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Pedigree Selection to Improve the Seed Yield in a Segregating Population of Sesame (*Sesamum indicum* L.)

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ABSTRACT

The present investigation was conducted at Arab El-Awammer Agricultural Research Station, Assiut, Egypt during 2012, 2013 and 2014 summer seasons. Two cycles of pedigree selection method were applied on a segregating population of sesame in the F_3, F_4 and F_5 generations to improve seed yield. The soil of the experiment site is sandy calcareous. Highly significant differences among F_3 families and a sufficient genotypic coefficient of variability (GCV) were obtained for all studied traits. The coefficient of variability decreased from 49.88 % in the F_3 population to 22.68 % in the F_5 for seed yield/plant. Broad sense heritability estimates were high for most traits and reached 93.32 % for seed yield/plant after two cycles of selection. The observed gain in seed yield/plant was significant ($P \leq 0.01$) and accounted for 80.27 % from the unselected bulk sample. All of the families in the F_5 generation showed significant increase in seed yield/plant. It could be concluded that pedigree selection was an efficient method to improve seed yield productivity in the studied population. Selection for productivity could be practiced in the early segregating generations and two cycles of selection were enough to detect the families with high productive. Otherwise, single trait selection accompanied with adverse effects on other traits, and selection index could be recommended to improve seed yield and other traits.

Keywords: Sesame (*Sesamum indicum* L.), pedigree selection, genetic advance, segregating generation.

INTRODUCTION

Sesame (*Sesamum indicum* L.) is an important oil seed crop not only in A.R.E. but also over all the world. It plays an important role as an industrial and food crop. The genus *Sesamum* belongs to small family Pedaliaceae, which consists of 16 genera and 35 species, found in tropical or subtropical regions (Kinman and Martin, 1954).

The total cultivated area in the world was 32 thousand hectare produced about 14 thousand tons of seeds, while in Egypt, the cultivated area about 10 million hectares (23.8 million fed.) produced about 5 thousand tons of seeds (FAO, 2016). Sesame is one of the most ancient cultured oil plants. It has an early origin in East Africa (in ancient Egyptian tombs dating back 4.000 years) and in India (since over 5.000 years ago) (Nayar and Mehra, 1970).

Sesame growing areas in Egypt are decreasing due to low seed yield compared to the other competitive crops in the crop rotation. Plant breeders are continuously searching for more effective and efficient method to improve yield. Although several selection methods were used to improve several traits, pedigree selection method has become the most popular of plant breeding procedures. Plant breeders prefer it because it is versatile, relatively rapid and makes possible the conducting of genetic studies along with the plant breeding work. Many investigations reported that the selection in segregating populations within local and exotic populations may gave promising results in improving sesame performance. Pathirana (1995) and Ismail *et al.* (2005) reported that the direct selection for seed yield was the most effective for improvement of yield in sesame. Abo-Elwafa and Ahmed (2005) found that the observed gain in seed yield of two population was better when selection practiced for seed yield *per se* (25.24 and 15.22% of the better parent) than selection for weight of capsules/plant after two cycles of pedigree selection. El-Shimy (2005) through two cycles of pedigree selection increased seed yield by 49.12 and 45.78% from the better parent in two populations. In another work, Ismail *et al.* (2005) reported because in seed yield of 28.64 and 31.53% from the bulk sample in two populations. Khan *et al.* (2007) reported heritability estimate and expected genetic advance from the mean for seed yield were 84.0 and 43.34%, respectively. Gangrade *et al.* (2009) recorded that high phenotypic and genotypic coefficient of variation were observed in the characters. Jadhav and Mohrir (2012) found high GCV, heritability and genetic advance as percent of mean were recorded for seed yield/plant. Kumar *et al.* (2012) observed maximum genetic gain for grain yield/plant. Ismail *et al.* (2013) reported that the phenotypic correlation coefficients between seed yield/plant and each of days to 50% flowering, plant height, length of fruiting zone, number of capsules/plant and 1000-seed weight accounted for 0.443, 0.246, 0.253, 0.466 and 0.293, respectively. The positive and negative correlations between seed yield and earliness in the previous researches proved that this correlation depends mainly upon the gene associations in the population under study, and gave a chance to improve earliness without great effect on seed yield.

The aims of the present work were to improve yielding ability of sesame through pedigree selection method and to study the effect of direct and indirect selection for seed yield/plant on the other traits.

MATERIALS AND METHODS

The present work was carried out at Arab El-Awammer, Agric. Res. Stn. Arc. Assiut, Egypt, during the three summer seasons of 2012, 2013 and 2014. The soil is sandy calcareous in the experiment site.

Genetic materials:

Two cycles of pedigree selection were achieved for seed yield/plant. The genetic materials were F_3, F_4 and F_5 generations of one population of sesame (*Sesamum indicum* L.) stemmed from the cross [Line 102-32-2 (NA 217 x G 25) x Shandaweel 3 (G 32 x NA 130)]. Growing seasons, planting dates, genetic materials and experimental design were as follows:

Seasons	Planting date	Generation	Experimental design
2012	18/5/2012	F_3	Non-replicated exp.
2013	22/5/2013	F_4	RCBD with three replications
2014	20/5/2014	F_5	RCBD with three replications

Season 2012 (F_3 generation):

The breeding materials were used in this study, 1000 F_3 families traced back to random F_2 plants from the population. The aforementioned population in the F_3-generation with non-replicated experiment were sown in 18/5/2012 at Arab El-Awammer Agric. Res. Station, ARC, Assiut Gov. in spaced plants; 30 rows, 50 cm apart and 10 cm between hills within a row. The parents were sown each in five rows. After full emergence, seedlings were thinned to one plant per hill. The recommended cultural practices for sesame production were adopted throughout the growing seasons. At harvest time, the following traits were recorded on 1000 guarded plants and 20 plants from each parent. The recorded traits were plant height (cm), height to first capsule (cm), number of branches/plant, number of capsules/leaf axel, number of capsules/plant, seed yield/plant (gm) and seed yield/plot (gm). After harvest, ten seeds from each of the 1000 plants were blended to give an unselected bulk sample. The first cycle of pedigree selection was applied on the F_3 population for seed yield/plant as a selection criterion. Seeds of the best 100 plants for seed yield/plant (10%) were selected based on seed yield/plant and saved to the next generation.

Season 2013 (F_4-generation), the first cycle of pedigree selection

The 100 selected F_4 families along with the unselected bulk sample and the two parents were sown in RCBD with three replications. The plot size was one row. The space between rows and hills were as in the previous season. The characters were recorded as in the previous season on ten guarded plant from each entry. The best 10 plants from the best 10 families for seed yield/plant were harvested separately for the next generation. Seeds of the unselected bulk sample were blended without selection.

Season 2014 (F_5-generation), the second cycle of pedigree selection

The 10 selected families along with the parents and the unselected bulk sample were sown and evaluated as in the previous season.

Statistical analysis:

The analysis of variance (Table 1) was performed following in F_5 generation with parents and bulk sample.

Table 1. The analysis of variance as well as mean squares expectations.

SOV	df	MS	Expected mean squares
Replications	r-1	M_3	
Genotypes	g-1	M_2	$\delta^2_e + r\delta^2_g$
Error	(g-1)(r-1)	M_1	δ^2_e

Where: r and g are number of replications and genotypes; respectively. δ^2_e is error variance, and δ^2_g is genetic variance component. Two analyses of variance were performed. The first was for all genotypes (selected families + parent + bulk sample), and the second one for the selected families to calculate heritability and coefficients of variations. The phenotypic (δ^2_p) and genotypic (δ^2_g) variances were calculated according to the following formulae as given by Al-Jibouri *et al.* (1958).

The genotypic variance, $\delta^2_g = (M_2 - M_1) / r$

The phenotypic variance $\delta^2_p = \delta^2_g + \delta^2_e = M_2 / r$

Heritability in broad sense was estimated as $(H) = (\delta^2_g/\delta^2_p) \times 100$.

The phenotypic (pcv) and genotypic (gcv) coefficient of variability were estimated using the formula developed by Burton (1952)

$$\text{PCV } \% = \frac{\sigma p}{\bar{x}} \times 100 \qquad \text{GCV } \% = \frac{\sigma g}{\bar{x}} \times 100$$

Where σ_p and σ_g are the phenotypic and genotypic standard deviations of the family means, respectively, and $\bar{x}$ is a family mean for a given trait.

Expected genetic gain AA = K δp h^2 based on 10% selection intensity.

$$K.H_b.\ \delta p$$

Where K = selection intensity, H_b = broad sense heritability and δp = phenotypic standard deviation of the population. Significance of the selected families was calculated using revised L.S.D. where, L.S.D. = Least significant differences between better parent or random sample and mean of the selected families and was calculated as; Rev. L.S.D$_\alpha$ = (t), $\sqrt{2MSE/r}$ (Al-Rawi and Khalafalla, 1980). Deviation of the observed direct and correlated response to selection in percentage from the better parent and the unselected bulk sample was measured using LSD test.

RESULTS AND DISCUSSION

Description of the F_3 base population:

Data in Table 2 represent the summary statistics of the F_3 base population. The criterion of selection; seed yield/plant ranged from 6.4 to 46.63 with an average of 17.15 (gm). The range in the population in seed yield/plant in the F_3 generation fell outside the range of their respective parents reflecting transgressive segregation and/or high level of heterozygosity among the F_3 families. This indicates the feasibility of selection for productivity. The phenotypic variance in the F_3 generation was high (73.21). Broad sense heritability estimates were high for plant height (94.65%), height to first capsule (94.89%), number of branches/plant (77.50%), number of capsules/leaf axel (77.50%), number of capsules/plant (94.27%), capsule length (60.57%), seed yield/plant (96.59%) and seed yield/plot (94.27%).

Table 2. Means, phenotypic variance (δ^2_p), genotypic variance (δ^2_g), phenotypic coefficient of variation (CV), heritability in broad sense (H) and expected genetic advance (ΔG) of the base population (F_3) and its parents of the studied traits season (2012).

Population 1	Plant height, cm	Height to first capsule, cm	No. of branches/ plant	Capsule length, cm	No. of capsules/ leaf axel	No. of capsules/ plant	Seed yield /plant, g	Seed yield /plot, g
Mean ± SE	177.6±1.16	59.2±0.93	3.993±1.29	2.90±0.02	1.16±0.031	153.6±3.69	17.15±0.49	209.9±3.86
Max.	245.16	110.35	12.21	4.09	3.0	340.00	46.63	407
Min.	130.03	10.10	1.01	2.18	1.0	57.14	6.4	85.6
CV%	11.34	27.34	55.83	11.55	46.85	41.65	49.88	31.86
σ^2_g	383.9	248.5	4.970	1.112	1.295	3857.1	70.71	4216.8
σ^2_p	405.6	261.9	6.413	1.836	2.01	4091.6	73.21	4473.3
H %	84.65	94.89	77.50	76.57	77.5	94.27	96.59	94.27
ΔG	39.33	31.68	4.05	1.693	2.267	124.4	17.05	130.07
ΔG/mean %	22.14	53.51	101.4	58.37	195.4	80.99	99.39	61.95
P_1								
Mean ± SE	180.0±2.89	53.33±8.82	2.00±0.58	2.70±0.10	1.0±0.0	80.00±2.89	8.36±0.388	117.4±9.46
Max.	185.0	70.13	3.54	2.8	1.0	85.01	9.0	135.0
Min.	175.0	40.05	1.04	2.5	1.0	75.31	7.69	102.6
P_2								
Mean ± SE	163.3±11.67	56.67±7.26	1.667±0.33	2.67±0.17	3.00±0.0	72.33±7.31	9.93±0.15	134.5±9.31
Max	185.3	70.31	2.06	3.0	3.0	82	10.16	152.2
Min.	145.0	45.10	1.0	2.5	3.0	58	9.64	120.7

ΔG = Expected genetic advance from selection 10% superior plants.

High estimates of broad sense heritability coupled with high or low δ^2_p gave high estimates of expected genetic advance from selection of 10% superior plants. The expected genetic advance ranged from 22.14% for plant height to 195.4% for number of capsules/leaf axel.

With respect to the F_3 generation mean, it could be noticed that means of all traits were better than the better parent except the plant height. These results are in agreement with those reported by Parameshwarappa *et al.* (2009), Menzir (2012), Sumathi and Muralidharan (2010), Ismaila and Usman (2012) and Mahdy *et al.* (2015a).

The correlation coefficient (Table 3), showed that the plant height had positive and highly significant correlation with number of branches/plant, height to first capsules, number of capsules/plant and seed yield/plant. These results indicate that selection for seed yield/plant could increase yield via its effect of number of capsules/plant. These results are in agreement with those obtained by Ibrahim and Khidir (2012).

Table 3. Simple correlation coefficients among the traits in the F_3 generation (base population).

	Plant height	**Height to first capsule**	**No. of branches / plant**	**Capsule length**	**No. of capsules / leaf axel**	**No. of capsules / plant**	**Seed yield /plant**	**Seed yield/plot**
Plant height	-	0.228**	0.194**	0.088	-0.032	0.196**	0.215**	-0.029
Height to first capsule		-	0.344**	-0.181**	-0.328**	0.093	-0.094	0.151**
No. of branches/ plant			-	-0.135*	0.078	0.310**	0.218**	0.103
Capsule length				-	0.308**	-0.184**	-0023	0.142*
No. of capsules/ leaf axel					-	-0.017	0.022	-0.170**
No. of capsules/ plant						-	0.349**	0.077
Seed yield/plant							-	-0.207**
Seed yield/plot								-

***, **, Significant at the 0.05 and 0.01 levels of probability, respectively.**

Seed yield/plant showed positive and highly significant correlations with plant height, number of branches/plant and number of capsules/plant. Aya Salah (2015) found that seed yield/plant showed significant correlations with number of capsules/plant, capsule length, height to first capsule and plant height. Sarwar *et al.* (2005), Chowdhury *et al.* (2010), Vanishree *et al.* (2011), Ibrahim and Khidir (2012) and Ismaila and Usman (2012) came to the same conclusion.

Pedigree selection for seed yield/plant:

1- Variability and heritability estimates in F_5 generation:

After two cycles of pedigree selection for seed yield/plant the entries mean squares (10 selected families + 2 parents + bulk sample) were highly significant ($P \leq 0.01$) for the criterion of selection and the other traits in the F_5 generation (Table 4). The GCV of seed yield/plant was 15.50, and it ranged from 9.44% for capsule length to 52.70% for height to first capsule. Two cycles of pedigree selection rapidly depleted the variability in the selection criterion (seed yield/plant). Its PCV was depleted from 49.88% in the F_3 to 22.68% in the F_5 generation. Therefore, further cycles of selection for seed yield/plant will not be fruitful, and selection for this trait should be practiced in the early segregating generations. The PCV and GCV of the other traits were (more than 10%) except for capsule length which were moderate. The small error variance for most traits cause very close estimates of phenotypic and genotypic variability, and resulted in unreliable high estimates of heritability. The other cause of very high estimates of heritability was the large mean squares of families compared to small error variance. This could be ascribed to evaluation of the selected families at one location for one season, which inflated the family's mean squares by the confounding effects of the interaction among families, years and locations. Reddy *et al.* (2001) found high GCV, PCV and heritability as percent of mean for seed yield per plant, total number of capsules per plant, capsule length, branches/plant and plant height. These results are in harmony with those reported by Solanki and Deepak (2003), Babu *et al.* (2004), Ganapathy *et al.* (2007) and Mahdy *et al.* (2015b).

Table 4. Mean squares, heritability estimates, genotypic (GCV%) and phenotypic (PCV%) coefficients of variability of the selected families for seed yield/plant in the F_5 generation in season 2014.

Pop. 1		**Mean square**							
S.V.	**d.f**	**Plant height, cm**	**Height to first capsule, cm**	**No. of branches / plant**	**Capsule length, cm**	**No. of capsules / leaf axel**	**No. of capsules / plant**	**Seed yield /plant, g**	**Seed yield /plot, g**
Reps.	2	29.94	254.1	0.949	0.042	0.0001	755.7	0.513	583.1
Entries	12	1237.8**	553.7**	18.15**	0.245**	1.676**	15278.5**	307.7**	7760.3**
Error	24	107.3	101.8	1.254	0.071	0.0001	226.2	20.56	492.7

Pop. 1		Mean square							
S.V.	d.f	Plant height, cm	Height to first capsule, cm	No. of branches/plant	Capsule length, cm	No. of capsules / leaf axel	No. of capsules/ plant	Seed yield/plant, g	Seed yield/plot, g
Reps.	2	40.83	272.5	1.600	0.012	0.0001	1005.4	740.9	1.478
Entries	9	1475.6**	732.3**	18.15**	0.306**	1.200**	11194.3**	7980.5**	98.87**
Error	18	93.61	90.09	1.452	0.086	0.0001	253.2	580.7	27.23
GVC %		11.52	25.90	46.26	9.44	52.70	29.75	26.85	15.50
PCV %		12.63	30.87	51.95	13.91	52.71	30.77	29.84	22.68
H %		83.11	70.38	79.31	70.73	99.98	93.51	80.94	46.73

***, **, Significant at 0.05 and 0.01 levels of probability, respectively. H= Heritability in broad sense.**

2- Means and direct observed selection gain in seed yield/plant:

Mean seed yield/plant of the ten selected families in the F_5 generation after two cycles of selection are shown in Table (5). The selection criteria; seed yield/plant ranged from 21.42 to 39.80 with an average of 31.53 g compared with 17.49 for the bulk sample and 9.93 for the better parent Shandaweel 3. All the selected families showed significant ($P \leq 0.01$) differences from both the unselected bulk sample and the better parent. The average observed selection gain in seed yield/plant was significant ($P \leq 0.01$) and accounted for 80.27% of the better parent compared to 76.13% from the first cycle (Table 6). The retained genetic variability (Table 4) was sufficient for success of further cycles of selection for seed yield/plant. These results are agreement with those obtained by Mahdy *et al*. (2015a,b) who indicated to the possibility of selection for seed yield/plant in the early segregating generations and two cycles of selection were enough to detect the highest productive families.

The correlated gains:

The average correlated gains from the bulk sample (Table 6) were significant ($P \leq 0.05$) for number of branches/plant (27.25%), number of capsules/axis (6.19%), number of capsules/plant (31.58%) and seed yield/plant (80.27%), while the average correlated gains decrease in capsule length. Pedigree selection was an efficient method to improve seed yield/plant in the population under study. However, it accompanied with adverse effects on some traits, especially when the correlated gain calculated in percentage of the better parent. All of the families under study showed significant increase in seed yield/plant of the better parent after two cycles of selection for seed yield/plant. It could be concluded that two cycles of single trait selection for seed yield/plant succeeded to improve the productive in the population under study but it caused adverse effects in another trait. Therefore, selection index involves important traits could be better in improving sesame. These results are in harmony with those obtained by Alake *et al*. (2010) and Yol *et al*. (2010).

Table 5. Means of the studied traits of the selected families for seed yield/plant in the F_5 generation, season 2014.

Selected Family No.	Plant height	Height to first capsule	No. of branches / plant	Capsule length	No. of capsules / leaf axel	No. of capsules/ plant	Seed yield/plant	Seed yield/plot
13	176.7	63.33	4.67	2.67	1.00	298.3	37.76	146.2
34	188.3	70.00	5.00	2.83	1.00	176.7	38.22	229.5
58	150.0	46.67	5.00	2.53	1.00	154.0	28.09	109.2
148	195.0	50.00	4.33	3.50	1.00	180.7	21.42	277.5
156	176.7	56.67	2.33	2.90	1.00	133.0	29.31	120.0
174	198.3	35.00	5.33	2.77	1.00	290.3	29.63	200.8
261	171.7	41.67	3.00	2.83	1.00	203.3	39.80	164.5
414	233.3	86.67	11.00	3.33	3.00	229.7	30.94	219.2
443	198.3	68.33	7.00	2.50	1.0	240.0	33.01	190.6
465	175.0	46.67	3.33	2.83	1.00	123.7	27.10	192.3
Mean	186.3	56.50	5.09	2.869	1.2	202.9	31.53	184.9
P1	180.0	53.33	2.00	2.70	1.00	80.00	8.36	117.4
P2 (Sh. 3)	163.3	56.67	1.67	2.67	3.00	72.3	9.93	134.5
Bulk	178.5	59.27	4.00	2.90	1.13	154.2	17.49	210.3
RL.S.D. 0.05	9.57	9.32	1.03	0.247	0.015	13.90	4.19	20.51

Table 6. Observed direct and correlated response after two cycles of pedigree selection for seed yield/plant in percentage from the unselected bulk sample; season 2014.

Selected Family No.	Correlated traits							
	Plant height	Height to first capsule	No. of branches / plant	Capsule length	No. of capsules / leaf axel	No. of capsules / plant	Seed yield/plot	Seed yield/plant
13	-1.01	6.85	16.75	-7.93	-11.50	83.45	-30.48	115.89
34	5.49	18.10	25.00	-2.41	-11.50	14.59	9.13	118.52
58	-15.97	-21.26	25.00	-12.76	-11.50	-0.13	-48.07	60.61
148	9.24	-15.64	8.25	20.69	-11.50	17.19	31.95	22.47
156	-1.01	-4.39	-41.75	0.00	-11.50	-13.75	-42.94	67.58
174	11.09	-40.95	33.25	-4.48	-11.50	88.26	-4.52	69.41
261	-3.81	-29.69	-25.00	-2.41	-11.50	31.84	-21.78	127.56
414	30.70	46.23	175.00	14.83	165.49	48.96	4.23	76.90
443	11.09	15.29	75.00	-13.79	-11.50	55.64	-9.37	88.74
465	-1.96	-21.26	-16.75	-2.41	-11.50	-19.78	-8.56	54.95
Bulk Mean	4.37	-4.67	27.25	-1.07	6.19	31.58	-12.08	80.27
Gain of 1st cycle								76.63
RLSD 0.05	16.60	16.04	2.07	0.502	0.0003	27.29	41.31	8.947
RLSD 0.01	22.74	21.97	2.83	0.687	0.0004	37.38	56.59	12.26

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

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الانتخاب المنسب لتحسين محصول البذرة في عشيرة انعزالية من السمسم

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قسم المحاصيل الزيتية – معهد بحوث المحاصيل الحقلية – مركز البحوث الزراعية – الجيزة

أجريت دورتين من طريقة الانتخاب المنسب على عشيرة انعزالية من الجيل الثالث إلي الخامس في السمسم لتحسين صفة محصول البذور في محطة البحوث الزراعية – عرب العوامر – أسيوط خلال المواسم الصيفية 2012 و2013 و2014 في أرض رملية جيرية. كانت الاختلافات الوراثية الظاهرية معنوية جداً في عائلات الجيل الثالث بما يكفي لإجراء الانتخاب. وأوضحت النتائج أن معامل الاختلاف نقص للصفة الانتخابية (وزن محصول النبات) من 49.88% في الجيل الثالث إلي 22.68% في الجيل الخامس. درجة التوريث بمعناها العام كانت عالية جداً لمعظم الصفات ووصل إلى 93.32% لصفة وزن محصول النبات بعد دورتين من الانتخاب المنسب. كان التقدم الوراثي المشاهد لمحصول البذور / النبات معنوياً (P≤0.01) 80.27% نسبة إلى العينة العشوائية. أظهرت كل العائلات المنتخبة في الجيل الخامس معنوية عالية في الزيادة في محصول النبات. من هذه الدراسة يمكن استنتاج أن الانتخاب المنسب كان فعالاً في تحسين الصفة المفردة وتحسين مستوي محصول البذور للنبات في العشيرة تحت الدراسة. ويمكن الانتخاب لهذه الصفة في الأجيال الانعزالية المبكرة كما أن دورتين من الانتخاب كانتا كافيتين للتعرف علي أعلي العائلات إنتاجية ولكن صحب الانتخاب لصفة واحدة تأثير سيء علي صفات أخري لذلك ينصح باستخدام أدلة الانتخاب التي تشمل مجموعة من الصفات الهامة في تحسين محصول وإنتاجية السمسم.