J. Plant Production, Mansoura Univ., Vol. 9 (12): 1063 - 1068, 2018

Performace of some Sesame (*Sesamum indicum* L.) Genotypes for Resistance to Wilt Disease Caused by *Fusarium oxysporum f.*sp. Sesami

Bedawy, I. M. A.[1]* and M. H. A. Moharam[2]
[1]Agronomy Dept. , Fac. Agric. Sohag Univ. Sohag, Egypt
[2]Plant Pathology Dept. Fac. Agric. Sohag Univ. Sohag, Egypt
***Corresponding author: ismail_bedawy@yahoo.com; Tel. 01003911668; Fax. 0932287558; New Campus at El-Kawamel, Sohag, Egypt, P.O. 82755**

ABSTRACT

Sesame is one of the important oil crops in Egypt. It can be infected by fungus *Fusarium oxysporum* f.sp. *sesami* which causing wilt disease. Among totally 6 isolates of *Fusarium* spp. isolated from diseased sesame plants, only isolates of *F. oxysporum* were found to be significantly pathogenic on sesame Giza-32 cultivar and showed the same ideal wilt symptoms. The objective of this investigation was aimed to; screened 86 sesame genotypes for wilt resistance during summer seasons of 2016 and 2017 under artificial infestation and field conditions with isolate FO2. In first season, a significant differences between genotypes under study in trait of disease infection %. Ten lines were resistance i.e. 71, 50, 44, 58, 28, 70, 79, 57, 24 and 80 which had a disease infection % with values of 13.77, 15, 15.29, 16.67, 17.59, 18.07, 18.33, 18.87, 19.12 and 20%, respectively. Forty eight lines had infection % varied from 20-40% considered as moderate resistance lines. In the second season, the resistance lines were 11 they were the same lines plus line number 49. Combined means over two seasons for wilt infection trait revealed that 12.5, 60, 16.25 and 18.75% from the total of 80 sesame lines were resistance, moderate resistance, moderate susceptible and susceptible, respectively. A significant and negative correlation was found between disease infection percent, number of days to 50% flowering and seed yield per plant was also negative and significant in both seasons. It could be recommended that, using the wilt resistance sesame lines in programs of new sesame cultivars or as a source for wilt resistance in sesame. The selection for lateness flowering genotypes in breeding programs for developing genotypes for *Fusarium* wilt resistance in sesame crop is very useful.

Keywords: Sesame genotypes, *Fusarium* wilt, resistance, protection.

INTODUCTION

Sesame (*Sesamum indicum* L.) is one of the oldest oil crops cultivated in the world, it has been grown in the Near East and Africa for over five thousand years for oil, cooking and medicinal purposes. It is considered as one of crops that can be sown successfully under reclaimed soils conditions in desert and gives high yield. A total of seed production 6.76 million tons of sesame seed was produced from 10.99 million ha worldwide. In Egypt, cultivated area was 32 thousand ha which produced 45 thousand tons. Egypt occupies the seventh position among the countries produced sesame in the world in the productivity of unit area with value of 1406.3 kg/ha (FAOSTAT, 2016).

Sesame has low yielding capacity compared to other crop plants, due to its low harvest index, susceptibility to diseases, seed shattering, indeterminate growth habit and asynchronous capsule ripening (Ashri, 1998; Yol and Uzun, 2012). Infection with diseases is one of the most important factor that restricts crop production in the whole world. Diseases infection in sesame production worldwide caused losses of 7 million tones yearly (Ara *et al*., 2017).Wilt disease of sesame caused by *Fusarium oxysporum* f.sp. *Sesami* (FOS) that is considered a series disease on sesame crop cultivated especially in upper Egypt because of highly temperature. It is one of the reasons caused decreased in the cultivated area of sesame yearly, due to farmer losing yield. FOS is a soil-borne fungus, infects root, grows and colonizes xylem vessels and blocking them completely to cause wilt (Bateman *et al*., 1996) and more than 50% yield losses in sesame (Gaber, *et al*., 1998; Khaleifa, 2003; El-Bramawy, 2006; El-Shakhess and Khalifa, 2007). Some of agricultural practices such as irrigation management and fertilization regimes, and application of systemic fungicides have been recommended to reduce disease affects (Mahdy *et al*., 2005), irrigation management needs experience from farmers to do, fertilization and fungicides costs more money and harmful for environment. Therefore, selection for new resistance sesame genotypes is more useful and sustainable way to reduce the yield loss and also safety, but it is only need more time (Bedigian, 2006).

Recently, breeding programs has concentrated on development of sesame high yielding and wilt disease resistant varieties (Mahdy *et al*., 2005). Selection for wilt resistance in sesame is most important toll in this field even is not easy because of it is two types of lives, plant and fungus with the interaction in between. Because of each fungal pathogen may have many strains which were developed by mutations and environment changes. Therefore, the aim of this study was screening a set of sesame genotypes against FOS to explore the resistant lines to wilt disease with high yield. It will be an initially step in establishment new sesame cultivars from testing promising lines.

MATERIALS AND METHODS

Isolation and identification of the causal pathogen of sesame wilt disease

Samples of wilt-infected plants of sesame Giza-32 and Shandweil-3 cultivars were collected at flowering period from different regions of Sohag governorate, Egypt during 2015 growing season to isolate the causal pathogen. Infected root and stem basal of each plant sample were washed thoroughly with tap water, cut into small segments (approximately 0.5-1.0 cm), surface sterilized by immersing in 5% sodium hypochlorite (SH) solution and 70% ethyl alcohol for 5 and 1 min, respectively (Jyothi *et al*., 2011) and then immediately rinsed for three times with sterile water (SW). Disinfected segments were dried between folds of sterile filter papers, placed on to Petri plates containing Komada's *Fusarium*-selective medium (Komada, 1975) supplemented with 400 mg streptomycin sulphate per liter of medium. Then plates were incubated at 25±5ºC for a week. During incubation, plates were examined daily and the growing fungal colonies were purified by single spore and hyphal tip techniques following sub-culturing onto a fresh prepared medium at the same conditions until pure colonies were formed. Isolated *Fusarium* species were identified according the morphological characteristics of mycelia and spores according to Domsch *et al*., (1980), Booth (1984) and Leslie and Summerell (2006). Pure cultures of all identified isolates of *Fusarium* species were coded and maintained at 5ºCon slopes of potato dextrose agar (PDA) medium for further studies.

Pathogenicity tests

The pathogenic capability of all isolates of *Fusarium* species to cause wilt disease was investigated on sesame

Giza-32 cultivar under greenhouse conditions in 2015 growing season. Inoculum of each tested isolate of *Fusarium* spp. was prepared by placing two disks (0.6 cm in diameter) taken from 7-day-old culture on autoclaved sorghum and washed sand medium (3: 1, respectively) in glass bottles tightly closed with cotton plugs. Then bottles were incubated at 28±5 ºC for 21 days. Formalin-sterilized pots (30 cm) each was filled with autoclaved loam soil (7.0 kg of each), infested with 70 g inoculum of each tested isolate and then slightly irrigated every other day for a week (Jyothi *et al*., 2011). Pots were treated with the same amount of sorghum and sand medium and free from fungal inocula served as control. Seeds were disinfected by dipping in 2% (SH) solution for 3 min, rinsed 3 times in SW for 5 min and then sowed at a rate of 10 seeds per each pot. Three pots as replicates of each tested fungal isolate were used in a completely randomized design. Pots were checked daily and irrigated when necessary.

Symptoms of wilt disease were noted from 20-110 days after sowing, the number of infected plants was counted in each replication and percent of infection was calculated. Also, individual plants in each replication were rated for severity of wilt using a scale of 0-3 described by Ha *et al.,* (2008), where 0= healthy plants, no visible symptoms; 1= weakly infected plants showing vascular discoloration but no leaf yellowing; 2= moderately infected plants showing leaf yellowing and wilted plants; 3= severely infected plants showing plant death. Then the disease severity (DS %) of each replicate of each tested fungal isolate was calculated using formula: $(\Sigma S_i \times N_i) \times 100 / (3 \times N_t)$, where S_i is the severity ratings 0-3, N_i is the number of plants in each ratting, and N_t is the total number of rated plants (Moharm and Negim, 2012). Finally, the main pathogen was also consistently re-isolated from infected plants showing wilt symptoms that were similar to the original symptoms developed on naturally infected plants.

Plant material and field experiments

The plant materials listed in Table 3 were 86 sesame genotypes (80 lines, parents of these lines Introduced No. 153515 from Venezuela, Introduced No. 158071 from China, and four check varieties Giza-25, Giza-32 Shandaweil-3 and Toshka1, were used to assess resistance to *Fusarium* wilt disease. These lines were selected previously in segregation generation for wilt and charcoal root rot diseases coupled with high yield (Mahdy *et al*., 2005).

Two field trials were performed in the successive growing summer seasons of2016 and 2017 at the Experimental Farm (El-Kawther), Faculty of Agriculture, Sohag University, Sohag, Egypt. The sowing date in both seasons was 1st May. In each experiment, sesame seeds of each genotype tested were sterilized as above mentioned and sown in hills of plots in a randomized complete block design of three replications. Seeds were sown in rows, each 4 m long with 0.6 m row width and 0.2 m between hills within rows. Each genotype was represented by one row in each replication. Inoculum amount (approx. 40 g) of isolate FO2 was added in hills with sesame seeds at same time of planting and covered with soil (Mahdy *et al*., 2005). Following full emergence, the growing seedlings were thinned to two per hill in each row and all cultural practices recommended for sesame production were carefully applied.

Assessment of sesame lines to wilt resistance and yield losses

At flowering stage, symptoms of wilt disease were noted and the infected plants were counted in each row (line) in the replicate to calculate disease infection percentage (Bedawy, 2004) as follow:

Disease infection % = the number of infected plants/ total number of plants in the row × 100.

Resistance level of each line tested was scored following the scale of disease rating (Table 1) described by El-Bramawy and Abd Al-Wahid (2007) and Jyothi *et al.,* (2011). The other traits studied were the number of days to 50% flowering that recorded to study the relation between wilt infection and flowering. Seed yield per plant was also measured as a mean of seed yield from 10 plants for each genotype in the three replicates. Yield losses were determined using data of seed yield per plant obtained from another experiment conducted at normal condition for the same lines (Bedawy and Mohamed, 2018) as follow:

Yield losses % = 100 - (seed yield under infection/ seed yield at normal condition) × 100.

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

Infection %	Category
0.0	Immune (I)
0.1 – 20%	Resistant (R)
20.1 – 40%	Moderately Resistant (MR)
40.1 – 50%	Moderately Susceptible (MS)
50.1 – 75%	Susceptible (S)
75-100 %	Highly Susceptible (HS)

Statistical analysis

The data of studied traits were analysed by using SAS program (SAS ver. 9.2, SAS 2008). Comparing of means for each trait was done by used the revised LSD (Petersen, 1985). Pearson correlation coefficient was calculated among studied traits in the two seasons.

RESULTS AND DISCUSSION

Isolation from diseased plants showing wilt symptoms collected from different localities in Sohag governorate resulted in 6 isolates of two species of *Fusarium*. Three isolates as *F. oxysporum* Schlecht. and 3 isolates as *F. solani* Mart. were identified. Results of pathogenicity tests in Table 2 revealed that among totally 6 isolates of *Fusarium* spp. obtained, only isolates of *F. oxysporum* were found to be significantly pathogenic on sesame Giza-32 cultivar and showed the same ideal wilt symptoms. Isolate FO2 was highly pathogenic ones and caused 36.67% and 25.56% of infection and DS%, respectively. However, isolate FO1 was a weak isolate and caused 23.33% and 12.22% of infection and DS, respectively. On the other hand, all isolates of *F. solani* did not induce wilt symptoms, but they caused damping-off or root rot. Results obtained were similarly and in agreement with those reported by (Abd-El-Ghany *et al*., 1974; El-Deeb *et al*., 1987; Khalifa, 1997; Alasee, 2006).

In first season of filed trails under artificial infestation with isolate FO2, analysis of variance showed highly significant differences between genotypes for all studied traits in two seasons (Table 3). The trait of disease infection % means varied from 13.77- 66.67% (Table 4). Ten lines described as resistance (R) viz. 71, 50, 44, 58, 28, 70, 79, 57, 24 and 80 had a disease infection % with values of 13.77, 15, 15.29, 16.67, 17.59, 18.07, 18.33, 18.87, 19.12 and 20%, respectively. Nineteen and twenty nine genotypes had infection % varied from 20-30% and 30-40%, respectively. Both considered as moderate resistance (MR) lines. Results also revealed that 13 and 15 genotypes were had disease degree of moderate susceptibility (MS) and susceptibility (S), respectively. Several research efforts for detecting the resistant genotypes of sesame against wilt disease caused by

F. oxysporum f.sp. *sesame* in different parts of the world were focused (Dinakaran *et al*., 1994; Kavak and Boydak, 2006; El-Bramawy *et al*., 2008; Jyothi *et al*., 2011). Also, seed yield per plant trait means varied from 9.82 to 16.53 g. Among the resistance lines group 8 from them had seed yield exceed 14 g per plant. Only two resistance lines (no. 28 and 44) had lower seed yield with values 12.44 and 12.33 g, respectively. The highly yield recorded for lines 50, 79 and 70 with values exceed 16 g these lines showed highly resistance degree in first year. Furthermore, the determine of yield losses in this year showed that 66 genotypes had yield losses percentage varied from 1.23 to 34.56% and, 20 lines had no loss of seed yield. All resistance lines had no loss of seed yield except line number 44 with 8.77%.

Table 2. Pathogenicity of all isolates of *Fusarium* spp. on sesame Giza-32 cultivar performed under open greenhouse in 2015 growing season.

Fusarium Species	Isolate				Infection (%)	Disease Severity (%)	Survival plants
	No.	Source	Cultivar	Code			
F. oxysporum	1	El-kawther	Giza-32	FO1	23.33	12.22	76.67
	2	Sakolta	Shandweil-3	FO2	36.67	25.56	63.33
	3	Tema	Giza-32	FO3	30.00	17.78	70.00
F. solani	1	Sakolta	Shandweil-3	FS1	0.0[a]	0.0	90.00
	2	Tema	Giza-32	FS2	0.0[a]	0.0	83.33
	3	Gerga	Shandweil-3	FS3	0.0[a]	0.0	86.67
L.S.D. $_{0.05}$					2.54	1.76	4.13

[a] means plants have no wilt, but they are infected with seed rot or damping-off or root rot (data not shown).

Table 3. Analysis of variance and general means for studied traits in two seasons under artificial infection by *Fusarium oxysporum*.

S.O.V	DF	MS first season			MS second season		
		Disease infection %	Number of days to 50% flowering	Seed yield	Disease infection %	Number of days to 50% flowering	Seed yield
Replication	2	2.38	2.84	1.32	7.20	2.42	0.057
Genotypes	85	531.11**	78.06**	8.96**	545.25**	88.68**	11.15**
Error	170	15.81	2.77	0.643	20.13	4.52	1.27
General mean		36.69	58.07	13.45	35.83	58.78	13.73

** significant at 0.01 level of probability.

Table 4. Means of studied traits of sesame genotypes under infection with FOS in first, second season and combined.

Genotype No.	First season					Second season					Combined means		
	DI%	DF	SY, g	YL%	RD	DI%	DF	SY, g	YL%	RD	DI%	DF	SY, g
1	32.8	56.3	12.6	5.2	MR	34.0	58.0	11.9	8.9	MR	33.4	57.2	12.2
2	38.3	59.3	13.1	6.4	MR	36.7	61.0	14.0	8.6	MR	37.5	60.2	13.5
3	28.3	64.3	15.6	5.4	MR	34.4	65.0	15.6	4.8	MR	31.4	64.7	15.6
4	28.3	61.3	15.5	6.7	MR	26.7	61.3	15.3	3.6	MR	27.5	61.3	15.4
5	53.3	63.0	15.1	9.2	S	46.7	63.0	15.2	9.6	MS	50.0	63.0	15.1
6	33.3	61.7	16.3	10.8	MR	35.0	63.3	17.5	7.5	MR	34.2	62.5	16.9
7	53.0	63.7	12.2	10.4	S	56.7	61.3	12.0	9.1	S	54.8	62.5	12.1
8	58.5	54.3	12.5	12.1	S	51.7	56.3	13.4	10.8	S	55.1	55.3	12.9
9	44.1	58.7	14.5	5.8	MS	41.7	58.7	14.7	5.8	MS	42.9	58.7	14.6
10	47.1	60.0	13.8	8.9	MS	53.3	61.7	14.6	9.5	S	50.2	60.8	14.2
11	48.3	59.7	15.6	6.6	MS	43.3	61.0	15.6	6.2	MS	45.8	60.3	15.6
12	35.0	62.3	15.4	7.9	MR	36.7	63.3	16.4	6.5	MR	35.8	62.8	15.9
13	28.3	56.7	14.3	3.8	MR	29.4	57.7	15.7	1.0	MR	28.9	57.2	15.0
14	31.1	56.3	15.1	0.0	MR	30.0	56.7	14.9	1.2	MR	30.6	56.5	15.0
15	24.0	60.7	14.4	1.3	MR	27.8	61.3	15.0	2.6	MR	25.9	61.0	14.7
16	30.0	55.0	14.4	6.1	MR	32.8	55.0	14.5	7.4	MR	31.4	55.0	14.5
17	48.3	54.3	10.9	2.7	MR	44.2	53.3	11.3	4.0	MS	46.3	53.8	11.1
18	61.8	52.0	12.1	3.7	MR	58.3	52.3	12.0	2.9	MS	60.0	52.2	12.1
19	33.3	58.0	9.8	22.4	MR	38.3	60.3	10.3	20.5	MR	35.8	59.2	10.0
20	31.7	61.0	11.9	4.5	MR	33.3	61.7	11.8	9.9	MR	32.5	61.3	11.8
21	41.3	56.3	14.4	9.3	MR	45.2	54.0	15.5	8.5	MS	43.2	55.2	15.0
22	33.3	56.7	15.4	2.1	MR	31.7	53.7	16.0	2.1	MR	32.5	55.2	15.7
23	30.9	51.0	13.1	9.0	MR	23.3	51.0	13.6	6.2	MR	27.1	51.0	13.4
24	19.1	56.3	14.7	0.0	R	17.8	56.3	15.0	0.0	R	18.5	56.3	14.9
25	33.3	67.7	12.7	0.0	MR	35.0	67.0	13.3	0.0	MR	34.2	67.3	13.0
26	36.7	68.7	10.9	11.2	MR	35.0	71.0	10.7	10.8	MR	35.8	69.8	10.8
27	25.0	59.0	11.1	17.5	MR	24.3	58.0	11.1	21.2	MR	24.6	58.5	11.1
28	17.6	53.3	12.4	13.7	R	13.3	56.0	12.5	12.6	R	15.5	54.7	12.4
29	40.0	51.7	11.4	34.6	MR	45.0	53.0	11.6	34.2	MS	42.5	52.3	11.5
30	43.2	54.7	11.8	30.6	MS	48.3	52.7	12.4	29.0	MS	45.7	53.7	12.1
31	55.0	50.3	14.6	0.0	S	48.3	52.7	15.4	0.0	MS	51.7	51.5	15.0
32	44.2	54.0	14.9	0.0	MS	39.2	53.7	15.1	0.0	MR	41.7	53.8	15.0
33	35.2	53.3	14.0	17.2	MR	26.0	54.3	13.9	23.1	MR	30.6	53.8	13.9
34	39.7	51.7	13.0	23.5	MR	36.1	54.0	13.4	20.9	MR	37.9	52.8	13.2
35	31.7	48.0	11.3	11.1	MR	30.0	52.3	11.6	10.0	MR	30.8	50.2	11.4
36	30.0	57.7	11.2	15.3	MR	35.0	58.0	11.1	10.0	MR	32.5	57.8	11.1
37	46.9	61.0	12.4	15.3	MR	42.4	64.0	13.0	11.4	MS	44.7	62.5	12.7
38	41.7	63.0	13.5	8.6	MR	46.7	66.0	13.1	17.1	MS	44.2	64.5	13.3
39	35.0	55.3	16.3	1.5	MR	27.8	54.0	16.7	4.5	MR	31.4	54.7	16.5
40	28.1	54.0	15.8	8.3	MR	28.3	56.0	16.3	4.6	MR	28.2	55.0	16.1
41	63.3	53.7	11.4	25.4	S	65.0	57.0	11.1	25.3	S	64.2	55.3	11.2
42	56.7	59.0	11.7	4.4	S	60.0	61.7	11.8	9.8	S	58.3	60.3	11.7
43	23.9	59.0	13.5	4.4	MR	20.9	57.3	14.0	5.9	MR	22.4	58.2	13.7
44	15.3	56.0	12.3	8.8	R	13.3	54.7	13.1	9.8	R	14.3	55.3	12.7
45	37.4	67.0	11.3	21.1	MR	41.7	70.0	11.5	21.4	MS	39.5	68.5	11.4

Table 4. Continued.

Genotype	First season					Second season					Combined means		
No.	DI%	DF	SY, g	YL%	RD	DI%	DF	SY, g	YL%	RD	DI%	DF	SY, g
46	41.7	63.7	12.8	8.3	MS	43.3	66.3	13.0	11.2	MS	42.5	65.0	12.9
47	58.3	49.7	15.2	0.0	S	53.3	51.0	15.6	0.0	S	55.8	50.3	15.4
48	35.0	52.7	14.7	0.0	MR	30.0	51.0	15.4	0.0	MR	32.5	51.8	15.1
49	25.0	64.0	16.2	4.7	MR	20.0	66.0	16.6	6.2	R	22.5	65.0	16.4
50	15.0	62.0	16.5	0.0	R	15.0	65.3	17.3	0.0	R	15.0	63.7	16.9
51	37.1	55.7	14.5	0.0	MR	35.0	55.0	14.5	0.0	MR	36.1	55.3	14.5
52	43.3	55.7	13.9	0.0	MS	38.3	54.7	14.7	0.0	MS	40.8	55.2	14.3
53	28.3	62.0	12.5	21.6	MR	26.7	61.3	12.3	27.3	MR	27.5	61.7	12.4
54	30.0	59.7	13.1	21.1	MR	28.3	61.0	12.5	27.3	MR	29.2	60.3	12.8
55	66.7	54.7	13.8	0.0	S	65.0	57.0	14.7	0.0	S	65.8	55.8	14.3
56	56.7	56.7	13.4	13.0	S	61.7	57.0	14.6	6.7	S	59.2	56.8	14.0
57	18.9	66.0	15.7	0.0	R	14.4	65.0	15.4	0.0	R	16.7	65.5	15.5
58	16.7	69.0	15.3	0.0	R	15.0	69.3	16.2	0.0	R	15.8	69.2	15.8
59	31.7	68.0	11.1	6.3	MR	31.7	71.0	11.9	1.4	MR	31.7	69.5	11.5
60	36.1	71.0	10.8	17.0	MR	36.7	70.7	11.0	16.7	MR	36.4	70.8	10.9
61	20.9	59.7	13.3	7.7	MR	21.7	61.3	12.9	11.0	MR	21.3	60.5	13.1
62	23.3	60.0	14.2	0.0	MR	21.7	63.7	14.7	0.0	MR	22.5	61.8	14.5
63	28.0	58.3	16.3	0.0	MR	31.1	61.3	17.2	0.0	MR	29.5	59.8	16.7
64	23.7	63.0	16.5	0.0	MR	26.7	61.3	16.7	0.0	MR	25.2	62.2	16.6
65	42.8	58.3	11.7	29.6	MS	41.7	57.0	12.2	28.0	MS	42.2	57.7	11.9
66	66.7	58.0	12.0	23.7	S	66.7	55.3	11.6	29.4	S	66.7	56.7	11.8
67	41.7	55.7	13.8	20.7	MS	35.0	57.0	13.8	23.2	MR	38.3	56.3	13.8
68	36.7	58.7	13.8	20.7	MR	33.3	60.3	14.6	20.5	MR	35.0	59.5	14.2
69	33.3	66.0	15.2	2.7	MR	31.1	66.7	15.8	0.3	MR	32.2	66.3	15.5
70	18.1	66.7	16.4	0.0	R	16.7	69.3	16.1	0.0	R	17.4	68.0	16.2
71	13.8	50.0	14.3	0.0	R	18.3	50.3	14.2	0.0	R	16.1	50.2	14.3
72	28.3	55.0	11.4	18.0	MR	26.7	56.0	12.0	8.6	MR	27.5	55.5	11.7
73	33.3	50.3	13.0	18.1	MR	31.7	51.3	14.0	12.5	MR	32.5	50.8	13.5
74	36.7	51.0	12.3	16.7	MR	38.3	49.0	13.3	14.8	MR	37.5	50.0	12.8
75	38.3	56.3	13.1	17.2	MR	37.2	58.0	13.8	11.3	MR	37.8	57.2	13.5
76	30.0	65.3	12.6	17.4	MR	28.3	63.0	12.9	23.2	MR	29.2	64.2	12.7
77	32.5	57.0	10.5	12.9	MR	33.3	56.7	10.3	21.0	MR	32.9	56.8	10.4
78	23.3	56.7	11.1	8.5	MR	25.0	58.3	11.2	9.5	MR	24.2	57.5	11.1
79	18.3	55.7	16.1	0.0	R	16.7	58.7	16.5	0.0	R	17.5	57.2	16.3
80	20.0	62.0	15.3	0.0	R	17.4	62.7	15.7	0.6	R	18.7	62.3	15.5
Intr. No. 153515	66.7	51.3	12.2	7.7	S	65.0	55.3	11.9	7.8	S	65.8	53.3	12.1
Intr. No. 158071	61.7	56.7	11.1	5.1	S	61.7	59.3	11.3	7.2	S	61.7	58.0	11.2
Giza25	56.7	54.0	12.6	3.2	S	58.3	52.7	12.5	8.6	S	57.5	53.3	12.5
Giza32	56.7	53.7	11.9	6.5	S	51.7	55.3	9.2	32.8	S	54.2	54.5	10.5
Shandaweil3	38.3	54.0	13.2	2.2	MR	31.7	50.7	13.7	6.4	MR	35.0	52.3	13.5
Toshka1	32.2	54.0	13.2	4.1	MR	30.0	52.0	14.0	5.5	MR	31.1	53.0	13.6
$RLSD_{05}$	5.64	2.41	1.18			6.47	3.06	1.68			6.98	2.87	1.47
$RLSD_{01}$	7.30	3.12	1.55			8.45	3.99	2.19			7.63	4.21	2.08

Whereas, DI%= disease infection %, DF = number of days to 50% flowering, SY = seed yield per plant, YL% = yield losses %, RD= resistance degree, R= resistance, MR= moderate resistance, MS = moderate susceptible, S = susceptible.

Results of second season had closer disease degree for the same genotypes except some differences like, the lines number 11 were R and line number 49 was changed the disease degree to be R with infection % 20 (Table 4). Also, same lines numbers 48 found to be MR in second season but in the last category (S) lines number decreased by one line. Results approved stable disease resistance degree from year to year in almost of sesame lines understudy these results are matching with El-Barmawy (2006). The genotypes means varied from 9.17 to 17.52 g for seed yield per plant trait. The resistance lines had the same trend form first year for high yield with the exception of lines number 28 and 44 with values of 12.45 and 13.06 g, respectively. Eighteen sesame lines recorded no loss of seed yield. In general, incidence of the *Fusarium* wilt disease of sesame in most lines tested was positively correlated with loss in yield. However, the resistant line number 44 was the only line from resistance group that recorded 9.7% yield losses in the second season.

Over two seasons wilt infection means (Fig. 1) revealed that 10, 48, 12 and 16 genotypes from the total of 86 sesame genotypes were resistance, moderate resistance, moderate susceptible and susceptible, and represented by 11.66, 55.81, 13.95 and 18.60 % of genotypes, respectively.

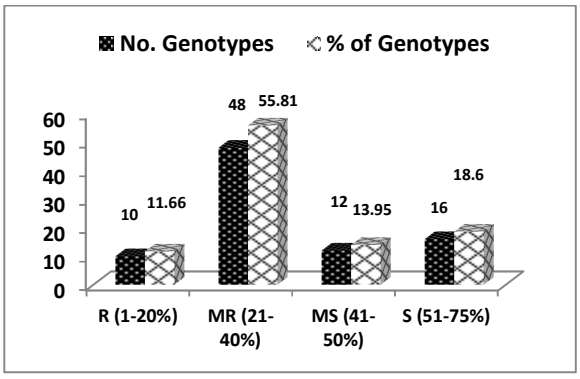

Fig. 1. Resistance degree of genotypes for wilt infection percentage over two seasons.

Similar results of the variation in wilt infection for the tested genotypes were reported (Mahdy *et al.*, 2005; El-Barmawy, 2006; El-Bramawy and Abd Al-Wahid, 2007; Jyothi *et al.*, 2011). Among the parents group and check varieties Toshka-1 recorded lower infection percentage with 31.11 followed by Shandweil-3 with 35 (MR), while

the rest were susceptible. In another study, 'Toshka-1' was MR and 'Giza-32' was MS and R in two seasons as a degree of resistance (El-Bramawy and Abd Al-Wahid, 2009). While, they found Giza-25 had a MR. These results matching with this study for Toshka-1 and Giza-25 cultivars.

Number of days to 50% flowering showed highly significant different and means ranged from 48 to 71 days in both season (Table 3, 4 and 5). Coupling of number of days to 50% flowering and disease infection% means showed that, the resistant lines had a variation in the number of days to 50% flowering trait. Lines 71, 24, 28, 44, 79, and 80 were early flowered with 51.33, 55.67, 56.67, 58, 59.67 and 60.33 days, respectively. Whereas, lines 50, 57, 70, 49 and 69.67 had a late flowered by 64, 66, 66.67, 66.67 and 69.67 days, respectively. This showed how breeding and selection for resistance lines is so complicated. Seed yield per plant trait under *Fusarium* infection showed highly significant differences and means ranged over two years from 10.04 to 16.93 g. Six lines from the resistant lines had a higher seed yield per plant, line 50, 58, 57, 70, 79 and 80 exceeded 15.51 g.

Correlation analysis coefficient among disease infection percentage, number of days to 50% flowering and seed yield per plant traits under disease infection were calculated in the first and second season (Table 5). The disease infection percentage and number of days to 50% flowering traits were correlated significantly and negatively with values (-0.279 and -0.214) in first and second season, respectively. These means the lines which were late in flowering are more wilt resistance. It is clearly from these results, selection for late flowering genotypes in wilt resistance breeding programs. Would be taken in account, previous studies in the correlation between wilt infection and flowering in sesame are very rare. But, Lyons *et al*., (2015) found a positive correlation among late flowering and resistance to *F. oxysporum* in *Arabidopsis thaliana* natural ecotypes. Correlation between disease infection % and seed yield was also significant and negative, it was -0.308 in first season and -0.312 in the second season. Very weak correlation values resulted between seed yield per plant trait and number of days to 50% flowering trait. El-Barmawy (2006) supported the significant and negative correlation in his study on F_3 and F_4 sesame segregation generation under field infection with *Fusarium* between infection percentage and seed yield trait.

Table 5. Correlation between studied traits under study (above) first season, (below diagonal) second season.

Item	Disease infection percentage	Number of days to 50% flowering	Seed yield
Disease infection percentage	1.000	-0.279**	-0.308**
Number of days to 50% flowering	-0.214*	1.000	0.113
Seed yield	-0.352**	0.072	1.000

***, ** significant and highly significant, respectively.**

Finally; it could be recommend that, most of the sesame resistant lines to wilt disease which had high yield could be used as new sesame cultivars or as a source for wilt resistance in sesame. Also, we can conclude that doing the selection for lateness flowering in genotypes would be very useful in breeding programs for developing genotypes for *Fusarium* wilt resistance.

ACKNOLEDGMENT

Authors are thankful to all members of Experimental Farm and Laboratories, Faculty of Agriculture, Sohag University for financial support to carry out the research work.

REFERENCES

Abd-El-Ghany, A. K.; M.B. Seoud; M.W. Azab; B. K. Mahmoud; K. A. A. El-Alfy and M. A. Abd-El-Gwad (1974). Tests with different varieties and strains of sesame for resistance to root rot and wilt diseases. Agric. Res. Rev., 52: 75-83.

Alasee, Najwa B. (2006). The use of transplanting as a method for control root rot of sesame with other control methods under greenhouse conditions. Ninth Arab Congress of Plant Protection, 19–23 November, Damascus, Syria, p. 196.

Ara, A.; A Akram; M. Ajmal; S. Akhund; B. G. Nayyar; W. Seerat and S. M. Chaudhry (2017). Histopathological studies of sesame (*Sesamum indicum*) seedlings infected with *Fusarium oxysporum*. Plant Pathology & Quarantine, (7)1: 82–90.

Ashri, A. (1998). Sesame breeding. Plant Breeding Review, 16:179-228.

Bateman, G. L.; H. Kwaśna and E. Ward (1996). Relationship among *Fusarium* spp. estimated by comparing restriction fragment length polymorphism in polymerase chain reaction amplified nuclear DNA. Can. J. Microbiol. 42: 1232-1240.

Bedawy, I. M. A. (2004). Pedigree selection for wilt resistance in some sesame populations, *Sesamum indicum* L. M. Sc. Assiut University.

Bedawy, I. M. A. and N. E. Mohamed (2018). Phenotypic and genotypic variability in some sesame (*Sesamum indicum* L.) genotypes. Egyptian Journal of Agronomy, 40 (3): 193- 205.

Bedigian, D. (2006). Assessment of sesame and its wild relatives in Africa. In: Ghazanfar, S.A. and H. Beentje (Editors). African plants: Biodiversity, Ecology, Phytogeography and Taxonomy. Royal Botanic Gardens, Kew, United Kingdom.

Booth, C. (1984). The *Fusarium* Problem: Historical, Economic and Taxonomic Aspects. (Ed.): The applied mycology of *Fusarium*. Moss, M. O. and J. E. Smith, Cambridge University Press, Cambridge, pp 264.

Dinakaran D.; V Manoharan and V. Dharmalingam (1994). Screening of sesame cultures against major diseases. Sesame and Safflower Newsletter, 9: 4-6.

Domsch, K. H.; W. Gams and A. Traute-Heidi (1980). Compendium of Soil Fungi. (Ed.) Academic Press. A Subbsidiary of Harcourt Brace Jovanovich, Publishers, London, pp 859.

El-Bramawy, M. A. S. (2006). Inheritance of resistance to *Fusarium*wilt in some crosses under field conditions. Plant Prot. Sci., 42 (2): 99-105.

El-Bramawy, M. A. S.; S. E. El-Hendawy and W. I. A. Shaban (2008). Assessing the suitability of morphological and phenological traits to screen sesame genotypes for *Fusarium* wilt and charcoal rot disease resistance. Journal of Plant Protection Research, 48 (4) :397-410.

El-Bramawy, M. A. S. and O. A. Abd Al-Wahid (2007). Identification of genetic resources to *Fusarium* wilt, charcoal root rot and *Rhizoctonia* root rot among sesame (*Sesamum indicum* L.) germplasm. African Crop Science Proceedings of African Crop Science Society, El-Minia, Egypt 8:1893-1900.

El-Bramawy, M. A. S. and O. A. Abd Al-Wahid (2009). Evaluation of resistance of selected sesame (*Sesamum indicum*) genotypes to *Fusarium* wilt disease caused by *Fusarium oxysporum* f. sp. *sesami*. Tunisian Journal of Plant Protection, 4: 29-39.

El-Deeb, A. A.; M. I. Elian; A. A. Hilal and A. A. Ali (1987). Sesame root-rot and wilt disease and methods to reduce their damage in Egypt. Zagazig J. Agric Res. 14(1):437-481.

El-Shakhess, S. A. M. and M. M. A. Khalifa (2007). Combining ability and heterosis for yield, yield components, charcoal-rot and *Fusarium* wilt diseases in sesame. Egypt J. Plant Breed., 11(1): 351-371.

FAOSTAT, 2016 [Internet] (2016) Rome, Italy: Food and Agriculture Organization (FAO); Available from: http://www.fao.org/faostat/en/#data/QC.

Gaber, M. R.; N. A. Hussein; O. I. Saleh and M. A. Khalil (1998). Susceptibility of certain varieties and genotypes and control of wilt and root rot diseases of sesame attributed to *Fusarium oxysporum* f. sp. *sesami* and *Macrophomina phaseolina*. Egypt. J. Microbiol., 33(3): 403-428.

Ha, M.T.; Y.-M. Hang and J.-W. Huang (2008). Influence of organic amendment and *Bacillus subtilis* on mineral uptake of asparagus bean in two field soils. Plant Pathology Bulletin, 17: 289-296.

Jyothi, B.; N. A. Ansari; Y. Vijay; G. Anuradha; A. Sarkar; R. Sudhakar and E.A. Siddiq (2011). Assessment of resistance to *Fusarium* wilt disease in sesame (*Sesamum indicum* L.) germplasm. Austr. Plant Pathol., 40: 471-475.

Kavak, H. and E. Boydak (2006). Screening of the resistance levels of 26 sesame breeding lines to Fusarium wilt disease. Plant Pathol. J., 5(2):157-160.

Khalifa, M. M. A. (1997). Studies on root-rot and wilt diseases of sesame (*Sesamum indicum* L.) M.Sc. Thesis, Fac. Agric., Zagazig University.

Khaleifa M. M. A. (2003). Pathological studies on charcoal rot disease of sesame. Ph.D. Thesis, Agron. Dept. Fac. of Agric., Moshtohor, Zagazig Univ., Benha, branch, Egypt, 295 pp.

Komada, H. (1975). Development of a selective medium for quantitative isolation of *Fusarium oxysporum* from natural soil. Rev. Plant Protect. Res., 8:114-125.

Leslie, J. F. and B. A. Summerell (2006). The *Fusarium* laboratory manual. Blackwell, Iowa, USA.

Lyons, R., A. Rusu, J. Stiller, J. Powell, J.M. Manners, K. Kazan (2015) Investigating the association between flowering time and defense in the Arabidopsis thaliana-*Fusarium oxysporum* Interaction. PLoS One., 10(6):e0127699. doi: 10.1371/

Mahdy, E. E.; R. R. Bakheit; M. M. Motawea and I. M. Bedawy (2005). Pedigree selection for resistance to *Fusarium oxysporum* in three sesame populations. Assiut J. Agric. Sci., 36(1): 141-157.

Moharam, M. H. A. and O. O. Negim (2012). Biocontrol of *Fusarium*-wilt disease in cucumber with improvement of growth and mineral uptake using some antagonistic formulations. Comm. Appl. Biol. Sci, Ghent University 77(3): 53-63.

Petersen, R.G. (1985). Design and analysis of experiments. Marcel Dekker, Inc., New York, USA.

SAS Institute (2008) The SAS system for Windows, release 9.2.SAS Institute, Cary, N.C. USA.

Yol, E. and B. Uzun (2012) Geographical patterns of sesame (*Sesamum indicum* L.) accessions grown under Mediterranean environmental conditions, and establishment of a core collection. Crop Sci., 52: 2206-2214.

أداء بعض التراكيب الوراثية للسمسم لمقاومة مرض الذبول المتسبب عن الفطر فيوزاريوم اوكسيسبوريم

إسماعيل محمود أحمد بديوي[1] و مصطفي حمدان أحمد محرم[2]

[1] قسم المحاصيل كلية الزراعة - جامعة سوهاج

[2] قسم امراض النبات كلية الزراعة جامعة سوهاج

السمسم يعد أحد أهم محاصيل الزيت في مصر والذي يصاب بمرض الذبول المتسبب عن فطر فيوزاريوم اوكسيسبوريم. أظهرت اختبارات القدرة المرضية أنه من بين عزلات انواع الفيوزاريوم المعزولة فقط عزلات النوع اوكسيسبوريم كانت ممرضة لنبات السمسم صنف جيزة 32 مسببة اعراض الذبول. أجريت هذه الدراسة خلال موسمين صيفيين 2016 و 2017 علي 86 تركيب وراثي من السمسم لتقييمهم للاصابة بمرض الذبول تحت ظروف العدوي الصناعية بالحقل باستخدام العزلة رقم 2 من فطر فيوزاريوم اوكسيسبوريوم. أظهر تحليل التباين في الموسم الاول لصفة الاصابة وجود 10 سلالات مقاومه لمرض الذبول وهم سلالات أرقام 71- 50- 44- 58- 28- 70- 79- 57- 24 و80 وكانت نسب الاصابة بهم 13.77- 15- 15.29- 16.67- 17.59- 18.07- 18.33- 18.87- 19.12 و 20% علي التوالي. بينما كانت ثمانية وأربعون سلالة متوسطه المقاومة للمرض وتراوحت نسبة الاصابة لهم ما بين 20- 40%. وفي الموسم الثاني كان عدد السلالات المقاومة 11 سلالة وهي نفسها سلالات العام الاول بالاضافة الي سلالة رقم 49. التقدير العام لمتوسط الموسمين اظهر انه من بين 80 سلالة سمسم كان: 12.5% مقاومين – 60 % متوسطين المقاومة – 16.25% متوسطين الحساسية و 18.75% حساسين للاصابة. اظهرت النتائج ايضا وجود أرتباط معنوي سالب بين النسبة المئوية للاصابة وكلا من صفة عدد الأيام حتي تزهير 50% وصفة المحصول/نبات. توصي هذة الدراسة بأن السلالات المقاومة من السمسم يمكن أستخدامها كأصناف مقاومة أو كمصدر للمقاومة في برامج التربية. ايضا بالانتخاب للتراكيب الوراثية متأخرة التزهير في برامج التربية لصفة مقاومة الذبول في محصول السمسم.