

Variability of yield and some morphological traits in sixteen sesame genotypes

M. W. Sh. Mahmoud¹, Zeinab, E. Ghareeb²

1- Oil crop Res., Field Crop Res., Inst., Agric. Res. Cen., Giza

2- Central Lab. For Design and Stat. Anal. Res., ARC, Giza, Egypt.

Abstract

The study was carried out during 2013 and 2014 growing seasons in order to determine the genetic behavior of sixteen sesame genotypes grown in East Ewinat Research Station Farm (as a new sandy soil), New Valley, Egypt. Results elucidated that the studied genotypes differed significantly for all characters, except number of branches/plant across seasons. Genotype x season interaction was insignificant for all studied traits, except for flowering date, No. of branches/plant, 1000- seed weight, seed yield /plant and seed yield /fed. Genotypes No.**F1013** and **F1004** followed by **Shandweel 3**, and **Giza 32** showed the highest number of capsules per plant, 1000-seed weight, seed yield/plant, seed yield/fed and oil yield (kg/fed). The highest estimates of broad sense heritability (h_b^2) and high genotypic coefficients of variation (GCV) coupled with high genetic advance (GS%) were obtained for number of capsules per plant, weight of 1000 seeds and seed yield per plant, which suggests the predominance of additive gene effects and selection would be useful for the improvement of these traits. Significant positive correlations were detected between seed yield and each of number of capsules per plant and the weight of 1000-seed. Oil yield showed highly significant and positive correlation with number of capsules per plant, 1000-seed weight, oil content % and seed yield per plant. Therefore, breeding for higher 1000-seed weight and number of capsules per plant leads to a high seed yield per plant; the corollary is true that breeding for higher seed yield is a useful approach to higher oil yield. These findings indicate that selection for each or both number of capsules per plant and the weight of 1000-seed would be accompanied by high yielding ability. The cluster I (**Shandweel 3**, **F1004**, **F1013** and **Giza 32**) which concluded that Shandweel 3 and Giza32 (local genotypes) was considered as cluster with highest yield. Meanwhile, F1004 and F1013 genotypes surpassed the seed and oil yield of Shandweel 3 and Giza32. Then, these selected superior genotypes will be useful in breeding program to improve sesame commercially important characters as seed and oil yield.

Key words: *Sesame, Genotypes, Variability, Heritability, Genetic advance.*

Introduction

Sesame (*Sesamum indicum* L.) is an important seed crop whose oil is desirable commercially and nutritionally. This plant is highly grown in the tropical and sub tropical regions (Azeez and Morakinyo 2009) for its edible oil, protein content and quality, as well as vitamins and amino acids. In Egypt, it is recognized as one of the oil crops; however, it has not attained the status of oil production. The sesame cultivated area is 32187.92 hectare, which represents about 0.49% of the total cultivated area. The production of sesame reaches about 1.15 ton per hectare (Anonymous 2005).

Seed yield is a complex trait, polygenic and highly influenced by environmental conditions. A successful breeding programme depends upon the genetic variability present among the different genotypes. Khidir (1997)

summarized one of the major problems facing sesame production to be: growing of poor and inferior genotypes with low yield and poor quality. To overcome the problems of low productivity of sesame, there must be a sound procedure for selection of high yielding varieties adapted to local environment. Many authors such as **Parameshwarappa *et al* (2009)** have reported a wide range of variability in most characters of the crop including seed yield and its components. **Ali *et al* (2003)** reported high heritability estimates (>80%) for days to 50% flowering, days to maturity and 1000-seed weight. High heritability coupled with high genetic advance was given by height to first capsule. **Gangadhara (2005)** reported high heritability and high genetic advance for plant height, number of capsules per plant and 1000-seed weight which indicate the additive gene action, whereas high heritability and low genetic advance were recorded for days to 50% flowering, days to maturity, number of branches per plant and seed yield per plant which indicate the importance of non-additive gene action. **Akpanlwo *et al* (2009)** reported that all characters studied had high heritability, except capsule length.

The major objective of increasing the genetic potential of yield for most, if not for all, can be achieved through breeding for higher yield or eliminating improper factors that reduce yield. The adaptability of a genotype over diverse environments is usually tested by the degree of its interaction with different environments under which it is planted (**Cooper *et al* 1999**). The success of an improvement programme for a crop essentially depends on the nature and the degree of variability in the attributes of that crop (**Sumathi and Muralidharan 2010**). Heritability of a trait influences the selection programme to a larger extent. Thus, gain from selection for a particular character is a function of its heritability, selection pressure and the variability existing in the base population (**Parameshwarappa *et al* 2009**). Correlation studies, according to **Azeez and Morakinyo (2009)**, provide reliable information on the nature, extent and direction of selection. **Parameshwarappa *et al* (2009)** reported that information on the association of plant characters is of great importance to breeders for selecting desirable genotypes.

Heritability, a measure of the phenotypic variance attributable to genetic causes, has predictive function of breeding crops (**Songsri *et al* 2008**). It provides an estimate of the genetic advance a breeder can expect from selection applied to a population under certain environment. High genetic advance coupled with high heritability estimates offers the most effective selection criteria for selection (**Larik *et al* 2000**). The magnitude of genetic inheritance and expected genetic advance are important for the prediction of response to selection in diverse environments and provide the basis for planning and evaluating breeding programs (**Ahmad *et al.* 2006 and Ahmed *et al.* 2013**). High heritability alone is not enough to make sufficient improvement through selection generally in advance generations unless accompanied by substantial amount of genetic advance (**Bhargava *et al.* 2003**). The utility of heritability therefore increases when it is used to calculate genetic advance, which indicates the degree of gain in a character obtained under a particular selection

pressure. The simplest way for the prediction of the variance components is the experimentation of a large number of genotypes for two or more years and at two or more locations (Mayo 1980).

Therefore, the objectives of the current study were to estimate the phenotypic and the genotypic coefficients of variation, heritability in broad sense, genetic advance and genetic advance as percentage of the mean for yield, yield components and other morphological traits in sixteen sesame genotypes to employ the most successful genotype(s) in a breeding program for the improvement of new faba bean cultivars.

Materials and Methods

Experimental procedures and treatments

A field experiment was conducted for two consecutive seasons: 2013 and 2014, at East Ewinat Research Station Farm (as a new sandy soil), New Valley, Egypt, and the soil properties are illustrated in **Table (1)**. In each season, a randomized complete block design with three replications was used for laying out the field experiment. Each replication was divided into sixteen plots, to which the genotypes were assigned randomly. The plot size was 2.4×5 m. Each genotype was represented by fourteen rows; each row was five meters long and 0.6 m apart. Sixteen sesame genotypes from Field crops Research Institute were used (**Table 2**). The seeds were sown in furrow along the row manually. Sowing date was 18 April 2013 for the first season and 14 April 2014 for the second season. The plants were trimmed to 24 plants/m² three weeks after sowing. The experimental area was kept free of weeds in both seasons. No pest's infestation or plant diseases were observed. Nitrogen fertilizer in the form of urea (46.5% N) was applied at a rate of 80 N kg/ha. Data were recorded on the following traits: days to 50% flowering, plant height (cm), length of fruiting zone (cm), number of branches/plant, number of capsules/plant, 1000-seed weight (g), seed yield/plant (g), seed yield (ard/fed), seed oil content (%) and oil yield (kg/fed).

Table 1. Some physical and chemical analysis of the East Ewinat experimental soil.

Soil characters	2013	2014
Practical size distribution		
Sand%	74.50	73.70
Silt%	18.50	17.90
Clay%	7.00	8.40
Texture grade	Sandy loam	Sandy loam
EC (1 : 1 extract) (dSm ⁻¹)	1.95	1.84
pH(1: 1 suspension)	7.59	7.64
Total Ca Co ₃ %	8.75	8.63
Ca ⁺ (ppm)	140.40	141.20
Mg ⁺⁺ (ppm)	18.60	17.90
Na ⁺ (ppm)	195.20	194.70
K ⁺ (ppm)	78.40	79.40
Cl ⁺ (ppm)	177.50	176.80

NaHCO ₃	(ppm)	423.50	427.20
So ₄	(ppm)	343.20	344.60

Table 2. Name, origin and pedigree for sixteen sesame genotypes used in the experiments.

No.	Name	Origin	Pedigree
1	Shandweel 3	Egypt 1987	A line selected from Giza 32x N.A. 130
2	Sohag 1	Egypt 2005	A line selected from Giza 32x N.A. 413
3	Shandweel 2000	Egypt 2005	A line selected from N.A777.x N.A. 413
4	Sohag 10	Egypt 2005	A line selected from N.A777.x N.A. 413
5	F1016	Egypt 2005	A line selected from N.A777.x N.A. 413
6	F1014	Egypt 2005	A line selected from N.A777.x N.A. 413
7	F1004	Egypt 2005	A line selected from N.A777.x N.A. 413
8	F1003	Egypt 2005	A line selected from N.A777.x N.A. 413
9	Giza 32	Egypt	B 32 (CAN 114 x Type29)
10	F1015	Egypt 2005	A line selected from N.A777.x N.A. 413
11	F1013	Egypt 2005	A line selected from N.A777.x N.A. 413
12	F1007	Egypt 2005	A line selected from N.A777.x N.A. 413
13	F1005	Egypt 2005	A line selected from N.A777.x N.A. 413
14	F8H8	Egypt 2005	A line selected from N.A777.x N.A. 413
15	HF65	Egypt 2005	A line selected from N.A777.x N.A. 413
16	RH1F3	Egypt 2005	A line selected from N.A777.x N.A. 413

Statistical analysis

Analysis of variance was carried out for the data in each season. Pooled analysis was carried out when the errors were homogeneous. The homogeneity of variances for the two seasons was checked by use of **Bartlett's test**, and then combined across the two seasons to test for significant differences among the sixteen genotypes, according to the standard statistical procedure described by **Steel and Torrie (1980)**. Phenotypic and genotypic coefficients of variation, heritability in broad sense (h_b^2) and the genetic advance (GA %) for each character were estimated by using variance components method (**Fehr 1987**).

The genotypic (GCV) and phenotypic (PCV) coefficients of variation were estimated according to the procedure outlined by **Johnson et al (1955)** thus: $PCV = \sigma_p / \bar{x} * 100$, $GCV = \sigma_g / \bar{x} * 100$, where \bar{x} = grand mean. The genetic advance expected under selection, assuming the selection intensity of 5% was calculated as suggested by **Allard (1960)**:

$GS = (K) \sigma_p (h_b^2)$, where: GS = Expected genetic advance K = Selection differential (2.06 at 5% selection intensity) σ_p = Phenotypic standard deviation. Genetic advance as percent of mean (GS %) was calculated using the formula: $GS\% = GS / \bar{x} * 100$.

Results and Discussion

Significance of mean performances due to different sources of variability for studied traits in separate analysis and combined ones are summarized in **Tables (3, 4 and 5)**. Results revealed that the studied genotypes

differed significantly for all traits in each season and combined analyses, except for number of branches/plant in both seasons and combined analyses. Combined analysis of variance across two seasons elucidates that years were significant or highly significant for plant height, number of capsules/plant, 1000- seed weight/plant, seed yield /plant, seed yield (ard/fed) and oil yield (kg/fed). Therefore, it could be concluded that environmental significantly affected the performance of the studied sesame genotypes. However, the evaluation for two seasons under the same location has led to narrower environmental fluctuation, which might have resulted in insignificant effects of season on the performance of some of the important components such as flowering date, length of fruiting zone, branches/plant and oil content (%). These results are in agreement with those obtained by **Parameshwarappa et al (2009)**, **Pham et al (2010)**, **Menzir (2012)**, **Shekhawat et al (2013)** and **Aladji Abatchoua et al (2014)**.

Results showed that genotype x season interaction was insignificant for all studied traits except for flowering date, no. of branches/plant 1000- seed weight, seed yield /plant and seed yield (ard/fed). All traits in both seasons revealed high significant differences among the studied genotypes. This indicates the presence of sufficient variability. This result was in conformity with the results reported by many authors **and Parameshwarappa et al (2009)**.

The mean performances for some agronomic traits of sixteen sesame genotypes are given in **Table (3)**. Data revealed that var. **Giza 32** and **F1015** possessed the earliest flowering genotypes (47.5 days). On the other hand, **F1004** and **F1013** possessed the latest ones (51.17 days). Regarding to plant height, **F1004** and **Sohag 10** possessed the tallest plants (172.50 and 170.83 cm) whereas; **F1004** and **F1005** exhibited the shortest plants (115.00 and 128.33 cm). **F1016** and **Giza 32** revealed shortest plant length of fruiting zone (78.33 and 95.83 cm), meanwhile **Sohag 10** and var. **Giza 32** revealed the tallest ones (135.83 and 133.33 cm). For number of branches per plant, var. **Giza 32** and **F1014** showed the profuse plants (1.55 and 1.36) whereas the var. **Shandweel 3** and **HF65** possessed the lowest branched plants (1.05 and 1.11).

Table 3. Mean performance of sixteen sesame genotypes for some agronomic traits during 2013, 20124 and combined data.

Genotype	Flowering date			Plant height (cm)			Length of fruiting zone(cm)			No. of branches/ pl		
	2013	2014	Comb.	2013	2014	Comb.	2013	2014	Comb.	2013	2014	Comb.
Shandweel 3	50.00	49.67	49.84	145.00	156.66	150.83	100.00	115.00	107.50	1.10	1.60	1.35
Sohag 1	49.00	50.00	49.50	160.00	155.00	157.50	133.33	125.00	129.17	1.00	1.10	1.05
Shandweel 2000	50.33	51.33	50.83	160.00	168.33	164.17	125.00	136.66	130.83	1.07	1.33	1.20
Sohag 10	48.00	49.00	48.50	175.00	166.66	170.83	146.66	125.00	135.83	1.03	1.40	1.22
F1016	48.67	48.33	48.50	110.00	120.00	115.00	70.00	86.66	78.33	1.07	1.17	1.12
F1014	50.33	50.33	50.33	138.33	148.33	143.33	115.00	118.33	116.67	1.37	1.34	1.36
F1004	50.33	52.00	51.17	175.00	170.00	172.50	135.00	131.66	133.33	1.00	1.39	1.20
F1003	48.00	50.33	49.17	151.67	151.66	151.67	125.00	133.33	129.17	1.00	1.24	1.12
Giza 32	47.00	48.00	47.50	120.00	140.00	130.00	90.00	101.66	95.83	1.63	1.46	1.55
F1015	47.00	48.00	47.50	133.33	133.33	133.33	110.00	106.66	108.33	1.33	1.18	1.26
F1013	51.67	50.67	51.17	145.00	145.00	145.00	121.66	123.33	122.50	1.00	1.23	1.12
F1007	48.00	48.00	48.00	125.00	138.33	131.67	100.00	113.33	106.67	1.00	1.25	1.13
F1005	50.00	50.00	50.00	130.00	126.66	128.33	108.33	105.00	106.67	1.03	1.47	1.25
F8H8	49.00	50.00	49.50	140.00	135.00	137.50	111.67	115.00	113.34	1.40	1.30	1.35
HF65	51.00	49.33	50.17	143.33	145.00	144.17	120.00	111.66	115.83	1.00	1.22	1.11

RHIF3	50.67	51.00	50.84	155.00	160.00	157.50	123.33	118.33	120.83	1.00	1.24	1.12
Mean	49.31	49.75	49.53	144.16	147.50	145.83	114.68	116.66	115.67	1.13	1.31	1.22
LSD Season (S)			NS			2.85			NS			NS
Genotype (G)	1.73	1.56	1.14	10.26	12.76	8.03	11.37	12.29	8.20	NS	NS	NS
S x G			NS			11.35			11.60			NS

Table (4) exhibited the mean performance of sixteen sesame genotypes for some sesame traits. The highest number of capsules per plant and 1000-seed weight (157.5 and 150.00, 3.37 and 3.27g) was recorded for **F1013** and **F1004**, respectively, whereas the lowest values (66.00 and 79.00, 1.90 and 1.95 g) was scored for **Sohag 1**, **F8H8**, **F1007** and **F8H8**, respectively. **Giza 32** and **F1015** exhibited the highest values of oil content which gave 53.47 and 53.33%, respectively, but **Sohag 1** and **Shandweel 2000** revealed the lowest values for this trait (40.19 and 42.25%, respectively).

Table 4. Mean performance of sixteen sesame genotypes for some seed traits during 2013, 20124 and combined data.

Genotype	No. of capsules/ plant			1000-seed weight (g)			Oil content (%)		
	2013	2014	Comb.	2013	2014	Comb.	2013	2014	Comb.
Shandweel 3	148.00	155.00	151.50	2.93	3.20	3.07	46.99	47.63	47.31
Sohag 1	57.00	75.00	66.00	2.33	2.66	2.50	40.97	43.52	42.25
Shandweel 2000	62.33	113.33	87.83	2.43	2.66	2.55	38.41	41.97	40.19
Sohag 10	95.67	138.33	117.00	2.17	2.50	2.34	38.34	52.70	45.52
F1016	62.67	96.66	79.67	2.20	2.20	2.20	51.20	49.43	50.32
F1014	132.00	116.00	124.00	3.17	2.76	2.97	47.87	45.67	46.77
F1004	160.00	140.00	150.00	3.33	3.20	3.27	43.90	53.90	48.90
F1003	57.67	103.33	80.50	2.13	2.23	2.18	44.15	46.90	45.53
Giza 32	105.00	145.00	125.00	2.23	2.80	2.52	53.30	53.63	53.47
F1015	86.67	108.33	97.50	2.37	2.66	2.52	52.09	54.57	53.33
F1013	153.33	161.66	157.50	3.40	3.33	3.37	52.17	49.37	50.77
F1007	68.33	94.33	81.33	1.80	2.00	1.90	53.08	53.53	53.31
F1005	111.67	125.00	118.34	2.10	2.13	2.12	47.94	53.97	50.96
F8H8	63.33	94.66	79.00	1.70	2.20	1.95	54.90	50.83	52.87
HF65	68.93	97.33	83.13	2.37	2.30	2.34	53.21	51.93	52.57
RHIF3	93.00	114.33	103.67	2.07	2.23	2.15	49.95	51.83	50.89
Mean	95.29	117.40	106.34	2.42	2.57	2.50	48.03	50.09	49.06
LSD Season (S)			8.80			0.08			NS
Genotype (G)	12.76	17.64	10.67	0.43	0.36	0.28	1.03	0.75	0.63
S x G			15.09			NS			0.88

Results in **Table (5)** showed that mean performance of sixteen sesame genotypes for some yield traits during the two seasons and combined. The highest yielder genotypes in combined across the two seasons were **F1013**, **Shandweel 3** and **F1004** which gave (21.90, 19.63 and 19.29 g/plant – 4.59, 4.27 and 4.21 ard/fed) for seed yield/plant and seed yield (ard/fed), respectively. Meanwhile, the lowest one was **F1016** (12.72 g and 2.83 ard/fed) for seed yield/plant and seed yield (ard/fed), respectively. **F1013** and **F1004** genotypes recorded the highest oil yield (272.70 and 264.83kg/fed), respectively. Whereas the lowest one was **Sohag 1** (151.65 kg/fed) (**Table 5**).

F1013 and **F1004** out yielded the overall mean, seed yield/plant by 34.57 and 41.70% in the first season and by 23.22 and 20.19% in the second season, respectively. Meanwhile, seed yield (ard/fed) differed from mean seed

yield (ard/fed) by 21.90 and 42.36% in the first season and by 21.90 and 20.75% in the second season, respectively. On the other hand, oil yield (Kg/fed) differed from mean oil yield (Kg/fed) by 25.35 and 32.58% in the first season and by 5.56 and 44.93% in the second season, respectively.

From the above-mentioned results, it could be concluded that **F1013** and **F1004** followed by **Shandweel 3**, and **Giza 32** showed the highest number of capsules per plant, 1000-seed weight, seed yield/plant, seed yield (ard/fed) and oil yield/fed (kg/fed). These results reflect that the selection prospects within these genotypes to improve the performance through breeding program.

Table 5. Mean performance of sixteen sesame genotypes for some yield traits during 2013, 2014 and combined data.

Genotype	Seed yield/plant (g)			Seed yield (ard/fed)			Oil yield (Kg/fed)		
	2013	2014	Comb.	2013	2014	Comb.	2013	2014	Comb.
Shandweel 3	18.33	20.93	19.63	3.93	4.61	4.27	210.65	242.03	226.34
Sohag 1	12.40	15.33	13.87	2.73	3.37	3.05	134.40	168.90	151.65
Shandweel 2000	14.77	16.73	15.75	3.20	3.68	3.44	147.57	186.41	166.99
Sohag 10	15.90	17.36	16.63	3.53	3.82	3.68	162.51	255.26	208.89
F1016	11.43	14.00	12.72	2.57	3.08	2.83	157.61	181.74	169.68
F1014	16.73	16.83	16.78	3.33	3.70	3.52	191.74	210.20	200.97
F1004	19.53	19.05	19.29	4.23	4.19	4.21	223.20	306.46	264.83
F1003	13.10	14.60	13.85	3.10	3.21	3.16	198.35	202.47	200.41
Giza 32	19.30	17.73	18.52	3.43	3.90	3.67	214.31	259.83	237.07
F1015	15.03	15.06	15.05	3.30	3.32	3.31	206.47	249.03	227.75
F1013	21.33	22.46	21.90	4.23	4.94	4.59	265.05	280.34	272.70
F1007	14.22	14.16	14.19	3.47	3.12	3.30	220.94	254.92	237.93
F1005	15.17	15.53	15.35	3.40	3.42	3.41	195.49	252.45	223.97
F8H8	11.50	13.66	12.58	2.90	3.01	2.96	191.07	207.38	199.23
HF65	11.30	15.33	13.32	2.63	3.37	3.00	168.08	195.07	181.58
RH1F3	14.33	14.10	14.22	3.23	3.10	3.17	193.98	232.35	213.17
Mean	15.27	16.43	15.85	3.33	3.62	3.47	192.59	230.31	211.45
LSD Season (S)			0.41			0.12			16.87
Genotype (G)	1.81	2.21	1.40	0.44	0.49	0.32	30.17	26.56	19.70
S x G			NS			NS			27.87

Genetic analysis

The variations among the genotypes were mostly due to genetic makeup or structure factors rather than environmental ones, as indicated by higher genetic variances which indicate that these traits were controlled by genes and are less influenced by the environment. The estimates of genetic variance (σ^2_g), phenotypic (σ^2_{ph}), genotypic (GCV) and phenotypic (PCV) coefficient of variability, broad-sense heritability and expected genetic advance under 5% selection intensity as percentage of the general mean (GS %) are presented in **Table (6)**. The phenotypic variance (σ^2_{ph}) was greater than the genotypic variance (σ^2_g) for all studied traits in both seasons and combined. The results of σ^2_{ph} and σ^2_g for flowering date were 6.88 and 5.79 in the first season, 5.14 and 4.26 in the second season and 1.46 and 1.28 in the combined, respectively, whereas, seed yield ard/fed recorded values of 0.80 and 0.73 for the variances, in the first season, 1.01 and 0.93 in the second season and 0.26 and 0.23 in the

combined, respectively (**Table 6**). The phenotypic variance (σ^2_{ph}) and genotypic variance (σ^2_g) values for number of capsules per plant and oil yield (kg/fed) were high in both and combined seasons. These results are in confirmatory with those of **Kumar and Sasivannan (2006)** and **El-Shakhess et al (2008)**.

The extent of coefficient of variation indicated that high estimates of (PCV) and (GCV) were recorded for the number of capsules/plant in both seasons and combined data (66.11 and 37.14), (65.62 and 36.02) and (28.69 and 25.82), respectively, for the 1000-seed weight in the first season (37.93 and 36.37), respectively and for the seed yield/plant in the first season (35.50 and 34.78), respectively. That is suggesting wide spectrum of genotypic variation for these trait. Similar results were obtained by **Prasad et al (2007)**, **Iwo et al (2007)** and **El-Shakhess et al (2008)**. Meanwhile, the lowest values were counted for the flowering date in both seasons (4.56, 4.15) and (5.32 and 5.32), respectively. These results are in harmony with those obtained by **Mothilal (2006)**, **Prasad et al (2007)**, **Iwo et al (2007)** and **El-Shakhess et al (2008)**.

Heritability (h_b^2) estimates were generally different for all studied traits at separate analyses and combined one, where season's effect was separated (ranged from 0.49 to 0.99). The high broad sense heritability was exhibited for all the characters studied except number of branches per plant in both seasons (52.00 and 54.00 %), respectively and oil content (%) in combined (49.00%). The highest broad sense heritability was exhibited for number of capsules per plant and oil content% (0.99 in separate analyses), and weight of 1000 seeds and plant height (0.94). These results are in harmony with those obtained by **Mothilal (2006)**, **Prasad et al (2007)** and **El-Shakhess et al (2008)**.

The high GCV recorded by the above mentioned traits alone is not sufficient for the determination of the extent of the advance to be expected by selection. **Burton (1952)** suggested that GCV together with heritability estimates would give the best picture of the extent of the advance to be expected by selection. Comparatively, the highest genetic advance as percent of mean was recorded for number of capsules per plant in both and combined seasons (134.18, 71.98 and 47.86), respectively, followed by weight of 1000 seeds (71.84, 54.35 and 34.82), respectively and seed yield per plant (70.19, 52.58 and 32.74), respectively. The magnitude of heritability in broad sense was low coupled with low genetic advance for flowering date. These results are in harmony with that obtained by **Kumar and Saivannan (2006)** and **Iwo et al (2007)**.

In addition, they reported that genotypic coefficient of variability was more important than heritability because characters showing maximum and minimum relative expected genetic advance possessed maximum and minimum genotypic coefficient of variability irrespective of the magnitude of heritability estimates. In the present study, it is obvious from **Table (6)** that characters with high GCV possessed high GS percent and vice versa irrespective of the heritability estimates indicating the importance of GCV. In both seasons, high heritability (h^2) estimates and high genotypic coefficients of variation (GCV)

coupled with high genetic advance (GS%) thus, these traits (number of capsule per plant, weight of 1000 seeds and seed yield per plant) seem to be highly heritable, points to the predominance of additive gene effect, easily fixable and can be taken as unit character for effective selection. The high estimates of GCV, h^2 and GS % were observed for number of capsule per plant, weight of 1000 seeds and seed yield per plant regardless of the seasons which suggests the predominance of additive gene effects and selection would be useful for the improvement of these characteristics. Similar results have also been reported by Dar and Sharma (2011).

Table 6. Variability, heritability (h^2 %) and genetic advance as percentage of the mean (GS %) for studied traits in sesame genotypes through the two seasons (2013 and 2014) and combined data.

Trait		σ^2_{ph}	σ^2_g	PCV%	GCV%	h_b^2	GS%
Flowering date	2013	6.88	5.79	5.32	4.88	0.84	9.23
	2014	5.14	4.26	4.56	4.15	0.83	7.79
	Comb.	1.46	1.28	2.44	2.28	0.87	4.39
Plant height	2013	1038.61	1000.69	22.36	21.94	0.96	44.37
	2014	703.59	644.87	17.98	17.22	0.92	33.95
	Comb.	263.52	246.67	11.13	10.77	0.94	21.46
Length of fruiting zone	2013	1082.39	1035.83	28.69	28.06	0.96	56.56
	2014	535.16	480.75	19.83	18.79	0.90	36.69
	Comb.	241.55	203.33	13.44	12.33	0.84	23.30
Number of branches/ plant	2013	0.17	0.09	36.37	26.17	0.52	38.80
	2014	0.07	0.04	20.78	15.25	0.54	23.05
	Comb.	0.008	0.006	7.549	6.446	0.73	11.337
Number of capsules/ plant	2013	3968.98	3910.30	66.11	65.62	0.99	134.18
	2014	1900.57	1788.40	37.14	36.02	0.94	71.98
	Comb.	930.80	753.80	28.69	25.82	0.81	47.86
1000-seed weight	2013	0.84	0.78	37.93	36.37	0.92	71.84
	2014	0.55	0.50	28.85	27.59	0.91	54.35
	Comb.	0.20	0.19	17.92	17.40	0.94	34.82
Oil content (%)	2013	89.10	88.70	19.65	19.61	0.99	40.31
	2014	46.88	46.60	13.67	13.64	0.99	28.04
	Comb.	22.50	11.07	9.67	6.78	0.49	9.80
Seed yield/plant (g)	2013	29.40	28.22	35.50	34.78	0.96	70.19
	2014	20.96	19.20	27.86	26.67	0.92	52.58
	Comb.	7.58	6.94	17.36	16.61	0.92	32.74
Seed yield (ard/fed)	2013	0.80	0.73	26.85	25.66	0.91	50.53
	2014	1.01	0.93	27.86	26.66	0.92	52.58
	Comb.	0.26	0.23	14.67	13.78	0.88	26.66
Oil yield (kg/fed)	2013	3452.58	3124.47	30.51	29.02	0.90	56.88
	2014	4647.41	4393.20	29.60	28.78	0.95	57.64
	Comb.	1188.20	1005.80	16.30	15.00	0.85	28.43

Correlation studies:

Correlation coefficients for all comparisons among the studied traits are presented in **Table (7)**. Significant differences were observed in the correlation

coefficients in terms of magnitude and direction. The values of correlation coefficient showed that number of capsules per plant and 1000-seed weight had a highly significant positive correlation with seed yield per plant ($r=0.793^{**}$ and $r=0.708^{**}$, respectively). These results suggest that selection for higher number of capsules per plant and the weight of 1000-seed would lead to increase seed yield in sesame. **Ong'injo and Ayiecho (2009)** and **Ismaila and Usman (2014)** obtained similar results in sesame. Length of fruiting zone and number of branches exhibited non significant positive correlation with seed yield per plant ($r=0.156$ and $r=0.183$, respectively), conversely, its association was insignificantly negative with oil content % ($r= -0.019$).

Table 7. Correlation coefficients among various traits in sixteen sesame genotypes across 2013 and 2014 seasons.

Trait	DF	PH	FZ	Bra	NC/P	SW	O%	SY/P
Plant height (PH)	0.364**							
Fruiting zone (FZ)	0.322**	0.867**						
No. of branches (Bra)	0.006	-0.096	-0.150					
No. of capsules (NC/P)	0.329**	0.216*	0.087	0.241*				
1000-seed weight (SW)	0.388**	0.295**	0.207*	0.035	0.683**			
Oil content (O %)	-0.104	-0.506**	-0.502**	0.237*	0.169	-0.125		
Seed yield /plant (SY/P)	0.223*	0.250*	0.156	0.183	0.793**	0.708**	-0.019	
Oil yield (OY)	0.151	0.040	0.012	0.240*	0.651**	0.392**	0.569**	0.607**

DF: days to 50% flowering; PH: Plant height; FZ: Length of fruiting zone, Bra: number of branches; NC/P: number of capsules per plant, SW: 1000-seed weight (g), O%: oil content (%), SY/P: Seed yield/plant (g) and OY: Oil yield (Kg/fed).

Oil yield per feddan showed highly significant positive correlation with number of capsule per plant ($r = 0.651^{**}$), 1000-seed weight ($r = 0.392^{**}$), oil content % ($r = 0.569^{**}$) and seed yield per plant ($r = 0.607^{**}$). Then, number of capsule per plant, 1000-seed weight, oil content % and seed yield per plant may be important yield predictors of oil for sesame improvement. Also number of capsules per plant showed significant positive correlation with flowering date ($r = 0.329^{**}$), plant height ($r = 0.216^{*}$), number of branches ($r = 0.241^{*}$) and 1000-seed weight ($r = 0.683^{**}$).

The results revealed significant and positive correlations of higher oil content %, number of capsules per plant and the weight of 1000-seed to oil yield per plant, also results suggest its importance for sesame seed yield improvement. Then, breeding for higher 1000-seed weight and number of capsules per plant leads to a high seed yield per plant, the corollary is true that breeding for higher seed yield is a useful approach to higher oil yield.

Cluster analysis

Cluster analysis seemed to be an efficient procedure for extracting the structured relationships among genotypes and provides a hierarchical classification of them (**Polignano et al 1989**). Hierarchical cluster analysis for the investigated 16 genotypes obtained with the average linkage procedure;

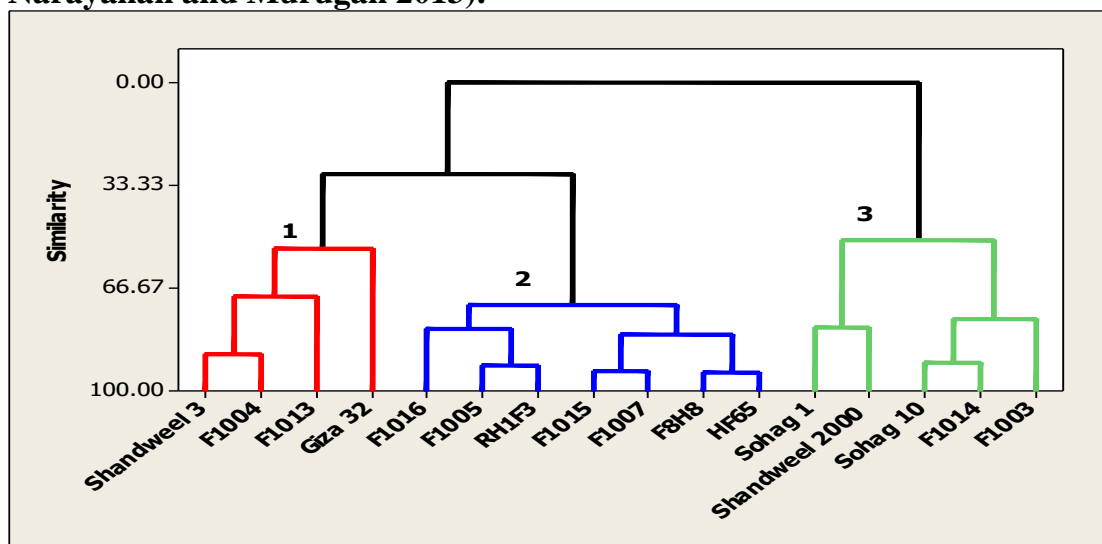
UPGMA (un-weighted pair group method using arithmetic average) is illustrated in **Table (7)** and **Fig (1)**.

Table 7. Level of different clusters for sesame studied yield traits (seed and oil).

Cluster No.	Similarity	No. of genotypes	Included genotypes
Cluster 1	53.88	4 genotypes	Shandweel 3, F1004, F1013 and Giza 32.
Cluster 2	71.90	7 genotypes	F 1016, F1005, RH1F3, F1015, F1007, F8H8.and HF65.
Cluster 3	50.89	5 genotypes	Sohag 1, Shandweel 2000, Sohag 10, F1014 and F1003.

Cluster analysis was used to further investigate the inter-relationships of the genotypes using all the studied yield traits. The genotypes were grouped into three main clusters (1, 2 and 3). Each of the main clusters was divided into sub clusters. The maximum number of genotypes (7) was grouped in cluster 2 followed by cluster 3 (5) and cluster 1 (4). Thus, in view of considerable genetic diversity in sesame found in the present study, their appearance had sufficient scope for genotypic improvement through hybridization between the genotypes from divergent clusters (**Ahmed *et al.* 2013, and Narayanan and Murugan 2013**).

Four genotypes were grouped in the same cluster 1 (Shandweel 3, F1004, F1013 and Giza 32), seven genotypes (F 1016, F1005, RH1F3, F1015, F1007, F8H8.and HF65) as cluster 2, and the rest of the six genotypes (Sohag 1, Shandweel 2000, Sohag 10, F1014 and F1003) were grouped in cluster 3. It is clear that genotypes Shandweel 3, F1004, F1013 and Giza 32 are related to each other, and are far from the rest of the other collection Giza35, Sohag 1, Shandweel 2000, Sohag 10, F1014 and F1003 (**Ahmed *et al* 2013 and Narayanan and Murugan 2013**).



Figure(1). Cluster analysis showing the relationship among sesame genotypes based on seed and oil yield traits.

Then, cluster I (**Shandweel 3, F1004, F1013 and Giza 32**) which concluded Shandweel 3 and Giza32 (local genotypes) was considered as cluster

with highest yield. Meanwhile, F1004 and F1013 genotypes surpassed the seed and oil yield of Shandweel 3 and Giza32.

References

- Ahmad, H. M., M. M. Kandhro, S. Laghari and S. Abro, (2006).** Heritability and genetic advance as selection indicators for improvement in cotton (*Gossypium hirsutum* L.). J. Biol. Sci. **6**: 96-99.
- Ahmed, Fadia, H. A., Aziza Hassanein M. and I. S. El-Demerdash (2013).** Evaluation and genetic diversity of eleven sesame lines. Egypt. J. Genet. Cytol., 42:205-222.
- Akpanlwo G., A.A. Idowu and S.M. Misari (2009).** Collection and evaluation of sesame (*Sesamum* spp.) germplasm in Nigeria. PGR. Newsletter 142: 59-62.
- Aladji Abatchoua M.M.I., J.B. Noubissié Tchiagam and N. Njintang Yanou (2014).** Genetic Analysis of Seed Yield Components in Sesame (*Sesamum indicum* L.) at Mora (Cameroon). Scholars Academic Journal of Biosciences (SAJB). 2(5): 318-325
- Ali K.H., A.S. Ibrahim, M.B. Taha and M.E. Ahmed (2003).** Performance, interrelationship and path analysis of some yield components in sesame. University of Khartoum. J. Agric. Sci., 11: 305-321.
- Allard, R.W. (1960).** Principles of Plant Breeding. John Wiley and Sons Inc., New York.
- Anonymous (2005).** Annual Statistical Book of Agricultural in Egypt, 213 pp. (in Arabic).
- Azeez, M. A. and J. A. Morakinyo (2009).** Genetic diversity of lipid and fatty acid profile in nine accessions of sesame (*Sesamum* and *Ceratotheca*). Proceedings of 33rd Annual Conference of Genetics Society of Nigeria, 27th -30th September: 35-45.
- Bhargava, A., S. Shukla, R. S. Katiyar and D. Ohri (2003).** Selection parameters for genetic improvement in *Chenopodium* grain on sodic soil. J. Appl. Hort. **5**: 45-48.
- Burton G.W. (1952).** Quantitative Inheritance of Grasses. Proc. the 6th Int. Grassland Congr. Pennsylvania State College, USA, 1: 277-283.
- Cooper, M., S. Rajatasereekul, S. Immark, S. Fukai and J. Basnayake (1999).** Rainfed lowland rice breeding strategies for Northeast Thailand I. Genotypic variation and genotype \times environment grain yield. Field Crops Res., **64**: 131-151.
- Dar R.A. and J.P. Sharma (2011).** Genetic variability studies of yield and quality traits in tomato (*Solanum lycopersicum* L.). International Journal of Plant Breeding and Genetics. **5**: 168-174.
- El-Shakhess, Samar A. M., Y. M. Abdel-Tawab and Nemat A. Nagib (2008).** Evaluation and differentiation of eleven sesame lines. Egypt. J. Plant Breed., 12: 1-25.
- Fehr, W.R. (1987).** Principles of Cultivar Development. Vol. I. Macmillan New York.

- Gangadhara R.S.V. (2005).** Genetic variability in sesame (*Sesamum indicum* L.). Sesame and Safflower Newsletter 20: 26-28.
- Ismail, A. and A. Usman (2014).** Genetic Variability for Yield and Yield Components in Sesame (*Sesamum indicum* L. International Journal of Science and Research (IJSR).9(3):63.66.
- Iwo, G. A., A. A. Idowu and S. Misari (2007).** Genetic variability and correlation studies in sesame (*Sesamum indicum* L.). Global J. of Pure and Applied Sciences. Nigeria, 13: 35-38.
- Johnson, H.W., H.E. Robinson and R.E. Camstolk (1955).** Estimation of genetic and environmental variability in soybean Agron. J., 47: 314-318.
- Khidir M.O. (1997).** Oil Crops in Sudan. Khartoum University Press 1st ed. pp. 103-120. (in Arabic).
- Kumar, P. S. and S. Sasivannan (2006).** Variability, heritability and genetic advance in sesame (*Sesamum indicum* L.). Crop Research 31: 258 -260.
- Larik, A. S., S. I. Malik, A. A. Kakar and M. A. Naz (2000).** Assessment of heritability and genetic advance for yield and yield components in *Gossypium hirsutum* L. Scientific Khyber 13: 39-44.
- Mayo, O. (1980).** The Theory of Plant Breeding. Clarendon Press-Oxford, New York.
- Menzir A. (2012).** Phenotypic variability, divergence analysis and heritability of characters in sesame (*Sesamum indicum* L.) genotypes. Nature and Science 10(10): 117-126.
- Mothilal, A. (2006).** Genetic variability and correlation studies for yield and its component characters in sesame (*Sesamum indicum* L.). J. of Ecobiology, Palani Paramount Publications, Palani, India, 18: 117-120.
- Narayanan, R. and S. Murugan (2013).** Genetic Divergence and Stability Analysis in Sesame (*Sesamum indicum*). International Journal of Advances in Doctoral Research, 2(11):16-19.
- Ong'Ingo, E.O. and P.O. Ayiecho (2009).** Genotypic variability in sesame mutant lines in Kenya. Afric. Crop Sci. J. 17(2): 101-107.
- Parameshwarappa S.G., M.G. Palakshappa, P.M. Salimath and K.G. Parameshwarappa (2009).** Studies on genetic variability and character association in germplasm collection of sesame (*Sesamum indicum*). Karnataka J. Agric. Sci., 22(2): 252-254.
- Pham, T. D., T. D. Thi Nguyen, A. S. Carlsson and T. Minh Bui (2010).** Morphological evaluation of sesame (*Sesamum indicum* L.) varieties from different origins. Australian Journal of Crop Science, 4(7): 498-504.
- Polignano, G. B., P. Ugenti and P. Perrino (1989).** Pattern analysis and genotypic x environment interactions in faba bean (*Vicia faba* L.) populations. Euphytica 40: 31-41
- Prasad, Y. V. N. S., N. D. Bangar and P. A. Navale (2007).** Genetic variability, correlation and path analysis in F2 and F3 populations of cross JLSV X Hawari in *Sesamum*. J. of Maharashtra Agric., 32: 59-61.

- Shekhawat R.S., S.S. Rajput, S.K. Meena and B. Singh (2013).** Variation and character association in seed yield and related traits in sesame (*Sesamum indicum* Linn.). Indian Research Journal of Genetics and Biotechnology 5(3): 186-193.
- Songsri, P., S. Jogloy, T. Kesmla, N. Vorasoot, C. P. A. Akkasaeng and C. Holbrook (2008).** Heritability of drought resistance traits and correlation of drought resistance and agronomic traits in peanut. Crop Sci., 48: 2245-2253.
- Steel R.G.D. and Torrie, S.H. (1980).** Principles and Procedures of Statistics. Mc Graw- Hill. Book Company, Inc., New York.
- Sumathi P. and V. Muralidharah (2010).** Analysis of genetic variability, association and path analysis in the hybrids of sesame (*Sesamum indicum* L.). Tropical Agricultural Research and Extension 13:63–67.

تنوع المحصول وبعض الصفات المورفولوجية في ستة عشر تركيباً وراثياً من السمسم

محمد وحيد شوقي أحمد محمود¹ - زينب السيد غريب²

1 - قسم بحوث المحاصيل الزيتية - معهد بحوث المحاصيل الحقلية - مركز البحوث الزراعية - الجيزة - مصر

2 - المعمل المركزي لبحوث التصميم والتحليل الإحصائي - مركز البحوث الزراعية - الجيزة - مصر

أجريت هذه الدراسة خلال الموسمين الصيفيين 2013 و 2014 بهدف تحديد السلوك الوراثي لستة عشر تركيباً وراثياً من السمسم منزرعة في محطة البحوث الزراعية بشرق العوينات (تربة رملية بالاراضى الجديدة)، الوادي الجديد، مصر. توضح النتائج أن التراكيب الوراثية تحت الدراسة اختلفت اختلافاً عالياً المعنوية في كلا الموسمين والتحليل المشترك لجميع الصفات باستثناء عدد الأفرع / نبات. كان تفاعل التركيب الوراثي في السنوات غير معنوي لجميع الصفات المدروسة باستثناء ميعاد الإزهار وعدد الفروع/النبات، وزن - 1000 بذرة، محصول البذور/النبات ومحصول البذور (اردب/ فدان). أظهرت التراكيب الوراثية F1004، F1013 ويليها شندويل 3، وجيزة 32 أكبر عدد من الكبسولات/النبات، ووزن - 1000 بذرة، محصول البذور/النبات، محصول البذور (اردب/ فدان) و محصول الزيت (كجم / فدان). وقد تم الحصول على أعلى تقديرات من كفاءة التوريث بالمعنى الواسع (h_b^2) ومعامل التباين الوراثي (GCV) إلى جانب التحسين الوراثي كنسبة من المتوسط العام (%GS) لكل من صفات عدد الكبسولات/النبات، ووزن - 1000 بذرة ومحصول البذور/النبات، والتي تقترح زيادة التأثيرات المضيفة للجينات، والانتخاب يكون مفيداً لتحسين هذه الصفات. تم تقدير معامل الارتباط بين الصفات وقد أوضح وجود ارتباطاً معنوياً موجباً بين محصول البذور وكل من عدد الكبسولات/النبات، ووزن - 1000 بذرة. أظهر محصول الزيت ارتباطاً إيجابياً معنويّاً مع عدد الكبسولات/ نبات، ووزن - 1000 بذرة، محتوى الزيت % ومحصول البذور/النبات. ومن ثم فإن الانتخاب لوزن - 1000 بذرة الأعلى، وعدد الكبسولات / النبات يؤدي إلى زيادة محصول البذور/النبات، والنتيجة الطبيعية الحقيقية هنا لزيادة محصول البذور هو الطريقة المثلى لارتفاع محصول الزيت. أن هذه النتائج تشير إلى أن اختيار أى من أو كلا من عدد الكبسولات/النبات، ووزن - 1000 بذرة تكون مصحوبة بالمحصول المرتفع. وقد اعتبرت المجموعة الاولى (شندويل 3، F1004، F1013 وجيزة 32) التي اشتملت على شندويل 3 و جيزة 32 (التراكيب الوراثية المحلية)، المجموعة ذات المحصول الأعلى. وفي الوقت نفسه، فقد تجاوزت التراكيب الوراثية F1004 و F1013 محصول البذور والزيت لكل من شندويل 3 و جيزة 32. لذا فإن هذه التراكيب الوراثية الممتازة المختارة سوف تكون مفيدة في برامج التربية لتحسين الصفات التجارية الهامة مثل محصول البذور والزيت في السمسم.