Fiki *et al.*, 2004; El-Bramawy, 2006a, b, 2008; Bayoumi and El-Bramawy, 2007; El-Shakhess and Khalifa, 2007; El-Bramawy *et al.*, 2008).

Sesame is a completely self pollinated crop however, an artificial pollination by man and insects (Knowles and Byron 1955; Weiss, 2000) made it cross pollinated. Therefore, the breeding methods of cross-pollinated crops can be used in sesame (Dajue and Miindel, 1996). Genetic variation and information regarding genetic control for different agronomic and disease resistance characters is needed to produce improved cultivars. Genetic variation for different characters including seed yield and its components as well as diseases (Fusarium wilt and charcoal root-rot) resistance has been previously reported in sesame germplasm by El-Shakhess (1998), El-Bramawy (2003), El-Fiki *et al.* (2004), Bayoumi and El-Bramawy (2007), El-Bramawy and Wahid (2007), El-Shakhess and Khalifa (2007) and El-Bramawy and Shaban (2008).

In general, diallel mating designs are used in plant breeding to get information on genetic effects for a fixed set of parental lines or estimates of General Combining Ability (GCA) and Specific Combining Ability (SCA) variance components as well as heritability. The four methods of Griffing (1956) have been used to obtain genetic information on the basis of data from only one year or one location, although multiple environment data were suggested to provide more reliable genetic information on material tested.

In addition, the diallel cross technique was reported to provide early information on the genetic behaviour of these attributes in the first (F_1) generation (Chowdhry *et al.*, 1999; Noorka *et al.*, 2007, 2009). Moreover, the diallel analysis fashion/modeling can provide the necessary genetic information for breeding programs (Hill *et al.*, 2001; Ghosh and Das, 2003; Maluwa and Gjerde, 2006) and has been frequently used to obtain the genetic information regarding various characters via yield and its components (Guines *et al.*, 2002) and diseases resistance in sesame crop (El-Bramawy, 2003; Bayoumi and El-Bramawy, 2007; El-Shakhess and Khalifa, 2007).

In many hermaphrodite plants, e.g., sesame in which it is difficult to produce F_1 seeds hybrid but it is easier to use F_2 progenies in diallel analysis (Mather and Jinks, 1982). Genetic analysis based upon F_1 progenies in diallel

crosses has been previously used in sesame but it seems that using F_2 progenies in diallel analysis has not been established so far. Since, there is not enough genetic information regarding seed yield, yield components and the wilt and charcoal root-rot diseases resistance of the sesame crop.

The importance of additive and non-additive genetic effects is well established in controlling many characters of sesame. It was shown that the additive and/or dominance effects of the genes played a major role variation, hence explained considerable amount of these variations in sesame seed yield and its components via plant height (cm), number of fruiting branches/plant, number of capsules/plant, 1000 seed weight (g) and oil content percentage in sesame (El-Bramawy, 2003; Ali, 2010). Also, the influence of both additive and non-additive effects of genes on resistance to Fusarium wilt (FOS) and charcoal root-rot (MPH) diseases in sesame has been reported (El-Bramawy, 2006a, b, 2008; Bayoumi and El-Bramawy, 2007; El-Shakhess and Khalifa, 2007; El-Bramawy *et al.*, 2008).

On the other hand, a high value of broad sense heritability in for seed yield as well as disease resistance in Fusarium wilt (FOS) and charcoal root-rot (MPH) in sesame was reported by El-Bramawy and Wahid (2007). While, heritability in narrow sense was detected and varied from low value (6.68%) to high value (68.48%) in sesame crop (El-Bramawy and Wahid, 2006).

Thus, keeping in view the said objectives the present study was initiated to estimate GCA, SCA and other genetic parameters by using F_1 and F_2 progenies in two set of diallel crosses, to compare the results from F_1 's and F_2 's diallel analyses and to determine phenotypic and genetic association between the characters studied.

MATERIALS AND METHODS

Plant materials: Seven sesame genotypes including six promising sesame lines, namely H_1 , H_6 , H_9 , S_2 , S_3 S_5 and Taka 2 variety (Table 1). These promising lines were derived by hybridization and selections through a breeding program in the Agronomy Department, Faculty of Agriculture, Suez Canal University while, Taka 2 variety considering to be a new variety was taken from Nuclear Research Center, Atomic Energy Authority in Egypt. These parental sesame genotypes were chosen on their genetic variation for seed yield and its components as well as their potential resistance to Fusarium wilt, (*Fusarium oxysporum* F. sp. *sesami*) (FOS) and charcoal root-rot (*Macrophomina phaseolina*) (MPH) diseases.

Table 1: Number, name, source and pedigree of sesame parental

No.	Name	Source	Pedigree
P ₁	H ₁	Egypt	Ismailia line 10 x Neu H.B
P ₂	H ₆	Egypt	A cross between two local lines
P ₃	H ₉	Egypt	A cross between two local lines
P ₄	S ₂	Egypt	Selection from local lines under breeding program at Agro. Dept., Agric. Fac., SCA*
P ₅	S ₃	Egypt	Selection from local lines under breeding program at Agro. Dept. Agric. Fac, SCA
P ₆	S ₅	Egypt	Selection from local lines under breeding program at Agro. Dept. Agric. Fac., SCA
P ₇	Taka 2	Egypt	Local line 2 produced by Nuclear Research Center, Atomic Energy Authority, Egypt

*SCA = Suez Canal University

Experiments sites and soil analysis: Three field experiments during three successive seasons of 2008-2010 were conducted in the experimental farm, Faculty of Agriculture, Suez Canal University and in a private Farm, Abou-Soltan village, Ismailia, Egypt. The soil of the experiments was sandy textured (94.5% sand, 2.5% silt and 3.0 clay) and (92.10% sand, 2.79% silt and 5.11 clay), respectively. The pH values of soil was 7.61 and 7.52 and contained 3.15 and 4.04 ppm available N, 1.80 and 1.96 ppm available P, 11.65 and 11.99 ppm available K and 0.049 and 0.078% organic matter in the both soil site, respectively. These analysis was done at the Department of Soil and Water according to Kilmer and Alexander (1949) methods.

The private farm (Abou-Soltan, village) was selected in this soil region due to infection of the disease through the complaints of farmers and scientist research during 2004 and 2005 (El-Bramawy, 2006a, b).

Crossing technique: During summer season of 2008, the sesame parental lines were crossed using half-diallel mating design to produce 21 F₁ hybrids. The seeds of F₁ progeny from each cross were planted and selfed to obtain F₂ seeds during crop season 2009.

Experimental designs and agronomic practices: During 2010 season, seeds of both F₁'s and F₂'s were sown in two separating experiments at Abou-Soltan village. Randomized Complete Block Designs (RCBD) with three replications was used in both experiments. In the first experiment (Exp. 1), (F₁'s) each experimental unit contained three rows, measuring 4 m long and 0.50 m wide while for Exp. 2 (F₂'s), it contained 6 rows, 4 m long with 0.50 m space. Recommended agriculture practices, e.g., irrigation, fertilization, weed control, etc., for same production were performed at proper time.

Agronomic characters data: Regarding to the agronomic characters, e.g., seed yield, number of days to maturity, plant height (cm), number of fruiting branches per plant, number of capsules per plant, 1000 seed weight (g), seed yield (g plant⁻¹) and seed yield (kg ha⁻¹) were recorded for each experimental unit. The oil content percentage of the seed was determined by Soxhlet method in which

n-hexane which was used as solvent according to AOAC (1990). The mentioned characters were considered for each plot and were calculated based on randomly chosen plants.

Diseases infection data: The infection of diseases by Fusarium wilt, *Fusarium oxysporum* F. sp. *sesami* (FOS) and charcoal root-rot, *Macrophomina phaseolina* (MPH), were done and percentage of infected plant per plot was calculated as follows:

Measurements of infection percentage: The percentage of diseased sesame plants infected with Fusarium wilt (FOS) or charcoal root-rot (MPH) were estimated according to specific disease symptoms for each fungus (*F. oxysporum* and *M. phaseolina*) and recorded weekly throughout the crop growth up to the stage from 30 days after sowing till the end of the experiment. The infected plants by *F. oxysporum* (FOS) were characterized by the internal vesicular discoloration, appearance of Fusarium wilt on plants and semi die considered wilted. However, the charcoal root-rot infection was expressed as root discoloration, black stem rot and pronounced reduction in root system of the sesame infected plants (Smith and Carvil, 1997).

Fungal pathogens isolates: To assure the existence of a relation between diseases pathogens (*F. oxysporum* (FOS) and *M. phaseolina* (MPH)) and the developed diseases, some of the wilted and rooted sesame plants from the diseased plant were considered as a sample to re-isolate the wilt (FOS) and root rot (MPH) pathogens which developed typical wilting and root rot symptoms. The re-isolation of *F. oxysporum* and *M. phaseolina* were carried out by Abdul Wahid (Smith and Carvil, 1997).

Scoring of sesame genotypes for resistance scale: Fusarium wilt and charcoal root-rot scores were measured using the own scale (Table 2). No definitive scales were recommended for evaluation of the sesame germplasm reaction with the *F. oxysporum* (FOS) and *M. phaseolina* (MPH) pathogens. Meanwhile, a 0-5 scale (Table 2) on sesame plot plants of F₁'s and F₂'s that were checked for any specific disease symptoms for each fungi (FOS and/or

Table 2: Evaluation scale used through the application work

Scores	Infection (%)	Categories
0	No infection	Immune (I)
1	0.10-5.00	Resistance (R)
2	15.0-5.10	Tolerance (T)
3	15.10-30	Moderately Susceptible (MS)
4	30.10-50	Susceptible (S)
5	>50	Highly Susceptible (HS)

MPH) according pervious disease symptoms in each plot. The genotype securing 0 scored were considered immune I (the damage ranged nothing); scoring 1 as resistant R (the damage ranged from 0.1-5%); scoring 2 as tolerance T (the damage ranged from 5.1-15%); scoring 3 as moderately susceptible MS (the damage ranged from 15.1-30%); scoring 4 as susceptible S (the damage ranged from 30.1-50%) and scoring 5 as highly susceptible HS (the damage ranged from >50%). This scale (Table 2) is based on the basis of the perception and in accordance results in the study area. The wilted and rotted sesame plants were counted and calculated as percentage of infected plants and then Arcsine values tables were used for the transformation of percentage numbers into numerical values according to Federer (1963).

Genetic parameters: Samples for each plot were analyzed in triplicate and their means were considered in statistical analyses. Since, the parental sesame genotypes were selected from different sources, the data were analyzed as a fixed model (Baker, 1978). For combining ability (GCA and SCA), Griffing's method 2, model I (Griffing, 1956) was used. For statistical analysis in both experiments (Exp. 1, F₁'s and Exp. 2, F₂'s), the below model was considered:

$$gijk = m + gi + gj + sij + eijk$$

Where:

- m = Mean of the experiment
- gi = GCA effects for the ith parent
- gj = The GCA effects for jth parent
- sij = The SCA effects for the ijth F₁'s or F₂'s progenies
- eijk = The residual

Narrow-sense heritability (h²n) was also calculated as:

$$h^2n = \sigma^2A / (\sigma^2A + \sigma^2D + \sigma^2e)$$

Where, σ^2A , σ^2D and σ^2e means component of variance due to additive effects; component of variance due to dominance effects and component of variance due to environment effects, respectively. These were estimated for each of F₁'s or F₂'s diallel analysis according to Kearsey and Pooni (1996).

The genotypic and phenotypic Pearson's correlation coefficients among the studied characters in both seasons were carried out by the method of Al-Jibouri *et al.* (1958).

Statistical analysis: The data was subjected to analysis of variance using General Linear Model (GLM) of the Statistical Analysis System program (SAS). The Least Significant Difference (LSD) test was used to determine the statistical difference between means when the F value was significant. The phenotypic and genetic Pearson's correlations was calculated using SAS program.

RESULTS AND DISCUSSION

Mean performance of sesame parents for all studied characters over both experiments (Exp. 1 and Exp. 2) were shown in Table 3. The parent S₉ (P₆) had the lowest mean of days to maturity (106) while the parent P₂ (H₆) possessed the highest value of plant height (191.47 cm), number of fruiting branches/plant (8.10), number of capsules/plant (112.39) and 1000 seed weight (4.02 g). The means of seed yield (g plant⁻¹) and seed yield (kg ha⁻¹) for parental sesame averaged over two experiments varied between 21.24 g and 1088.38 kg (P₂ = H₆) to 10.67 g and 855.85 kg (P₅ = S₃), respectively (Table 3). Parental sesame genotypes P₁ (H₁) and P₆ (S₉) had the highest (58.10%) and the lowest (53.20%) oil content among all parents, respectively.

The genotype parent P₂ (H₆) showed lowest infection percentage (2.05%) by FOS (*Fusarium wilt, F. oxysporum*) and scored as Resistance (R) while it scored the Susceptible rank (S) with MPH (charcoal root-rot, *M. phaseolina*) and possessed highest infection percentage (30.25%).

On the other hand, the parent P₅ (S₃) scored highest infection percentage (15.86%) by FOS and had Moderately Susceptible (MS) rank but possessed the Resistance (R) rank with infection percentage (3.41%) of MPH (Table 3). However for instance, both sesame parents (S₉ P₆ and Taka 2 P₇) keeping their resistance characters in reaction with both fungi pathogens whereas scored Tolerance (T) rank with 8.50 and 11.15 in case of FOS and scored Resistance (R) rank with 3.20 and 2.05 in case of MPH, respectively (Table 3). On the other hand, no immune sesame genotype was found among all sesame parents.

The effects of sesame genotypes including parental sesame and their crosses in both Exp. 1 (F₁'s) and Exp. 2 (F₂'s), diallel analysis were significant for all of the studied characters (Table 4). The mean squares of GCA in F₁ and F₂ diallel experiments were highly significant for all

Table 3: Mean performance of studied traits for the seven sesame parental

Traits	Days to maturity	Plant height (cm)	No. of fruiting branches/plant	No. of capsules/plant	1000 seed weight (g)	Seed yield (g plant ⁻¹)	Seed yield (kg ha ⁻¹)	Oil seed content (%)	Infection (%) by FOS		Infection (%) by MPH	
									Values	Rank	Values	Rank
Parents												
P ₁	116	164.31	4.01	56.24	3.21	10.20	796.28	58.10	4.89	R	8.95	T
P ₂	111	191.47	8.10	112.39	4.02	21.24	1088.38	55.39	2.05	R	30.25	S
P ₃	118	163.39	5.10	80.36	3.63	16.13	942.33	56.13	7.18	T	4.01	R
P ₄	124	158.24	4.91	70.20	3.36	11.34	931.00	57.39	2.98	R	3.95	R
P ₅	120	152.91	5.12	60.38	3.41	10.67	855.85	57.11	15.86	MS	3.41	R
P ₆	107	179.11	7.10	89.87	3.84	19.01	1007.58	53.20	8.50	T	11.15	T
P ₇	115	180.33	6.18	91.14	3.37	14.12	900.80	56.42	3.20	R	2.05	R
Significant	**	**	**	**	**	**	**	**	**	---	**	-
L.S.D 0.05	2.19	3.45	2.91	4.09	0.50	1.92	11.76	1.49	2.02	---	2.91	-
L.S.D 0.01	3.33	5.22	4.41	5.48	0.76	2.91	17.82	2.56	2.70	---	4.40	-

P₁ = H₁, P₂ = H₂, P₃ = H₃, P₄ = S₁, P₅ = S₂, P₆ = S₃ and P₇ = Taka 2. FOS = *Fusarium oxysporum* f. sp. *sesami*. MPH = *Macrophomina phaseolina*. R = Resistance, T = Tolerance, S = Susceptible and MS = Moderately Susceptible * and ** significant at 0.05 and 0.01 of probability levels, respectively

Table 4: Mean square for the diallel analysis and computes of the important genetic parameters in Exp. 1 (F₁'s) and Exp. 2 (F₂'s)

Source of variation	Experiment or generation	DF	Days to maturity	Plant height (cm)	No. of fruiting branches/plant	No. of capsules/plant	1000 seed weight (g)	Seed yield (g plant ⁻¹)	Seed yield (kg ha ⁻¹)	Oil seed content(%)	Infection(%) by FOS	Infection(%) by MPH
Rep.	Exp. 1 (F ₁ 's)	2	2.89	1.39	2.06	1.42	0.32	4.36*	9.32**	2.19	3.12	2.89
	Exp. 2 (F ₂ 's)	2	1.69	2.49	3.01	1.06	0.60	10.97**	21.39**	1.89	2.11	5.17**
Crosses	Exp. 1 (F ₁ 's)	27	51.42**	431.62**	2.10*	253.98**	0.18**	58.11**	1.98**	6.23**	41.67**	37.61**
	Exp. 2 (F ₂ 's)	27	63.12**	378.09**	3.47**	301.54**	0.21**	71.34**	2.11**	7.14**	39.57**	31.98**
GCA	Exp. 1 (F ₁ 's)	6	34.17**	264.68**	1.09**	179.25**	0.11**	21.69**	0.58**	2.91**	27.26**	29.17**
	Exp. 2 (F ₂ 's)	6	28.13**	176.14**	1.87**	137.98**	0.06**	17.98**	0.31**	2.57**	21.98**	24.87**
SCA	Exp. 1 (F ₁ 's)	21	6.36	57.98	1.02**	31.12	0.04**	26.31**	0.51**	1.89*	22.39**	18.97*
	Exp. 2 (F ₂ 's)	21	23.20*	151.69**	0.91**	120.69**	0.01**	21.35**	0.45**	2.04**	11.97*	16.98*
Error	Exp. 1 (F ₁ 's)	27	0.39	3.19	0.17	5.98	0.11	1.54	0.05	0.06	7.08	6.98
	Exp. 2 (F ₂ 's)	27	0.56	6.47	0.54	2.89	0.14	1.38	0.03	0.04	3.97	4.31
δ ² GCA/δ ² SCA	Exp. 1 (F ₁ 's)	---	5.37	4.56	1.07	5.76	2.75	0.82	1.14	1.54	1.22	1.54
h ² _{narrow}	Exp. 2 (F ₂ 's)	---	1.21	1.16	2.05	1.14	6.00	0.84	0.69	1.26	1.84	1.46
	Exp. 1 (F ₁ 's)	---	81.21	89.14	51.35	61.39	40.39	21.69	23.08	24.69	54.38	56.98
h ² _{broad}	Exp. 2 (F ₂ 's)	---	76.98	51.14	37.98	29.33	20.39	12.24	8.97	21.97	34.59	21.69
	Exp. 1 (F ₁ 's)	---	92.37	96.21	75.32	79.65	84.98	69.10	74.69	91.22	74.99	67.32
	Exp. 2 (F ₂ 's)	---	95.61	97.28	86.32	70.39	90.69	73.21	63.28	94.13	64.95	71.69

*and ** significant at 0.05 and 0.01 of probability levels, respectively; GCA = General Combining Ability. SCA = Specific Combining Ability; h²_b = Bored-sense heritability. h²_n = Narrow-sense heritability

characters (Table 4). In Exp. 1 (F₁'s) diallel analysis, SCA mean squares were significant for all characters except for days to maturity (6.36), plant height (57.98) and number of capsules per plant (31.12). However in analysis of F₂'s progenies, mean square of SCA was significant for all of the traits (Table 4).

The GCA/SCA ratio of mean squares ranged from 1.07 (for fruiting branches number/plant) to 6.00 (for capsules number/plant) in F₁'s diallel analysis. While in F₂'s diallel, the lowest and the highest ratios of GCA/SCA were 0.69 for seed yield (kg ha⁻¹) and 5.76 for 1000 seed weight, respectively.

In the first generation (F₁'s) diallel analysis, narrow sense heritability (h²_{narrow}) was relatively low to moderate for all of the studied traits except for days to maturity and plant height (Table 4). The lowest narrow sense heritability in F₁'s diallel was observed for seed yield g plant⁻¹ (21.69) and seed yield kg ha⁻¹ (23.08) and oil seed content (24.69). A moderate to high narrow sense heritability was found for all traits in F₂ diallel analysis except for days to maturity character where high and

scored 76.98 (Table 4). All the characters (except for plant height, number of fruiting branches per plant, number of capsules per plant and infection percentage by FOS) were almost consistent in terms of their narrow sense heritability in F₁'s and F₂'s analysis (Table 4). The plant height (cm) showed a high (89.14 %) and a moderate (51.14 %) narrow sense heritability in F₁'s and F₂'s diallels, respectively. The narrow sense heritability for infection percentage by MPH was 56.98% in F₁'s and 21.69% in F₂'s progenies.

The values of narrow sense heritability in all characters were increased a relatively in F₁'s compared in F₂'s diallels analysis. On the other hand in terms of broad sense heritability (h²_{broad} sense) all the characters had a relatively high heritability (>70%) in both analyses with few exception (Table 4). These exception cases represented in seed yield (g plant⁻¹) in F₁'s (69.10) and seed yield (kg ha⁻¹) in F₂'s (63.28) as well as each of infection percentage by FOS (54.99 and 64.95) and infection percentage by MPH (67.32 and 61.69) in F₁'s and F₂'s progenies, respectively (Table 4). In case of General

Table 5: General Combining Ability (GCA) effects for the seven sesame parents in Exp. 1 (F₁'s) and Exp. 2 (F₂'s)

Sesame parental or generation	Experiment	Days to maturity	Plant height (cm)	No. of fruiting branches/plant	No. of capsules/plant	1000 seed weight (g)	Seed yield (g plant ⁻¹)	Seed yield (kg ha ⁻¹)	Oil seed content (%)	Infection (%) by FOS	Infection (%) by MPH
P ₁	Exp.1 (F ₁ 's)	2.33	3.36	-1.05	6.25	-0.03	-0.98	0.41-	0.89	-0.97	1.36
	Exp.2 (F ₂ 's)	2.58	3.58	-0.99	7.01	0.01	-0.80	-0.94	1.00	-0.58	1.21
P ₂	Exp.1 (F ₁ 's)	-1.44	4.12	0.41	-9.45	0.21	1.01	0.21	-0.58	-0.86	-0.51
	Exp.2 (F ₂ 's)	-1.29	4.02	-0.65	-6.67	-0.03	1.24	0.78	-1.01	-1.09	-0.59
P ₃	Exp.1 (F ₁ 's)	3.47	6.13-	0.46	2.14	0.31	0.91	0.09	-0.91	1.99	1.05
	Exp.2 (F ₂ 's)	3.56	-8.04	0.69	3.39	0.51	1.11	-0.49	-0.88	2.38	0.86
P ₄	Exp.1 (F ₁ 's)	1.99	8.99-	-0.58	-3.95	-0.41	1.13-	-0.19	0.37	-1.68	-2.86
	Exp.2 (F ₂ 's)	1.43	-9.40	-0.48	-0.86	-0.63	1.49-	-0.50	0.49	-2.09	-3.51
P ₅	Exp.1 (F ₁ 's)	0.84	-10.16	-0.71	-4.97	-0.18	-0.55	-0.13	0.67	1.89	0.68
	Exp.2 (F ₂ 's)	1.44	-8.09	-0.14	-5.91	0.01	0.15-	0.19	-0.36	1.50	0.49
P ₆	Exp.1 (F ₁ 's)	-3.08	11.34	0.89	6.34	0.11	0.63	0.31	-0.25	1.22	1.83
	Exp.2 (F ₂ 's)	-2.66	13.23	0.59	5.38	0.23	0.84-	0.59	0.89	1.09	2.91
P ₇	Exp.1 (F ₁ 's)	-4.11	7.46	0.58	3.64	-0.01	0.11	0.12	-0.19	-1.59	-1.55
	Exp.2 (F ₂ 's)	-5.03	4.70	0.98	-2.34	-0.10	0.93	0.37	-0.13	-1.21	-1.37

P₁ = S₁, P₂ = S₂, P₃ = S₃, P₄ = S₄, P₅ = S₅, P₆ = S₆ and P₇ = Taka 2 *and*** significant at 0.05 and 0.01 of probability levels, respectively

Combining Ability (GCA) effects in both F₁'s and F₂'s diallels for all of the characters studied were shown in Table 5. The results showed that the behavior of the parents varied from one parent to another as well as from characters to character. The estimates of GCA effects which give a broad view of combinations between such particular parental lines indicating that the best general combiner parents with highly significant effects for both of F₁'s and F₂'s were P₂ (S₂) for days to maturity (-1.44, -1.29), plant height (4.12, 4.02), seed yield g plant⁻¹ (1.01, 1.24), seed yield kg ha⁻¹ (0.21, 0.78), respectively. Also, the parent P₆ (S₆) appeared good combiner with significant effects in positive direction for days to maturity, plant height (cm), number of fruiting branches/plant, number of capsules/plant, 1000 seed weight (g) and seed yield (g plant⁻¹) through both generations (experiments).

The parent P₄ (S₄) was a good combiner for only oil seed content (%) and resistance to infection percentage by FOS and MPH due to the significant effects for these characters. These scored values were 0.37, -1.68 and -2.36 in F₁'s, while scored values were 0.49, -2.09 and -3.01 in F₂'s, respectively.

Highly significant GCA effects through each of F₁'s and F₂'s for days to maturity, plant height (cm), number of fruiting branches/plant and resistance to infection percentage by FOS and MPH in F₁'s and F₂'s progenies (Table 5). The minimum and maximum values of GCA were belonged to the parental varieties in both F₁'s and F₂'s analysis, respectively for most studied characters, i.e., seed yield (g plant⁻¹) and seed yield (kg ha⁻¹). Whereas, there was more instability for GCA effects for seed yield (g plant⁻¹) and seed yield (kg ha⁻¹).

However, relatively consistent estimates of GCA effects for different characters over each of F₁'s and F₂'s diallels were observed in sesame parental P₂ (S₂) and P₇ (Taka 2). GCA for number of capsules per plant had a variation of 6.24 (P₆ = S₆) to -9.45 (P₂ = S₂) in F₁'s diallel

and between 7.01 (P₁ = S₁) to -5.91 (P₅ = S₅) when estimated by F₂'s progenies (Table 5). However among all sesame parental lines only P₁ (S₁) and P₄ (S₄) were significant and positive GCA effects for oil content during the both generations (Table 5).

Correlation coefficient between means of sesame parents and their General Combining Ability (GCA) effects shown in Table 6. The GCA effects estimates had significant positive correlations with parental values for all of the characters under study in both generations experiments except for days to maturity (0.631) in F₁'s and resistance to infection percentage by FOS (0.659) in F₂'s diallel where did not reach to the significant level (Table 6).

For phenotypic (r_{ph}) and genotypic correlation (r_g) among the characters under study in Exp. 1 (F₁'s) and Exp. 2 (F₂'s) are shown in Table 7. In general, the phenotypic (r_{ph}) and genotypic (r_g) correlation values are relatively different in the majority of the characters. The phenotypic and genotypic correlation coefficients for days to maturity, plant height, number of capsules/plant, 1000 seed weight (g) and oil seed content (%) were highly significant with negative values while positive values were observed for the trait resistance to infection (%) by FOS and by MPH in Exp. 1 (F₁'s) and Exp. 2 (F₂'s). However, days to maturity correlated genetically (r_g) significantly with seed yield (g plant⁻¹) in F₁'s (0.230*) and F₂'s (220*) but did not reach to the level of significant in case of phenotypic correlation (r_{ph}).

The phenotypic (r_{ph}) and genotypic correlation (r_g) between plant height and number of fruiting branches/plant was highly significant and positive values in both generations (F₁'s and F₂'s) while with the other characters, e.g., number of capsules/plant and oil seed content (%) was significant correlated phenotypically only in Exp. 1 (F₁'s) where varied from positive to negative values but in the F₂'s (Exp. 2), the most of characters showed non significant correlation

Table 6: Correlation coefficient between means of sesame parents and their General Combining Ability (GCA) effects in Exp. 1 (F₁'s) and Exp. 2 (F₂'s)

Traits	Days to maturity	Plant height (cm)	No. of fruiting branches/plant	No. of capsules/plant	1000 seed weight (g)	Seed yield (g plant ⁻¹)	Seed yield (kg ha ⁻¹)	Oil seed content (%)	Infection (%) by FOS	Infection (%) by MPH
Exp. 1 (F ₁ 's)	0.631	0.954**	0.769*	0.804**	0.851**	0.712*	0.801**	0.903**	0.814**	0.870**
Exp. 2 (F ₂ 's)	0.941**	0.910**	0.799*	0.817**	0.903**	0.893**	0.851**	0.961**	0.659	0.864**

*and** significant at 0.05 and 0.01 of probability levels, respectively

Table 7: Phenotypic (r_{ph}) and genotypic correlations (r_g) among the studied characters in Exp. 1 (F₁'s) and Exp. 2 (F₂'s)

Characters	BOG	Plant height (cm)		Plant no. of fruiting branches/plant		No. of capsules/plant		1000 seed weight (g)		Seed yield (g plant ⁻¹)		Seed Yield (kg ha ⁻¹)		Oil seed conten. (%)		Infection (%) by FOS		Infection (%) by MPH	
		F ₁ 's	F ₂ 's	F ₁ 's	F ₂ 's	F ₁ 's	F ₂ 's	F ₁ 's	F ₂ 's	F ₁ 's	F ₂ 's	F ₁ 's	F ₂ 's	F ₁ 's	F ₂ 's	F ₁ 's	F ₂ 's	F ₁ 's	F ₂ 's
Days to maturity	r _{ph}	-0.418**	-0.451**	-0.169	-0.209**	-0.247**	-0.189	-0.512**	-0.479**	0.113	0.134	0.128	0.148	-0.526**	-0.480**	0.528**	0.484**	0.391**	0.417**
	r _g	-0.315*	-0.324*	0.318*	0.401**	-0.368**	-0.287*	-0.563**	-0.526**	0.231*	0.220*	-0.241*	-0.149	-0.403**	-0.288*	0.541**	0.603**	0.472**	0.308**
Plant height (cm)	r _{ph}	-	-	0.518**	0.537**	0.209	0.138	0.047	0.112	-0.124	0.113	-0.121	0.101	0.254*	-0.048	-0.254*	-0.289**	-0.147	-0.217*
	r _g	-	-	0.528**	0.547**	0.199	0.303*	0.128	0.149	-0.143	0.106	-0.101	0.113	0.146	-0.142	-0.143	-0.127	-0.179	-0.100
Number of fruiting branches/plant	r _{ph}	-	-	-	0.417**	0.399**	0.123	0.114	0.189	0.221*	0.186	0.329*	0.139	-0.083	-0.133	0.111	0.347*	-0.267*	-
	r _g	-	-	-	0.489**	0.615**	0.143	0.236*	-0.314*	-0.244*	-0.264*	-0.294*	0.177	-0.104	-0.121	0.152	0.412**	-0.213*	-
Number of capsules/plant	r _{ph}	-	-	-	-	-	-0.388**	-0.376**	0.547**	0.701**	0.630**	0.513**	0.413	-0.389**	0.369**	0.431**	0.410**	0.341*	
	r _g	-	-	-	-	-	-0.441**	-0.342**	0.604**	0.573**	0.581**	0.577**	0.387**	-0.423**	-0.216*	-0.362**	-0.513**	-0.268*	
1000 seed weight (g)	r _{ph}	-	-	-	-	-	-	-	0.369**	0.493**	0.417**	0.521**	-0.489**	-0.347*	0.123	0.148	0.254*	0.230*	
	r _g	-	-	-	-	-	-	-	0.612**	0.303**	0.405**	0.630**	-0.314*	-0.297*	0.125	0.199	-0.321*	0.314*	
Seed yield (g plant ⁻¹)	r _{ph}	-	-	-	-	-	-	-	-	0.391**	0.713**	0.398**	0.473**	-0.269	-0.158	-0.321*	-0.140	-	
	r _g	-	-	-	-	-	-	-	-	0.304**	0.640**	0.367**	0.406**	-0.143	-0.263*	-0.301*	-0.169	-	
Seed Yield (kg ha ⁻¹)	r _{ph}	-	-	-	-	-	-	-	-	-	0.304**	0.640**	0.367**	0.406**	-0.143	-0.263*	-0.301*	-0.169	
	r _g	-	-	-	-	-	-	-	-	-	0.304**	0.640**	0.367**	0.406**	-0.143	-0.263*	-0.301*	-0.169	
Oil seed content (%)	r _{ph}	-	-	-	-	-	-	-	-	-	-	-	0.304**	0.640**	0.367**	0.406**	-0.143	-0.263*	
	r _g	-	-	-	-	-	-	-	-	-	-	-	0.304**	0.640**	0.367**	0.406**	-0.143	-0.263*	
Infection (%) by FOS	r _{ph}	-	-	-	-	-	-	-	-	-	-	-	-	0.521**	0.489**	0.364**	0.217*	-	
	r _g	-	-	-	-	-	-	-	-	-	-	-	-	0.798**	0.449**	0.308**	0.357**	-	
Infection (%) by MPH	r _{ph}	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.412**	0.471**	-	
	r _g	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.406**	0.517**	-	

* and ** significant at 0.05 and 0.01 of probability levels, respectively. Normal no. = Phenotypic correlation (r_{ph}), Bulled no. = genotypic correlations (r_g). BOG = Experiment or Generation

phenotypically nor genotypically with plant height (Table 7). Number of branches per plant had a positive and relatively high phenotypic and genotypic correlation with number of capsules per plant where possessed 0.417**, 0.589** (r_{ph}) and 0.489**, 0.615** (r_g) through both generations. Negative with significant genotypic correlation was noticed in case of branches number per plant with seed yield (g plant⁻¹) and seed yield (kg ha⁻¹) in both Exp. 1 (F₁'s) and Exp. 2 (F₂'s) as well as with resistance to infection (%) by MPH (-0.213*) but only in Exp. 2 (F₂'s) (Table 7).

Number of capsules per plant showed consistency in terms of direction and magnitude of phenotypic and genotypic correlation (r_{ph} and r_g) with other studied traits over the two types of progenies (Table 7). Highly significant correlation with positive values was cleared between capsules number per plant and the most of characters in each of Exp. 1 (F₁'s) and Exp. 2 (F₂'s), except 1000 seed weight (g) where this correlation was negatively. These except values were -0.388**, -0.441** (F₁'s) and -0.376**, -0.342** (F₂'s). Also, a significant negative genotypic correlation (r_g) was found between number of capsules per plant and resistance to infection (%) by FOS (-0.216*, -0.362**) and resistance to infection (%) MPH (-0.513**, -0.268*) in each of F₁'s and F₂'s (Table 7).

Positive with highly significant values of phenotypic and genotypic correlation between 1000 seed weight and each of seed yield (g plant⁻¹) and seed yield (kg ha⁻¹). However, this correlation with oil seed content (%) scored negative values (Table 7). Also, 1000 seed weight was correlated phenotypically and genotypically significant with resistance to infection (%) MPH but did not reach to the level of significant with resistance to infection (%) by FOS (Table 7). Seed yield (g plant⁻¹) showed a highest

positive and considerable phenotypic (r_{ph}) and genotypic (r_g) correlation with each of seed yield (kg ha⁻¹) and oil seed content (%) through both of Exp. 1 (F₁'s) and Exp. 2 (F₂'s). On the other hand, seed yield (g plant⁻¹) correlated phenotypically (r_{ph}) and genotypically (r_g), negatively with significant and non-significant values with resistance to infection (%) by FOS as well as by MPH (Table 7). Seed yield (kg ha⁻¹) was correlated phenotypically (r_{ph}) and genotypically (r_g) negatively and significant with oil seed content (%), resistance to infection (%) by FOS and resistance to infection (%) by MPH (Table 7) in F₁'s and F₂'s, except resistance to infection (%) by FOS in Exp. 2 (F₂'s) which scored non significant genotypic (r_g) correlation values 0.199 in Exp. 1 (F₁'s) and 0.148 in Exp. 2 (F₂'s).

Oil seed content (%) possessed significant and positive phenotypic (r_{ph}) and genotypic (r_g) correlation with resistance to infection (%) by FOS and by MPH (Table 7). However, the both correlations (r_{ph} and r_g) between resistance to infection (%) by FOS and resistance to infection (%) by MPH was positive and significant and scored in respectively, 0.412** and 0.406** in F₁'s and 0.471** and 0.517** in F₂'s.

The superiority of parental lines may not depend so much on their performance as on their ability to combine well and through transgressive segregates. The concept of combining ability is important for plant breeders for testing procedures to compare the performance of sesame lines in hybrid combinations as well as the nature of gene action. In practice often a plant breeder carries out a diallel cross experiment by selecting parental lines from a random population consisting of a large number of lines. In such a case, the expected values of an observation for the general combining ability and specific combining ability, arising out of cross involving, lines, e.g., sesame parents

under this study. There was considerable genetic variability among the sesame parents for all evaluated characters including infection (%) by *Fusarium oxysporum* F. sp. *sesami* (FOS) and infection (%) by *Macrophomina phaseolina* (MPH) as shown in Table 3. The presence of sufficient variability for a characters studied could be considered valuable for further biometrical assessments. This was not surprising, since these sesame genotypes originated from different genetic backgrounds as in Table 1.

The existence of genetic variation for the different studied characters in sesame has been previously reported by El-Shazly *et al.* (1999), Ammar *et al.* (2004), El-Fiki *et al.* (2004), Bayoumi and El-Bramawy (2007), El-Bramawy and Shaban (2008), El-Shakhess and Khalifa (2007) and Ali (2010). This genetic variation can be used in breeding programs to improve the potential of seed yield and its yield components with resistance to infection (%) by FOS and MPH for sesame cultivars.

In regarding to the behavior of the sesame parents with *F. oxysporum* (FOS) and *M. phaseolina* (MPH), the results showed some points of interest. For instance, some parents such as S₅ (P₆) and Taka 2 (P₇) keeping their tolerance characters against fungi pathogens. Such parents might be helpful for breeding program due to their tolerant or resistant stability. Parent H₆ (P₂) possessed the Resistance (R) rank with FOS while lost their resistance to have the Susceptible (S) rank with MPH. In contrast, the parent S₃ (P₅) had the Moderately Susceptible (MS) rank with *F. oxysporum* (wilt disease) and the Resistances (R) rank with *M. phaseolina* (charcoal root rot disease). Therefore according the present results, the sesame parent were resistance or tolerance to wilt disease (*F. oxysporum*) or charcoal root rot disease (*M. phaseolina*) could be considered as a source of resistance or tolerance in breeding programs or directly to economic production under field conditions. These findings are in harmony with the results by El-Bramawy (1997, 2003), El-Shazly *et al.* (1999), Ammar *et al.* (2004), El-Fiki *et al.* (2004), Bayoumi and El-Bramawy (2007), El-Bramawy and Shaban (2008), El-Bramawy and Wahid (2007) and El-Shakhess and Khalifa (2007). On the other hand, the absent of immune plants in sesame genotypes were reported before by Li *et al.* (1991) while in contrast, El-Bramawy (1997) reported before existence of the immune plants in sesame genotypes through their studied sesame materials.

In both Exp. 1 (F₁'s) and Exp. 2 (F₂'s) diallels, it was found that GCA had contributions in genetic variation of the characters. Therefore, the additive effects of the genes were so clearing important in genetic variation of these studied characters hence in this case, the selection

programs can improve them for use in breeding programs for a reception sesame crop. For almost all of these characters, GCA variation among the sesame parents had an acceptable consistency in two types of diallel analyses. Therefore, it seems that each of Exp. 1 (F₁'s) and Exp. 2 (F₂'s), diallel analysis can provide almost the same results for estimating genetic parameters such as GCA. This conclusion is in agreement with a findings indicating that using F₁'s and F₂'s progenies provided similar results of bread wheat, *Triticum aestivum* (Abdel-Sabour *et al.*, 1996; Hassan *et al.*, 1996) and in sesame, *Sesamum indicum* (El-Bramawy, 2003; Ammar *et al.*, 2004) as well as in safflower, *Carthamus tinctorius* (Pahlavani *et al.*, 2004). On the other hand, significant to highly significant SCA mean squares were noticed for most of studied characters such as number of fruiting branches per plant 1000 seed weight (g), seed yield (g plant⁻¹), seed yield (kg ha⁻¹), oil seed content (%), infection (%) by FOS and infection (%) by MPH in Exp. 1 (F₁'s) crosses and for all of the characters with non-exception one in Exp. 2 (F₂'s) progenies as shows in Table 4.

This considerable genetic variation among these crosses indicates that it is possible to find suitable combinations of the parental considering this research for hybrid cultivar production. Significant SCA mean squares for different sesame traits were also reported by El-Bramawy (2003), El-Shakhess and Khalifa (2007) and Ali (2010).

The mean squares of SCA for the characters such as days to maturity, plant height and number of capsules per plant were not significant in Exp. 1 (F₁'s) diallel although their values were so considerable somewhat (Table 4). The inconsistency in statistically being significant of SCA in the two diallel analyses was observed in another study as well (Meredith, 1990).

For seed yield (kg ha⁻¹) and oil seed content (%) and also infection (%) by FOS and infection (%) by MPH, the mean squares of GCA and SCA were the same in terms of magnitude (Table 4). This finding indicates that both selection and hybridization programs could be used for producing high seed yielding cultivars of sesame which are possessed high oil seed content (%) with resistance to the infection (%) by each of FOS and MPH.

The same results regarding equality of GCA and SCA mean squares have been reported for seed yield and its yield components including resistance to wilt (*F. oxysporum*, FOS) and charcoal root-rot (*M. phaseolina*, MPH) diseases. The ratio of GCA/SCA mean squares indicates the ratios of VA/(VA+VD) in Exp. 1 (F₁'s) and VA/(VA+½VD) in Exp. 2 (F₂'s) generation, respectively and these ratios express the relative

importance of additive and dominance effects (Baker, 1978). The GCA/SCA ratio for all studied characters in Exp. 1 (F₁'s) and Exp. 2 (F₂'s) diallels were higher than unity (1) except for seed yield (g plant⁻¹) in F₁'s (0.82) and in F₂'s (0.84) as well as seed yield (kg ha⁻¹) only in F₂'s (0.69) analysis. Therefore, this means that greater considerable role with contribution of additive effects of genes in the genetic expressions which controlling these characters. In contrast, non-additive gene action was found to be more important for the exception characters indicated that dominance gene effects mainly controlled in the inheritance of these characters and selection can be effective in their improvement. However, it could be emphasized that $\delta^2\text{GCA}/\delta^2\text{SCA}$ ratio may not always project the true picture of the gene action for a particular characters. This state is due to the deferential of parental ability to combine well with each other. On the other hand, such combination depends considerably upon complex interaction among genes and genotype by environment. The obtained results also concluded that mean squares of genotypes in Exp. 2 (F₂'s) were higher than Exp. 1 (F₁'s) for the most of the studied characters. These finding is expected, since F₂'s generation is the first segregating generation. These results are in a harmony with the findings which reported before by each of Sharaan and Ghallab (1998), El-Bramawy (2003) and El-Shakhess and Khalifa (2007). In the same respect, Saravanan *et al.* (2000), Ali (2001), Hoballah *et al.* (2001) and Bayoumi and El-Bramawy (2007) had the same results and concluded that additive and non-additive gene action played a great role in the gene expression of theses characters.

In regard to heritability (narrow sense or board sense) estimates as shown in Table 4, high estimates of narrow sense heritability in Exp. 1 (F₁'s) for days to maturity and plant height indicated that additive genetic variances for these traits were relatively large (Table 4) and this was in agreement with findings of Bayoumi.

On the other side, medium of values of narrow sense heritability were scored number of capsules/plant (61.39), resistance infection (%) by FOS (54.38) and resistance infection (%) by MPH (56.98) in Exp.1 (F₁'s). However, estimation of very low narrow sense heritability for 1000 seed weight (g) seed yield (g plant⁻¹), seed yield (kg ha⁻¹) and oil seed content (%) in this study contradicts the findings of Sajjanar *et al.* (1995). In Exp. 2 (F₂'s), all studied characters possessed low values of narrow sense heritability (h^2_{narrow}), except days to maturity (76.98). The low heritability narrow sense of seed yield and its components including resistance to diseases (wilt and chocolate root rot) were reported (El-Bramawy, 2003; El-Shakhess and Khalifa, 2007). On the other hand, high estimates of broad sense heritability (h^2_{broad}) for

seed yield and its components as well as r esistance to infection by wilt pathogen (*F. oxysporum*, FOS) and charcoal root-rot pathogen (*M. phaseolina*, MPH) in this study (Table 4). This results obtained indicated that other types of genetic effects such as dominance or epitasis might be involved in their variation (Mather and Jinks, 1982).

As mentioned earlier by Kearsey and Pooni (1996), GCA effects provide a measure of the general potential of genetic material, such as what is in the current research. Hence, based on GCA of parental sesame lines (Table 5), it is concluded that for improvement of seed yield (g plant⁻¹), seed yield (kg ha⁻¹), days to maturity and plant height (cm) as well as resistance to infection (%) by FOS (*F. oxysporum*) and infection (%) by MPH (*M. phaseolina*), the genotype P₂ (S₂) have good genetic potential for these pervious characters through each of F₁'s and F₂'s. This genotype (S₂) was also good combiner for breeding to earliness, since scored negative with significant GCA values, -1.44 in F₁'s and -1.29 in F₂'s for days to maturity character. Also, the parent S₄ (P₄) gave highest values of GCA with highly significant among parents for oil seed content (%), resistance to infection (%) by FOS and infection (%) by MPH in the favorable direction during both generations. This genotype was a line selected from a local population and it has a good genetic potential for oil content improvement with resistance to both pathogen diseases (FOS and MPH). On the other hand, highest and positive GCA effect for plant height, number of fruiting branches per plant, number of capsules per plant, 1000 seed weight (g) and seed yield (kg ha⁻¹) was for S₆ (P₆) which was the good source for improving these characters (Table 5).

Taka 2 (P₇) was the best combiner parents in terms of days to maturity (-4.11 and -5.03) plant height (7.46 and 7.46), number of fruiting branches per plant (0.58 and 0.98) resistance to infection (%) by wilt pathogen, *F. oxysporum* (-1.09 and -1.2) and infection (%) by charcoal root-rot pathogen, *M. phaseolina* (-1.55 and -1.37) in F₁'s and F₂'s diallels, respectively. On the other hand, the positive direction (negative GCA values) which observed in some parents in the infection (%) by FOS and infection (%) by MPH were indicating that these parents possessed significant susceptibility to its offspring. Similar findings were reported in other crosses by Ganesh *et al.* (1999), Chakrabortti and Basu (2000), Hoballah *et al.* (2001), El-Bramawy (2003) and El-Shakhess and Khalifa (2007). Regarding to poor General Combining Ability (GCA) of P₅ (S₅) for most of the characters considering, i.e., plant height, number of fruiting branches per plant, number of

capsules per plant, seed yield (kg ha^{-1}) in both F_1 's and F_2 's diallels since, it was had a negative and significant GCA for these above mentioned (Table 5).

It is worth to mention that aforementioned sesame genotypes in addition to possessing higher GCA and good general combiners (favorable genes) have the highest mean performance (Table 3) of these characters. In this connection, Khorgagde *et al.* (1988) detected that some parents or crosses were identified as a good combiners on the basis of seed yield per plant on the basis of high mean. Therefore according to the present results, it can be said that parents P_2 (S_2), S_4 (P_4) and Taka 2 (P_7) proved the best parents and could be used in hybridization programme for future improvement of seed yield and most of its components including the resistance to infection (%) by wilt pathogen, *F. oxysporum* (FOS) and infection (%) by charcoal root-rot pathogen, *M. phaseolina* (MPH).

The trend of GCA effects for seed yield and most of its components and also for resistance to infection (%) by FOS and by MPH were more or less in agreement with the results reported by several investigators, i.e., El-Shakhess (1998), Das and Choudhury (1999), Bakheit *et al.* (2001), El-Bramawy (2003) and El-Shakhess and Khalifa (2007).

Considerable association between GCA effects and mean characters of parental lines (Table 6) imply that the value can be used to choose parents with better combining ability instead of using the GCA effects. In general, the association between GCA effects and mean characters of the parental sesame lines were highly significant with positive in all cases. These positive correlation coefficients implied that parental sesame lines with high values of the characters can have superior combining ability.

Regarding to phenotypic (r_{ph}) and genotypic correlation (r_g) among the all studied characters in each of Exp. 1 (F_1 's) and Exp. 2 (F_2 's) are shown in Table 7. The relatively different between the phenotypic (r_{ph}) and genotypic (r_g) correlation values in the majority of the studied characters could be due to the effects of the environmental factors on the inheritance of these characters. There was reasonable consistency between genetic and phenotypic correlations among the traits which indicates limited effects of environmental factors (Guines *et al.*, 2002).

The negative and considerable phenotypic and genetic correlation which detected between days to maturity and each of plant height, number of capsules per plant, 1000 seed weight (g) and oil seed content (%), indicated the importance the selection for earliness (days to maturity) character for improving the mentioned characters. Similar results were reported before in this

connection (El-Bramawy, 2003). The phenotypic (r_{ph}) and genotypic correlation (r_g) between plant height and number of fruiting branches/plant was highly significant and positive values in both generations (F_1 's and F_2 's) and also with number of capsules/plant and oil seed content (%) which correlated phenotypically significant. These correlations indicate that the plant height could be used as selection criteria in improving these characters, hence increasing seed yield/plant (Table 7) which agreed with the results of Arameshwarappa *et al.* (2009).

The positive and considerable of number of branches per plant with number of capsules per plant (Table 7) implies that selection for increased number of branches per plant should have no deleterious impact on number of capsules per plant. This finding was agreement with the results reported by Pawar *et al.* (2002).

Significant and very high positive association between number of capsules/plant and most of characters in each of Exp. 1 (F_1 's) and Exp. 2 (F_2 's) indicate that this character was a reliable yield component characters. Tomar *et al.* (1999) also found similar observations. However, a significant negative correlation genotypic correlation (r_g) which was found between number of capsules per plant and resistance to infection (%) by FOS and by MPH confirmed that selection of high number of capsules/plant will be at the expense of the infection (%) by FOS as well as the infection (%) by MPH. This result was harmony with the result reported by El-Bramawy (2003, 2006a, b), Ammar *et al.* (2004), El-Shakhess and Khalifa (2007) and El-Bramawy and Wahid (2007).

The genotypes which have highest weight of 1000 seed could be gave a high seed yield (g plant^{-1}) and seed yield (kg ha^{-1}) while, it gave low oil seed content (%) and low resistance to infection (%) by each of FOS and MPH. These results are in accordance with El-Shakhess (1998), El-Bramawy (2003) and Onginjo and Ayiecho (2009).

The positive and considerable correlation of seed yield (g plant^{-1}) with each of seed yield (kg ha^{-1}) and oil seed content (%) (Table 7), implies that selection for increased seed yield should have no deleterious impact on these both characters. The results therefore indicate that these characters has importance in sesame improvement. This also confirm with the findings of Dharmalingam and Ramanathan (1993), Van Zanten (2001), Pawar *et al.* (2002) and Onginjo and Ayiecho (2009).

Due to the negative and significant values of seed yield (g plant^{-1}) or seed yield (kg ha^{-1}) with each the infection (%) by FOS infection (%) by MPH (Table 7), it is said that on the basis of selection of high seed yield (g plant^{-1}) or seed yield (kg ha^{-1}), it should be at the expense the infection (%) by each of FOS and MPH. This

confirms with earlier findings of El-Bramawy (2003, 2006a, b), El-Shakhs and Khalifa (2007) and El-Bramawy and Wahid (2007). Since sesame is primarily grown for oil, yield of oil is also considered as important. Therefore, selection for both seed yield and oil content simultaneously would be plausible if the two are positively correlated. These results are in harmony with results reported by El-Bramawy (2003) and Onginjo and Ayiecho (2009).

Highest positive and considerable phenotypic (r_{ph}) and genotypic (r_g) correlation was detected between oil seed content (%) and each of infection (%) by FOS as well as MPH through both of Exp. 1 (F_1 's) and Exp. 2 (F_2 's) confirmed the selection for high oil seed content (%) with the high resistance degree to wilt caused by *Fusarium oxysporum* F. sp. *sesami* (FOS) and charcoal root-rot caused by *Macrophomina phaseolina* (MPH).

CONCLUSION

In general, there was considerable consistency for the results obtained from analysis of F_1 's and F_2 's progenies in terms of GCA, SCA, heritability in narrow and broad sense as well as phenotypic (r_{ph}) and genetic (r_g) correlation. It is expected that the results of analysis for F_1 's and F_2 's progenies in a diallel set of crosses should not be different in terms of theoretical aspects (Mather and Jinks, 1982). The results of this study indicated that there are some consistencies between results of F_1 's and F_2 's diallel analyses. Therefore, it seems that F_2 's diallels may provide similar results as F_1 's diallels in other crops. One of the most important advantages of the F_2 's diallel is to have sufficient seeds to overcome the difficulties regarding artificial crossing and F_1 's seed production in many hermaphroditic plants such as sesame. Also, sufficient F_2 's seeds provide the opportunity to have more replication or environments in the experiments.

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