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RESEARCH ARTICLE

Selection in two segregating populations of sesame under artificial infection of *Macrophomina phaseolina* (Tassi) Goid

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Abstract

The root rot/stem "rot/charcoal rot" disease caused by *Macrophomina phaseolina* (Tassi.) Goid is one of the most destructive disease in all sesame growing areas. To improve tolerance and/or resistance of sesame to this pathogen, two cycles of pedigree selection under artificial infection of were done at Fac. Agric. Assiut Univ. Expr. Farm. Assiut, Egypt. The genetic materials were the F_2, F_3 and F_4 generations of two populations. The experiments were done in the three successive seasons of 2018 to 2020. The F_2 was sown in nor-replicated experiments, and the F3 and F4 were raised in RCBD of three replications. The selection criteria were days to 50% flowering (earliness), plant height (PH), height to first capsule (HFC), length of fruiting zone (LFZ) and seed yield/plant (SY/P). The infection % in the F_2 ranged from 53.67 to 80.43%. The remained genotypic coefficient of variation in the F_4 was high and enough for further cycles of selection for HFC, LFZ and SY/P. Heritability in broad sense of the selection criteria in the F_4-generation was very high and unreliable. However, the narrow sense heritability was low to moderate. After two cycles of selection, the direct observed genetic gain from the mid-parent was significant ($p \leq 0.01$) and reached -6.06 and -12.15% for earliness,14.66 and 5.82% for PH, -20.78 and -16.50% for HFC, 32.35% and 19.19% for LFZ and 43.89 and 36.67% for SY/P for pop1 and pop2, respectively. The infection% decreased significantly by selection. Single trait selection was an effective method to improve the selection criterion, but in some cases, it was accompanied with adverse effects on the other correlated traits. To overcome this problem selection index combined the favorable traits could be recommended.

Keywords: Narrow sense heritability; Observed genetic gain; *Sesamum indicun L.;* Single trait selection.

1. Introduction

Sesame crop (*Sesamum indicum L.*) is one of the oldest oilseed crops grown from 3050-3500 B.C.(Bedigian and Harlan, 1986). It is grown between 40° N latitude to 40° S latitude (Bedigian D., 2003; Attibayeba *et al.*, 2010; Ashri, 1998). Sesame is a diploid species with 2n= 26 chromosomes under the family *Pedaliaceae*. It is a self-pollinated crop (Menzir, 2012). Sesame is known as "the queen of oil seeds" because of its nutritive value (protein 25% and carbohydrates 13.5%) and oil quality and quantity (45-60%) with the highest antioxidant content as a high-quality digestible oil (Iman *et al.*, 2011). Its oil is rich in vitamin E and has a significant amount of linoleic acid that can control blood cholesterol levels (Banerjee and Kole, 2009; Boureima *et al.*, 2011; Engin *et al.*, 2010; Renuka *et al.*, 2011; Revathi *et al.*, 2012). The root rot/stem "rot/charcoal rot" disease caused by *Macrophomina phaseolina* (Tassi.) Goid is one of the most destructive disease in all sesame growing areas occurs from seedling to maturity stage and causes about 5–100% yield loss (Maiti *et al.*, 1988). The most common symptom of the disease is the sudden wilting of growing plants, mainly after the flowering stage, the stem and roots become black due to severe infection. The pathogen survives as sclerotia in the soil and crop residues and has also been reported to be seed-borne characteristics that make it difficult to control. To overcome this problem, developing resistance genotypes by breeding is a must. Evaluation and selection for resistance to *Macrophomina phaseolina* in contaminated field could improve resistance. Ranganatha (2014)

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reported heavy yield losses up to 55% or more. Wherever, sesame is grown it is liable to attack by root rot and wilt diseases. Therefore, the area of sesame in Egypt was decreased. Meena *et al.* (2018) screened several entries under field (sick plot) conditions and found that the disease severity of root rot ranged between 8.2% and 62.4%. Aremu *et al*. (2011), Vanishree *et al.* (2011) and Ibrahim and Khidir (2012) stated that number of capsules and seeds per capsule are the principal yield components, and selection for these traits may be useful in improving seed yield in sesame. Menzir (2012) found significant difference ($p \leq 0.01$) among 64 genotypes for all the characters studied. The phenotypic coefficient of variation was high for most traits. Heritability was high for days to maturity followed by thousand seed weight and oil content. Moderate heritability coupled with high genetic advance was recorded for number of branches per plant and plant height. Selection for yield and its components could improme sesame yield (Abate, 2018; Lalpantluangi and Shah, 2018; Ramprasad and Senthilvel, 2019). Observed genetic gains in seed yield of sesame were achieved by pedigree selection for two cycles in segregating generations of different populatins (Abo-Elwafa and Ahmed, 2005; EL-Shimy, 2005; EL-Shimy *et al.*, 2005; Ismail *et al.*, 2014; Mahdy *et al.*, 2005 and 2015; Abd-ElAziz, 2018). Furthermore, the researches indicated that single trait selection for seed yield was accompanied in most cases with adverse effects on other traits, and selection index could be recommended to improve seed yield and other traits. This work aimed to improve seed yield and tolerance and/or resistance to *Macrophomina phaseolina* (Tassi.) Goid through pedigree selection for earliness, plant height, height to first capsule, length of fruiting zone and seed yield under artificial infection.

2. Materials and methods

The present work was achieved at Fac. Agric. Assiut Univ. Expr. Farm. Assiut, Egypt (Longitude: 31.125 N, Latitude: 27.25 E, Elevation :45m/148 Feet) in the three successive seasons of 2018 to 2020. The genetic materials were the F_2, F_3 and F_4 generations of two populations of sesame (*Sesamum indicun* L). The first population stemmed from the cross of "Shamdaweel3 x Sohag 2000" (pop1), and the second one stemmed from the cross "Int.562 x Int.688" (pop2). Shamdaweel3 and Sohag 2000 are Egyptian local cultivars. Introduction 562 was imported from FAO in 1983, and introduction 688 was imported from Israel in 1988. Two cycles of pedigree selection were achieved for days to 50% flowering (earliness), plant height (PH, cm), height to first capsule (HFC, cm), length of fruiting zone (LFZ=PH-HFC) and seed yield/plant (SY/P, g). The experimental site was artificial inoculated yearly by *Macrophomina phaseolina* (Tassi) Goid. The soil was clay (sand 27.4%, silt 24.3%, clay 48.3%, EC (1:1 extract) dSm^{-1} 1.07, pH 8.2, Organic matter 0.24%, Soluble K (mg kg^{-1}) 39, Soluble Ca (mg kg^{-1}) 190, Soluble HCO_3 (mg kg^{-1}) 427, Soluble Na (mg kg^{-1}) 140, Total nitrogen 0.08% and Soluble Mg (mg kg^{-1}) 72.

2.1 First season (F_2 - generation)

Planting date in the three-season ranged from April 12th to 15th. The two populations and the parents were sown in rows 4m long, 60cm apart and 10cm between hills, 15 rows each (non-replicated experiment). Seeds were dibbled in holes and covered with equal amount (approximately 40 g) of pathogen inoculum at the ratio of 1% soil weight. Seedlings were thinned to one plant/hill two weeks later. The recommended cultural practices for sesame production were followed throughout the growing season. The studied traits were recorded on 100 guarded survival plants in each population and on 30 plants from each parent. The traits were days to 50% flowering (earliness), plant height (PH), height to the first capsule (HFC), length of the fruiting zone (LFZ), number of capsules/ plant (NC/P), seed yield/plant (SY/P) and infection % (Inf % = 1- (number of survival plants at harvest/ number of seedlings after thinning) x 100. The better 10 plants for each selection criterion from each population were saved for the second season.

2.2. The second season (F_3 - generation)

The selected plants of the two populations and parents were sown in families in a randomized complete block design (RCBD) with three replications in two separate experiments. The distances between rows and hills were as in the

previous season. The plot size was three rows. The best plant from each of the best five families (Within family selection) for each selection criterion was saved as the second cycle selections.

2.3. The third season(F_4)

The five selected families for each selection criterion along with the parents in both populations were evaluated in RCBD as in the previous season. Oil percentage was determined according to the official method (A.O.A.C. 1980).

2.4. Isolation and identification of the causal pathogen

Macrophomina phaseolina (Tassi) Goid. used in this study was isolated from naturally diseased sesame plants showing typical symptoms of charcoal rot. Diseased samples were collected from Assiut Governorate- Egypt during 2017 growing season. Diseased tissues were cut into small pieces (2-3 mm), washed thoroughly with tap water, the surface was sterilized with 3% sodium hypochlorite (NaOCL) for 3 minutes, washed two times with sterilized water. The sterilized pieces were placed into Petri dishes containing Potato Dextrose Agar (PDA) and incubated at 28±2°C for 3-5 days. Pure cultures of the developing fungi were obtained using single spore and hyphal-tip isolation techniques. Identification of the isolated fungi was carried out on 5-12 days old culture using the morphological and microscopic characteristics of mycelium and spores according to Booth (1971) and Mahmoud (2016). Inoculum of the tested pathogen were prepared by growing in sterilized conical flasks (500 ml) containing barley medium (100g barley supplemented, with 2g glucose + 1g yeast extract + 100 ml distilled water) and incubated at 28±2°C for two weeks.

2.5. Statistical analysis

The analysis of variance, phenotypic variance (σ^2_p) and genotypic variance (σ^2_g) were performed as Steel *et al*. (1997). The analysis of variance of infection percentage was done on Arcsine transformed data. Two analyses of variance were performed. The first was for all entries (selected families + parents) to calculate the direct and indirect gains from selection, and the second for the selected to estimate heritability and coefficients of variation (not included). Heritability in broad sense (H%) = (σ^2_g / σ^2_p) ×100, heritability in narrow sense (h^2) was calculated as Smith and Kinman (1965). Expected genetic gain = k σ_p h^2 based on 10% selection intensity (Falconer, 1989). The phenotypic and genotypic coefficients of variation were estimated using the formula developed by (Burton, 1952). Deviation of the observed direct and correlated genetic advance to selection in percentage from the better parent and the mid-parent was measured using LSD test. The infection% was Arcsine transformed before the analysis of variance.

3. Results

3.1. Description of the base population (F_2 generation)

The characteristics of the base populations and their parents are shown Table 1. Days to 50% flowering (earliness) in the F_2-generation was later than the two respective parents in both populations; however, the range was wider in the F_2 than in the parents. Means of the other four selection criteria (PH, HFC, LFZ and SY/P) were better in the F_2-generation than in the parents except for SY/P in pop1. The phenotypic coefficient of variation (PCV%) was higher in both populations than in their respective parents. It reached to 8.34, 14.40, 25.70, 23.52, and 67.69% for earliness, PH, HFC. LFZ and SY/P, respectively in population 1, and 7.43, 15.48, 33.18, 21.97, and 64.58% for the respective traits in population 2. The heritability in broad sense was high for PH (61.73%) and HFC (79.68%), moderate for LFZ and low for earliness and SY/P in pop1. However, in pop2 it was low for HFC (11.0%) and moderate for SY/P (60.0%). The expected genetic advance in percentage of the mean, from selection 10% superior plants ranged from 7.07% for earliness to 44.74% for SY/P in pop 1, and from 2.24 %for HFC to 52.35% for SY/P in pop2. The infection percentage of *Macrophomina phaseolina* in the F_2-gneration showed partial dominance towards susceptibility in both populations.

Table 1. Means of the studied traits, genotypic (GCV) and phenotypic (PCV) coefficients of variations, heritability in broad sense (Hb) and expected genetic advance(ΔG) in the two base populations (F_2) evaluated under artificial infection of *Macrophomina phaseolina*.

`Item	50% Flow.	PH, cm	HFC, cm	LFZ, cm	SY/P, g	Inf.%
			F_2-population Shandaweel 3/Sohag 2000			
Mean±SE	69.47 ±0.58	122.55 ±1.76	57.09 ±1.47	66.09 ±1.55	9.26± 0.63	70.42
Max.	82.00	170.00	105.00	120.00	28.01	
Min.	50.00	90.00	25.00	35.00	4.30	
GCV%	4.9	11.31	13.02	17.22	39.92	
PCV%	8.34	14.40	25.79	23.52	67.69	
Hb	34.54	61.73	79.68	53.60	37.57	
ΔG	3.52	19.17	23.01	22.15	4.14	
ΔG/mean%	5.07	15.64	4.49	33.51	44.74	
			(Parent) Shandaweel.3			
Mean±SE	57.1 ±1.43	114 ±3.54	63.2 ±2.26	50.8 ±3.96	12.68 ±1.53	53.67
Max.	62.00	130.00	77.00	74.00	14.50	
Min.	50.00	100.00	55.00	38.00	7.80	
CV%	7.93	9.81	11.29	24.65	38.15	
			(Parent) Sohag 2000			
Mean±SE	56.2 ±1.53	87.2 ±3.37	33 ±1.93	54.2 ±2.60	10.29 ±1.60	80.43
Max.	63.00	105.00	41.00	68.00	13.70	
Min.	49.00	75.00	22.00	40.00	8.20	
CV%	8.61	12.21	18.47	15.16	49.17	
			F_2- population Int.562/Int.688			
Mean±SE	70.63 ±0.52	113.37 ±1.75	41.39 ±1.37	71.98 ±1.58	11.21 ±0.72	67.52
Max.	75.00	170.00	85.00	125.00	33.97	
Min.	50.00	80.00	15.00	35.00	4.50	
GCV%	4.46	11.61	11.99	14.64	49.87	
PCV%	7.43	15.48	33.18	21.97	64.58	
Hb	36.02	56.24	11.37	44.37	59.64	
ΔG	2.00	13.03	0.93	8.23	5.87	
ΔG/mean%	2.82	11.49	2.24	11.43	52.35	
			(Parent) Int.562			
Mean±SE	65.5 ±1.36	111 ±3.96	52 ±3.63	59 ±3.27	9.52 ±1.41	70.81
Max.	68.00	130.00	65.00	78.00	13.50	
Min.	58.00	85.00	33.00	46.00	7.30	
CV%	6.57	11.27	22.07	17.52	46.86	
			(Parent) Int.688			
Mean±SE	60.7 ±1.29	112.5 ±3.36	46 ±4.5	66.5 ±4.14	11.14 ±1.50	60.78
Max.	63.00	130.00	65.00	90.00	15.70	
Min.	56.00	100.00	23.00	53.00	8.30	
CV%	6.73	9.45	30.95	19.69	42.48	

ΔG; expected genetic advance from selection 10% superior plants.

PH= plant height, HFC= height to the first capsule, LFZ= length of fruiting zone, SY/P= seed yield/plant, INF%= infection%

3.2. Variability and heritability after two cycles of selection (F_4-generation)

After two cycles of pedigree selection in the F_4-generation the entries mean squares (5-selected families + two parents) was significant ($p \leq 0.05$ - $p \leq 0.01$) for all traits except for SY/P in pop1 when selection practiced for earliness (Table 2). The PCV% of the selection criterion decreased from 8.34 in the F_2 to 5.1 in the F_4 in pop1 when selection practiced for earliness (Table 3). The PCV% and GCV% decreased by selection for PH and LFZ, however they increased when selection

practiced for HFC and SY/P. Results indicated that after two cycles of pedigree selection, the retained variability as measured by GCV was moderate for earliness (5.09 % in pop1 and 8.42 % in pop2). However, it was high and enough for further cycles of selection for HFC (28.30% for pop1 and 15.33% for pop 2), LFZ (15.11% for pop 1 and 14.20% for pop2) and SY/P (78.63% for pop1 and 24.46% for pop 2).

Table 2. Pertinent of mean squares of the studied traits for the two populations in the F_4 generation under artificial infection of *Macrophomina phaseolina.*

Selection criterion	Population	Item	50% Flow	PH, cm	HFC, cm	LFZ,cm	NC/P	SY/P, g	1000-SW, g	Oil %	Inf%
50% Flow.	Sohag2000 /Shand3	Entries	20.43**	185.43**	249.38**	238.09**	1402.13**	30.23	0.65**	0.21	5.61**
		Error	0.04	28.84	9.10	10.32	18.40	10.91	0.04	3.78	0.27
	Int.512 /Int. 688	Entries	68.97**	762.06**	344.31**	877.19**	1158.70**	30.16**	0.75**	0.76	21.93**
		Error	9.23	60.21	29.61	144.86	26.97	0.58	0.03	3.35	0.69**
PH	Sohag2000 /Shand3	Entries	62.49**	269.27**	391.38**	662.44**	674.27**	150.35**	0.18**	0.51	7.78
		Error	2.56	20.5	6.658	46.389	38.5	5.96	0.03	1.87	0.42
	Int.512 /Int. 688	Entries	180.94**	108.20**	239.78**	337.27**	1565.37**	66.25**	0.54**	0.18	10.01**
		Error	12.555	20.5	32.235	48.45	41.516	1.888	0.086	3.08	0.86
HFC	Sohag2000 /Shand3	Entries	11.89*	120.64**	359.64**	253.34**	2015.61**	36.33**	0.33**	0.20	152.68**
		Error	3.032	19.444	7.32	36.836	42.1	1.79	0.06	0.88	0.52
	Int.512 /Int. 688	Entries	57.00	644.16**	130.41**	818.56**	446.75**	58.18**	0.81**	0.40	11.01**
		Error	11.45	48.25	15.43	42.20	42.05	0.79	0.04	2.10	0.80
LFZ	Sohag2000 /Shand3	Entries	66.49**	228.16**	270.89**	304.65**	892.95**	46.75**	0.15**	0.07	6.44**
		Error	2.1	23.592	4.5	33.858	31.688	1.68	0.02	0.61	0.23
	Int.512 /Int. 688	Entries	178.22**	138.8**	237.31**	473.34**	231.91**	29.26**	0.43**	0.41	11.12**
		Error	10.913	44.844	17.911	60.200	22.605	1.398	0.077	2.71	1.06
SY/P	Sohag2000 /Shand3	Entries	97.63**	197.15**	400.59**	585.76**	660.98**	120.9**	0.23*	0.12	15.01**
		Error	2.45	16.50	9.60	21.50	20.02	2.10	0.06	0.78	0.50
	Int.512 /Int. 688	Entries	194.30**	190.44**	70.33	272.54**	269.21**	38.54**	0.35**	0.41	14.23**
		Error	11.21	23.83	46.55	62.09	30.24	1.92	0.02	1.90	0.69

*and **; significant at 0.05 and 0.01 level of probability, respectively. PH= plant height, HFC= height to the first capsule, LFZ= length of fruiting zone, NC/P= number of capsules/plant, SY/P= seed yield/plant, INF%= infection%.

Table 3. Genotypic (GCV%) and phenotypic (PCV%) coefficients of variation for the studied traits for the two populations in the F_4 generation under artificial infection of *Macrophomina phaseolina.*

Selection criterion	Population	Item	50%Flow	PH,cm	HFC,cm	LFZ,cm	NC/P	SY/P,g	1000-SW, g	Inf%
50% Flow.	Sohag 2000 /Shand 3	GCV%	5.09	7.51	20.46	16.61	23.92	ns	11.62	2.88
		PCV%	5.10	8.17	20.85	16.99	24.07	ns	12.00	2.95
	Int.512 /Int. 688	GCV%	8.42	14.50	22.12	26.39	29.58	33.26	12.93	5.28
		PCV%	9.05	15.11	23.14	28.89	29.93	33.59	13.22	5.36
PH	Sohag 2000 /Shand 3	GCV%	7.82	8.29	26.47	21.36	12.34	42.63	5.41	3.45
		PCV%	7.99	8.62	26.70	22.15	12.70	43.50	5.93	3.55
	Int.512 /Int. 688	GCV%	11.04	4.23	17.56	12.19	21.21	30.17	9.51	3.54
		PCV%	11.44	4.70	18.88	13.17	21.50	30.61	10.38	3.71
HFC	Sohag2000 /Shand 3	GCV%	3.28	6.48	28.30	16.53	29.90	29.22	7.89	15.11
		PCV%	3.80	7.07	28.60	17.89	30.22	29.97	8.73	15.13
	Int.512 /Int. 688	GCV%	6.16	13.88	14.40	31.17	15.51	40.23	14.09	3.67
		PCV%	6.89	14.44	15.33	32.00	16.30	40.50	14.46	3.82
LFZ	Sohag 2000 /Shand3	GCV%	8.26	7.48	19.82	15.11	15.33	28.04	4.90	3.15
		PCV%	8.40	7.90	19.98	16.03	15.61	28.56	5.27	3.21
	Int.512 /Int. 688	GCV%	11.01	4.26	17.56	14.20	8.17	22.43	8.51	3.69
		PCV%	11.37	5.18	18.26	15.20	8.60	22.98	9.38	3.88
SY/P	Sohag 2000 /Shand 3	GCV%	15.97	12.70	45.26	37.04	22.41	78.63	11.61	8.56
		PCV%	16.04	12.88	45.44	37.27	22.53	78.85	12.15	8.60
	Int.512 /Int. 688	GCV%	11.91	5.65	ns	9.92	8.60	24.46	7.91	4.17
		PCV%	12.27	6.05	ns	11.29	9.13	25.10	8.12	4.28

ns; insignificant differences among families. PH= plant height, HFC= height to the first capsule, LFZ= length of fruiting zone, NC/P= number of capsules/plant, SY/P= seed yield/plant, INF%= infection%.

The heritability in broad sense of the selection criteria was very high and ranged from 81.05 to 99.80% in both populations. However, the narrow sense heritability calculated by parent-offspring regression of F_4/F_3 was low to moderate. It was 0.5102 and 0.4651 for earliness, 0.4216 and 0.4472 for HFC, 0.3744 and 0.3925 for PH, 0.1941 and 0.2606 for LFZ and 0.2241 and 0.2180 for SY/P for pop1 and pop 2, respectively (Table 4).

Table 4. Heritability in broad (H) and in narrow sense (h^2) as estimated by parent- offsping regression (F_4/F_3) for the selection criteria for both populations under artificial infection of *Macrophomina phaseolina*.

Population	Shan.3/Sohag 2000		Int.562/Int.688	
Sel.criterion	H	h^2	H	h^2
50% flow.	99.80	0.5102	86.62	0.4651
Plant height	92.39	0.3744	81.05	0.3925
HFC	97.96	0.4216	88.17	0.4472
LFZ	88.89	0.1941	87.28	0.2606
SY/P	99.42	0.2241	95.01	0.2180

HFC= height to the first capsule, LFZ= length of fruiting zone, SY/P= seed yield/plant

3.3. Observed direct and correlated genetic gains after two cycles of pedigree selection

3.3.1. Selection for days to 50% flowering (earliness)

Observed direct and correlated gains in the F_4-generation are presented in Table 5. Two cycles of pedigree selection for earliness gave significant ($p \leq 0.01$) genetic gain towards earliness of -6.06 and -12.15% from the mid-parent in pop 1 and pop2, respectively, and -1.56% from the earlier parent in pop1. Unfavorable significant decreases were obtained in the correlated traits; NC/P, SY/P and PH from both of mid- and the better parent in pop 2. Selection for earliness in pop1 caused deleterious effects in NC/P from the better parent. The decrease in SY/P in pop1, and 1000 seed weight and oil% in both populations was not significant. Selection for earliness decreased ($p \leq 0.05$ - $p \leq 0.01$) the infection % from mid-and better parent in pop1 and mid-parent in pop 2.

3.3.2. Selection for plant height

The observed genetic gain in PH (Table 5) was significant ($p \leq 0.01$) and reached 14.66 and 5.82% of the mid-parent in pop1 and pop2, respectively. However, selection for PH adversely affected earliness by 4.83 and 12.49% from the mid-parent in pop1 and pop2, respectively, but it showed favorable observed correlated genetic gains in HFC of -11.49 and -8.04%, LFZ of 41.26 and 16.11%, NC/P of 23.04 and 17.25% and SY/P of 24.74 and 27.11% from the mid-parent in pop1 and pop2, respectively, and 10.45% for 1000-seed weight in pop2. Oil% was not affected.

3.3.3. Selectin for HFC

The direct response of selection for HFC was significant ($p \leq 0.01$) and reached -20.78 and -16.50% from the mid- parent in both populations. The indirect effects on earliness, 1000-seed weight, and oil% were not significant. In pop2, selection for HFC caused deleterious decrease of -25.55 and 30.25% in LFZ, -17.40 and -18.13% in NC/P from mid- and better parent, respectively, and decrease of -16.93% from the better parent in SY/P.

3.3.4. Selection for LFZ

The direct observed genetic gains from selection for LFZ (Table 5) were significant ($p \leq 0.05$ - $p \leq 0.01$) and were 32.35% and 19.19% from the mid-parent in pop 1 and pop 2, respectively. Selection for LFZ accompanied with adverse effects on earliness and caused significant lateness by 7.82% from the earlier parent in pop1, and 12.38 % from the mid-parent, and 23.27% from the earlier parent in pop2. But selection for LFZ caused favorable significant indirect gain from the mid-parent in PH of 15.22 and 8.69%, 15.25 and 12.83% for NC/P and 23.65 and 20.94% for SY/P in pop1 and pop2, respectively.

3.3.5. Selection for SY/P

The direct genetic response from selection for SY/P (Table5) after two cycles of selection was significant ($p \leq 0.01$) and reached 43.89 and 36.67% from the mid-parent for pop1 and pop2, respectively. Selection for SY/P caused unfavorable significant effects on earliness of 13.03 and 8.73% from the mid-parent of pop1 and

pop2, respectively. However, it caused significant increase from the mid-parent of 13.72 and 9.08% for PH, 36.70 and 21.79% for LFZ, 19.00 and 14.53% for NC/P, -18.11 and -5.10% for infection % in pop1 and pop2, respectively.

Table 5. The observed genetic advance (GA) in percentage from the mid- parent (GA. MP%) and better parents (GA. BP%) after two cycles of pedigree selection for the two populations.

Population	Selection Criterion	Item	50% Flow	PH, cm	HFC, cm	LFZ, cm	NC/P	SY/P, g	1000 SW, g	Oil%	Inf%
Sohag2000/ Shand.3	50% Flow	Mean	51.20	96.18	43.73	52.44	89.80	10.85	3.88	58.01	46.38
		GA.MP%	-6.06**	0.36	-9.52*	10.41*	-6.37	ns	-1.77	ns	-15.67**
		GA.BP%	-1.56**	-5.40	31.20	-7.45	-15.93**	ns	-7.62	ns	-2.58*
INT.562/ INT.688		Mean	53.00	105.49	46.30	59.20	65.67	9.44	3.78	57.79	50.44
		GA.MP%	-12.15**	-12.70*	-10.11	-14.62	-27.55	-15.97**	2.53	ns	-5.96**
		GA.BP%	-3.64	-15.61**	-9.23	-20.01	-28.19	-27.88**	-4.71	ns	-1.40ns
Sohag2000/ Shand.3	PH	Mean	57.13	109.88	42.78	67.10	118.00	13.77	4.13	58.20	45.38
		GA.MP%	4.83*	14.66**	-11.49*	41.26**	23.04**	24.74*	3.77	ns	-17.48**
		GA.BP%	9.87**	8.08*	-33.46**	75.04**	10.47*	5.37	-3.12	ns	-4.67**
INT.562/ INT.688		Mean	67.87	127.87	47.36	80.50	106.27	14.28	4.07	57.91	49.30
		GA.MP%	12.49*	5.82**	-8.04	16.11*	17.25	27.11**	10.45*	ns	-8.08
		GA.BP%	23.39**	2.29	-7.13	8.79	16.21	9.09	2.66	ns	-3.63
Sohag2000/ Shand.3	HFC	Mean	52.40	89.67	38.29	51.38	85.78	11.43	3.80	57.79	47.15
		GA.MP	-3.85	-6.43	-20.78**	8.16	-10.56*	2.28	-3.80	ns	-14.27**
		GA.BP	0.77	-11.80	14.87*	-9.33	-19.69**	-13.60	-9.52	ns	-0.96ns
INT.562/ INT.688		Mean	63.27	101.51	43.00	51.62	74.87	10.87	3.59	57.85	50.19
		GA.MP%	4.86	-15.99*	-16.50**	-25.55**	-17.40**	-3.21	-2.73	ns	-6.43**
		GA.BP%	15.03*	-18.79**	-15.69*	-30.25**	-18.13**	-16.93*	-9.60*	ns	-1.89ns
Sohag2000/ Shand.3	LFZ	Mean	56.07	110.42	47.56	62.87	110.53	13.64	4.25	58.04	45.65
		GA.MP%	2.87	15.22**	-1.61	32.35**	15.25**	23.65*	7.51*	ns	-17.00**
		GA.BP%	7.82*	8.61*	42.67**	10.94	3.48	3.48	1.11	ns	-4.10**
INT.562/ INT.688		Mean	67.80	131.33	48.70	82.64	102.27	13.59	4.06	57.83	49.65
		GA.MP%	12.38**	8.69*	-5.45	19.19*	12.83**	20.94*	10.00	ns	-7.43**
		GA.BP%	23.27**	5.07	-4.52	11.67	11.83*	3.79	2.24	ns	-2.94ns
Sohag2000/ Shand.3	SY/P	Mean	61.60	108.98	44.04	64.93	114.13	16.09	3.95	57.87	45.04
		GA.MP%	13.03**	13.72**	-8.87	36.70**	19.00**	43.98*	-0.08	ns	-18.11**
		GA.BP%	18.46**	7.19*	32.13**	14.59*	6.85	21.62*	-6.03	ns	-5.39**
INT.562/ INT.688		Mean	65.60	131.80	47.36	84.44	103.80	15.35	4.23	57.53	50.90
		GA.MP%	8.73*	9.08*	ns	21.79*	14.53**	36.67**	14.65**	ns	-5.10**
		GA.BP%	19.27**	5.44	ns	14.11	13.51*	17.29*	6.55*	ns	-0.50

*and **; significant at 0.05 and 0.01 level of probability, respectively, ns; insignificant differences among entries. PH= plant height, HFC= height to the first capsule, LFZ= length of fruiting zone, NC/P= number of capsules/plant, SY/P= seed yield/plant, INF%= infection%.

4. Discussion

4.1 Description of the base population (F_2 generation)

The range in the F_2- generation (Table1) of all selection criteria based on the maximum and minimum values was located outside the range of the parents, and the PCV% in the F_2's was higher than in their respective parents. This could be due

to low variability in pure lines (parents), and the maximum variability generally obtained in the F_2-generations, and some plants showed transgressive segregation. Except for earliness, these results indicate enough variability and feasibility of selection.

The expected genetic advance in percentage of the mean, from selection 10% superior plants ranged from 7.07% for earliness to 44.74% for SY/P in pop 1, and from 2.24 %for HFC to 52.35% for SY/P in pop 2 (Table 1). It could be noticed that the expected genetic advance was more affected by PCV than heritability estimates. Mahdy *et al.* (2005) found coefficient of variation ranged from 4.12- 4.83% for earliness, 5.54 - 7.42% for PH, 10.80-15.66% for HFC, 14.35-15.63% for LFZ and 15.25 - 26.38% for SY/P for three base populations in the F_5-generation under artificial infection of *M. phaseolina.* However, he noted very high estimates of broad sense heritability (more than 90%) for most traits. Mahdy *et al.* (2015) recorded estimates of heritability in broad sense of 96.38, 94.31, 85.13, 91.05, and 64.52% in an F_2-population, and 92.08, 82.82, 75.15, 85.57 and 45.45% in another population for days to flowering, PH, HFC, LFZ and SY/P, respectively. Abd-Elaziz (2018) noted coefficient of variation in the F_2- generation of 11.34, 27.34 and 49.88% for PH, HFC and SY/P and heritability of 84.65, 94.89 and 96.59% for the same respective traits. The infection percentage of *Macrophomina phaseolina* in the F_2-gneration showed partial dominance towards susceptibility in both populations. Mahdy *et al.* (2005**)** noted infection percentage ranged from 9.15 to 21.55% in the F5 of three populations under artificial infection of *M. phaseolina.*

4.2. Variability and heritability after two cycles of selection (F_4-generation)

The PCV% and GCV% of the selection criteria (Table3) are expected to decrease by selection because of the selection was for the plants of the highest values, and the similarity of the selected plants increased cycle after cycle, in consequence the selection differential decreased (Falconer, 1989). The results indicated decrease in PCV% and GCV% for earliness, PH and LFZ. However, the variability increased by selection for HFC and SY/P. The materials herein were under two forces, the pressure of selection and the pressure of the pathogen effects, and selection was for the survival plants. The pathogen may kill the high or low yielding plants. Therefore, the variability in the selected plants could not be expected. (El-Shimy, 2005; El-Shimy *et al.*, 2005; Ismail *et al*., 2014; Mahdy *et al*., 2015; Abd-ElAziz, 2018) found that selection decreased both of GCV and PCV. Results indicated that after two cycles of pedigree selection, the retained variability as measured by GCV was moderate for earliness. However, it was high and enough for further cycles of selection for HFC, LFZ and SY/P.

Heritability in broad sense of the selection criteria was very high and ranged from 81.05 to 99.80% in both populations (Table 4). This could be due to that evaluation of selected families at one location for one year inflated the families mean squares by the confounding effects of the interactions of families with locations and years. However, the narrow sense heritability calculated by parent-offspring regression of F_4/F_3 was moderate for earliness and HFC and low for PH (0.3744 and 0.3925), LFZ (0.1941 and 0.2606) and for SY/P (0.2241 and 0.2180) for pop1 and pop2, respectively.

4.3. Observed direct and correlated genetic gains after two cycles of pedigree selection

4.3.1. Selection for days to 50% flowering (earliness)

Two cycles of pedigree selection for earliness gave significant ($p \leq 0.01$) genetic gain towards earliness of -6.06 and -12.15% from the mid-parent in both populations (Table 5) and decreased ($p \leq 0.05$ - $p \leq 0.01$) the infection %. Otherwise, it caused unfavorable significant decrease in the correlated traits; NC/P, SY/P and PH. It could be concluded that two cycles of selection for days to 50% flowering improve the selection criterion and cause deleterious effects on PH, NC/P and SY/P.

4.3.2. Selection for plant height

The observed genetic gain in the PH from the mid-parent was significant ($p \leq 0.01$) and showed favorable correlated genetic gains in HFC, LFZ, NC/P and SY/P. However, it adversely affected

earliness. Ramprasad and Senthilvel (2019) indicated that yield improvement would be possible via selection for plant height.

4.3.3. Selection for HFC

The direct response of selection for the HFC was significant ($p \leq 0.01$) and reached -20.78 and -16.50% from the mid- parent in both populations. Selection for HFC causes deleterious decrease in LFZ, NC/P and SY/P. This could be due to that the selected families for HFC resulted in short plants of short LFZ, in consequence low NC/P and Low SY/P.

4.3.4. Selection for LFZ

The direct observed genetic gains in the LFZ were significant ($p \leq 0.05$ - $p \leq 0.01$) and were 32.35% and 19.19% from the mid-parent in pop1 and pop2, respectively. Favorable significant indirect gain from the mid-parent was attained in the PH, NC/P and SY/P in both populations. However, selection for the LFZ accompanied with significant adverse effects on earliness.

4.3.5. Selection for SY/P

The direct genetic response from selection for SY/P after two cycles of selection was significant ($p \leq 0.01$) and reached 43.89 and 36.67% from the mid-parent for pop1 and pop2, respectively. Selection for SY/P caused favorable indirect gains in PH, LFZ, NC/P, and infection %. But, it caused unfavorable significant effects on earliness in both populations. These results agree with those found by Abo-Elwafa and Ahmed (2005), EL-Shimy (2005), EL-Shimy *et al*. (2005), Mahdy *et al*. (2005 and 2015) and Abd-Elaziz (2018).

It could be concluded that two cycles of pedigree selection for earliness, PH, HFC, LFZ, and SY/P in these materials under artificial infection of *Macrophomina phaseolina* deceased the infection percentage and increased the selection criteria. Pedigree selection was an effective method to improve the selection criterion, but in some cases, it accompanied with adverse effects on the other correlated traits. To overcome this problem selection index combined the favorable traits could be recommended.

5. Conclusion

Two cycles of pedigree selection for different traits under artificial infection of *Macrophomina phaseolina* decreased the infection% at harvest in the two populations. The decrease in INF% ranged from -5.39 to 17.48% of the mid-parent in population 1 when selection practiced for SY/P and PH, respectively, and from 15.10 to 18.08% for the same selection criteria in population 2. The highest genetic response from selection for SY/P was significant ($p \leq 0.01$) and reached 43.89 and 36.67% from the mid-parent for pop1 and pop2, respectively when selection practiced for SY/P per se followed by selection for PH, and LFZ, while the lowest was for HFC and 50% flowering. The highest observed genetic gain in a selection criterion was for the selection criterion per se. To overcome this problem selection index combined the favorable traits could be recommended.

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