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Pedigree Selection in Improving Seed Yield and Tolerance of Sesame to *Macrophomina phaseolina* (Tassi) Goid

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CHARCOAL rot caused by *Macrophomina phaseolina* (Tassi) Goid is the most destructive among major pathological constraints to sesame production in Egypt and worldwide. The objective of the current study was to improve high seed-yielding lines of sesame tolerant to charcoal rot through two cycles of pedigree selection for eight selection criteria under artificial infection. The base population consisted of 185 families at the F_3-generation. Broad sense heritability was very high and ranged from 0.79 to 1. Tall plants gave large number of capsules/plant (NC/P), long fruiting zone (LFZ), high yielding ability and low infection% of *Macrophomina*. Number of capsules/plant gave sizeable genotypic (0.52) and phenotypic (0.49) correlations with seed yield/plant (SY/P). After the second cycle of selection, highly significant differences were noted for the eight selection criteria. The results revealed that the selection for days to 50% flowering improved earliness, but it was better if it restricted by SY/P. Meanwhile, selection for oil% restricted by SY/P gave the best improvement from the mid-parent in SY/P (70.16%**) followed by selection for 1000SW (62.14%**), SY/P *per se* (55.80%**) and selection for days to 50% flowering restricted by SY/P (39.76%**). The inclusion of a trait as an independent culling level improves the efficiency of the selection. Therefore, selection index incorporating favorable traits is recommended. The eight different methods of pedigree selection decreased the infection% at harvest ranged from -3.31%** to -15.45%** from the mid-parent.

Keywords: Genotypic correlation, Narrow sense heritability, Observed gain, Restricted selection.

Introduction

Sesame (*Sesamum indicum* L., 2n= 26) is recognized as the queen of oil seeds owing to its high-value of oil quality and the plethora of nutritive substances (Al-Khayri et al., 2019; Goshme, 2021). It is nearly one of the oldest oilseed crops known to mankind with an oil content of 50–60% and a protein content of 20–30% (Bedigian & Harlan, 1986; Ashri, 1998; Anilakumar et al., 2010; Prasad et al., 2012; Makinde & Akinoso, 2014).

The cultivated area of sesame in Egypt in the summer season of 2020 was about 29 thousand hectare which produced about 38 thousand tons (FAOSTAT, 2022). Through this production, Egypt came as the twentieth country in the global production of sesame seeds. Compared to previous seasons, the area and productivity of sesame have been decreased in Egypt, due to a number of factors, perhaps the most important one is the infection of pathogens, especially fungi.

Macrophomina phaseolina Tassi (Goid) is a

destructive generalist soil-borne fungus present all over the world. It causes diseases such as stem and root rot, charcoal rot and seedling blight and cause substantial yield losses in some crops including that of sesame, leading to high (> 50%) yield losses (Dutta et al., 2020; Marquez et al., 2021). Several symptoms are common like the sudden wilting of growing plants which occurs after the flowering stage and under severe infection, the stem and roots become black (Mahdy, 2021). Additionally, Ibrahim & Abdel-Azeem (2015) stated that *M. phaseolina* survives as microsclerotia in the soil and infected plant debris. Moreover, *M. phaseolina* is of high incidence in Egypt, predominately during the hot period. Interestingly, it was reported that this fungus can infect about 500 plant species (including sesame) in more than 100 families throughout the world (Khare et al., 2011; Mihail & Taylor, 2011; Marquez et al., 2021).

Breeding a cultivar resistant to charcoal rot of sesame seems to be the most cost-effective, economic and eco-friendly (Al-Khayri et al., 2019; Goshme, 2021). However, breeding for tolerance and/or resistance is difficult because most diseases are quantitatively inherited and controlled by multiple genes (St.clair, 2010). Therefore, understanding the resistance mechanisms, identify resistant genotypes, the genetic variability, magnitude of heritability estimates, and the association with the agronomic traits play a vital role in the success of breeding programs (St.clair, 2010; Myint et al., 2020).

The conventional and mutation breeding methods have focused on germplasm characterization and recommendation (Teklu et al., 2022). Bedawy & Moharm (2019) found highly significantly differences among eighty-six sesame genotypes for resistance to charcoal rot disease. Mahdy (2021) noted significant decrease in the infection of *Macrophomina phaseolina* after two cycles of pedigree selection under artificial infection. Therefore, the objective of the current study was to improve high seed-yielding lines of sesame tolerant to charcoal rot disease through the pedigree selection method.

Materials and Methods

Plant material and the experimental design
The current study was conducted at Faculty of Agriculture Farm, Assiut University (Longitude:

31.125 N, Latitude: 27.25 E, Elevation :45m/148 Feet) during the three successive summer seasons of 2016-2018. A population of sesame (*Sesamum indicum* L.) in the F_3- generation (stemmed from crossing between the cultivar Shandaweel 3 and the introduction 688) was provided by Oil Crops Research Department, Agriculture Research Center. Before applying selection in the F_2 generation, the population was subjected to the artificial infection of *Macrophomina phaseolina* (Tassi) Goid, in the field. The experiment in the F_3, F_4 and F_5 generation was laid out in randomized complete block design (RCBD) with three replications. The details of growing seasons and planting dates can be found in Mahdy et al. (2021).

Isolation and preparation of Macrophomina phaseolina (Tassi) Goid
The preparation and isolation of the *Macrophomina phaseolina* (Tassi) Goid fungus was done according to Booth (1971), and Mahmoud (2016) (See Mahdy et al., 2021).

Season 2016; F_3- generation
Seeds of the F_3- families along with the parents were sown on April 21st 2016 in rows, 4.0 m long and 10 cm between hills. The experimental unit was one row for each family of the population and five rows for each the parents. After full emergence, seedlings were thinned to one plant per hill. The recommended cultural practices for sesame production were adopted throughout the three growing seasons. The number of families was 200. At harvest, the total survival families were 185. Data were recorded on ten random plants from each family in each replication for days to 50% flowering, plant height (PH, cm), height to the first capsule cm (HFC, cm), length of the fruiting zone (LFZ, cm), number of capsules/ plant (NC/P), seed yield/ plant (SY/P, g), 1000-seed weight (SW, g), seed oil% (according to A.O.A.C., 1980) and infection% (Inf%) (the wilted plants were recorded at seedling stage and at harvest). The selection criteria were days to 50% flowering, days to 50% flowering restricted by SY/P (the earliest families that gave SY/P not less than the average of the families), LFZ, LFZ restricted by HFC, 1000-seed weight, SY/P, seed oil%, seed oil% restricted by SY/P. At harvest, the best survival plant from each of the top 10 families based on yield was saved for the next season.

Season 2017, F₄- generation

The ten selected plants tolerant to *M. phaseolina* for each selection criterion were evaluated along with the parents in the field under artificial infection as in the previous season. Sowing date was July 7ᵗʰ 2017. At the end of the season, seeds of the top 4 plants for each selection criterion were saved.

Season 2018, F5- generation

The selected tolerant families to *M. phaseolina* along with the parents were evaluated in the field under artificial infection as in the previous season. Sowing date was July 7ᵗʰ 2018.

Statistical analysis

The two-way analysis of variance (randomized complete block design; RCBD) for the F_3, F_4, and F_5 generations, 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. Broad sense heritability (H%) was calculated as $(\sigma^2_g / \sigma^2_p) \times 100$, narrow sense heritability in (h²) was calculated as Smith & Kinman (1965). Expected genetic gain in the $F_3 = k \sigma_p H$ was estimated based on 10% selection intensity (Falconer, 1989). The phenotypic and genotypic coefficients of variation were estimated. 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. Genotypic and phenotypic correlations were estimated according to Miller et al. (1958).

Results and Discussion

Description of the base population; season 2016 (F₃- generation)

Means and variances

The analysis of variance revealed highly significant differences among all entries for all the investigated traits (Table 1). The phenotypic (PCV) and genotypic (GCV) coefficients of variability indicated that the low variability was recorded for days to 50% flowering. However, high GCV's were obtained for the other traits. These results are in line with those reported by many authors through evaluation of sesame genotypes. Kalaiyarasi et al. (2019) recorded high PCV and GCV% for seed yield per plant (26.95 and 26.82) and number of capsules per plant (24.94 and 24.84), respectively. Kehie et al. (2020) observed highest genotypic coefficient of

variation for seed yield/plant (53.65%), while the highest phenotypic coefficient of variation was recorded for the stem height from base to first branch (77.75%). Patidar et al. (2020) indicated that seed yield (kg/ha) showed moderate level of GCV and PCV. Also, Shammoro et al. (2020) and Saravanan et al. (2020) found high GCV and PCV% for seed yield and contributing traits.

Estimates of broad sense heritability were very high and ranged from 0.79 to 1.0. These estimates of heritability are considered biased upward, because the evaluation in one location for one season inflated families mean squares by the confounding effects of the interactions of families with locations and years. Furthermore, the maximum and minimum values in the F_3-generation which located outside the parental means indicated to the feasibility of selection for all traits. These results are in line with those reported by Aladji et al. (2014), Ismail et al. (2014), Fazal et al. (2015), Mahdy et al. (2015b) and Patil & Lokesha (2018). Kanak & Rajani (2016) recorded high heritability and genetic advance in percentage of the mean for seed yield per plant (97.5, 6.83%) followed by number of capsules per plant (96.6, 1.72%) indicating that selection could be effective for improvement these characters.

Genotypic and phenotypic correlations in the base populations (F₃-generation)

Days to 50% flowering showed weak and negligible correlations with all traits, negative with PH, HCF, NC/P and SY/P at both of genotypic and phenotypic levels, while it was positive with LFZ, 1000SW and infection% at harvest (Table 2). This indicates that the later flowering families had long fruiting zone and high infection%. However, such weak correlations with 50% flowering will not be an obstacle in improving SY/P or any favorable trait. Plant height showed positive correlations with HFC, LFZ, SY/P, and NC/P at genotypic and phenotypic levels and negative correlations with infection%. Tall plants gave large NC/P, long FZ, high yielding ability and low infection%. Number of capsules /plant gave sizeable genotypic (0.52) and phenotypic (0.49) correlations with SY/P. Height to first capsule gave negative weak correlations with LFZ and SY/P, and positive with PH at genotypic and phenotypic levels, indicating that to improve seed yield in these materials multiple traits selection including PH, LFZ, NC/P and HFC must be considered. These results are in

line with those noted by Ramprasad et al. (2019), Disowja et al. (2020) and Saravanan et al. (2020). Negative genetic correlations between days to 50% flowering (-0.463**), plant height (-0.010), single plant yield and oil content were reported by Kiruthika et al. (2020). Patidar et al. (2020) indicated that the direct effect of number of seeds/capsule (0.661) on seed yield (kg/ha) was positive and highly significant followed by number of capsules/plant (0.524), oil content (0.181) and 1000 seed weight (0.117).

Evaluation of the second cycle selection, season 2018 under artificial infection by M. phaseolina
    Variability and heritability estimates
    The analysis of variance revealed significant differences among the tested entries for the eight selection criteria after two cycles of selection (Table 3). This result indicates the presence of

sufficient vitiation in these selection criteria for further cycles of selection. The remained variability after selection expressed as GCV and PCV could be considered low for all traits except for SY/P, LFZ, and LFZ restricted by yield (Table 4). The low values of both GCV% and PCV% for oil% and 1000 SW indicates the inability to select for these traits again. Similar results were obtained by Mahdy et al. (2021). It worth to mention that the variation in the 5th generation was declined for LFZ, SY/P and oil%, compared to those in the base population. Saravanan et al. (2020) reported PCV and GCV% for yield/plant of 68.97 and 45.68%, respectively. Also, Iqbal et al. (2016) recorded GCV% and PCV% of 26.11 and 26.30, respectively for yield per plant. Our results are in harmony with those obtained by Aladji et al. (2014), Bharathi et al. (2014) and Mahdy et al. (2015a, b).

TABLE 1. Mean squares, broad sense heritability (H), genotypic (GCV %) and phenotypic (PCV %) coefficients of variability of the families in the F_3-generation season 2016, F_3- mean, parental means, maximum (Max) and minimum (Min) values under artificial infection by *Macrophomina phaseolina* (Tassi) Goid

S.V.	d.f	50% FLOW.	PH; cm	HFC; cm	LFZ; cm	NC/P	SY/P; g	1000SW	OIL%	INF% at harvest
Reps	2	2.88	481.0	129.19	1023.5	153600.0	160.20	0.12	0.81	83.38
Entries	186	38.87**	1265.4**	395.5**	1068.8**	105416**	2591.4**	6535**	80.37**	222.8**
Error	372	0.59	87.72	83.36	102.36	19307.66	131.42	0.13	0.59	5.53
PCV%		5.84	13.13	28.58	16.24	43.46	54.95	906.26	9.74	12.55
GCV%		5.79	12.67	25.39	15.44	39.28	53.53	906.26	9.71	12.39
H		0.98	0.93	0.79	0.90	0.82	0.95	1.00	0.99	0.98
F_3-Mean		61.68	156.41	40.18	116.23	431.29	53.49	5.15	53.12	68.67
Max		76.67	208.33	90.00	165.00	1120.3	211.67	6.57	65.67	80.00
Min		54.00	98.33	15.00	65.00	63.50	6.78	4.35	37.00	22.50
GA		6.24	33.64	15.95	30.04	269.49	49.10	82.14	9.04	14.79
GA/mean*100		10.12	21.51	39.69	25.84	62.48	91.80	1595.0	17.02	21.54
Mean Shandaweel 3		63.00	148.33	53.33	95.00	414.00	47.38	5.44	54.00	40.00
Mean Int 688		63.00	111.67	26.67	85.00	443.67	50.82	5.35	60.67	60.00

*, **, significant at 0.05 and 0.01 levels of probability; respectively. GA= expected genetic advance from selection 10% superior families, 50% flow= days to 50% flowering, PH= plant height, HFC= height to first capsule, LFZ= length of fruiting zone, NC/P= number of capsules/plant, SY/P= seed yield/plant, 1000SW=1000 seed weight, INF%= infection %.

TABLE 2. Genotypic (above) and phenotypic (below diagonal) correlation coefficients among the traits in the F$_3$-generation under artificial infection by *Macrophomina phaseolina* (Tassi) Goid fungus

Traits	50% FLOW	PH, cm	HFC, cm	LFZ, cm	NC/P	SY/P, g	1000SW	OIL%	INF% at harvest
50% Flow	-	-0.05	-0.12	0.01	-0.07	-0.27	0.07	-0.06	0.12
PH, cm	-0.05	-	0.43	0.86	0.29	0.16	-0.04	0.05	-0.18
HFC, cm	-0.10	0.42	-	-0.09	0.02	-0.04	-0.06	0.10	-0.19
LFZ, cm	0.01	0.83	-0.15	-	0.31	0.20	0.00	0.00	-0.09
NC/P	-0.07	0.26	0.04	0.26	-	0.52	-0.03	-0.02	-0.14
SY/P, g	-0.26	0.15	-0.03	0.18	0.49	-	0.05	0.14	-0.06
1000SW	0.06	-0.03	-0.05	0.00	-0.02	0.04	-	0.16	-0.08
OIL%	-0.06	0.05	0.09	0.00	-0.02	0.14	0.14	-	-0.13
INF% at harvest	0.12	-0.17	-0.16	-0.09	-0.12	-0.05	-0.07	-0.13	-

50% flow= days to 50% flowering, PH= plant height, HFC= height to first capsule, LFZ= length of fruiting zone, NC/P= number of capsules/plant, SY/P= seed yield/plant, 1000SW=1000 seed weight, INF%= infection %.

TABLE 3. Mean squares of the selected families for the eight selection criteria in the F$_5$-generation, season 2018 under artificial infection by *Macrophomina phaseolina* (Tassi) Goid

Population									
				Mean squares of the selection criteria					
S.V.	d.f	50% flow	50% Flow. restricted by yield	Seed yield/ plant	Oil%	Oil% restricted by yield	LFZ	LFZ restricted by HFC	1000 SW
Reps	2	0.67	0.06	40.83	0.16	1.056	68.06	104.14	0.004
Entries	5	49.70**	49.42**	370.98**	39.20**	12.456**	318.06**	733.33**	0.05*
Error	10	1.067	1.06	3.24	0.77	0.856	6.39	12.49	0.02

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

High estimates of heritability in broad sense were observed for the selection criteria and ranged from 71.15% (1000 SW) to 99.13% (seed yield/ plant) (Table 4). These high estimates of heritability could be considered unreliable because the evaluation for one season and one location inflated the mean squares of families by the confounding effects of the interactions of families with years and locations. Otherwise, heritability estimates in narrow sense in most of selection criteria were increased from F$_3$ to F$_5$ generations. It is well known that heritability increased with increasing homozygosity. In contrast, LFZ and Oil% restricted by yield showed remarkable decrease in narrow-sense heritability values when it estimated by regression of F$_4$ on F$_3$ compared to regression of F$_5$ on F$_4$ generation. Such low variability in the F$_5$ may not allow further cycles of selection. Interestingly, Mahdy et al. (2021) estimated high values of heritability in broad sense for the same selection criteria of the same genetic materials which evaluated for resistance to *Fusarium*

oxysporum f. sp. *sesame.* Fazal et al. (2015) and Mahdy et al. (2015b) estimated high values of heritability in the broad sense of 89.20% for days to flowering and 89.16% for days to maturity, while days to first flower showed 94.86% after two cycles of selection in the two populations. Mohanty et al. (2020) reported a range in heritability from 25.0 to 47.11% for oil% with GCV of 15.37% and PCV of 15.44%. Singh et al. (2018) noted PCV of 7.03% and GCV of 2.82% and heritability in broad sense of 88.40% for oil%. Prithviraj & Parameshwarappa (2017) noted GCV (3.19%) and PCV (3.32%) and heritability of 92.20% for oil%.

Means and direct observed genetic gain in days to 50% flowering

After the second cycle selection (F$_5$), the direct genetic response in days to 50% flowering was significant from the mid-parent (-1.74%) followed by positive significant (P≤0.05) correlated gain in HFC of 8.33% from the mid-parent and 13.04% from the better parent (Table

5a). Positive correlated gains from the mid-parent were also found for NC/P and SY/P. Otherwise, significant (p≤0.05 or p≤0.01) negative correlated gains were recorded for 1000SW and oil%. The infection % was significant (p ≤0.01) decreased from both of the mid- parent (-6.87%) and better – parent (-5.18%). The best selected family showed significant (p ≤0.01) observed genetic gain in SY/P from the better parent of 19.37%. Mahdy et al. (2015b) found that the observed gain in days to first flower was significant (p≤0.01) and reached -35.31 and -34.06% in pop1, and 37.18 and -9.75% in pop2 from the unselected bulk sample and the better parent; respectively.

Means and direct observed genetic gain in days to 50% flowering restricted by yield

The inclusion of seed yield as a restricted trait with days to 50% flowering was better than selection or days to 50% flowering *per se*. It led to a significant (p≤0.01) increase in yield (reached 39.76% from the mid-parent and 34.43% from the better parent), number of capsules, plant height and a desirable decrease in infection rate. However, it accompanied by an undesirable increase in the height of the first capsule. The best selected family (39.25g/plant) showed significant (p≤0.01) increase in SY/P from the better parent (Table 5a).

Mahdy (2021) reported that selection for earliness in pop1 caused deleterious effects in NC/ and favorable decreased the infection % in two populations. Mahdy et al. (2015b) concluded that two cycles of pedigree selection were enough to detect the early families and could be practiced in the early segregating generations.

Means and direct observed gain in seed yield/ plant

Mean seed yield/ plant was 24.60 g compared to 15.16 and 16.42g for the two parents (Table 5a).

The direct significant (P≤0.01) observed genetic gain in SY/P reached 55.80% from the mid-parent and 49.86% from the better parent. The increase in yield followed by significant decrease in correlated gains in days to 50% flowering (-6.23 and -5.41%), in HFC (-10.42 and -6.52%), in 1000SW (-6.13 and -8.86%), oil% (4.68 and -7.91%) and infection % at harvest (-3.31 and -1.56) from the mid and better parent, respectively. It could be noticed that pedigree selection for SY/P accompanied with favorable decrease in days to 50% flowering, HFC, and infection% at harvest, and adversely affected oil%, and 1000SW. It is the main drawback of single trait selection. These results are in line with those found by Ismail et al. (2014), Mahdy et al. (2015a, b), Abd-ElAziz (2018), and Mahdy (2021).

Means and direct observed genetic gain in oil%

After two cycles of selection, mean selected families of oil% was 63.0% compared to 55.00 and 59.00% for the two parents (Table 5a). The genetic direct observed gain in oil% was significant (P≤ 0.01) from the mid-parent (10.53%) and from the better parent (6.78%). Selection for oil% accompanied with significant delay in flowering, increase in HFC and decrease in 1000SW. Otherwise, selection for oil% showed significant observed correlated gain from the mid and better parent of 36.67 and 30.16% for PH, 36.11 and 22.50% for LFZ, 38.36 and 13.64% for NC/P, 45.67 and 40.12% for SY/P, -9.87 and -15.97 and -14.45% for infection% at harvest, respectively. Baydar et al. (1999) and Baydar (2005) succeeded to isolate sesame lines high in oil content using line selection method in a segregating population of sesame. Mohanty et al. (2020) reported high to moderate genetic advance in percentage of the mean for 1000 seed weight, oil content%, oil yield/plant and seed yield/ plant.

TABLE 4. Genotypic (GCV%), phenotypic coefficients of variability (PCV%), heritability in broad (H%) and in narrow sense (h²) for the selection criteria in the F₅- generation

Selection criterion	GCV%	PCV%	H%	$h^2(F_5/F_4)$	$h^2(F_4/F_3)$
50% Flowering	7.13	7.20	97.85	0.5471	0.0085
50% Flow. restricted by yield	7.10	7.17	97.86	0.9550	0.7491
Seed yield/plant	45.01	45.21	99.13	0.3623	0.0379
Oil%	5.68	5.74	98.04	0.7109	0.3391
Oil% restricted by yield	3.28	3.40	93.13	0.0990	0.6493
LFZ	13.98	14.12	97.99	0.2824	0.4920
LFZ restricted by HFC	18.79	18.95	98.30	0.8533	0.7702
1000 SW	2.04	2.42	71.15	0.3723	0.2710

LFZ=length of fruiting zone. 1000 SW= 1000 seed weight.

TABLE 5a. Selected family means (C2 mean), the best family (B. fam), observed gain from the mid-parent (GA-MP%) and better parent (GA-BP%) for 50% Flow, 50% Flow restricted by yield, seed yield/plant and oil% as selection criteria and correlated traits in the F5- generation under artificial infection by *Macrophomina phaseolina* (Tassi) Goid

Sel. criterion	Fam. No.	Item	50% Flow	PH; cm	HCF; cm	LFZ; cm	NC/P	SY/P; g	1000SW; g	Oil%	INF% at harvest
50% Flow	73	B. fam	64.00	100.00	55.00	45.00	142.32	19.37††	4.80	60.00	71.59
		C2 mean	56.50	104.58	43.33	61.25	82.25	16.82	4.99	56.00	67.88
		GA-MP%	-1.74*	4.58	8.33**	2.08	20.65*	6.55*	-7.73**	-1.75*	-6.87**
		GA-BP%	-0.88	-0.40	13.04**	-8.13	-0.91	2.49	-10.41**	-5.09**	-5.18**
50% FLOW R by yield	19	B. fam.	56.33	145.00††	41.67	103.33††	58.34	39.25††	4.92	52.00	74.18
		C2 mean	56.58	117.08	45.42	71.67	88.25	22.07	5.01	56.00	69.09
		GA-MP%	-1.59*	17.08**	13.54**	19.44**	29.46**	39.76**	-7.39**	-1.75*	-5.20**
		GA-BP%	-0.73	11.51	18.48**	7.50	6.32	34.43**	-10.08**	-5.09**	-3.48**
SY/P	19	B. fam.	56.33	145.00††	41.67	103.33††	58.34	39.25††	4.92	52.00	74.18
		C2 mean	53.92	118.33	35.83	82.50	61.33	24.60	5.07	54.33	70.47
		GA-MP%	-6.23**	18.33**	-10.42**	37.50**	10.03**	55.80**	-6.13**	-2.70**	-3.31**
		GA-BP%	-5.41**	12.70*	-6.52	23.75**	6.11	49.86**	-8.86**	-2.28**	-1.56
Oil%	72	B. fam.	56.00	145.00††	65.00	80.00††	98.19**	37.60††	5.36	64.00††	61.71
		C2 mean	60.25	136.67	55.00	81.67	94.32	23.00	5.36	63.00	61.24
		GA-MP%	4.78**	36.67**	37.50**	36.11**	38.36**	45.67**	-0.75**	10.53**	-15.97**
		GA-BP%	5.70**	30.16**	43.48**	22.50**	13.64	40.12**	-3.64**	6.78**	-14.45**
Shandaweel 3			57.00	105.00	38.33	66.67	53.33	16.42	5.57	3.93	55.00
Introduction 688			58.00	95.00	41.67	53.33	83.00	15.16	5.24	3.90	59.00

*, **, significant at 0.05 and 0.01 levels of probability; respectively; 50% flow=days to 50% flowering, PH=plant height, HFC=height to first capsule, LFZ=length of fruiting zone, NC/P=number of capsules/plant, SY/P=seed yield/plant, 1000SW=1000 seed weight, INF%= infection %, †† significant at 0.01 level of probability from the better parent.

Means and observed genetic gain in seed oil% restricted by seed yield/ plant

Mean oil% of the selected families was 59.92%, and 26.87% for SY/P. The selected families for oil% after two cycles of selection were homogeneous (Table 5b). After two cycles of pedigree selection for oil% restricted by seed yield, the observed direct genetic gains in oil% were 5.12%** and 1.55%, while they were 70.16%** and 63.67%** for SY/P from the mid- and better parent, respectively, accompanied by significant (p≤0.01) increase of 34.58 and 28.18% for PH, 44.79 and 51.09% for HFC, 27.78 and 15.00% for LFZ, 69.54 and 39.24% for NC/P and favorable decrease in infection% of -14.53 and -12.98% at harvest from both the mid- and better parent, respectively. Selection caused significant (p≤0.01) decrease in 1000SW. Inclusion of SY/P as a restricted selection for oil% significant (p≤0.01) increase SY/P, LFZ, and NC/P. It is worth noting that the selection oil% gave the best reduction in the infection% of *Macrophomina.* Singh et al. (2018) estimated the expected genetic advance in seed oil% of 12.81%. Mohanty et al. (2020) estimated also the expected genetic from the mean for oil% of 31.50%.

Means and direct observed gain in length of the fruiting zone

Mean LFZ of the selected families after the second cycle was 72.92 cm (Table 5b). The direct observed genetic gain was 21.53%** from the mid-parent and 9.38%** from the better parent. The favorable correlated gains were 13.33%** and 7.94%** for PH, 9.73%** and 5.55% for SY/P, and favorable decrease in infection % of -9.00** and -7.36** from the mid-and better parent, respectively. Otherwise, selection for LFZ significantly (p≤0.01) decreased 1000SW and oil%. This could be due to the positive genotypic correlation of LFZ with PH and SY/P and negative with 1000SW in the base population (Table2). These results are in harmony with those reported by Mahdy et al. (2021).

Means and direct observed gain in LFZ restricted by HFC

Mean selected families was 82.50 cm for LFZ and 46.67cm for HCF (Table 5b). After two cycles of pedigree selection for LFZ restricted by HCF the observed direct genetic gain in LFZ was 37.50**, and 23.75**, 16.67** and 21.74**for HFC from the mid- and better parent, respectively, accompanied by significant increase

of 29.17** and 23.02**% for PH and decrease infection% of -11.59** and -9.99** at harvest from both the mid- and better parent, respectively. Selection caused significant (P≤0.01) decrease in 1000SW and oil%. Mahdy et al. (2021) found that selection for LFZ restricted by HFC under artificial infection of *Fusarium* accompanied by favorable increase from the mid-parent in PH (9.86%*), NC/P (58.89%**), SY/P (19.35%**), and 1000- SW (1.46%**).

Means and direct observed gain in 1000-seed weight

Mean 1000SW of the selected families was 5.43g (Table 5b). After two cycles of pedigree selection for 1000SW the observed direct genetic gain in 1000SW was 0.52**, and -2.40** from the mid- and better parent, respectively, accompanied with significant increase of 44.17 and 37.30**% for PH, 4.78** and 5.70**in 50% flowering, 29.17** and 34.78**for HFC, 54.17** and 38.75** for LFZ,113.42** and75.28** for NC/P,62.14** and 55.96**for SY/P, and significant decrease of -9.14** and 7.49%** for infection % at harvest from the mid and better parent, respectively. These results were in line with those obtained by Mahdy et al. (2021). Mohanty et al. (2020) reported high to moderate genetic advance in percentage of the mean for 1000 seed weight, oil content%, oil yield/plant and seed yield/ plant.

Comparison between the eight selection methods under artificial infection of Macrophomina phaseolina (Tassi) Goid

Looking at the results in Tables 5a and b and Fig. 1, we could observe that two cycles of selection for days to 50% flowering improved earliness from the mid-parent (-1.74*) followed by significantly improve in the correlated traits, HFC (8.33%**), NC/P (20.65%*-*), SY/P (6.55%**) and INF% at harvest (-6.87%) . This could be due to negative correlation between these traits and days to 50% flowering in the base population (Table 2). However, negative significant decrease was obtained in 1000SW (-7.73%**) and oil% (-1.75%*). Otherwise, the best improvement in days to 50% flowering (-6.23%**) was obtained from selection for SY/P because of the negative genotypic correlation between them in the base population. Pedigree selection is an efficient method to improve selection criterion (Mahdy et al. 2015a, b).

TABLE 5b. Selected family means (C2 mean), the best family (B. fam), observed gain from the mid-parent (GA-MP%) and better parent (GA-BP%) for oil% restricted by yield, length of fruiting zone, length of fruiting zone restricted by height of first capsule, and 1000 seed weight as selection criteria and correlated traits in the F5– generation under artificial infection by *Macrophomina phaseolina* (Tassi) Goid.

Sel. criterion	Fam. No.	Item	50% Flow	PH, cm	HCF; cm	LFZ; cm	NC/P	SY/P; g	1000SW, g	Oil%	INF% at harvest
Oil% R. by yield	128	B. fam	59.00	146.67 ††	55.00	91.67 ††	106.33 ††	31.90 ††	5.13	60.67 †	59.19 ††
		C2 mean	58.25	134.58	57.92	76.67	115.57	26.87	4.95	59.92	62.29
		GA-MP%	1.30	34.58**	44.79**	27.78**	69.54**	70.16**	-8.50**	5.12**	-14.53**
		GA-BP%	2.19*	28.18**	51.09**	15.00**	39.24	63.67**	-11.15	1.55	-12.98**
LFZ	21	B. fam.	60.00	130.00 ††	48.33	81.67 ††	79.69**	24.94 ††	4.53	57.00	69.31
		C2 mean	57.58	113.33	40.42	72.92	63.31	17.33	5.13	48.92	66.32
		GA-MP%	0.15	13.33**	1.04	21.53**	-7.13**	9.73**	-5.07**	-14.18**	-9.00**
		GA-BP%	1.02	7.94**	5.44	9.38*	-23.72*	5.55	-7.83**	-17.09**	-7.36**
LFZ R by HFC	21	B. fam.	60.00	130.00 ††	48.33	81.67 ††	79.69**	24.94 ††	4.53	57.00	69.31
		C2 mean	56.17	129.17	46.67	82.50	66.07	16.41	5.10	51.25	64.44
		GA-MP%	-2.32**	29.17**	16.67**	37.50**	-3.08	3.95	-5.63**	-10.09**	-11.59**
		GA-BP%	-1.46	23.02**	21.74**	23.75**	-20.40	-0.02	-8.38**	-13.14**	-9.99**
1000 SW	296	B. fam.	58.00	156.67 ††	45.00	111.67 ††	135.51 ††	31.24 ††	5.40	58.00	59.19 ††
		C2 mean	60.25	144.17	51.67	92.50	145.48	25.60	5.43	54.50	66.22
		GA-MP%	4.78**	44.17**	29.17**	54.17**	113.42**	62.14**	0.52**	-4.39**	-9.14**
		GA-BP%	5.70**	37.30**	34.78**	38.75**	75.28**	55.96**	-2.40**	-7.63**	-7.49**
Shandaweel 3			57.00	105.00	38.33	66.67	53.33	16.42	5.57	3.93	55.00
Introduction 688			58.00	95.00	41.67	53.33	83.00	15.16	5.24	3.90	59.00

*, **, significant at 0.05 and 0.01 levels of probability; respectively; 50% flow= days to 50% flowering, R= restricted, PH= plant height, HFC=height to first capsule, LFZ=length of fruiting zone, NC/P=number of capsules/plant, SY/P=seed yield/plant, 1000SW= 1000 seed weight, INF%= infection %, †† significant at 0.01 level of probability from the better parent.
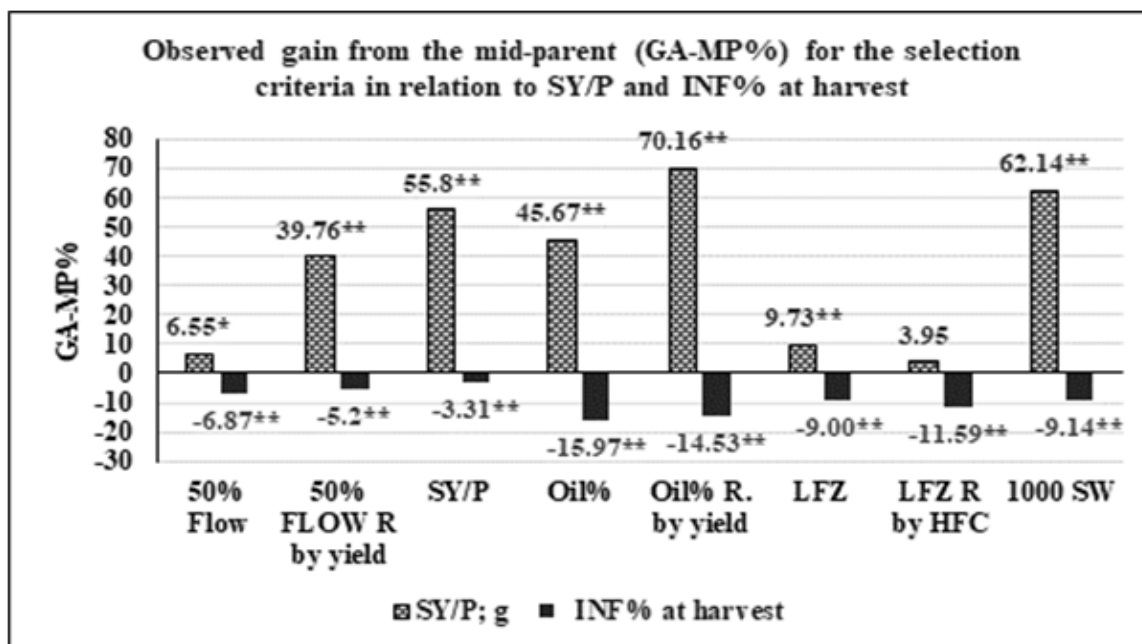
Fig. 1. Observed gain from the mid-parent (GA-MP%) for the selection criteria in relation to SY/P and INF% at harvest

Selection for days to 50% flowering restricted by SY/P, reduced the improvement of 50% flowering and increase SY/P (39.76%**) compared to selection for days to 50% flowering per se. Mostly, all the characters showed positive correlation with SY/P in the base population were improved. The correlated gains measured from the mid-parent were 17.08%** (PH), 13.54%** (HFC), 19.44%** (LFZ), and 29.46%** (NC/P). Otherwise, negative reduction was obtained in 1000SW (-7.39%**) and -1.75% (oil%). This means that incorporation of valuable trait with the selection criterion improved genetic gain. The direct observed genetic gain from selection for SY/P was positive from both of mid-parent (55.80%**) and better parent (49.86%**). The observed correlated gain from the mid-parent was favorable in days to 50% flowering (-6.23%**), 18.33** in plant height, -10.42%** in HFC, 37.50%** in LFZ and -3.31**for INF%. The other correlated traits gave negative unfavorable gains.

The direct observed genetic gain from selection for oil% was positive from both of mid-parent (10.53%**) and better parent (6.78%**). The observed correlated gain from the mid-parent was unfavorable in days to 50% flowering (4.78**), and (37.50**) in HFC, and favorable in PH (36.67%**), LFZ (36.11%**), NC/P (38.36%**) and INF% at harvest (-15.97%**).

The other correlated traits gave negative unfavorable gains. Selection for oil% restricted by SY/P gave direct observed genetic gain from the better parent of 5.12%** (lower than selection for oil% per se), and 70.16%** for SY/P. Favorable correlated gains were obtained in PH (34.58%**), LFZ (27.78%**), NC/P (69.54%**), and INF% at harvest (-14.53%**). The other correlated traits gave unfavorable gains. Selection for LFZ gave direct observed genetic gain from the mid-parent of 21.53%** and 9.38%** from the better parent. Favorable correlated gains from the mid-parent were obtained in PH (13.33%**), SY/P (9.73%**) and INF% at harvest (-9.00%**). The other correlated traits gave unfavorable gains from selection. Selection for LFZ restricted by HFC increased LFZ by 37.50%** from the mid-parent and 23.75%** from the better parent, followed by unfavorable increase in HFC. Selection for LFZ only was better than selection for LFZ restricted by HFC.

Direct selection for 1000SW slightly increased seed weight, while it gave sizeable favorable correlated gains from the mid-parent in SY/P (62.34%**), PH (44.17%**), LFZ (54.17%**), NC/P (113.42%**) and INF% at harvest (-9.14%**). The other correlated traits were adversely affected. Ismail et al. (2014) improved SY/P by 46.68% of the better parent after two cycles of selection. Mahdy et al. (2015a)

noted direct observed gain in SY/P after two cycles of selection -56.71 and -56.17% for height to first capsule, 43.21 and 81.52 % for number of capsules/plant and 30.68 and 45.18% for seed yield from the better parent for population 1 and 2; respectively. Mahdy et al. (2015b) found significant (P≤0.01) observed gain in days to first flower of -35.31 and -34.06% in pop1, and 37.18 and -9.75% in pop2 from the unselected bulk sample and the better parent; respectively after two cycles of selection.

Conclusion

It could be concluded that single trait selection was an efficient method to improve selection criterion, but it had adverse effect on some correlated traits. Moreover, selection for days to 50% flowering improved earliness, but it was better if it restricted by SY/P. Additionally, selection for oil% restricted by yield gave the best improvement from the mid-parent in SY/P (70.16%**) followed by Selection for 1000SW (62.14%**), SY/P per se (55.80%**) and selection for days to 50% flowering restricted by yield (39.76%**). Inclusion of a trait as independent culling level improve the efficiency of selection. Therefore, selection index incorporating favorable traits is recommended. The correlation coefficients among traits help the breeder to select for few favorable traits. The eight different methods of pedigree selection decreased the infection% at harvest ranged from -3.31%** to -15.45%** from the mid-parent.

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الأنتخاب المنسب لتحسين صفتي محصول البذور وتحمل السمسم لفطر ماكروفومينا فاصولينا (تاسي) جويد

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يعد مرض التعفن الفحمي والمتسبب عن فطر ماكروفومينا فاصولينا (تاسي) جويد هو الأكثر تدميراً وفتكاً من بين المسببات المرضية الأخرى لإنتاج السمسم في مصر والعالم. وتهدف الدراسة الحالية إلي تطوير سلالات من السمسم عالية الأنتاجية لمحصول البذور ومتحملة للعفن الفحمي من خلال دورتين من الأنتخاب المنسب لثمانية صفات انتخابية تحت ظروف العدوى الصناعية. أحتوت العشيرة القاعدية على 185 عائلة في الجيل الثالث. كانت درجة التوريث بمعناها الواسع عالية جداً وتراوحت بين 0.79 إلى 1. وقد أعطت النباتات الطويلة أكبر عدد من الكبسولات للنبات الفردي, أطول منطقة ثمرية, قدرة محصولية عالية ومعدل إصابة منخفض بالنسبة للفطر ماكروفومينا. وأرتبطت صفة عدد الكبسولات للنبات الفردي وراثياً (0.52) ومظهرياً (0.49) بمحصول البذور للنبات الفردي. بعد الدورة الأنتخابية الثانية، لوحظ إختلافات عالية المعنوية للصفات الأنتخابية الثمانية وكان الانتخاب للصفة المفردة كان فعالاً في تحسين الصفة. إضافة إلى ذلك، أدى الأنتخاب لصفة عدد الأيام حتى 50% تزهير إلى تحسين التبكير ولكنه كان أفضل عندما كان مقيداً بمحصول البذور. أدى الأنتخاب لنسبة الزيت والمقيد بمحصول البذور إلى تحسين نسبة الزيت مقارنة بمتوسط الأباء بالنسبة لمحصول البذور (70.16%**) تلاه الأنتخاب لصفة وزن الألف بذرة (62.14%**) و محصول البذور (55.80%**) ثم الأنتخاب لعدد الأيام حتى 50% تزهير المقيد بالمحصول (39.76%**). وجد أن إدخال صفة مقيدة إضافية إلى الصفة الانتخابية أدى إلى تحسين كفاءة الأنتخاب. لذلك ، يوصى باستخدام دليل انتخابي يشتمل على الصفات المرغوبة. وقد قللت الطرق الأنتخابية الثمان نسبة الإصابة بالفطر عند الحصاد بنسب تراوحت بين -3.31% إلى 15.45% عن متوسط الآباء.