

**COMPARISON BETWEEN PEDIGREE SELECTION AND INDEPENDENT
CULLING LEVELS TECHNIQUES FOR IMPROVING SEED YIELD
AND ITS COMPONENTS IN SESAME**

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ABSTRACT

The current experiments were carried out at El-Mattana Agricultural Research Station, Luxor Governorate, Egypt, during the three summer seasons from 2016 to 2018, to compare the relative efficiency of two selection procedures, namely pedigree selection and independent culling level (ICL), for improving seed yield and its components in sesame. The genetic materials were the F₃, F₄ and F₅ generations. This study was carried out on 182 of F₃ families derived from a single cross between Introduction 688 X hybrid 102 family 2, and added F₃ bulked random sample. Variations among the F₃ families were highly significant for all the studied traits. The results indicated that pedigree selection decreased the genetic variability measured as genotypic coefficient of variability (GCV) of seed yield/plant and other studied traits. The GCV of seed yield/plant decreased from 28.22 % in the base population to 7.79 % after two cycles of selection, from 32.89 to 13.37 % for capsules No./plant, from 11.11 to 7.63 % for fruiting zone length, and from 13.24 to 9.20 % for 1000-seed weight. Heritability in the broad sense after two cycles of selection was high for seed yield/plant (85.69 %), capsules No./plant (96.55 %), fruiting zone length (89.78 %) and 1000-seed weight (76.40 %). The realized heritability for pedigree selection increased, indicating that increasing seed yield was accompanied with increases in related traits, and the realized heritability increased after the two cycles of ICL technique by 33.9 % from the bulk sample for grain yield/plant. Heritability in the broad sense after two cycles of (ICL) was high for all the studied traits.

Key words: *Sesamum indicum*, Selection methods, Segregating generations, Heritability.

1. INTRODUCTION

Sesame (*Sesamum indicum* L., Pedaliaceae), a self-pollinated crop, is an ancient cultivated oil crop (Ashri, 2007), better known as "queen of oil seed crops" by virtue of its high oil quality.

Sesame growing areas in Egypt are decreasing due to low seed yield and prices compared to the other competitive summer crops in the crop rotation, and its susceptibility to root-rot diseases. Plant breeders are continuously searching for more effective and efficient methods to improve seed 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. Abo-Elwafa and Ahmed (2005) found that the observed gain in seed yield of two populations was better when selection was 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. In addition, the positive relationship between seed yield and the other traits such as capsules number, fruiting zone length and 1000-seed weight proved rewarding in breeding for high yield in sesame (El-Shakhess *et al.*, 2002). El-Shimy (2005) found that the observed gain in seed yield/plant reached 49.12 and 45.78 % of the better parent when selection was practiced for seed yield in two populations after two cycles. However, the correlated gains were 40.29 and 3.87 %, and 29.90 and 6.19 % when selection was exerted for

fruiting zone length and capsules No./plant, respectively. In another two populations, El-Shimy *et al.* (2005) found great depletion of genetic coefficient of variability from F₃ (22.5 and 22.82 %) to F₆ generation (3.66 and 4.18 %) and recorded observed gain of 28.64 and 31.53 % of the bulk sample of the two populations after three cycles of pedigree selection for seed yield. High heritability, phenotypic and genotypic coefficients of variability for plant height, capsules No./plant, days to 50 % flowering and seed yield/plant were reported by Parameshwarappa *et al.* (2009), Chowdhury *et al.* (2010), and Akbar *et al.* (2011). And, high expected gain were reported by Sumathi and Muralidharam (2010), Ismaila and Usman (2012) and Menzir (2012). On the contrary, Sivaprased and Yadavalli (2012) found low genotypic variability, heritability and expected gain in seed yield/plant in the F₂ and F₃ generations. Many investigators reported high genotypic and phenotypic coefficients of variability and genetic advance in seed yield and its components in sesame (Gidey *et al.*, 2013; and Ismail *et al.*, 2013).

The efficiency of a breeding program is largely dependent on the efficiency of selection criteria and the selection method used. The present study was carried out to compare the efficiency of two selection methods, namely pedigree method and independent culling levels method in one population of sesame.

2. MATERIALS AND METHODS

The present study was carried out at El Mattana Agricultural Research Station, Luxor Governorate, Egypt, during the three successive summer seasons 2016, 2017 and 2018. The breeding material used in this study was 180 F₃ families traced back to random F₂ plants from the cross: Introduction 688 X hybrid 102 family2 (Table 1).

sample (a mixture of equal No. of seeds from each plant to represent the generation mean) were sown on April 15th in a randomized complete block design with three replications according to Steel *et al.* (1997). Each plot was a single row of 4 m long, 55 cm apart, and 10 cm between hills within a row. Each parent was sown in two rows, in addition to F₃ family was sown in one row and the bulked population was sown in two rows each replicate. The recommended cultural practices were adopted throughout the growing season. The following traits were measured on ten guarded random plants in each plot:

Plant height (cm), fruiting zone length (cm), branches No./plant, capsule length (cm); capsules No./plant, seed yield/plant (g), 1000-seed weight (g) (calculated from the selected plants), seed oil percentage: determined by using petroleum ether (Bp 40-60°) as solvent in Soxhlet apparatus according to the method of A.O.A.C. (1980).

Concerning the pedigree selection method, the best 30 plants of the base F₃ population based on superiority of seed yield/plant were saved to give the F₄ families. Furthermore, the best 30 plants fulfilled the following ICL method for the three traits were selected for the next cycle of the population and selection was applied for the studied traits according to the following levels (fruiting zone length ≥ 103 cm, capsules No./plant ≥ 82 and seed yield/plant ≥ 22 g).

In 2017 season (F₄ generation), the 30-families selected for pedigree selection and independent culling levels along with the parents and F₄ bulk sample were sown on May 15th in two separate experiments in a randomized complete block design with three replications. Each group of families (30 families) for seed yield/plant (pedigree selection) and independent culling levels were analyzed separately. The best 10 families for seed yield/plant and independent

Table (1): The details of the studied sesame genotypes in this experiment.

No .	Genotype	Origin	Main description	
			Capsules No./ leaf axel	Branching habit
1	Introduction 688	FAO	Single	Non branched
2	Hybrid 102 family 2	Egypt	Three	Branched

In 2016 season, the 182 F₃ families with the original parents and F₃ bulked random

culling levels were saved to give the F₅ families.

In 2018 season, the 10-F₅ families covering all selection procedures with the the parents and F₅ bulk sample were sown as previous seasons. The data were scored as in the earlier experiments.

2.1. Statistical analysis

For each season, estimates of phenotypic (σ_{ph}^2) and genotypic variance (σ_g^2) and covariance, as well as broad sense heritability estimates were calculated from expected mean square (EMS) of the variance and covariance components of the selected families as presented in Table (2).

Table (2): The analysis of variance and mean square expectations.

S.O.V	d.f	MS	Expected mean squares
Replications	r- 1		
Genotypes	g - 1	M ₂	$\sigma^2 e + r\sigma^2 g$
Error	(r-1)(g-1)	M ₁	$\sigma^2 e$

Where: r and g = replications No. and genotypes No., respectively.

σ_e^2 = error variance. σ_g^2 = genetic variance.

The phenotypic (σ_{ph}^2) and genotypic (σ_g^2) variances were estimated as given by Al-Jibouri *et al.* (1958):

The genotypic variance $\sigma_g^2 = (M_2 - M_1) / r$

The phenotypic variance $\sigma_{ph}^2 = \sigma_g^2 + \sigma_e^2 / r$

The genetic covariance (cov. g₁₂) and phenotypic covariance (cov. p₁₂) between pairs of traits (1 and 2) were calculated according to Steel *et al.* (1997) as follows:

-Broad sense heritability $H = (\sigma_g^2 / \sigma_{ph}^2) * 100$

- The phenotypic (PCV %) and genotypic (GCV %) coefficients of variability were estimated according to Burton (1952).

Phenotypic coefficient variability (PCV):

$$PCV\% = \left(\frac{\sigma_{ph}}{\bar{x}} \right) * 100$$

Genotypic coefficient of variability:

$$PCV\% = \left(\frac{\sigma_g}{\bar{x}} \right) * 100$$

Where: σ_{ph} and σ_g are the phenotypic and genotypic standard deviations of the families, respectively, and \bar{x} is the family mean for a given trait.

Realized heritability was calculated according to Falconer (1989) from the equation of response, i.e. $R = S h^2$, which were discussed earlier from the point of view of predicting the response to selection, the heritability being estimated as the ratio of the $h^2 = R/S$, where:

R = is response to selection

S = is selection differential.

3. RESULTS AND DISCUSSION

3.1. Description of the base population

The analysis of variance (Table 3) indicated highly significant differences among F₃- families for all the studied traits, indicating the presence of variability among the genotypes. The results of (GCV) and (PCV) are presented in Table (4). The traits of the starting population had a significant effect on early generation selection and the slight difference between (GCV) and (PCV) resulted in high estimates of broad sense heritability for most studied traits.

Greater response to selection could be expected in a population having greater phenotypic and genotypic variances. These data resulted in wide ranges and high estimates of broad sense heritability (more than 64 %) for all studied traits in base population (F₃ generation).

High genotypic and phenotypic variations and heritability for yield and its components were reported by Parameshwarappa *et al.* (2009), Sumathi and Muralidharan (2010) Ismaila and Usman (2012) and Kumar *et al.* (2012).

Table (3): Mean squares for the studied traits of the base population (F₃).

S.O.V	d.f	Mean squares							
		Plant height	Fruiting zone length	Capsule length	Branches No./ plant	Capsules No./ plant	Seed yield/ plant	1000-seed weight	Oil %
Replication	2	2500.65	3122.51	0.90	1.59	16919.13	372.19	24.15	1.23
Genotypes	181	1429.65**	817.64**	0.57**	1.64**	3067.09**	202.62**	1.09**	139.54**
Error	362	358.94	274.59	0.20	0.41	658.65	72.02	0.32	34.38

**significant at the 0.01 level.

Table (4): Means, phenotypic (PCV %), genotypic (GCV %) coefficients of variability and heritability in broad-sense for the studied traits in the F₃ families.

Item	Plant height (cm)	Fruiting zone length (cm)	Capsule length (cm)	Branches No./plant	Capsules No./plant	Seed yield/plant (g)	1000-seed weight (g)	Oil %
Mean	186.27	121.12	3.49	3.48	86.14	23.38	3.83	50.57
Maximum	253.33	157.67	5.40	7.67	191.67	46.10	6.67	66.58
Minimum	123.33	68.67	2.33	1.00	50.40	10.07	2.73	32.67
P ₁	189.33	116.67	3.63	3.67	79.00	19.33	3.12	57.69
P ₂	245.00	153.33	4.00	4.00	95.33	22.40	2.90	55.00
Bulk	179.70	121.12	3.49	3.48	86.14	23.38	3.83	48.72
CV%	10.17	13.68	12.71	18.49	29.79	36.30	14.66	11.59
GCV %	10.14	11.11	10.03	18.35	32.89	28.22	13.24	11.71
PCV %	11.72	13.63	12.43	21.23	37.12	35.15	15.71	13.49
Heritability %	74.89	66.42	65.14	74.72	78.53	64.46	70.97	75.36

3.2. Pedigree selection

The pedigree selection was practiced on the population of sesame for seed yield/plant.

3.2.1. Variances and means

The analysis of variance for the selected families for seed yield/plant and other traits in cycle 1 (F₄ generation) and cycle 2 (F₅ generation) is presented in Table (5). The results indicated highly significant differences among genotypes. This result reflected the genetic make-up of those selected families in population; consequently offer good chance for selection.

The average seed yield/plant of the selected families in Table (6) increased from 34.74 g in F₄ generation (cycle 1) to 41.49 g in F₅ generation (cycle 2). The average seed yield/plant for the bulk population was 20.00 and 27.00 g in the F₄ and the F₅ generations, respectively.

The results indicated that pedigree selection

decreased the genetic variability measured as genotypic coefficient of variability of the selection criterion and other traits after two cycles of selection. This may due to the low No. of selected families (ten families out of 30 families) and increasing the percentage of the homozygosity than in the F₅ generation. However, the (GCV) of seed yield/plant decreased from 28.22 % in the base population (Table 6) to 7.79 % after two cycles of selection from 32.89% to 13.37% for capsules No./plant, from 11.11 % to 7.63 % for fruiting zone length, and from 13.63 to 7.96 % for capsule length. The phenotypic coefficients of variation (PCV) values were in line with those recorded for (GCV) in population. Falconer (1989) stated that selection reduces genotypic variance of the following generation. The results indicated that pedigree selection decreased the genetic variability measured as genotypic coefficient of variability for seed yield/plant the studied traits

Table (5): Analysis of variance after the first and second cycles of pedigree selection for seed yield/plant.

Cycle No.	S.O.V	d.f	Mean squares							
			Plant height	Fruiting zone length	Capsule length	Branches No. / plant	Capsules No. / plant	Seed yield/plant	1000-seed weight	Oil %
C ₁ (F ₄)	Replication	2	72.12	506.80	5.26	0.67	6157.33	10.52	1.08	13.16
	Genotypes	29	1037.34**	466.65**	0.74**	1.39**	2220.57**	2135.02**	0.72**	123.95**
	Error	58	141.97	52.48	0.19	0.42	225.24	1023.64	0.12	16.77
C ₂ (F ₅)	Replication	2	441.23	295.61	1.19	0.13	1997.65	35.47	2.47	8.93
	Genotypes	9	846.19**	334.11**	0.46**	1.18**	1018.23**	85.60**	0.60**	83.60**
	Error	18	86.40	49.54	0.09	0.27	94.20	17.24	0.14	8.57

**significant at 0.01 level.

of the two cycles of selection which is in agreement with Abo-Elwafa and Ahmed (2005), El-Shimy (2005), Ismail *et al.*(2013) and Mahdy *et al.* (2015).

3.2.2. Heritability and realized heritability estimates

Theoretically, heritability estimate of family means increases with the increase in homozygosity. The results in (Table 6) indicated that heritability estimates increased from the F₄ (cycle 1) to the F₅ generation (cycle 2) for all studied traits. Estimates of heritability in broad sense after two cycles of selection were high for seed yield/plant (85.69 %), 1000-seedweight (95.98 %) capsules No./plant (96.55 %) and fruiting zone length (89.78 %).

The realized heritability estimated from the realized gain in both cycles of single trait selection in the studied population decreased

from C₁ to C₂ for seed yield/plant and all studied traits, revealing the less genetic variation in C₂ comparing to C₁ (Table 6).

3.2.3. The expected genetic gain from selection

Results in Table (7) show the expected genetic gain (ΔG) based on the proportion of the selected families in population after carrying out two cycles of pedigree selection. High and moderate estimates of broad sense heritability were coupled high estimates of expected genetic gain from selection of 16.5 % and 33 % superior plants of pedigree selection for seed yield/plant in the F₄ and F₅ generations, respectively (Table 7). With respect to the expected genetic gain from selection calculated from bulk means and better parents, the data clearly demonstrate high percentage of the expected genetic gain in relation to better parents in most studied traits.

Table (6): Means, range, phenotypic (PCV %), genotypic (GCV %) coefficients of variability, heritability in broad-sense (H.B.S) and realized heritability in the two cycles of pedigree selection for seed yield/plant.

Cycle No.	Item	Plant height (cm)	Fruiting zone length (cm)	Capsule length (cm)	Branches No./ plant	Capsules No./ plant	Seed yield/plant (g)	1000-seed weight (g)	Oil %	
C ₁ (F ₄)	Range	Min.	185.00	112.00	2.73	2.47	82.00	28.00	2.91	37.60
		Max.	253.33	169.00	5.10	5.30	182.67	47.03	4.90	61.00
	F ₄ selected families	212.39	132.57	4.20	3.59	120.95	34.74	4.02	52.94	
	P ₁	189.33	116.67	3.63	3.33	80.67	17.67	3.12	57.69	
	P ₂	232.33	147.33	4.00	3.67	95.33	20.90	2.90	55.50	
	Bulk	203.33	138.33	4.00	4.00	106.00	20.00	3.80	51.93	
	CV%	5.61	5.46	10.36	17.96	12.41	12.09	9.94	7.74	
	GCV %	8.13	8.86	10.21	15.89	21.32	12.43	11.11	11.29	
	PCV %	8.76	9.41	11.83	18.97	22.49	14.26	12.20	12.14	
	H.B.S %	86.31	88.75	74.46	70.13	89.86	76.03	82.90	86.47	
Realized heritability		0.63	0.87	0.79	0.49	0.96	0.88	0.70	0.24	
C ₂ (F ₅)	Range	Min.	174.00	122.67	3.82	2.77	117.33	36.80	3.47	42.15
		Max.	233.50	163.67	5.06	4.64	172.67	46.50	4.87	59.26
	F ₅ selected families	213.07	136.77	4.42	3.67	135.35	41.49	4.26	53.97	
	P ₁	189.33	116.67	3.63	3.67	79.00	17.00	3.12	57.69	
	P ₂	220.00	153.33	4.00	4.00	95.33	20.47	2.90	55.00	
	Bulk	203.33	138.33	4.00	4.00	106.00	27.00	3.20	48.50	
	CV%	4.36	5.13	6.62	14.20	7.17	9.98	8.86	5.43	
	GCV %	7.47	7.63	7.96	15.01	13.37	7.79	10.32	9.27	
	PCV %	7.88	8.06	8.83	17.10	13.61	8.42	10.53	9.78	
	H.B.S %	89.79	89.78	81.27	77.01	96.55	85.69	95.98	89.74	
Realized heritability		0.91	0.17	0.28	0.36	0.32	0.24	0.59	0.54	

Table (7): Expected genetic advance (ΔG) of the population and as percentage from bulk mean and better parent after F₄ (cycle 1) and F₅ (cycle 2) generation of pedigree selection for seed yield/plant and independent culling levels (ICL).

Item	Generation	Expected gain estimates	Plant height (cm)	Fruiting zone length (cm)	Capsule length (cm)	Branches No./plant	Capsules No./plant	Seed yield/plant (g)	1000-seed weight (g)	Oil %
SY/PL	F ₄ generation	ΔG	24.08	16.60	0.56	0.72	36.67	5.65	0.60	8.34
		ΔG /bulk	11.84	12.00	13.89	17.93	34.59	28.25	15.67	16.05
		ΔG /better	10.36	11.27	13.89	19.56	38.47	27.03	19.08	14.45
	F ₅ generation	ΔG	17.49	10.43	0.37	0.56	19.39	4.95	0.40	5.50
		ΔG /bulk	8.60	7.54	9.19	14.02	18.30	18.33	12.44	11.33
		ΔG /better	7.95	6.80	9.19	14.02	20.34	24.18	12.75	9.53
ICL	F ₄ generation	ΔG	32.19	27.90	0.46	0.90	48.35	12.52	0.72	6.97
		ΔG /bulk	15.83	20.17	11.41	22.48	45.62	62.61	18.90	13.42
		ΔG /better	12.87	23.92	12.56	24.52	61.21	96.32	12.88	11.96
	F ₅ generation	ΔG	14.09	19.36	0.49	0.79	30.75	4.76	0.44	5.95
		ΔG /bulk	6.93	14.00	12.20	19.82	29.01	23.81	12.45	11.46
		ΔG /better	6.41	12.63	12.20	19.82	32.26	23.26	15.31	10.81

SY/PL= Seed yield/plant, ICL= Independent culling level, ΔG = Population expected genetic gain, ΔG /bulk= Bulk mean expected genetic gain, ΔG /bulk = Better mean expected genetic gain.

Concerning the genetic advance as percentage of bulk mean after carrying out two cycles of pedigree selection for seed yield/plant was high for seed yield/plant (18.33%) followed by capsules No. (18.30 %), branches No./plant (14.02 %) and 1000-seeds weight (12.44%). It was minimum for each of fruiting zone length (7.54 %) and plant height (8.60 %). Similarly, genetic advance as percentage of better parent was high for seed yield/plant (24.18 %) followed by capsules No. (20.34 %) after carrying out two cycles of pedigree selection (Table 7).

3.2.4. Observed direct and correlated responses after carrying out two cycles of pedigree selection for seed yield/plant

Results in Table (8) show the means (observed direct) of the best 10 families selected according to seed yield/plant and correlated response after carrying out two cycles of pedigree selection in the F₅ generation. The correlated response was estimated as percentage from bulk mean and better parent. The pedigree selection method succeeded to isolate superior genotypes in seed yield/plant with one or more effective attributed traits.

Plant height ranged from 184.0 cm for family No.52 to 243.5 cm for No.115. Nine and eight families out of ten were significantly taller than the bulk mean and the taller parent, respectively (Table 8). Likewise, the highest length of the fruiting zone length of the selected families ranged

from 122.7 cm for family No.52 to 163.7 cm for No.128 with an average of 136.8 cm. Branches No./plant of the selected families ranged from 2.8 for No.111 to 4.6 branches for No.127. All families had branches No./plant than the better parent, except only three families (No.52, No.127 and No.128).

The results revealed that there was a wide range in capsules No./plant, i.e. from 117.3 for No.122 to 155.2 for No.128 with an average of 135.4 capsules. Most of the selected families were significantly higher in capsules No./plant than both of bulk sample and the better parent. It is also clear that the family No.127 was superior from bulk sample and better parent by 62.9 and 81.1 %, respectively. The seed yield of the ten selected families ranged between 37.3 and 46.5 g with an average of 41.5 g. All families did not differ significantly and the family No. 122 was the best family from them and recorded increase of about, 72.2 and 127.2 % in seed yield than bulk mean and better parent, respectively (Table 8).

Concerning 1000-seed weight, the ten selected families ranged between 3.5 and 4.9 g with an average of 4.3 g. The family No. 115 differed significantly and had heavier 1000-seeds weight than both of bulk sample and better parent, and recorded an increase of 52.1 and 56.0 %, respectively. For oil percentage trait, eight

Table (8): Observed direct and correlated responses after two cycles of pedigree selection for seed yield/plant (SY/P) in percentage of the bulk and better parent (P).

Families	Plant height			Fruiting zone length			Capsule length			Branches No./plant		
	Mean	Better P	Bulk	Mean	Better P	Bulk	Mean	Better P	Bulk	Mean	Better P	Bulk
51	226.0	2.73	11.15	136.0	-11.30	-1.69	4.1	6.75	1.42	3.64	-9.08	3.90
52	184.0	-16.36	-9.51	122.7	-20.00	-11.33	4.4	15.53	9.75	4.30	7.58	22.95
61	230.0	4.55	13.11	138.3	-9.78	0.00	4.4	15.53	9.75	3.27	-18.25	-6.57
109	222.0	0.91	9.18	133.0	-13.26	-3.86	4.6	22.11	16.00	3.94	-1.58	12.48
111	225.5	2.50	10.90	131.2	-14.46	-5.18	3.8	0.61	-4.42	2.77	-30.75	-20.86
115	243.5	10.68	19.75	141.7	-7.61	2.41	4.6	22.11	16.00	3.97	-0.75	13.43
122	222.0	0.91	9.18	135.3	-11.74	-2.17	4.6	22.11	16.00	2.94	-26.58	-16.10
127	233.0	5.91	14.59	138.7	-9.57	0.24	5.1	33.07	26.42	4.64	15.92	32.48
128	231.0	5.00	13.61	163.7	6.74	18.31	3.9	2.37	-2.75	4.14	3.42	18.19
166	207.7	-5.61	2.13	127.2	-17.07	-8.07	4.6	22.11	16.00	3.10	-22.42	-11.33
Average	222.5	1.12	9.41	136.8	-10.80	-1.13	4.4	16.23	10.42	3.67	-8.25	4.86
P ₁	189.3			116.7			3.6			3.67		
P ₂	220.0			153.3			4.0			4.00		
Bulk	203.3			138.3			4.0			4.00		
RLSD _{0.05}	14.72			11.15			0.48			0.92		
Families	Capsules No./plant			Seed yield/plant (g)			1000-seed weight (g)			Oil %		
	Mean	Better P	Bulk	Mean	Better P	Bulk	Mean	Better P	Bulk	Mean	Better P	Bulk
51	120.9	26.8	14.1	40.0	95.4	48.1	4.0	28.7	25.5	56.0	-3.0	15.4
52	136.1	42.7	28.4	36.8	79.8	36.3	3.5	11.1	8.3	58.3	1.1	20.2
61	121.7	27.6	14.8	42.7	108.5	58.0	4.5	45.5	41.9	54.0	-6.4	11.3
109	134.0	40.6	26.5	39.9	95.0	47.8	4.5	43.2	39.6	48.3	-16.4	-0.5
111	119.7	25.6	12.9	40.0	95.2	48.0	4.1	30.3	27.1	55.2	-4.3	13.9
115	150.0	57.3	41.5	45.7	123.1	69.1	4.9	56.0	52.1	57.0	-1.2	17.5
122	117.3	23.1	10.7	37.3	82.4	38.3	3.8	20.7	17.7	59.3	2.7	22.2
127	172.7	81.1	62.9	46.5	127.2	72.2	4.7	51.2	47.4	42.2	-26.9	-13.1
128	155.2	62.8	46.4	45.8	123.5	69.4	4.1	31.9	28.6	52.0	-9.9	7.2
166	126.0	32.1	18.8	40.3	97.1	49.4	4.6	48.0	44.3	57.6	-0.2	18.7
Average	135.4	42.0	27.7	41.5	102.7	53.7	4.3	36.7	33.3	54.0	-6.4	11.3
P ₁	79.0			17.0			3.1			57.7		
P ₂	95.3			20.5			2.9			55.0		
Bulk	106.0			27.0			3.2			48.5		
RLSD _{0.05}	14.74			6.58			0.60			4.64		

and two families out of ten showed P't significant increase than the bulk mean and the better parent, respectively.

3.3. Independent culling levels procedure

3.3.1. Variances and means

The analysis of variance for the selected families of independent culling levels for cycle 1 (F₄ generation) and cycle 2 (F₅ generation) is shown in Table (9). The results indicated highly significant differences among genotypes.

Means, genotypic and phenotypic coefficients of variability and heritability in broad-sense (H.B.S) of cycles 1 and 2 of

independent culling levels for studied traits are presented in Table (10).

The average seed yield/plant of the selected families (Table 10) increased from 36.01 g in F₄ generation (cycle 1) to 42.20 g in F₅ generation (cycle 2). The length of the fruit zone increased from 148.09 cm in F₄ generation (cycle 1) to 165.02 in F₅ generations (cycle 2). While, increasing the length of the fruit zone and the number of capsules per plant from (148.09 cm and 122.32) in F₄ generation (cycle 1) to (165.02 and 140.16) in F₅ generation (cycle 2), respectively.

Table (9): Analysis of variance after the first and the second cycles for independent culling levels.

Cycle No.	S.O.V	d.f	Mean squares							
			Plant height	Fruiting zone length	Capsule length	Branches No. / plant	Capsules No. / plant	Seed yield/plant	1000-seed weight	Oil %
C ₁ (F ₄)	Replication	2	242.14	884.44	4.36	4.06	3087.14	485.64	1.53	6.66
	Genotypes	29	1671.30**	1315.58**	0.61**	1.46**	3521.48**	7721.85**	0.89**	80.39**
	Error	58	151.97	146.87	0.20	0.20	208.25	1759.07	0.11	8.26
C ₂ (F ₅)	Replication	2	142.97	410.91	0.31	0.10	310.89	192.99	0.35	0.19
	Genotypes	9	627.50**	1099.68**	0.67**	1.64**	2329.63**	581.05**	0.53**	90.74**
	Error	18	100.41	140.91	0.07	0.13	113.38	133.86	0.05	6.15

After two selection cycles of independent culling levels procedure, the (GCV) of seed yield/plant, fruiting zone length and capsules No./plant were decreased to 10.40, 10.83 and 18.68 %, respectively, compared to 11.47, 7.10 and 12.97 % in single trait selection for seed yield/plant, respectively. El-Shimy (1995) found that the realized seed yield/plot was 46.34, 26.83 and 21.95 % in population I and 22.95, 36.07 and 40.16 in population II using selection index, independent culling levels and pedigree selection, respectively after two cycles of selection.

In general, it could be concluded that the genetic variability retained after

independent culling levels was larger than that obtained from single trait selection. These results were expected because single trait selection was exerted and directed to one trait only (selection criterion), however, independent culling levels was directed to all traits incorporated. El-Shimy (2005) found that the genetic variability retained after (ICL) was larger than that after single trait selection.

3.3.2. Heritability and realized heritability estimates

The results in Table (10) showed that estimates of heritability in the broad sense after two cycles of independent culling

Table (10): Means, range, phenotypic (PCV %), genotypic (GCV %) coefficients of variability, heritability in broad-sense (H.B.S) and realized heritability in the two cycles of independent culling levels.

Cycle No.	Item		Plant height (cm)	Fruiting zone length (cm)	Capsule length (cm)	Branches No. / plant	Capsules No. / plant	Seed yield/plant (g)	1000-seed weight (g)	Oil %
	C ₁ (F ₄)	Range	Min.	123.33	68.67	2.33	1.00	50.40	10.07	2.73
Max.			253.33	157.67	5.40	7.67	191.67	46.10	6.67	66.58
F ₄ selected families		206.52	148.09	3.78	3.84	122.32	36.01	4.10	49.32	
P ₁		189.33	116.67	3.63	3.67	79.00	19.33	3.12	57.69	
P ₂		245.00	153.33	4.00	4.00	95.33	22.40	2.90	55.00	
Bulk		179.70	121.12	3.49	3.48	86.14	23.38	3.83	48.71	
CV%		5.97	8.18	11.84	11.75	11.80	15.29	8.10	5.83	
PCV %		10.90	13.33	9.80	16.84	27.17	24.63	12.48	9.94	
GCV %		11.43	14.14	11.95	18.15	28.01	26.16	13.33	10.50	
H.B.S %		90.91	88.84	67.27	86.03	94.09	88.61	87.69	89.73	
Realized heritability		0.33	0.66	0.30	0.87	0.82	0.94	0.73	0.70	
C ₂ (F ₅)	Range	Min.	202.17	138.33	3.42	1.67	110.37	38.33	3.54	42.15
		Max.	247.33	204.33	5.06	4.64	187.47	52.33	4.72	63.64
	F ₅ selected families		231.70	165.02	4.04	3.47	145.54	42.20	4.09	53.17
	P ₁		189.33	116.67	3.63	3.67	79.00	17.00	3.12	57.69
	P ₂		220.00	153.33	4.00	3.67	95.33	20.47	2.90	55.00
	Bulk		203.33	138.33	4.00	4.00	106.00	20.00	3.57	51.90
	CV%		4.32	7.19	6.73	10.23	7.32	6.50	5.30	4.66
	PCV %		5.72	10.83	11.05	20.51	18.68	9.96	9.80	9.99
	GCV %		6.24	11.60	11.72	21.35	19.15	10.32	10.27	10.34
	H.B.S %		84.00	87.19	89.00	92.34	95.13	93.03	91.12	93.23
Realized heritability		0.37	0.15	0.91	0.68	0.58	0.16	-0.76	0.43	

levels procedure were high for all traits. The realized heritability estimated from the realized gain in both cycles of independent culling levels selection in the studied population decreased from C₁ to C₂ and all correlated traits, revealing the less genetic variation in C₂ comparing to C₁. El-Shimy (1995) and Ismail *et al.* (2013) reported similar results.

3.3.3. The expected genetic gain from selection

The expected genetic gain from selection in relation to bulk mean and better parents (Table 7), revealed high percentage in most studied traits. Genetic advance as percentage of bulk means after carrying out two cycles of independent culling levels was high for capsules No./plant (29.01 %) followed by seed yield/plant (23.81 %) and fruiting zone length (14.0 %). Similarly, genetic advance as percent of better parent

was high for capsules No./plant (32.26 %) followed by seed yield/plant (23.26 %) after carrying out two cycles of independent culling levels selection.

3.3.4. Observed direct and correlated responses after applying two cycles of independent culling levels selection.

Table (11) shows the means (observed direct) of the best 10 families selected according to the selection independent culling levels and correlated responses after carrying out two cycles in F₅ generation. The correlated responses were estimated as percentage from bulk's mean and better parent. Results show that the independent culling levels selection succeeded to isolate superior genotypes in seed yield/plant with one or more effective attributed traits.

After two cycles of selection, all the selected families were highly significantly improved than the bulk sample and the best parent for length of

Table (11): Observed direct and correlated responses after two cycles of pedigree selection for independent culling levels in percentage of the bulk and better parent (P).

Families	Plant height			Length of fruiting zone			Capsule length			Branches No. /plant		
	Mean	Better P	Bulk	Mean	Better P	Bulk	Mean	Better P	Bulk	Mean	Better P	Bulk
34	202.2	-8.11	-0.57	156.7	2.17	13.25	3.4	-10.09	-14.58	3.5	-12.50	0.00
35	239.0	8.64	17.54	172.7	12.61	24.82	4.0	5.26	0.00	1.7	-58.33	-52.38
39	241.5	9.77	18.77	161.5	5.33	16.75	4.3	11.84	6.25	3.3	-16.67	-4.76
49	234.0	6.36	15.08	168.0	9.57	21.45	4.0	5.26	0.00	3.7	-8.33	4.76
52	220.0	0.00	8.20	162.3	5.87	17.35	3.9	3.07	-2.08	3.4	-14.17	-1.90
56	222.0	0.91	9.18	138.3	-9.78	0.00	4.4	15.53	9.75	3.3	-18.25	-6.57
87	247.3	12.42	21.64	204.3	33.26	47.71	4.0	5.26	0.00	3.8	-4.17	9.52
122	223.0	1.36	9.67	138.7	-9.57	0.24	5.1	33.07	26.42	4.6	15.92	32.48
130	245.0	11.36	20.49	169.7	10.65	22.65	3.9	3.07	-2.08	3.7	-6.67	6.67
142	243.0	10.45	19.51	178.0	16.09	28.67	3.4	-10.09	-14.58	3.6	-10.00	2.86
Average	231.7	5.32	13.95	165.0	7.62	19.29	4.0	6.22	0.91	3.5	-13.32	-0.93
P ₁	189.3			116.7			3.6			3.7		
P ₂	220.0			153.3			4.0			4.0		
Bulk	203.3			138.3			4.0			4.0		
LSD 0.05	16.61			19.68			0.43			0.56		
Families	No. of capsules/plant			Seed yield/plant (g)			1000-seed weight (g)			Oil %		
	Mean	Better P	Bulk	Mean	Better P	Bulk	Mean	Better P	Bulk	Mean	Better P	Bulk
34	110.4	15.8	4.1	40.5	98.0	102.7	4.6	46.6	28.2	53.4	-7.4	2.9
35	187.5	96.6	76.9	38.7	88.9	93.3	3.7	18.8	3.9	63.6	10.3	22.6
39	116.8	22.5	10.2	38.3	87.3	91.7	4.1	30.0	13.7	53.7	-6.9	3.5
49	135.1	41.7	27.4	41.9	104.8	109.5	3.5	13.5	-0.7	51.7	-10.4	-0.4
52	160.9	68.7	51.8	52.3	155.7	161.7	4.0	28.4	12.3	49.1	-15.0	-5.5
56	121.7	27.6	14.8	42.7	108.5	113.3	4.5	45.5	27.3	54.0	-6.4	4.0
87	156.4	64.1	47.5	42.5	107.7	112.6	4.3	36.4	19.3	51.7	-10.3	-0.3
122	172.7	81.1	62.9	46.5	127.2	132.5	4.7	51.2	32.2	42.2	-26.9	-18.8
130	173.5	81.9	63.6	38.3	87.3	91.7	3.9	25.2	9.5	56.9	-1.4	9.6
142	120.7	26.6	13.8	40.2	96.4	101.0	3.6	15.4	0.9	55.5	-3.8	6.9
Average	145.5	52.7	37.3	42.2	106.2	111.0	4.1	31.1	14.7	53.2	-7.8	2.5
P ₁	79.0			17.0			3.1			57.7		
P ₂	95.3			20.5			2.9			55.0		
Bulk	106.0			20.0			3.6			51.9		
LSD 0.05	16.2			4.3			0.3			3.9		

the fruiting zone, number of capsules No./plant and seed yield/plant. It is important to remark that the selected family No.35 exceeds significantly its best parent and bulk for seed yield/plant and branches No./plant %. It has been observed that there are common families between the pedigree method of selection and the method of independent culling levels. Of these families, are No.56 and No. 122, which were considered good families selected to achieve high potentiality of seed yield/plant trait.

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مقارنة بين الانتخاب بطريقة تسجيل النسب وطريقة المستويات المستبعدة المستقلة في تحسين محصول البذور ومكوناته في السمسم

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ملخص

أجرى هذا البحث بمحطة البحوث الزراعية بالمطاعة – محافظة الأقصر- مصر خلال ثلاث مواسم صيفية من 2016 إلى 2018، لمقارنة الكفاءة النسبية لتأثير طريقتين من الانتخاب وهما طريقة الانتخاب المنسب باستخدام صفة محصول البذور كصفة إنتخابية والانتخاب للمستويات المستبعدة المستقلة باستخدام ثلاث صفات محصولية لتحسين محصول البذور ومكوناته في عشيرة إنعزالية من أحد هجن السمسم. كانت المواد الوراثية هي أجيال F₃، F₄، F₅. كانت الإختلافات بين عائلات F₃ ذات أهمية كبيرة لجميع الصفات. وأشارت النتائج إلى أن طريقة الانتخاب المنسب قد قللت من التباين الوراثي الذي تم قياسه كمعامل وراثي لصفة محصول البذور للنبات وغيرها من الصفات المدروسة، كما إنخفض معامل الإختلاف الوراثي (GCV) لصفة محصول البذور للنبات من 28.22% في العشيرة الأساسية إلى 7.79% بعد دورتين من الانتخاب، أيضاً من 32.89% إلى 13.37% لصفة عدد الكبسولات/ نبات ومن 11.11% إلى 7.10% لصفة طول المنطقة الثمرية ومن 13.24% إلى 10.32% لصفة وزن الألف بذرة. كانت كفاءة التوريث بالمعنى الواسع بعد دورتين من الانتخاب عالية بالنسبة لمحصول البذور للنبات (85.69%)، وعدد الكبسولات/ النبات (96.55%)، وطول المنطقة الثمرية (89.78%) ووزن الألف بذرة (95.98%). كما زادت كفاءة التوريث المحققة للإنتخاب المنسب، وكذلك زادت كفاءة التوريث بعد أن تم حساب دورتين من تقنية المستويات المستبعدة المستقلة (ICL) بنسبة 33.9% من العينة السائبة (الخلطة) لمحصول البذور/ نبات. وكانت كفاءة التوريث بالمعنى الواسع بعد دورتين من (ICL) عالية لجميع الصفات.