RESISTANCE OF SOME SESAME (*SESAMUM INDICUM* L.) COLLECTIONS AGAINST ROOT ROT DISEASE (*RHIZOCTONIA SOLANI* KÜHN) UNDER FIELD CONDITIONS

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Abstract: The investigation was conducted in 2004 and 2005 to test 28 sesame genotypes for resistance and susceptablity to *Rhizoctonia solani* under artificial infection conditions at the Plant Breeding Experimental Farm of the Faculty of Agriculture, Suez Canal University, Ismailia, Egypt. All screened sesame genotypes showed varied significant degrees of infestation with the root rot pathogen. It is worth to mention that some of sesame genotypes kept their resistance characterestic classes as moderately resistant (MR) or resistant (R) during the two successive seasons. Such genotypes might be useful for breeding programs due to stability of their resistant character as well as their seed yield. Phenotypic coefficients of variation (P.C.V.) and genotypic coefficients of variation (G.C.V.) were of high value regarding resistance characters during both seasons and comparable to seed yield character. The heritability estimates indicate that selection is a suitable way for picking up sesame genotypes that have high chance for resistance character to root rot disease (*R. solani*) with high seed yield potential. The genetic advance and heritability estimates in all cases supported the selection of some sesame genotypes to be used in next breeding programs for root rot resistance, they also showed a high seed yield potential.

Key words: sesame, root rot, *Rhizoctonia solani,* resistance, heritability, genetic advance

INTRODUCTION

Sesame (*Sesamum indicum* L.) is an important oilseed crop being cultivated in the tropical and the temperate zones all over the world for its edible oil, protein content and quality, as well as vitamins and amino acids. It is probably the first oilseed crop known and used by man and it dates back to 2130 BC (Weiss 1983). Its recorded

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history in Egypt returns to 1300 BC (Burkill 1953). In recent years, the local interest in sesame has increased, owing to its luxurian bakery foodstuffs, different palatable snacks and food recipes. In Egypt, it is recognized as one of the oil crops, however, it has not attained the status of oil production. The sesame cultivated area is 32187.92 hectare, which represents about 0.49% of the total cultivated area. The production of sesame reaches about 1.15 ton per hectare (Anonymous 2005). Wherever sesame is grown, it is liable to the attack by various pathogenic fungi, which cause at least eight fungal diseases (Kolte 1985). *Rhizoctonia solani* causing root rot is a serious fungal disease in Egypt that limits sesame production (El-Marzok 1982; El-Barougy 1990; El-Shakhess 1998). In this context, breeding works could be effective by finding the best genotype, which would be superior for having a high yield potential with high degree of resistance to the above-mentioned disease. Thus, the aim of the present work was to screen the available sesame germplasm for resistance against the root rot pathogen (*R. solani*) under artificial infection conditions and determining the genetic coefficients of variation and heritability in the broad sense as well as genetic advance for the resistance character among all tested genotypes.

MATERIALS AND METHODS

Field study was conducted to evaluate twenty-eight sesame genotypes under artificial infection by the root rot pathogen (*R. solani*) during two successive seasons (2004 and 2005) at the Experimental Farm of Plant Breeding, Faculty of Agriculture., Suez Canal University, Ismalia, Egypt. These sesame genotypes are listed in Table 1 and include 10 local cultivars, 3 introduced cultivars and 15 promising lines originated by hybridization and selection through previous breeding program. These genotypes were characterized by being branched, early flowering except no. 10, 13 and 16 and have high yielding capacity with regard to the number of capsules per axis, however, some of them have a low number capsules per axis. The experiment laid out in design of randomized complete blocks with four replications. Plots consisted of one row of 4 m in length with spacing of 60 cm between rows, and seed spacing of 15 cm. Uninoculated rows were used as control. All recommended agronomic practices were carried out regularly as needed.

The isolation of *R. solani* using diseased plants collected from different sesame growing fields at Ismailia Governorate and pathogenicity tests were carried out at Botany Department, Faculty of Science, Suez Canal University. Reisolation of the root rot pathogen from the diseased plants which developed typical root rot symptoms was carried out to assure the presence of the pathogen and the disease. The diseased plants were counted and presented as percentage of disease, then transformed to Arcsine values and prepared for statistical analysis.

The experiment was established in a sand soil (94.46% sand, 2.50% silt and 3.04% clay) with 7.8 pH value. Soil analysis was carried out according to the method outlined by Kilmer and Alexander (1949). The reaction of sesame accessions with the root rot pathogen (*R. solani*) was determined according to the scale presented in Table 2.

The data obtianed were subjected to the statistical analysis, described by Snedecor and Cochran (1969) and the differences among tested sesame genotypes were determined using Duncan's Multiple Range Test at 0.05 level of probability (Duncan 1955). The genetic coefficient of variation was estimated according to Burton (1952). Heritability in the broad sense and genetic advance were calculated according to Johnson *et al.* (1955).

Table 1. Origin and pedigree of the varieties and lines of sesame accessions

No.	Name	Origin	Pedigree
1	Toshka 1	Egypt	M2 A1 B11 (CAN 114 x Type29) x NA413
2	Toshka 2	Egypt	M2 A2 B11 (CAN 114 x Type29) x NA413
3	Toshka 3	Egypt	M2 A3 B11 (CAN 114 x Type29) x NA413
4	Mutants 48	Egypt	Giza 24 D 20 M 3 R-10
5	Mutants 8	Egypt	Giza 24 D 20 M 6 R -12
6	Taka 1	Egypt	not available
7	Taka 2	Egypt	not available
8	Taka 3	Egypt	not available
9	Giza 25	Egypt	Giza white x Type 9
10	Giza 32	Egypt	B 32 (CAN 114 x Type29)
11	$U_{N.A\,130}$	U.S.A	unknown
12	$G_{N.A\,574}$	Greece	unknown
13	$K_{N.A\,592}$	Korea	unknown
14	H_1	Egypt	Ismailia line 10 x Neu H.B
15	H_2	Egypt	Oro x Local line 274
16	H_3	Egypt	U C. R 10 x Giza 32
17	H_4	Egypt	U C. R 11 x Giza 25
18	H_5	Egypt	Ismailia line 8 x Ismailia line 20
19	H_6	Egypt	a cross between two local lines
20	H_7	Egypt	a cross between two local lines
21	H_8	Egypt	a cross between two local lines
22	H_9	Egypt	a cross between two local lines
23	H_{10}	Egypt	a cross between two local lines
24	S_1	Egypt	selection from local lines under breeding program
25	S_2	Egypt	selection from local lines under breeding program
26	S_3	Egypt	selection from local lines under breeding program
27	S_4	Egypt	selection from local lines under breeding program
28	S_5	Egypt	selection from local lines under breeding program

U – originated in USA, G – originated in Greece, K – originated in Korea
H – originated by hybridization, S – originated by selection

Table 2.   The scale of evaluation used through the study

Score	Percentage of infected plant	Category
0	0.00	immune (I)
1	0.1–20	resistant (R)
2	20.1–40	moderately resistant (MR)
3	40.1–50	moderately susceptible (MS)
4	50.1–75	susceptible (S)
5	75.1–100	highly susceptible (HS)

RESULTS AND DISCUSSION

The screening for resistance against root rot will help identify sesame genotypes with resistance as well as high yield potential, which can be directly used for large scale cultivation. In addition, it will help in hybridization programs for incorporating resistance in agronomically suitable cultivars. Highly significant variations were noticed among screened sesame genotypes concerning the degree of infestation with *R. solani* as well as the seed yield (Table 3). These findings give an overview on presence of sufficient genetic variability for the evaluated sesame genotypes. In addition, these genotypes seem to have different genes controlling the resistance to *R. solani.*

Results showed some interesting points. In the first season (2004), the percentage of infestation by *R. solani* varied from 44.00% (Giza 25) to 4.40% (H_9). Both genotypes were ranked as moderately susceptible (MS) with 244.78 kg seed yield per plot and resistant (R) with 377.83 kg seed yield per plot, respectively, while under non-infestation conditions, they gave 374.33 and 399.75 kg seed yield per plot, respectively. On the other hand, in the second season (2005), the percentage of infestation ranged from 30.90% (H_4) with 261.97 kg seed yield to 4.00% (H_6) with 376.94 kg seed yield per plot. These two genotypes gave 305.92 and 390.83 kg seed yield per plot under non-infestation conditions, respectively.

The results showed that sesame genotypes Giza 25 and H_{10} ranked as moderately susceptible with 244.78 and 241.03 kg seed yield per plot, in the season 2004, and changed to moderately resistant with 326.88 kg and resistant with 226.67 kg seed yield per plot, in the second season 2005. It is worth to mention that some of sesame genotypes kept their resistance characteristic classes as moderately resistant or resistant during the two successive seasons. Such genotypes may be helpful for breeding programs due to their resistant or moderately resistant stability as well as their seed yield stability. This finding was in agreement with the results obtained by Gupta (1995) and Munoz Valenzuela (1996).

Correlation coefficient (r) between sesame genotypes, resistant to root rot disease and seed yield are presented in Table 3. The correlation was negative in both seasons with significant low value (–0.133) in the second season and highly significant value (–0.799) in the first season.

Coefficients of variation (P.C.V. and G.C.V.), heritability (Tb) and genetic advance presented as per cent of means (G.A.%) are given in Table 4. The phenotypic and genotypic coefficients of variation were of high value for resistance characteristics to root rot disease (*R. solani*) during the first and second season and comparable to seed yield. This could be due to lesser effect of environmental conditions on resistance character than on seed yield.

The estimates of heritability in a broad sense (Tb) was high (more than 85%) in all cases during the two seasons, indicating that selection will be the best step for selecting sesame genotypes that have high possibility for resistance to root rot disease (*R. solani*) with high seed yield potential.

High genetic advance (G.A.%) coupled with high heritability estimates indicated additive gene nature of the resistance genes and consequently a high gain yield, also when expressed as seed yield in kg per plot. These enable to choose sesame genotypes for the further breeding programs concerning root rot resistance with high seed yield potential.

Tables 3. Percentage of infection by the root rot pathogen (*R. solani*) and seed yield of sesame genotypes grown through the seasons of 2004 and 2005

No.	Genotypes Name	2004				2005			
		mean	category	seed yield/kg under infestation conditions	seed yield/kg without infestation	mean	category	seed yield/kg under infestation conditions	seed yield/kg without infestation
1	Toshka 1	22.10 (28.03) cde	MR	292.47 i	367.67 gh	9.50 (17.96) ijkl	R	356.67 def	380.0 j
2	Toshka 2	25.40 (30.28) cd	MR	292.61 i	377.83 defgh	19.50 (26.20) cde	MR	301.19 k	393.58 cdef
3	Toshka 3	16.10 (23.66) def	MR	332.39 e	387.18 abcdef	22.52 (28.35) bc	MR	293.89 k	386..67 ghi
4	Mutants 48	31.80 (34.32) bc	MR	257.65 k	372.96 fgh	7.10 (15.40) lmno	R	355.19 ef	393.08 def
5	Mutants 8	16.60 (24.05) def	MR	340.58 de	321.75 jk	11.60 (19.89) fghijk	R	348.33 fg	387.50 fghi
6	Taka 1	17.10 (24.42) def	MR	294.00 i	362.00 hi	26.00 (30.62) ab	MR	325.67 ij	365.00 lm
7	Taka 2	12.02 (20.90) efg	MR	354.08 bc	397.25 ab	7.41 (15.82) klmn	R	190.00 o	400.12ab
8	Taka 3	28.70 (32.36) c	MR	255.73 kl	387.18 abcdef	20.31 (26.76) bcd	MR	302.33 k	388..25 fghi
9	Giza 25	44.00 (41.53) a	MS	244.78 lm	374.33 efgh	13.60 (21.64) fghi	MR	326.88 ij	390.65 efgh
10	Giza 32	30.67 (33.61) bc	MR	250.89 klm	347.67 i	14.70 (22.51) efgh	MR	327.61 ij	387.83 fghi
11	U$_{N.A\ 130}$	22.50 (28.32) cde	MR	276.33 j	349.00 i	16.30 (23.78) defg	MR	341.56 gh	384.67 hij
12	G$_{N.A\ 574}$	23.30 (28.86) cd	MR	300.73 ghi	367.18 gh	6.70 (16.10) jklm	R	367.50 bcd	380.00 j
13	K$_{N.A\ 592}$	30.90 (33.78) bc	MR	274.97 j	364.93 gh	9.61 (18.06) ijkl	R	210..00 n	371.41 j
14	H$_1$	23.01 (28.63) cd	MR	253.42 kl	400.25 a	4.80 (12.66) mno	R	213..33 n	402.10 a
15	H$_2$	24.80 (29.86) cd	MR	320.86 f	332.58 j	17.80 (24.96) cdef	MR	325.89 ij	367.67 k
16	H$_3$	31.30 (34.03) bc	MR	310.97 fg	347.93 i	23.20 (28.78) bc	MR	322.08 j	360.00 m
17	H$_4$	39.98) ab)41.30	MR	185.23 n	310.68 k	30.90 (33.78) a	MR	261.971	305.92.n
18	H$_5$	10.70 (19.66) fg	R	333.81 de	366.42 gh	11.90 (20.18) ghij	MR	345.17 fgh	380.50 j
19	H$_6$	8.58 (17.01) gh	R	374.58 a	398.75 a	4.00 (11.54) o	MR	376.94 ab	390.83 efgh
20	H$_7$	25.42 (30.29) cd	MR	298.64 hi	385.92 abcdef	10.30 (18.71) hijkl	R	351.07 fg	385.72 ghij
21	H$_8$	13.01 (21.14) fg	MR	308.33 gh	380.00 cdefg	8.19 (16.58) jklm	R	233.75 m	397.55 abcde
22	H$_9$	4.40 (11.12) h	R	377.83 a	399.75 a	6.48 (14.73) lmno	R	356.47 def	384.42 ij
23	H$_{10}$	43.80 (41.41) a	MS	241.03 m	373.08 fgh	9.31 (17.77) ijkl	R	226.67 m	399.10 abc
24	S$_1$	30.80 (33.69) bc	MR	260.50 k	381.50 bgdefg	4.78 (12.98) mno	R	372.78 ab	388..33 fghi
25	S$_2$	5.00 (12.91) h	R	358.56 b	395.67 abc	7.20 (15.57) lmno	R	363.64 cde	394..67bcde
26	S$_3$	4.50 (12.24) h	R	379.14 a	393.43 abcd	4.19 (11.78) no	R	382.17 a	391.50 efg
27	S$_4$	23.10 (28.01) cde	MR	293.50 i	390.25 abcde	30.60(33.53) a	MR	262.531	385.08 hij
28	S$_5$	12.64 (20.82) fg	MR	343.94 cd	384.33 abcdef	13.90 (21.88) fghi	MR	334.97	389.92 efghi
	Mean square of genotypes	409.48 **	–	11720.26 **	2228.02**	133.30 **	–	35978.00 **	1338.31**
	Correlation (r)	–0,799 **				–0,133 *			

U – originated in USA, G – originated in Greece, K – originated in Korea, H – originated by hybridization, S – originated by selection, R – resistant, MR – moderately resistant, MS – moderately susceptible *and **significant at 0.05 and 0.01 levels of probability, respectively means marked with the same letter are not significantly different

Table 4. Variability, heritability and genetic advance of root-rot disease (*R. solani*) resistance and seed yield in sesame genotypes through the two seasons evaluation (2004 and 2005)

Parameters	Season 2004			Season 2005		
	disease infestation	seed yield		disease infestation	seed yield	
		under infestation conditions	without infestation		under infestation conditions	without infestation
Mean ±SE	22.23±2.11	299.93±9.03	372.05 ±4.46	13.30±1.49	317.33±10.52	383.28±3.46
P.C.V.%	0.96%	0.39%	0.13%	0.93%	0.60%	2.01%
G.C.V.%	0.91%	0.36%	0.12%	0.87%	0.60%	2.00%
Tb	89.29%	99.59%	95.50%	86.65%	99.53%	98.99%
G.A.% of mean	39.26%	222.35%	92.90%	21.95%	387.75%	74.23%

SE – standard deviation, P.C.V.% – phenotypic coefficients of variation,
G.C.V.% – genotypic coefficients of variation, Tb – heritability in a broad sense,
G.A.% – genetic advance

CONCLUSIONS

It is worth to mention that some of sesame genotypes kept their resistance characteristic classes as moderately resistant or resistant during the two successive seasons. Such genotypes might be useful for breeding programs due to stability of their resistance as well as satisfactory seed yield. Selection is a good criterion for choosing sesame genotypes that have high chance for satisfactory resistance characteristics to root rot pathogen, *R. solani*, and high seed yield potential.

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POLISH SUMMARY

ODPORNOSĆ NIEKTÓRYCH KOLEKCJI SEZAMU WSCHODNIEGO (*SESAMUM INDICUM* L.) W WARUNKACH POLOWYCH NA ZGNILIZNĘ KORZENI WYWOŁANA *RHIZOCTONIA SOLANI* KÜHN

W latach 2004–2005 przeprowadzono badania nad odpornością i wrażliwością 28 kolekcji sezamu wschodniego na zgniliznę korzeni (*Rhizoctonia solani*). Badania były wykonane w polu w warunkach sztucznej infekcji, w Stacji Doświadczalnej Hodowli Roślin Wydziału Rolniczego UniwersytetuKkanału Sueskiego, Ismailia, Egipt. Testowane genotypy sezamu wykazały zróżnicowany, istotny poziom występowania choroby. Niektóre z nich były średnio odporne (MR) lub odporne w kolejnych 2 latach badań. Takie genotypy mogą być użyteczne w programach hodowlanych dzięki stabilnemu charakterowi odporności, jak również dobrym parametrom plonowania. Współczynnik genotypowej korelacji (P.C.V.) oraz współczynnik genotypowej korelacji (G.C.V.) dotyczące cech odporności stwierdzonych w obydwu sezonach wegetacyjnych były wysokie oraz porównywalne z wysokością plonu nasion. Przeprowadzone badania dziedziczenia cech wskazywały na selekcje jako właściwą metodę pozyskiwania perspektywicznych genotypów sezamu w aspekcie odporności na zgniliznę korzeni (*R. solani*). oraz plonowanie. Dokonana ocena postępu genetycznego oraz możliwości dziedziczenia były uzasadnione we wszystkich przypadkach wyboru do przyszłych programów hodowli genotypów sezamu wysoko plonujących i odpornych na zgniliznę korzeni.