RESEARCH ARTICLE

Pedigree selection in sesame under artificial infection of *Fusarium oxysporum* f. sp. sesami

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Abstract

Fusarium is one of the most dangerous fungal diseases that cause great loss of the sesame yield worldwide. The present work aimed to improve tolerance and/or resistance to *Fusarium* through two cycles of pedigree selection on sesame population for eight selection criteria started in the F_3-generation. Genotypic coefficient of variability in the F_3 varied from 4.34% for days to 50% flowering to 38.15% for seed yield (SY/P). Days to 50% flowering showed negative correlations with all traits except height to first capsule (HFC). Height to first capsule was negatively correlated with length of fruiting zone (LFZ), 1000-SW, oil% and infection%, and positively correlated with capsules/plant (NC/P) and SY/P. Single trait selection was an efficient method to improve selection criterion, but it caused adverse effects on some correlated traits. Selection for days to 50% flowering improved earliness, but it was better in improving yield if the selection was restricted by SY/P. Selection for oil% restricted by yield was better in improving yield than selection for oil% per se. Therefore, the inclusion of a trait as independent culling level improved the efficiency of selection. The best genetic gain in SY/P in percentage from the mid-parent was obtained from selection for days to 50% flowering restricted by SY/P (35.56**), LFZ restricted by HFC (19.53**), days to 50% flowering (19.32**), oil% restricted by SY/P (19.02**), SY/P (17.38**), 1000 SW (14.09**) and LFZ (14.032**). Therefore, selection index incorporating favorable trait is recommended.

Keywords: Sesame; *Fusarium oxysporum*; Pedigree selection; Genotypic correlation; Observed gain.

1. Introduction

Sesame (*Sesamum indicum* L., belongs to family *Pedaliaceae*) is one of the most ancient oilseed crops known to mankind (Nayar, 1984; Bedigian and Harlan, 1986). Its cultivation goes back to 2130 B.C.(Weiss, 1983). It is cultivated in the tropical and subtropical regions of the world (Ashri,1994) as a source of excellent vegetable oil, and has one of the highest oil contents (35–63%) among oil crops (Ashri, 2010; and Baydar *et al.,* 1999). The oil is very stable due to the presence of a number of antioxidants such as

sesamin, sesamolin and sesamol (Suja *et al.,* 2004). Therefore, it has a long shelf life and can be blended with less stable vegetable oils to improve their stability and longevity (Chung *et al.,* 2006). The cultivated area in the world was 11,743,382 ha in 2018. The production was 6015573t (FAO. 2019). Wherever sesame is grown, it is infected by various pathogens. *Macrophomina phaseolina* (Tassi) Goid and *Fusarium oxysporum* f. sp sesami are serious pathogens that cause root rot and wilt diseases and decrease yield. Many authors worked on evaluation and selection in sesame. Bharathi *et al. (*2014), (Iqbal, 2016) and Saravanan *et al.* (2020) indicated that the magnitude of GCV and PCV was high for seed yield per plant , number of capsules per plant and number of branches

per plant. Mahdy *et al.* (2015a) and Ismail *et al.* (2014) found slight discrepancy between GCV and PCV. Patil and Lokesha (2018) and Shammoro *et al*. (2020) came to the same conclusion.

High heritability and genetic advance in percentage of the mean was recorded for seed yield per plant and number of capsules per plant, indicating that selection could be effective for improving these characters (Abatchoua *et al.,* 2014**;** Ismail *et al.,* 2014**;** Fazal *et al.,* 2015; Mahdy *et al.,* 2015b)**.** 1000 seed weight exhibited a high heritability along with a high genetic advance in percent of the mean (Vanishree *et al.,* 2011**;** Kanak and Rajani, 2016 and Singh *et al.,* 2018)**.** Mohanty *et al.* (2020) estimated expected genetic from the mean for oil% of 31.50%. Jyothi *et al.* (2011) **s**creened 35 sesame germplasm accessions. All the accessions displayed some percent infection rate, and none could be described as immune.

Capsules/Plant showed positive significant (p≤0.01) correlation with SY/P (Mahdy *et al* 2015b, Sopundharya *et al.* 2017 and Disowja *et al.,* 2020) and days to maturity showed negative correlation with yield/plant. Patidar *et al.* (2020) reported 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).

This study aimed to improve tolerance and/or resistance of sesame to *F. oxysporum* through two cycles of pedigree selection under artificial infection in the field using one population in the F_3- generation, gather information's on variability, correlation, heritability, and genetic gain from selection.

2. Materials and methods

The present work was carried out at Fac. Agric. Farm, Assiut University during the three summer seasons of 2016-2018. The experimental site was artificially infected each

year by the pathogen *Fusarium oxysporum* f. sp. sesami.

2.1. Genetic Materials

The materials used was one population of sesame (*Sesamum indicum* L.) in the F_3-generation provided by Agriculture Research Center. This population was subjected in the F_2-generation to artificial infection in the field and selection was for resistance to *F. oxysporum.* The population stemmed from the cross Shandaweel 3/ Introduction 688. The growing seasons, planting dates, and experimental design were as follows

Season	Date	Generation	Experimental design
2016	21/4/2016	F_3	RCBD with three replications
2017	3/7/2017	F_4	RCBD with three replications
2018	3/7/2018	F_5	RCBD with three replications

2.2. Season 2016; F3- generation
2.2.1. Isolation and preparation of *Fusarium oxysporum* f. sp. sesame.

Fungus was grown on a media of Potato Dextrose Agar (PDA) which consisted of (200g potatoes, 20g dextrose, 20g agar and 1000 ml distilled water). The media was autoclaved at 120°C for 20 minutes. The media was poured in Petri dishes (9cm diameter×1.5cm) under sterilized conditions and was inoculated by the fungus under these sterilized conditions and then incubated at 25- 30°C in the dark for 15 days. Inoculum of the tested isolate was prepared by growing in sterilized glass bottles (500-ml) containing barley medium (150 g barley seeds, 4g glucose, and 200ml water) and autoclaved in two consecutive days. A7 mm disk was cut from the margin of 5-day-old actively growing culture of the isolate and placed at the barley medium and incubated at 28 ±2° for two weeks. Inoculum for the isolate was prepared by inoculating sterilized 1000 ml conical flasks containing barley medium (150 g barley+ 4g

glucose +200 ml water) with the tested fungal isolate followed by incubation at 28 ±2° for two weeks. Soil infestation was carried out by adding the inoculum of isolate to soil at the rate 2% barley medium contains fungus. Identification of the isolated fungus 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)

2.2.2. Sowing and data collection
Seeds were sown in rows, 4.0 m long and 10 cm between hills. The parents were sown each in five rows. The experimental unit was one row except for 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 along with the parents. At harvest, data were recorded on ten random survival plants for 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) , capsule length (CL, cm) , capsule width (CW, cm), number of capsules/plant (NC/P), seed yield/ plant (SY/P, g), 1000-seed weight (SW, g), seed oil% and infection% (Inf%) (the wilted plants were recorded at seedling stage and at harvest). The total survival families were 188. The selection criteria were days to 50% flowering, days to 50% flowering restricted by SY/P (the earliest families that gave SY/P that was 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.

2.3. Second season, F4- generation
The ten selected plants tolerant to *F. oxysporum* for each selection criterion were evaluated along with the parents in the field under artificial infection as in the previous season. At the end of the season, seeds of the top 5 plants for each selection criterion were saved.

2.4. Third season, F₅- generation
The selected families tolerant to *F. oxysporum* along with the parents and were evaluated in the field under artificial infection as in the previous season.

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. Heritability in broad sense (H%) = (σ^2_g / σ^2_p) ×100, and expected genetic gain=k σ_p h^2 based on 10% selection intensity was estimated as Falconer (1989)**,** heritability in narrow sense (h^2) was calculated as (Smith and Kinman, 1965)**.** 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 and the mid-parent was measured using LSD test. Genotypic and phenotypic correlations were estimated according to (Miller *et al.*, 1958)

3. Results and discussion

3.1. Description of the base populations; season of 2016 (F₃- generation)
3.1.1. Means and variances
The analysis of variance (Table1) of the morphological traits, yield, and yield components was done on the survival families (F₃- generation). Families mean squares were significant (p≤0.01) for all the studied traits in the population except capsule length and capsule width. Therefore, capsule length and width were omitted from all analyses. The phenotypic (PCV) coefficient of variability (Table1) indicated that the lowest variability was recorded for days to 50% flowering (5.37%).

However, moderate to high GCV was obtained variability varied from 4.34% for days to 50% flowering to 38.15% SY/P. These results are in line with many authors. Bharathi *et al* (2014) indicated that the magnitude of GCV and PCV, respectively, was high for seed yield per plant (47.18 and 50.26%), number of capsules per

for the other traits. Genotypic coefficient of plant (37.12 and 41.02%) and number of branches per plant (33.84 and 38.56%). (Mahdy *et al.* 2015a) found slight discrepancy between GCV and PCV. Iqbal (2016a), Patil and Lokesha, (2018) and Shammoro 2020 et al.(2020) came to the same conclusion.

Table 1. Mean squares, heritability in broad sense (H), genotypic (GCV %) and phenotypic (PCV %) coefficients of variability of the families in the F3-generation season 2016, F3- mean, parental means, maximum and minimum values under artificial infection by *F. oxysporum*

S.V.	d.f	50%flow	PH, cm	HFC, cm	LFZ, cm	NC/P	SY/P, g	1000S W	OIL%	INF% Seedling	INF% at harvest
Reps	2	0.25	974.01	40.69	1406.00	1188.00	373.25	0.10	3.00	0.81	32.88
Entries	189	33.39**	1375.54 **	324.39*	1512.90 *	62862.78**	1314.25*	0.64*	98.37*	172.13*	173.05 **
Error	378	0.349	127.83	91.32	142.68	7826.69	59.48	0.05	0.87	6.32	6.07
PCV%		5.37	12.70	22.80	18.26	36.09	39.05	9.09	10.93	16.41	10.67
GCV%		5.34	12.10	19.33	17.38	33.77	38.15	8.75	10.88	16.11	10.48
H%		98.95	90.71	71.85	90.57	87.55	95.47	92.56	99.12	96.33	96.50
F$_3$- mean		62.11	168.56	45.60	122.95	401.07	53.60	5.10	52.40	46.15	71.17
Max		76.67	208.33	83.33	178.33	1174.00	114.04	6.59	66.00	57.50	82.50
Min		54.33	105.00	26.67	55.00	121.17	6.12	4.18	25.00	25.00	50.00
GA		5.81	34.18	13.15	35.79	223.04	35.17	0.76	9.99	12.84	12.90
GA/mean*100		9.35	20.28	28.83	29.11	55.61	65.61	14.81	19.07	27.82	18.12
Mean Shandaweel 3		59.67	138.33	45.00	93.33	227.33	29.81	5.46	59.33	52.50	77.50
Mean Int688		69.33	151.67	41.67	110.00	378.00	39.60	5.34	54.00	45.00	72.50

*, **, significant at 0.05 and 0.01 levels of probability; respectively. GA=expected genetic advance from selection 10% superior families.

Heritability estimates in broad sense in the F$_3$- generation were high and ranged from 71.85 % for PH to 96.50% for infection%. 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 interaction of families with locations and years. The expected genetic advance from selection of 10% superior families in percentage of the F$_3$- generation mean ranged from 9.35% for 50% flowering to 65.61% for SY/P, it depended mainly on phenotypic variance rather than heritability. These results are in line with those reported by

Abatchoua *et al.* (2014)**,** Fazal *et al.* (2015), Ismail *et al.* (2014), Mahdy *et al.* (2015b**)** and Vanishree *et al.* (2011**).** Kanak and Rajani (2016) recorded high heritability and genetic advance in percentage of the mean for seed yield per plant (97.5 and 6.83%, respectively) followed by number of capsules per plant (96.6 and 1.72%, respectively) indicating that selection could be effective for improving these characters

The F$_3$- mean and parental means are shown in Table 1. The number of survival families that could be considered tolerant to *F. oxysporum* was 188 out of 215 families. Furthermore, the

two parents Shandaweel 3 and Introduction 688 were severely damaged by *F. oxysporum*. The maximum and minimum values in the F_3-generation survival families indicated the feasibility of selection for 50% flowering, PH, HFC. LFZ, NC/P, SY/P, 1000-SW and oil%. Family means ranged in days to 50% flowering from 54.33 to 76.67, plant height from 105.00 to 208.33 cm, height to the first capsule from 26.67 to 83.33 cm, length of the fruiting zone from 55.00 to 178.33 cm., 1000-seed weight from 4.18 to 6.59g, capsules/plant from 121.17 to 1174.00, seed yield/plant from 6.12 to 114.04g, seed oil percentage from 25.00 to 66.00%. Such wide range of variability was sufficient for selection.

3.1.2. Genotypic and phenotypic correlations in the base populations (F_3-generation)

Days to 50% flowering showed negative correlations with all traits except HFC at genotypic and phenotypic levels (Table 2), indicating that the early families had the favorable traits. Likewise, PH gave positive correlations with all traits except INF%, meaning that the tall plants were favorable in all traits. The highest correlation of PH was with LFZ (0.9120 r_g, 0.8887 r_p). Tall plants gave large NC/P, long FZ, high yielding ability and low infection%. Height to first capsule negatively correlated with LFZ, 1000 SW, oil% and INF%, and positively correlated with NC/P and SY/P, meaning that the high yielding plants with high NC/P had high first capsule. These findings recommended the use of multiple trait selection. Length of fruiting zone showed positive correlations at genotypic and phenotypic levels with NC/P, SY/P, 1000 SW and oil% and negative with INF%. Seed yield/plant gave high correlations with NC/P (r_g= 0.6324, r_p=0.6087). These findings are in line with those of many authors. Mahdy *et al.* (2015b) showed positive significant (p≤0.01) correlation of NC/P with seed yield/plant in two populations (0.183 and 0.538). Otherwise, days to first flower showed negative significant correlation with number of capsules/plants. (Soundharya *et al.*, 2017) found

Table 2. Genotypic (above) and phenotypic correlation coefficients (below diagonal) among the traits in the F_3-generation in population under artificial infection of *Fusarium oxysporum.*

Traits	DFF	PH,cm	HFC,cm	LFZ,cm	NC/P	SY/P,g	1000SW	OIL%	INF % Seedling	INF% at harvest
DFF	-	-0.1467	0.1151	-0.1875	-0.1858	-0.2947	-0.1884	-0.0518	-0.0211	-0.0171
PH;cm	-0.1399	-	0.1026	0.9120	0.1594	0.1326	0.1924	0.1047	-0.2957	-0.2969
HFC;cm	0.0987	0.1401	-	-0.3145	0.1624	0.1070	-0.1454	-0.0326	-0.0981	-0.1040
LFZ;cmp	-0.1791	0.8887	-0.3295	-	0.0851	0.0824	0.2436	0.1133	-0.2417	-0.2404
NC/P	-0.1750	0.1454	0.1245	0.0809	-	0.6324	0.1413	-0.0905	0.1392	0.1389
SY/P;g	-0.2875	0.1308	0.0935	0.0814	0.6087	-	0.1115	0.0215	0.1019	0.0997
1000SW	-0.1795	0.1714	-0.1136	0.2160	0.1382	0.1046	-	0.1442	-0.1004	-0.0970
OIL%	-0.0503	0.0991	-0.0210	0.1042	-0.0827	0.0220	0.1388	-	-0.0412	-0.0488
INF% Seedling	-0.0202	-0.2792	-0.0761	-0.2310	0.1311	0.0973	-0.0937	-0.0413	-	1.0138
INF% at harvest	-0.0166	-0.2797	-0.0836	-0.2280	0.1284	0.0952	-0.0898	-0.0482	0.9971	-

that Number of capsules/plants showed positive significant (p≤0.01) correlation with seed yield/plant in two populations (0.183 and 0.538). (Disowja *et al.,* 2020) indicated that the capsules/plant recorded a high positive and significant genetic correlation with yield/plant.

Maturity days showed negative correlation with yield / plant (0.162 rg, 0.120 rp). Patidar et al. (2020) reported 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).

3.2. Evaluation of the second cycle selection, season 2018

Variability and heritability estimates

Mean squares of the entries (families + parents) of all the selection criteria were significant ($p \leq 0.01$) after two cycles selection (Table 3) indicating the presence of variability in the selection criterion for further cycles of selection. The remained variability after selection expressed as GCV% and PCV% could be considered low (Table 4) for flowering and oil%, moderate for LFZ restricted by HFC and

1000 SW, and high for SY/P and LFZ. The significant differences of the entries, which in the analysis of variance of the low GCA and PCV caused by the inclusion of the two parents in the analysis.

Heritability in broad sense of the selection criteria were very high and unreliable (Table 4) because the evaluation for one season and one location inflated families mean squares by the confounding effects of the interaction of families, years and locations. Otherwise, heritability in narrow sense as estimated by regression was considered high in the F_5 for flowering, SY/P and Oil% and very low for the other traits in both of F_4 and F_5-generations. This is due to the fact that the pathogen kills susceptible families regardless of their performance in any trait.

Table 3. Mean squares of the selected families for the eight selection criteria in the F_5-generation, season 2018.

S.V.	d.f	50% flow	Flow.Res. by yield	SY/P	Oil%	Oil% Res. by yield	LFZ	LFZ. Res. by HFC	1000sw
Reps	2	3.7619	3.76	0.810	4.3333	4.332	72.62	72.62	0.10
Entries	6	13.4286**	21.76**	82.193**	48.7460**	37.826**	666.27**	348.41**	0.55**
Error	12	0.4286	0.43	8.346	0.2220	0.111	53.17	74.01	0.004

Res. =restricted, **, significant at 0.01 levels of probability

Table 4. Genotypic (GCV %), phenotypic coefficients of variability (PCV%), heritability in broad (H%) and in narrow sense (h^2) for the selection criteria in the F_5- generation.7/15

Selection criterion	GCV%%	PCV%	H%	$h^2(F_4/F_3)$	$h^2(F_5/F_4)$
50% Flowering	4.14	4.21	96.81	0.90	0.23
50% Flow. restricted by yield	5.20	5.25	98.03	0.90	0.75
Seed yield/plant	16.47	17.38	89.85	0.81	0.18
Oil%	6.41	6.43	99.54	0.75	0.93
Oil% restricted by yield	5.80	5.81	99.71	0.61	0.39
LFZ	14.94	15.58	92.02	0.05	0.86
LFZ restricted by HFC	9.69	10.92	78.76	0.15	0.23
1000-SW	7.92	7.95	99.19	0.19	0.10

Many authors are in line with these findings. (Ismail *et al.*, 2014) noted that the slight discrepancy between (GCV) and (PCV)

resulted in high estimates of broad sense heritability for most studied traits in the two base populations. (Aladji *et al.*, 2014),

(Bharathi *et al.*, 2014) and (Mahdy *et al.*, 2015a,b). (Iqbal *et al.,* 2016) and (Saravanan *et al.*, 2020) noted high GCV and PCV% of (26.11 and 26.30) for yield per plant. (Fazal *et al.*, 2015) found that heritability in the broad sense was high for days to flowering (89.20%). (Kanak and Rajani, 2016) found high heritability and genetic advance in percentage of the mean seed yield per plant (97.5 and 6.83%, respectively) followed by number of capsules per plant (96.6 and 1.72%, respectively) indicating that selection could be effective for improvement of these characters.

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

After the second cycle (F_5) selection for days to 50% flowering, the five selected families become alike to large extent. They ranged from 50.00 to 51.00 day indicating the great depletion of variability, and the significantly in families mean square caused by the inclusion of the parents in the analysis of variance.

The direct genetic response in days to 50% flowering (Table 5) was significant from the mid-parent (-7.77%[**]) and from the better-parent (-6.91%[**]) followed by positive significant correlated gain from the mid-parent in PH (16.99%[**]), HFC (51.83%[**]), SY/P (19.32%[**]), and 1000 SW (7.47%[*]). Otherwise, significant negative correlated gains were recorded for oil% (-6.08%[**]) and infection% at harvest (-1.7%[**]). These results are in line with those of Mahdy *et al.* (2015b).

Table 5. Selected family means of days to 50% flowering and correlated traits in the F_5-generation, observed gain from the mid-parent (GA-MP %) and better parent (GA-BP %) under artificial infection of *Fusarium oxysporum*.

Fam. No.	§0.50 Flow	PH, cm	HFC, cm	LFZ, cm	NC/P	SY/P, g	1000SW	OIL%	INF % Seedling	INF% at harvest
19	51.00	171.67	75.00	96.67	104.33	19.48	5.49	54.00	41.90	44.29
138	50.33	141.67	55.00	86.67	83.03	26.64	5.30	52.00	58.93	61.71
152	50.00	163.33	61.67	101.67	144.33	19.48	5.35	52.00	61.41	62.57
195	50.00	133.33	51.67	81.67	133.52	32.53	5.40	49.00	53.53	54.51
210	50.00	101.67	35.00	66.67	82.43	21.18	5.63	60.67	55.00	55.26
Average	50.27	142.33	55.67	86.67	109.53	23.86	5.44	53.53	54.15	55.67
M-P	54.50	121.67	36.67	85.00	108.78	20.00	5.06	57.00	54.41	56.68
GA-MP%	-7.77**	16.99**	51.82**	1.96	0.69	19.32**	7.47**	-6.08**	-0.47**	-1.78**
GA-BP%	-6.91**	6.75	85.56**	-3.70	-32.53	4.46	-5.84**	-12.24**	10.34**	9.61**
Shandaweel 3	55.00	133.33	43.33	90.00	162.33	17.15	5.77	53.00	49.08	50.79
Introduction 688	54.00	110.00	30.00	80.00	55.22	22.84	4.34	61.00	59.74	62.57
MP LSD0.05%	1.01	10.16	6.79	11.42	25.81	4.99	0.11	0.73	0.05	0.12
MP LSD 0.01%	1.41	14.24	9.53	16.02	36.18	7.00	0.15	1.02	0.07	0.17
BP LSD 0.05%	1.17	11.73	7.85	13.19	29.80	5.77	0.13	0.84	0.06	0.14
BP LSD 0.01%	1.63	16.44	11.00	18.49	41.78	8.09	0.18	1.18	0.08	0.19

§ = selection criterion, *, **, significant at 0.05 and 0.01 levels of probability; respectively.

3.2.2. Means and direct observed genetic gain in days to 50% flowering restricted by SY/P

After the second cycle (F_5) selection for days to 50% flowering restricted by SY/P, the five

selected families become similar except one. They ranged from 50.00 to 56.00 day indicating the great depletion of variability. The direct genetic response in days to 50% flowering (Table 6) was significant from the mid-parent (-5.93%**) and from the better- parent (-5.06%**) followed by positive significant correlated gain from the mid-parent in PH (14.26%**), HFC (44.55%**), SY/P (35.56%**), and 1000 SW (4.54%*). Otherwise, significant negative correlated gains were recorded for oil% (-4.68%**) and infection% at harvest (-1.68%**). These results are in line with those of Mahdy *et al.* (2015b).

Table 6. Selected family means of days to 50% flowering restricted by seed yield and correlated traits in the F$_5$-generation, observed gain from the mid-parent (GA-MP%) and better parent (GA-BP%).

Fam. No.	Selectom criteria		Correlated traits							
	0.50	SY/P, g	PH, cm	HFC, cm	LFZ, cm	NC/P	1000 SW	OIL%	INF % Seedlin	INF% harvest
138	50.33	26.64	141.67	55.00	86.67	83.03	5.30	52.00	58.93	61.71
152	50.00	19.48	163.33	61.67	101.67	144.33	5.35	52.00	61.41	62.57
195	50.00	32.53	133.33	51.67	81.67	133.52	5.40	49.00	53.53	54.51
199	56.00	84.85	155.00	61.67	93.33	294.00	4.75	58.00	46.79	54.10
210	50.00	21.18	101.67	35.00	66.67	82.43	5.63	60.67	55.00	55.26
Average	51.27	36.93	139.00	53.00	86.00	147.46	5.29	54.33	55.13	57.63
M-P	54.50	20.00	121.67	36.67	85.00	108.78	5.06	57.00	54.41	56.68
GA-MP%	-5.93**	84.69**	14.25**	44.55**	1.18	35.56**	4.54**	-4.68**	1.33**	1.68**
GA-BP%	-5.06**	61.69**	4.25	76.67**	-4.44	-9.16	-8.41**	-10.93**	12.33**	13.47**
Shandaweel 3	55.00	17.15	133.33	43.33	90.00	162.33	5.77	53.00	49.08	50.79
Introduction	54.00	22.84	110.00	30.00	80.00	55.22	4.34	61.00	59.74	62.57
MP LSD0.05%	1.01	7.26	9.61	6.06	11.69	18.70	0.13	0.89	0.28	0.37
MP LSD0.01%	1.41	10.18	13.47	8.50	16.39	26.22	0.19	1.25	0.39	0.52
BP LSD0.05%	1.16	8.39	11.09	7.00	13.50	21.59	0.15	1.03	0.32	0.42
BP LSD0.01%	1.63	11.76	15.56	9.81	18.92	30.27	0.21	1.44	0.45	0.60

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

3.2.3. *Means and direct observed genetic gain in seed yield/plant*

After two cycles of selection for SY/P, wide range of variation in SY/P was found (Table 7). Family means ranged from 21.18 to 34.34 g/plant with an average of 30.13g. A wide range of variation was observed in the other correlated traits. Infection% at harvest, the family means ranged from 50.70 to 62.5% with an average of 55.20%. The direct significant (p≤0.01) observed genetic gain in SY/P was 17.38% from the mid-parent, while it was not significant from the better parent. The increase in yield followed by significant decrease in days to 50% flowering (-2.02 and -1.11%), in LFZ (-14.12 and -18.89%), oil% (-7.84 and -13.88%) and infection % at harvest (-2.2 and 9.0%) from the mid and better parent, respectively. It could be noticed that the pedigree selection for SY/P accompanied with favorable decrease in days to 50% flowering, and infection% at harvest, and adversely affected LFZ and Oil%. It is the main drawback of single trait selection, it is efficient in changing the mean of the selection criterion,

and adversely affects some correlated characters. These results are in line with those found by (Ismail *et al*., 2014) and (Mahdy *et al.*, 2015a). In a study of 15 populations in the F_3 and F_4 EL-Bramawy (2006) indicated that selection for both *Fusarium* wilt resistance and seed yield could be feasible and lead to resistant cultivars with seed yield potential. El-Bramawy and Abd Al-Wahid (2007) noticed that the high resistance entries gave the lowest seed yield. so, great care should be taken during selection for breeding program. (Jyothi *et al.*, 2011) screened 35 sesame germplasm accessions. All the accessions displayed some percent infection rate, and none could be described as immune. (Ngamba *et al.*, 2020) stated that the genotypes

differed significantly (P≤0.001) for disease incidence.

3.2.4. Means and direct observed genetic gain in seed oil%

Mean oil% after two cycles of selection ranged from 60.33 to 65.0% with an average of 62.73% compared to 53.00 and 61.00% of the two parents (Table 8). The genetic direct observed gain in oil% was significant (p≤ 0.01) from the mid-parent (10.06%) and from the better parent (2.84%). Selection for oil% accompanied with significant delay in flowering, increase in HFC, 1000-SW, and INF% was observed. Otherwise, selection for oil% showed insignificant decrease of the observed correlated gain from the mid parent in LFZ, NC/P and SY/P.

Table 7. Selected family means for seed yield/ plant and correlated traits in the F_5-generation, observed gain from the mid-parent (GA-MP%) and better parent (GA-BP%) under artificial infection by *Fusarium oxysporum*.

Fam. No.	Sel.cri		Correlated traits								
	SY/P, g	50% flow	PH, cm	HFC, cm	LFZ, cm	NC/P	1000 SW	OIL%	INF % Seedling	INF% at harvest
21	32.88	56.67	110.00	38.33	71.67	200.83	4.44	51.00	60.58	62.57
41	29.70	55.33	135.00	65.00	70.00	196.47	5.31	45.00	53.53	53.77
50	34.34	55.00	120.00	45.00	75.00	202.44	5.34	57.00	49.08	50.79
195	32.53	50.00	133.33	51.67	81.67	133.52	5.40	49.00	53.53	54.51
210	21.18	50.00	101.67	35.00	66.67	82.43	5.63	60.67	55.00	55.26
Average	30.13	53.40	120.00	47.00	73.00	163.14	5.23	52.53	54.34	55.38
M-P	25.67	54.50	121.67	36.67	85.00	108.78	5.06	57.00	54.41	56.68
GA-MP%	17.38**	-2.02**	-1.37	28.18**	-14.12**	49.98**	3.31**	-7.84**	-0.12**	-2.29**
GA-BP%	3.25	-1.11**	-10.00	56.67**	-18.89**	0.50	-9.49**	-13.88**	10.72**	9.04**
Shandaweel 3	22.15	55.00	133.33	43.33	90.00	162.33	5.77	53.00	49.08	50.79
Introduction 688	29.18	54.00	110.00	30.00	80.00	55.22	4.34	61.00	59.74	62.57
MP LSD0.05%	4.45	0.45	9.26	8.12	9.95	20.07	0.10	0.46	0.07	0.10
MP LSD0.01%	6.24	0.64	12.98	11.39	13.94	28.14	0.14	0.64	0.10	0.14
BP LSD0.05%	5.14	0.53	10.69	9.38	11.48	23.17	0.11	0.53	0.08	0.11
BP LSD0.01%	7.21	0.74	14.99	13.15	16.10	32.49	0.16	0.74	0.11	0.16

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

Table 8. Selected family means for seed oil% and correlated traits in the F_5-generation, observed gain from mid-parent (GA-MP%) and better parent (GA-BP%).

Fam. No.	Sel.criterion	Correlated traits								
	Oil%	50%flow	PH, cm	HFC, cm	LFZ, cm	NC/P	SY/P, g	1000SW	INF % Seedling	INF% at harvest
5	65.00	55.00	141.67	45.00	96.67	74.95	12.51	5.33	64.97	69.31
46	65.00	59.00	126.67	45.00	81.67	161.49	35.54	5.87	62.28	62.57
168	62.00	58.33	100.00	36.67	63.33	73.67	22.18	4.67	57.34	59.19
185	60.33	56.33	133.33	45.00	88.33	65.71	22.71	5.23	65.94	66.25
327	61.33	56.33	135.00	51.67	83.33	144.44	32.25	5.84	58.12	60.03
Average	62.73	57.00	127.33	44.67	82.67	104.05	25.04	5.39	61.73	63.47
M-P	57.00	54.50	121.67	36.67	85.00	108.78	25.67	5.06	54.41	56.68
GA-MP%	10.06[**]	4.59[**]	4.66	21.82[**]	-2.75	-4.34	-2.44	6.56[**]	13.45[**]	11.98[**]
GA-BP%	2.84[**]	5.56[**]	-4.50	48.89[**]	-8.15	-35.90[**]	-14.18[**]	-6.64[**]	25.77[**]	24.97[**]
Shandaweel 3	53.00	55.00	133.33	43.33	90.00	162.33	22.15	5.77	49.08	50.79
Introduction 688	61.00	54.00	110.00	30.00	80.00	55.22	29.18	4.34	59.74	62.57
MP LSD0.05%	0.73	0.48	8.52	5.66	9.23	16.43	7.48	0.11	0.08	0.17
MP LSD0.01%	1.02	0.67	11.94	7.94	12.95	23.03	10.48	0.16	0.12	0.24
BP LSD0.05%	0.84	0.55	9.84	6.54	10.66	18.97	8.63	0.13	0.10	0.20
BP LSD0.01%	1.18	0.77	13.79	9.16	14.95	26.59	12.11	0.18	0.14	0.27

**, significant at 0.01 levels of probability; respectively.

3.2.5. *Means and direct observed genetic gain in seed oil% restricted by SY/P*

Mean oil% of the selected families (Table 9) ranged from 59.67 to 65.00% with an average of 61.13%, and SY/P ranged from 20.84 to 35.54g/P with an average of 26.58%. It could be noticed the homogeneity of the selected families in oil% after two cycles of selection. After two cycles of pedigree selection for oil% restricted by seed yield the observed direct genetic gains in oil% were 7.25%[**], and 0.22%, and in SY/P were 19.02%[**], and 2.85% from mid- and better parent, respectively. Significant (p≤0.05 or p≤0.01) correlated gains of 16.71[**] and 6.50%[**]

3.2.6. *Means and direct observed gain in LFZ*

Mean LFZ of the selected families (Table 10) ranged from 88.38 to 106.67cm with an average of 98.67cm. After two cycles of pedigree selection for LFZ, the observed direct genetic gain in LFZ was 16.78%[**] and 9.36%[**] from the mid and better parent, respectively. The observed genetic gain in percentage of the mid-parent was favorable for PH (20.27[**]), NC/P (50.09[**]), SY/P (14.05[**]), and 1000 SW (6.86[**]), while it was unfavorable for 50% flowering (0.55[**]), oil% (-10.16[**]) and infection% at harvest (5.27[**]).

for PH, 39.09[**] and 70.0%[**] for HFC, 6.08[**] and -7.06%[**] for 1000 SW, 9.01[**] and 4.60%[**] for CL and 3.93[**] and 15.21%[**] for infection% at seedling stage from both the mid- and better parent, respectively. It should be indicated that selection for oil% only (Table 8) insignificantly decrease LFZ, SY/P and NC/P, however, selection for oil% restricted by SY/P significantly increased SY/P (Table 9). These results are in line with those reported by Singh *et al.* (2018) who estimated expected genetic advance in seed oil% of 12.81%. Mohanty *et al.* (2020) estimated expected genetic from the mean for oil% of 31.50%.

3.2.7. *Means and direct observed genetic gain in LFZ restricted by HFC*

Mean LFZ of the selected families ranged from 75.0 to 110.00cm with an average of 95.67cm, and from 30.00 to 43.33cm with an average of 38.00cm for HFC (Table 11). The direct observed genetic gain from the mid-parent for LFZ was 12.549%[**] and from the better parent was 6.29%. Otherwise, the observed gain in HFC was not significant. Selection for LFZ restricted by HFC 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%[**]). However, unfavorable genetic correlated gains were obtained for 50% flowering (2.395[**]), oil % (-3.63%[*]) and infection% at harvest (8.38%[**]). Results proved the efficiency of single trait selection in changing the mean of the selection criterion, and adversely affected some correlated traits. It is of interest to indicate that selection for LFZ restricted by HFC was better in improving yield and NC/P than selection for LFZ *per se*. Otherwise; single trait selection for LFZ was more efficient in changing the mean of the selection criterion.

Table 9. Selected family means for seed oil% restricted seed yield/ plant and correlated traits in the F_5-generation, observed gain from the mid-parent (GA-MP%) and better parent (GA-BP%) under artificial infection by *Fusarium oxysporum*.

Fam. No.	Selection crieriteria				Correlated traits					
	OIL%	SY/P, g	50%flow	PH, cm	HFC, cm	LFZ, cm	NC/P	1000 SW	INF % Seedling	INF% at harvest
46	65.000	35.543	59.000	126.667	45.000	81.667	161.487	5.873	62.280	62.567
73	59.667	20.913	57.000	143.333	36.667	106.667	110.037	5.753	55.773	56.813
125	60.000	29.870	58.000	156.667	55.000	101.667	76.562	5.530	49.817	50.050
252	60.667	20.843	57.000	135.000	58.333	76.667	88.444	4.463	60.580	60.850
270	60.333	25.723	55.000	148.333	60.000	88.333	151.806	5.208	54.270	54.513
Average	61.133	26.579	57.200	142.000	51.000	91.000	117.667	5.366	56.544	56.959
M-P	57.000	22.332	54.500	121.667	36.667	85.000	108.778	5.058	54.408	56.678
GA-MP%	7.251**	19.018**	4.954**	16.712**	39.091**	7.059	8.172**	6.076**	3.925**	0.495**
GA-BP%	0.219	2.845	5.926**	6.500	70.000**	1.111	-27.515*	-7.061**	15.208**	12.145**
Shandaweel 3	53.000	18.820	55.000	133.333	43.333	90.000	162.333	5.773	49.080	50.790
Introduction 688	61.000	25.843	54.000	110.000	30.000	80.000	55.222	4.343	59.737	62.567
MP LSD0.05%	0.513	6.368	0.336	9.608	6.022	10.203	20.302	0.084	0.067	0.112
MP LSD0.01%	0.720	8.928	0.471	13.471	8.444	14.305	28.463	0.118	0.094	0.156
BP LSD0.05%	0.593	7.353	0.388	11.094	6.954	11.781	23.442	0.097	0.078	0.129
BP LSD0.01%	0.831	10.309	0.544	15.555	9.750	16.518	32.866	0.137	0.109	0.181

**, significant at 0.01 levels of probability.

3.2.8. Means and direct observed gain in 1000-seed weight

Mean 1000-SW of the selected families (Table 12) ranged from 5.31 to 5.50g with an average of 5.39g. After two cycles of pedigree selection for 1000 SW the observed direct genetic gain in 1000 SW was 18.14[**], and 12.82%[**] from the mid- and better parent, respectively, accompanied by observed correlated gain of 14.25[*] and 4.25%% for PH, 3.61[**] and 4.57[**] in 50% flowering, 53.64[**] and 87.78%[**] for HFC, -2.75 and - 8.15 for LFZ, 52.24[**], and 2.02 for NC/P, 14.09[**] and 0.36[**] for SY/P, 2.07[**], 1.29[**] and -5.36[**] for oil% and 9.32[**] and 21.99%[**] for infection % at harvest from the mid and better parent, respectively. Mohanty *et al.*, 2020 reported high to moderate phenotypic and genotypic coefficients of variation accompanied by high heritability and high to moderate genetic advance in percentage of the mean for 1000 seed weight, oil content%, oil yield/plant and seed yield/ plant.

Table 10. Selected family means for length of the fruiting zone and correlated traits in the F$_5$-generation, observed gain from the mid-parent (GA-MP%) and better parent (GA-BP%).

Fam. No.	Sel. criterion LFZ, cm	Correlated traits								
		HFC, cm	DFF	PH, cm	NC/P	SY/P, g	1000 SW	OIL%	INF % Seedling	INF% at harvest
72	88.33	41.67	55.33	130.00	83.690	13.653	5.88	64.00	59.74	60.85
152	101.67	61.67	50.00	163.33	144.333	16.147	5.35	52.00	61.41	62.57
183	108.33	65.00	57.33	173.33	192.395	30.080	4.91	48.00	61.41	61.71
239	88.33	40.00	56.33	128.33	165.043	34.260	5.70	55.00	51.28	51.49
281	106.67	30.00	55.00	136.67	230.909	52.213	5.18	55.00	58.93	61.71
Average	98.667	47.667	54.80	146.333	163.274	29.27	5.40	54.80	58.55	59.67
M-P	85.000	36.667	54.50	121.667	108.778	25.67	5.06	57.00	54.41	56.68
GA-MP%	16.078[**]	30.000[**]	0.55*	20.274[**]	50.099[**]	14.05[**]	6.82[**]	-3.86[**]	7.62[**]	5.27[**]
GA-BP%	9.630[**]	58.889[**]	1.48[**]	9.750	0.580	0.32	-6.41[**]	-10.16[**]	19.30[**]	17.48[**]
Shandaweel 3	90.00	43.33	55.00	133.33	162.333	22.153	5.77	53.00	49.08	50.79
Introduction 688	80.00	30.00	54.00	110.00	55.222	29.177	4.34	61.00	59.74	62.57
MP LSD0.05%	13.255	7.099	0.48	10.476	29.346	5.63	0.10	0.91	0.04	0.12
MP LSD0.01%	18.584	9.953	0.67	14.688	41.143	7.89	0.14	1.28	0.06	0.16
BP LSD0.05%	15.306	8.198	0.55	12.097	33.886	6.50	0.11	1.05	0.05	0.14
BP LSD0.01%	21.459	11.493	0.77	16.960	47.508	9.11	0.16	1.47	0.07	0.19

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

3.3. Comparison between the eight selection methods under artificial infection of F. oxysporum

Two cycles of selection for days to 50% flowering (Table 13) improved earliness from the mid-parent (-7.77[**]) and - 6.91[**] from the better-parent followed by improve in the correlated traits in percentage of mid-parent; PH (16.99[**]), SY/P (19.32), 1000 SW (7.47[**]), and favorable decrease in INF% at harvest (-1.78[**]). This could be due to negative correlation between these traits and days to 50% flowering in the base population (Table 2). However, negative decrease from the mid-parent was obtained in oil% (-6.08[**]).

Selection for days to 50% flowering restricted by SY/P, reduced days to 50% flowering (-5.93[**]) and increase SY/P (35.56%[**]) 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 in percentage from the mid-parent were 14.25[**] (PH), 44.55[**] (HFC), 1000-SW (4.54[**]), and 84.69[**] (NC/P). Otherwise, negative reduction was obtained in oil% (-4.68[**]). This means that single trait selection proved to be an efficient method in improving selection criterion, and the incorporation of valuable traits with the selection criterion improved genetic correlated gains. (Mahdy *et al.*, 2015a,b) stated that pedigree selection is an efficient method to improve selection criterion and improved the direct observed gain in days to first flower by - 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. The direct observed genetic gain from selection for SY/P

was positive from the mid-parent (17.38%[**]). The observed correlated gain in percentage of the mid-parent was favorable in days to 50% flowering (-2.02%[**]), 49.98[**] in NC/P, 3.31[**] in 1000-SW, 4.04[**] in CL, and -2.29 in Inf % at

harvest. The other correlated gains in HFC, LFZ, CW, and oil% were unfavorable. Mahdy *et al.* (2015a) improved SY/P throw two cycles of selection by 30.68 and 45.18% from the better parent in two populations.

Table 11. Selected family means for length of the fruiting zone restricted by HFC and correlated traits in the F_5-generation, observed gain from the mid-parent (GA-MP%) and better parent (GA-BP%).

Fam. No.	Sel.criterion			Correlated traits						
	LFZ, cm	DFF	PH, cm	HFC, cm	NC/P	SY/P, g	1000SW	OIL%	INF % Seedling	INF% at harvest
89	75.00	53.00	115.00	40.00	136.31	21.28	5.30	57.33	54.27	57.59
184	80.00	58.00	126.67	46.67	151.33	24.82	4.95	56.33	55.77	58.40
271	110.00	55.00	140.00	30.00	232.13	47.14	5.35	56.33	67.92	74.18
281	106.67	55.00	136.67	30.00	230.91	36.88	5.18	55.00	58.93	61.71
347	106.67	58.00	150.00	43.33	113.50	23.26	4.87	49.67	55.00	55.26
Average	95.667	55.80	133.667	38.000	172.84	30.68	5.13	54.93	58.38	61.43
M-P	85.000	54.50	121.667	36.667	108.78	25.67	5.06	57.00	54.41	56.68
GA-MP%	12.549[*]	2.39[**]	9.863[*]	3.636	58.89[**]	19.53[**]	1.46[**]	-3.63[**]	7.30[**]	8.38[**]
GA-BP%	6.296	3.33[**]	0.250	26.667[**]	6.47	5.15	-11.11[**]	-9.95[**]	18.95[**]	20.94[**]
Shandaweel 3	90.00	55.00	133.33	43.33	162.33	22.15	5.77	53.00	49.08	50.79
Introduction 688	80.00	54.00	110.00	30.00	55.22	29.18	4.34	61.00	59.74	62.57
MP LSD0.05%	11.236	0.43	8.949	7.673	17.83	5.51	0.10	0.75	0.12	0.34
MP LSD0.01%	15.752	0.61	12.546	10.758	25.00	7.73	0.14	1.05	0.17	0.48
BP LSD0.05%	12.974	0.50	10.333	8.860	20.59	6.37	0.11	0.87	0.14	0.39
BP LSD0.01%	18.189	0.70	14.487	12.422	28.87	8.92	0.16	1.22	0.19	0.55

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

The direct observed genetic gain from selection for oil% was positive from both of mid-parent (10.06%[**]) and better parent (2.84%[**]). The observed correlated gain from the mid-parent was unfavorable for SY/P (-2.44), days to50% flowering (4.59[**]), HFC (21.82[**]), infection% at seedling stage (13.45[**]) and infection% at harvest (11.98%[**]), and favorable in 1000 SW (6.56%[**]).

Selection for oil% restricted by SY/P gave direct observed genetic gain from the mid-parent of 7.25%[**] (lower than selection for oil% *per se*), and 19.02%[**] for SY/P. Favorable correlated

gains were obtained in PH (16.71%[**]), NC/P (8.17%[**]), and 1000 SW (6.08%[**]). The other correlated traits, days to 50% flowering, HFC, and INF% showed unfavorable gains. Inclusion of SY/P with oil% in selection increased SY/P, 1000 SW, and NC/P. Selection for LFZ gave direct observed genetic gain from the mid-parent of 16.08%[**] and 9.63%[**] from the better parent. Favorable correlated gains from the mid-parent were obtained in PH (20.27%[**]), NC/P (50.10%[**]), SY/P (14.05%[**]) and 1000 SW (6.82%[**]). The other correlated traits gave unfavorable gains from selection.

Table 12. Selected family means for 1000-seed weight in the F_5-generation, observed gain from the mid-parent (GA-MP%) and better parent (GA-BP%).

Fam. No.	Sel.crit.		Correlated traits							
	1000S W, g	50% flow	PH, cm	HFC, cm	LFZ; cm	NC/P	SY/P, g	OIL%	INF % Seedling	INF% at harvest
5	5.33	55.00	141.67	45.00	96.67	74.95	12.51	65.00	64.97	69.31
24	5.40	56.33	115.00	55.00	60.00	272.46	46.49	60.33	60.58	62.57
125	5.53	58.00	156.67	55.00	101.67	76.56	29.87	60.00	49.82	50.05
127	5.31	63.00	118.33	65.00	53.33	259.72	38.05	51.33	64.07	65.31
152	5.35	50.00	163.33	61.67	101.67	144.33	19.48	52.00	61.41	62.57
Average	5.39	56.47	139.00	56.33	82.67	165.60	29.28	57.73	60.17	61.96
M-P	4.56	54.50	121.67	36.67	85.00	108.78	25.67	57.00	54.41	56.68
GA-MP%	18.14**	3.61**	14.25*	53.64	-2.75	52.24**	14.09**	1.29**	10.59**	9.32**
GA-BP%	12.82**	4.57**	4.25	87.78	-8.15	2.02	0.36	-5.36**	22.59**	21.99**
Shandaweel 3 Introduction	4.77	55.00	133.33	43.33	90.00	162.33	22.15	53.00	49.08	50.79
688	4.34	54.00	110.00	30.00	80.00	55.22	29.18	61.00	59.74	62.57
MP LSD0.05%	0.10	1.01	11.11	5.78	13.24	22.21	6.64	0.87	0.07	0.17
MP LSD0.01%	0.14	1.41	15.58	8.11	18.56	31.14	9.31	1.22	0.10	0.24
BP LSD0.05%	0.12	1.16	12.83	6.68	15.29	25.65	7.67	1.00	0.08	0.20
BP LSD0.01%	0.17	1.63	17.99	9.36	21.43	35.96	10.75	1.41	0.11	0.28

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

Selection for LFZ restricted by HFC increased LFZ (12.55%[**]) and SY/P (19.53%[**]) from the mid-parent, followed by favorable increase in NC/P, 1000-SW, Cl, and CW. Selection for LFZ only was less efficient than selection for LFZ restricted by HFC in improving correlated traits. Direct selection for 1000 SW increased seed weight (18.14%[**]) and gave sizeable favorable correlated gains from the mid-parent in SY/P (14.08%[**]), PH (14.25%[**]), NC/P (52.24%[**]). 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 after two cycles of selection of -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 pop 2 from the unselected bulk sample and the better parent; respectively after two cycles of selection.

Table 13. Means of the selected families, observed gain from the mid-parent (GA-MP%) and better parent (GA-BP%) for the eight selection criteria in the F_5- generation under artificial infection by *Fusarium oxysporum*.

Selection criterion	Item	50% flow	PH,cm cm	HCF,cm cm	LFZ,cm cm	NC/P	SY/P,g g	1000-SW,g sw,g	Oil%	INF% seeling	INF% harvest
50 50% flowering	C₂ mean	50.27	142.33	55.67	86.67	109.53	23.86	5.44	53.53	54.15	55.67
	GA-MP%	-7.77**	16.99**	51.82**	1.96	0.69	19.32**	7.47**	-6.08**	-0.47**	-1.78**
	GA-BP%	-6.91**	6.75	85.56**	-3.70	-32.53*	4.46	-5.84**	-12.24**	10.34**	9.61**
50% flow. Restricted By yield	C₂ mean	51.27	139.00	53.00	86.00	36.93	147.46	5.29	54.33	55.13	57.63
	GA-MP%	-5.93**	14.25**	44.55**	1.18	84.69**	35.56**	4.54**	-4.68**	1.33**	1.68**
	GA-BP%	-5.06**	4.25	76.67**	-4.44	61.69**	-9.16	-8.41**	-10.93**	12.33**	13.47**
SY/P	C₂ mean	53.40	120.00	47.00	73.00	163.14	30.12	5.23	52.53	54.34	55.38
	GA-MP%	-2.02**	-1.37	28.18**	-14.12**	49.98**	17.38**	3.31**	-7.84**	-0.12**	-2.29**
	GA-BP%	-1.11**	-10.00*	56.67**	-18.89**	0.50	3.25	-9.49**	-13.88**	10.72	9.04**
Oil%	C₂ mean	57.00	127.33	44.67	82.67	104.05	25.04	5.39	62.73	61.73	63.47
	GA-MP%	4.59**	4.66	21.82**	-2.76	-4.34	-2.44	6.56**	10.06**	13.45**	11.98**
	GA-BP%	5.56**	-4.50	48.89**	-8.15	-35.90**	-14.18*	-6.64**	2.84**	25.77**	24.97**
Oil% restricted .by yield	C₂ mean	57.20	142.00	51.00	91.00	117.67	26.58	5.37	61.13	56.54	56.96
	GA-MP%	4.95**	16.71**	39.09**	7.06	8.17**	19.02**	6.08**	7.25**	3.93**	0.50**
	GA-BP%	5.93**	6.50	70.00**	1.11	-27.52*	2.85	-7.06**	0.22	15.21**	12.15**
LFZ	GA-MP%	0.55*	20.27**	30.00**	16.08**	50.10**	14.05**	6.82**	-3.86**	7.62**	5.27**
	GA-BP%	1.48**	9.75	58.89**	9.63**	0.58	0.32	-6.41**	-10.16**	19.30**	17.48**
	C2 mean	55.8	133.667	38	95.667	172.84	30.68	5.13	54.93	58.38	61.43
LFZ Restrict By HFC	GA-MP%	2.39**	9.86*	3.64	12.55*	58.89**	19.53**	1.46**	-3.63**	7.30**	8.38**
	GA-BP%	3.33**	0.25	26.667**	6.296	6.47	5.15	-11.11**	-9.95**	18.95**	20.94**
	C2 mean	56.47	139.00	56.33	82.67	165.60	29.28	5.39	57.73	60.17	61.96
1000-SW	GA-MP%	3.61**	14.25*	53.64	-2.75	52.24**	14.09**	18.14**	1.29**	10.59**	9.32**
	GA-BP%	4.57**	4.25	87.78	-8.15	2.02	0.36	12.82**	-5.36**	22.59**	21.99**
	GA-MP%	0.55*	20.27**	30.00**	16.08**	50.10**	14.05**	6.82**	-3.86**	7.62**	5.27**

4. Conclusion

Single trait selection was an efficient method to improve selection criterion, but it caused adverse effects on some correlated traits. Selection for days to 50% flowering improved earliness, but it was better in improving yield if it restricted by SY/P. Selection for oil% restricted by yield was better in improving yield than selection for oil% pe se.

Inclusion of a trait as independent culling level improves the efficiency of selection. Therefore, selection index incorporating favorable trait is recommended. The correlation coefficients among traits help the breeder to select for few favorable traits. The best genetic gain in SY/P in percentage from the mid-parent was obtained from selection for days to 50% flowering restricted by SY/P (35.56**) [because of the negative genotypic correlation between

them), LFZ restricted by HFC (19.53^{**}), days to 50% flowering (19.32^{**}), oil% restricted by SY/P (19.02^{**}), SY/P (17.38^{**}), 1000-SW (14.09^{**}) and LFZ (14.032^{**}).

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