Egypt. J. Plant Breed. 12(1): 1-25(2008)

EVALUATION AND DIFFERENTIATION OF ELEVEN SESAME LINES

Samar A. M. El Shakhess[1], Y.M. Abdel- Tawab[2] and Nemat A. Naguib[2]

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

ABSTRACT

Eleven sesame lines were used during two successive seasons, 2006 and 2007. Results revealed that line S_5 had longest fruiting zone, number of capsules/pl, seed yield/pl., seed yield / fed. and oil yield /fed. line S_{33} recorded the highest germination%, seed vigor index and electrical conductivity. Accelerated ageing germination ranged from 74.0 to 84.3. Radical length, shoot length and seed vigor index showed slight difference among different lines. Variation in the chemical components was related to genetic constitution of different genotypes. Crude oil ranged from 50.36 to 54.58.Crude protein ranged from 21.94 to 25.45. Total carbohydrate ranged from 10.07 to 12.75.Oleic acid ($C_{18:1}$) and linoleic acid ($C_{18:2}$) were the major unsaturated fatty acid in sesame oil. Number of branches/pl., number of capsules/pl. and seed yield/pl. had high coefficient of variation at the genotypic (GCV) and (PCV) levels. The value of (GCV) and (PCV) were nearly equal for seed vigor index, electrical conductivity, seed index, seed coat/whole seed ratio, crude oil, crude protein, and total carbohydrate. However, high heritability coupled with high genetic advance were recorded for length of fruiting zone, number of branches/pl., number of capsules/pl., seed yield/pl., seed vigor index, electrical conductivity, seed index, seed coat/ whole seed ratio, crude carbohydrate, crude protein and crude oil. This indicated that mass selection could be effective an improving these characters. SDS-PAGE was generated 12 bands, ten from which were polymorphic. Four bands were observed as specific unmakes. Five random primers used for RAPD analysis were generated 44 bands, 33 from which were polymorphic. Nine bands were found to be useful as genotype-specific markers. Cluster dendrogram classified the lines into two main groups.

Key world: ***Sesame, Agronomic characters, Yield, Seedling characters, Seed characters, Chemical characteristics,Fatty acid, SDS-PAGE.***

INTRODUCTION

Sesame (*Sesamum indicum* L) is recognized as one of the oldest oil crops in the world. Knowledge on genetic variability is very important in selection of parents in hybridization programmes for identifying heterotic crosses and obtaining desirable segregates. Many sesame investigators such as Das and Samanta (1998) indicated that additive effect were significant for oil content and four fatty acids (palmitic, stearic, olic and linoleic) except arachidic acid. Also, Tamina Begum and Dasgupta (2003), reported that phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for plant height, days to flowering, flower duration, days to maturity, number of branches/pl., number of capsules/pl, number of seeds/cap., capsules length, seed index, protein percentage, harvest index and seed yield/ fed. Raghuwanshi (2005) studied genetic

variability for days to 50% flowering, days to maturity, plant height, number of branches/pl., number of capsules/ pl., seed yield, seed index and oil content in 100 genotypes of sesame. He found a wide range and high variability for seed yield and its components, except seed index that showed low to moderate variability. Sonali Senguota and Datta (2004), Babu *et al* (2005), Ganesan (2005), Mothilal (2006) and Iwo *et al* (2007) found high heritability combined with high genetic advance for plant height, number of branches/pl., number of capsules /pl. and seed index. They added that high heritability combined with high genetic advance for these traits. Indicated that additive gene action is of high magnitude and phenotypic selection could be effective for improving these characters.

The importance of seed quality in realizing full potential of a cultivar is well known. Seed quality includes seed viability and seedling vigor, which are considered as two interrelated characters. The standard germination test is the universal test for seed quality, evaluates the maximum potential of a particular seed under favorable conditions (ISTA 1987). High standard germination does not always result in rapid and uniform emergence or vigorous stand under actual planting conditions. On the other hand, seed vigor denotes the ability of a seed to germinate rapidly and produce a normal seedling under a wide range of conditions (Dornbos, 1995). Perry (1989) suggested that a vigor test would provide a better indication of seed performance in the filed than the standard germination test. There is no one universal vigor test for all seeds. A wide array of testing methods has been used to characterize seed vigor. According to Ellis (1992), seed vigor can be assessed in laboratory and various procedures can be used to detect high and low vigor seed. Several examples of seed vigor test include the accelerated ageing test and electrical conductivity test.

Genetic fingerprinting is a useful method for identification of germplasm, planning breeding programs through marker-assisted selection (MAS), taxonomic studies and protection of plant breeder's rights. Sodium dodecyle sulfate polyacrylamide gel electrophoresis (SDS-PAGE) is considered a low cost, reproducible and rapid technique for the identification and characterization of different genotypes. Randomly amplified polymorphic DNA (RAPD) –PCR technique can be successfully used to identify genotypes, and to enhance and determine the genetic purity of genotypes.

Therefore, the main objectives of this work was to study 1) The performance, heritability, genotypic and phenotypic variability. 2) Sesame seed quality by using some vigor, viability test and to determine the major chemical and fatty acid compositions of oil. 3) Determine the genetic purity of different sesame genotypes, in order to obtain reliable information for recommending desired genotypes and making decisions concerning the proper breeding methods for improving yield and yield components.

MATERIALS AND METHODS

Field trial

Ten sesame lines and one commercial cultivars (Shandweel$_3$), namely: S_4,S_5,S_8,S_{11},S_{13},S_{15},S_{27},S_{28}, S_{33} and S_{34}. The pedigree of these lines is shown in Table (1). The lines were planted during the summer seasons in 2005 and 2006 at Giza Research Station (ARC). The experiment was laid out using a randomized complete block design with three replications. Each entry was grown in plot area of 8 m^2 (4.0 × 2.0 m). The cultural practices were done according to the recommended methods. The observations were recorded on ten randomly selected plants per plot for the following agronomic characters:

1. Morphological characters: (plant height, length of fruiting zone, number of branches/pl., number of capsules/pl.).
2. yield parameters: At harvest, seed yield/pl. Seed yield / fed (ard.) and oil yield/fed. (Kg) were determined.

Table 1. Pedigree of sesame lines studied.

Liens	Origin	pedigree
Line S_4	Egypt	A line selected from B14x line178
Line S_5	Egypt	A line selected from B14x line180
Line S_8	Egypt	A line selected from N.A579 x line178
Line S_{11}	Egypt	A line selected from line 102-23-2 x line178
Line S_{13}	Egypt	A line selected from N.A370-1 x line178
Line S_{15}	Egypt	A line selected from line178 x line180
Line S_{27}	Egypt	A line selected from GSM103x line109-7
LineS_{28}	Egypt	A line selected from GSM103 x B21
Line S_{33}	Egypt	A line selected from GSM104x line102-7 x MGS104
Line S_{34}	Egypt	A line selected from GSM104x line102-7 x line102-7
Shandweel$_3$	Egypt	A line selected from Giza32 x N.A130

Laboratory tests

Before starting seed- laboratory tests, initial moisture content and seed index of each seed sample were determineded.

Germination test: one – hundred pure seeds of each sample were placed on Petri dishes containing filter paper soaked with distilled water. The Petri dishes were placed in an incubator at 25 ±1°C for 6 days. Normal seedlings were counted according to the international rules of (ISTA ,1993). Germination percentage was calculated using the formula by Krishnasamy and Seshu (1990).

$$\text{Germination (\%)} = \frac{\text{number of normal seedlings}}{\text{number of seed tested}} \times 100$$

Ratio of seed coat to whole, seed color at maturity and vigor index was calculated using the formula of Copeland (1976).

Seed vigor index= $\frac{\text{Number of seeds germinated (1}^{st}\text{ count)}}{\text{Number of days to first count}} + \frac{\text{Number of seeds germinated (last count)}}{\text{Number of days to last count}}$

Evaluation of seedlings: Normal seedlings obtained from standard the germination test were used for seedling evaluation according to the rules of the Association of Official Seed Analysis (AOSA, 1983). Seedling shoot and root length were measured after 6 days of germination test. Twenty-five seedlings from each Petri dish were randomly selected and shoot and root length of individual seedlings were recorded. The shoots and roots were also dried at 70°C for 72h. seedling vigor index was calculated using data recorded on germination percentage and seedling growth according to (ISTA,1985) by the formula:

Seedling vigor index = seedling length (cm) × germination percentage

Electrical conductivity test: The electrical conductivity of the leachate was determined according to procedures described by AOSA (1983). Four sub- samples of 50 seeds of each cultivar were weighed to 0.001g, placed into plastic cups with 250 ml of distilled water, and held at 25°C. After 24h, the electrical conductivity of the leachates was determined using Ec meter. The mean values were expressed in $\mu S\ cm^{-1}\ g^{-1}$ seed weight.

Accelerated ageing: The seeds were kept in an aging chamber at 45°C and 100% relative humidity for 3 days. After aging, the seeds were dried up in the sun and percentage survival of the seeds was determined by standard germination test at 20°C and the mean normal seedling percentage was calculated according to (AOSA, 1983).

Chemical composition: Samples of about 50g of air dried seeds of each genotype were randomly chosen from two replications and fine ground for estimating chemical composition i.e. total nitrogen was determined using Kjeldahl Method (AOAC, 2000), crude protein was calculated by multiplying the total nitrogen by factor of 6.25. Total carbohydrates were evaluated according to (AOAC, 2000). Crude oil percentage was determined using Soxhlet apparatus and hexane as solvent according to (AOAC, 2000) and Iodine value was also estimated. Ash was determined according to the methods of (AOAC, 2000). Samples were ashed at 650°C until a light gray ash was obtained in muffle. Fiber and moisture content were determined according to the methods of (AOAC, 2000). Analysis of fatty acid methyl esters was performed by GLC for oil.

SDS-protein electrophoresis

SDS-polyacrylamide gel electrophoresis (SDS-PAGE) procedure was carried out according to Laemmli (1970). Protein bands were visualized by staining the gel with 0.25% Coomassie Brilliant Blue R-250. Protein

band sizes were determined by comparisons with the high molecular weight protein marker.

DNA extraction : DNA was extracted from 100 mg of young leaves (after 7 days of planted) for each line using mi-Plant Genomic DNA Isolation Kit (metabion). The concentration and purity were determined by spectrophotometer.

RAPD-PCR analysis: RAPD analysis was carried out according to Williams *et al* (1990). The ten primers used were 10-mer oligonucleotide selected as potentially useful. The codes and sequences of the used primers are shown in Table (2).

Table 2. Summary of data obtained by RAPD analysis for the eleven sesame lines.

Primer	Sequence 5→3	TAB	PB	Genotypes 1		2		3		4		5		6		7		8		9		10		11		TSM
				ab	sm	ab	sm	ab	sm	ab	sm	ab	sm	ab	sm	ab	sm	ab	sm	ab	sm	ab	sm	ab	sm	
A09	GGGTAACGCC	8	5	6	0	5	0	7	0	7	0	7	0	5	0	5	0	6	0	3	0	5	0	5	0	0
A11	CAATCGCCGT	13	10	8	0	4	0	7	0	8	0	7	0	8	0	4	1	8	0	7	0	7	0	5	0	1
B05	TGCGCCCTTC	6	5	4	0	5	1	5	0	4	0	5	0	4	0	1	3	4	0	4	0	4	0	4	0	4
B15	GGAGGGTGTT	10	9	4	0	2	0	3	0	5	0	9	2	6	0	7	0	5	0	5	0	6	0	5	0	2
B18	CCACAGCAGT	7	4	5	0	5	0	4	0	3	0	4	1	3	0	4	1	3	0	4	0	4	0	5	0	2
Total		44	33																							9

TAB= Total amplified bands, PB= Polymorphic bands, TSM= Total specific markers AB= amplified band and SM= specific marker

PCR reactions were optimized and mixtures (25 µl total volume) were composed of dNTPs (200 µM), Mg Cl2 (1.5 mM), 1x buffer, primer (0.2 µM), DNA (50 ng), Taq DNA polymerase (2 units). Amplification was carried out in a Thermo Cycler (PTC 200) programmed for 94 °C for 3 min (one cycle); followed by 94 °C for 30 sec, 36 °C for 1 min and 72 °C for 2 min (36 cycle); 72 °C for 10 min (one cycle), then 4 °C (infinitive). Amplification products (15 µl) were mixed with 3 µl loading buffer and separated on 1.3% agarose gel and stained with 0.5 µg/ml ethidium bromide, and visualized under ultraviolet light and photographed. DNA fragment sizes were determined by comparisons with the 100 bp DNA Ladder marker.

Data analysis

The results of SDS-PAGE and RAPD analysis were entered in a computer file as binary matrices where 0 stand for the absence of a band and 1 stand for the presence of a band in each individual sample. Similarity, coefficients were calculated according to Dice matrix (Nei and Li 1979). Construction of the dendrogram tree was performed using the unweighted pair group method based on arithmetic mean (UPGMA) as implemented in the SPSS program version 10.

Analysis of variance was calculated for each season separately according to Mather and Jinks (1982).

RESULTS AND DISCUSSION

Mean performance

Agronomic characters

Table (3) illustrates that wide range of variability was recorded for some agronomic characters. The differences among lines were significant for plant height, length of fruiting zone, number of branches/pl. and number of capsules/pl.

Table 3. Mean performance, Range for agronomic characters of eleven genotypes in 2006 and 2007 seasons.

Genotypes	Plant height (cm)		Length of fruiting zone (cm)		Number of branches/pl.		Number of capsules/pl	
	2006	2007	2006	2007	2006	2007	2006	2007
Line S_4	209.00	209.67	123.33	130.00	4.53	5.40	195.20	211.00
Line S_5	227.67	234.67	184.67	189.67	3.60	4.40	471.27	460.00
Line S_8	220.67	216.33	138.00	140.67	5.00	5.60	277.00	319.80
Line S_{11}	209.00	211.00	137.00	138.00	5.20	7.20	358.00	366.40
Line S_{13}	246.33	244.33	181.67	188.67	5.67	5.87	434.33	433.67
Line S_{15}	237.67	237.00	178.33	179.67	6.40	6.73	368.87	238.40
Line S_{27}	184.67	187.33	102.67	111.33	6.20	5.33	246.67	368.33
Line S_{28}	250.67	249.33	153.33	165.00	3.47	5.00	382.33	408.93
Line S_{33}	222.00	238.00	166.33	178.33	8.60	9.47	370.13	355.73
Line S_{34}	231.67	237.33	170.00	176.67	4.80	6.13	307.17	323.20
$Shandweel_3$	203.00	192.67	154.00	152.67	1.00	1.00	186.17	191.83
L.S.D	13.58	12.45	16.87	14.91	1.61	1.65	55.32	42.10
Mean	222.03	223.42	153.58	159.15	4.93	5.65	327.01	3.34
Range	184.67-250.67	187.33-249.33	102.67-184.67	111.33-189.67	1.00-8.60	1.00-9.47	186.17-471.27	191.83-460.00

Ranges for plant height were from 184.67 to 250.67 cm. with mean 222.03 cm. in 2006 and from 187.33 to 249.33 cm. with mean 223.42 cm. in 2007.The line S_{28} recorded the tallest genotype in both seasons. Meanwhile, the line S_{13} recorded the shortest genotype in both seasons.

Length of fruiting zone ranged from 102.67 to 184.67 cm. and the 111.33 to 189.67 cm. in 2006 and 2007 seasons, respectively. The line S_5 had longest fruiting zone in both seasons. In contrast, line S_{27} had the shortest fruiting zone in both seasons.

With respect to number of branches/pl. It ranged from 1.00 to 8.60 in 2006 and from 1.00 to 9.47 in 2007.

Ranges for number of capsules/pl., were 181.17 to 471.27 and from 191.83 to 460 with mean 327.01 and 334.30 in 2006 and 2007 seasons, respectively. The line S_5 produced greatest number of capsules/pl. followed by line S_{13} in both seasons. In other hand, cv. Shandweel$_3$ had lowest number of capsules/pl.

Yield

Fig. (1) shows seed yield/pl. distributions based on the means obtained in 2006 and 2007 seasons. It is obvious that the range is 37.67 - 74.09 g., suggesting large variability in genes controlling seed yield /pl. It is well known that heterosis based on hybrids between lines depends mainly on the difference in the gene frequency between the parents used for breeding (heterosis in $F_1 = \Sigma dy^2$ for all possible combinations of lines, where d = the degree of dominance, y = the difference in gene frequency of any two lines). The line S_5 gave the highest seed yield/pl. in both seasons. Mean seed yield/pl. for highest genotype was high by 77.8 % in 2006 and 91.1% in 2007 over Shandweel$_3$ (a commercial variety).

1	
2	
3	7.67
4	2.93 8.80 2.93 1.63 2.67 6.0 3.0
5	7.73 2.67 2.00 8.67 6.00 3.0 1.67 7.67
6	9.13 9.67
7	4.09 3.13 1.60 2.00
8	
9	
10	

Fig1. Seed yield/plant distribution (g) via stem and leaf display (Turkey, 1977) for the mean eleven lines, in both 2006 and 2007.

With respect, seed yield/fed Fig. (2), the range was 6.53-9.53 ardb. in both seasons. The line S_5 gave the greatest seed yield/fed, being slightly higher than the line S_{13}.It is obvious that the highest seed yield/fed was higher by 42.0% over commercial variety.

5	
6	.77 .53
7	.51 .11 .50 .10 .53 .50
8	.67 .70 .50 .50 .50 .10 .70 .87 .86
9	.53 .13 .13 .10 .28 .27
10	

Fig. 2. Seed yield/fed distribution (ardb) via stem and leaf display(Turkey, 1977) for the mean eleven lines in both 2006 and 2007 seasons.

Results in Fig. (3) showed the oil yield/fed. distribution. It was obvious that high oil yield/fed. was obtained from line S_5 (592kg) in 2006 and (580.81kg) in 2007. Meanwhile, the line S_{27} gave the lowest oil yield/fed in both seasons.

410	3.0
420	
430	5.1
440	
450	5.5 6.5 4.6
460	2.3
470	
480	
480	7.9
490	1.3 4.3
500	
510	
520	
530	
540	6.6 9.8 3.5
550	8.9 3.0
560	0.5 3.1
570	3.6 7.1
580	0.8
590	0.0 2.0

Fig.3. Oil yield/fed. distribution (kg) via stem and leaf display for mean oil yield of eleven lines in both 2006 and 2007 seasons.

Germination characters

Data in Table (4 showed standard germination % ranged from 88.67 to 98.00 and from 92.67 to 98.67 in 2006 and 2007, respectively. The line S_{33} gave the highest standard germination % in 2006. Meanwhile, the line S_{13} recorded the highest standard germination % in 2007. With respect to seed vigor index, it varied significantly in 2006 and 2007. It was ranged from 39.22 to 47.89 with mean 44.20 in 2006 and from 40.44 to 46.89 with mean 43.54 in 2007. The line S_{33} recorded the highest seed vigor index in both seasons. In contrast, the line S_{34} gave the lowest seed index vigor in 2006 and 2007.

Table 4. Mean performance and range of standard germination%, seed vigor index, accelerated ageing germination and electrical conductivity for eleven sesame genotypes in 2006 and 2007 seasons.

Genotypes	Standard germination%		Seed vigor index		Accelerated ageing germination%		Electrical conductivity $\mu Scm^{-1}g^{-1}$	
	2006	2007	2006	2007	2006	2007	2006	2007
Line S_4	92.67	96.67	42.78	42.00	82.67	80.67	43.11	41.53
Line S_5	97.33	95.67	46.89	43.72	83.00	80.00	32.10	34.00
Line S_8	94.67	97.67	46.03	45.17	78.00	83.33	40.57	40.15
Line S_{11}	94.67	96.67	43.56	43.00	78.67	80.33	42.45	43.52
Line S_{13}	96.67	98.67	45.00	45.00	81.00	84.33	32.83	33.23
Line S_{15}	96.67	97.33	46.56	45.78	80.67	82.67	38.49	38.94
Line S_{27}	95.33	96.67	42.11	41.67	80.33	76.00	40.67	41.79
Line S_{28}	90.00	94.67	40.89	41.00	80.33	76.67	46.11	46.20
Line S_{33}	98.00	97.30	47.89	46.89	80.33	83.00	33.02	34.72
Line S_{34}	88.67	95.33	39.22	40.44	74.00	74.67	47.34	47.50
Shandweel$_3$	95.33	92.67	45.22	44.22	81.67	83.33	38.68	38.61
L.S.D	NS	NS	2.57	1.80	NS	3.70	3.35	1.27
Mean	94.55	96.30	44.20	43.54	80.06	80.45	39.57	40.02
Range	88.67-98.00	92.67-98.67	39.22-47.89	40.44-46.89	74.00-83.00	74.67-84.33	32.10-47.34	33.23-47.5

Range for accelerated ageing germination were from 74.0 to 83.0 and 74.67 to 84.33 in 2006 and 2007, respectively. Table (4) shows that electrical conductivity is more commonly used for determining seed vigor of crops. It is based on the principle that seeds which are losing vigor release materials, such as sugars or other electrolytes in solution into the soil which may increase the activity of soil fungi, which in turn may infect and interfere with the development of seedling growth, especially under cold and wet conditions. Electrical conductivity after 24 hours varied among different genotypes. Ranges were 32.1 to 47.34 in 2006 and from 33.23 to 47.50 in 2007. Electrical conductivity was much higher in the line S_{34} (47.34 and 47.5 $\mu Scm^{-1}g^{-1}$ in 2006 and 2007, respectively).The higher electrical conductivity of seed was associated with initial moisture content. Higher moisture content might have increased respiratory activities of seed and shortened seed lives. Cellular membranes of short- lived seeds become weaker and permit cell contents to easy escape into water, which increase electrical conductivity of seed. The electrical conductivity of seeds in all genotypes increased with increasing soaking time. The ion leakage increased by passage of imbibitions time. Higher electrical conductivity of deteriorated seeds was also observed by Schuttle and Loepold (1984) in soybean. There is a negative relationship between electrical conductivity and seed germination which indicated that more cell leachates escaped from deteriorated seed and lowered the germination% of seed.

Seedling characters

Data in Table (5) revealed that the line S_5 had the longest radical length with average 4.02 and 3.87cm in 2006 and 2007, respectively. It is worth noting that this line showed the highest seed and oil yield per unit area. While line S_{27} and $Shandweel_3$ had the shortest radical length with average 2.97 and 3.08 cm in 2006 and 2007, respectively. The range of shoot length were 20.15-3.52 and 2.85-3.61cm in 2006 and 2007, respectively. The line S_{34} was 3.52 and 3.61 cm in 2006 and 2007, respectively. Meanwhile, the line S_4 was 2.15 and 2.85 cm in 2006 and 2007, respectively.

Line S_{34} had the greatest seedling length being 6.98 cm in 2006. Meanwhile, line S_5 had the greatest seedling length in 2007. On the other hand, the line S_{27} in 2006 and $shandweel_3$ in 2007 expressed the lowest value of this trait (5.68 and 6.05 cm, respectively).

Lines S_{13} in 2006 and S_{28} recorded the greatest dry weight with an average of 4.07 and 4.21g, respectively.

With respect to seedling vigor index ranged from 542.20 in S_{27} to663.03 in S_4 in 2006 and from 561.23 in $shandweel_3$ to 717.30 in S_{13} in 2007.

Table 5. Mean performance and range of seedling characters in 2006 and 2007 Seasons.

Genotypes	Radical length (cm)		Shoot length (cm)		Seedling length 9cm)		Seedling dry weight(mg)		Seedling vigor index	
	2006	2007	2006	2007	2006	2007	2006	2007	2006	2007
Line S_4	3.90	3.83	2.15	2.85	6.05	6.68	3.07	3.55	560.17	645.41
Line S_5	4.02	3.87	2.80	3.42	6.82	7.28	3.11	3.76	663.03	696.80
Line S_8	3.85	3.68	2.73	3.40	6.58	7.08	2.93	3.22	624.27	697.52
Line S_{11}	3.42	3.23	2.68	2.99	6.10	6.22	3.51	4.10	574.40	601.91
Line S_{13}	3.80	3.68	2.75	3.58	6.55	7.27	4.07	3.42	633.50	717.30
Line S_{15}	3.42	3.13	2.82	3.42	6.23	6.55	3.47	3.85	602.27	636.07
Line S_{27}	2.97	3.20	2.72	3.20	5.68	6.40	3.44	3.35	542.20	617.81
Line S_{28}	3.80	3.37	2.62	2.97	6.42	6.33	3.49	4.21	577.73	598.93
Line S_{33}	3.83	3.67	2.72	3.21	6.55	6.87	3.79	3.19	642.20	669.31
Line S_{34}	3.47	3.15	3.52	3.61	6.98	6.76	3.38	3.39	617.10	644.03
Shandweel$_3$	3.17	3.08	3.10	2.97	6.28	6.05	3.80	3.67	598.60	561.23
L.S.D	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
Mean	3.45	2.78	2.78	3.24	6.38	6.68	3.46	3.61	603.22	643.67
Range	2.97-4.02	3.08-3.87	2.15-3.52	2.85-3.61	5.68-6.98	6.05-7.28	2.93-4.07	3.19-4.21	542.2-663.03	561.23-717.30

Seed characters

Data presented in Table (6) show the mean performance and range for seed index and seed coat/ whole seed of eleven sesame genotypes.

Range for seed index was 3.65-4.41 and 3.58-4.30 g in 2006 and 2007, respectively. The line S_5 followed by line S_{11} and line S_{13} had significantly, the greatest seed index in 2006 and 2007. In contrast, S_{34} recorded the lowest seed index in both seasons.

Range for seed coat/whole seed were from 14.70 – 18.21in 2006 and from 14.55 – 18.23 in 2007. The line S_{28} recorded significantly, the greatest seed coat/ whole seed being 18.21 and 18.23 in 2006 and 2007, respectively. While line S_8 showed the lowest value of this trait recording 14.70 and 14.55 in 2006 and 2007, respectively.

Table 6. Mean performance and range of seed characters in 2006 and 2007seasons.

Genotypes	Seed index		Seed coat/ whole ratio	
	2006	2007	2006	2007
Line S_4	3.77	3.70	16.52	16.43
Line S_5	4.41	4.30	17.20	17.44
Line S_8	3.68	3.71	14.70	14.55
Line S_{11}	4.24	4.30	14.82	14.67
Line S_{13}	4.10	4.13	16.84	16.82
Line S_{15}	3.98	4.11	15.25	15.26
Line S_{27}	3.81	3.84	15.59	15.78
Line S_{28}	4.17	4.15	18.21	18.23
Line S_{33}	3.83	3.91	15.72	15.51
Line S_{34}	3.65	3.58	17.77	17.79
Shandweel$_3$	4.04	4.01	15.75	15.65
L.S.D	0.12	0.12	0.39	0.34
Mean	3.97	4.00	16.22	16.19
Rang	3.65 – 4.41	3.58 – 4.30	14.70 – 18.21	14.55 - 18.23

Chemical composition

The variations in chemical components of sesame are mainly related to genotypes, planting date, location, soil structure, crop maturity and other environmental conditions, as reported by Gupta *et al* (1998).

Results in Table (7) showed that crude oil content ranged from 50.36 – 54.54 and 50.71 – 54.58 in 2006 and 2007, respectively. The line S_{11} recorded the highest crude oil in both seasons. Meanwhile, the line S_{28} had lowest crude oil in both seasons. These results are in agreement with those obtained byAshri (1998), Bayder *et al* (1999 a and b), El-Shakhess *et al* (2003) and Hiremath *et al* (2007).

It was also obvious from results in Table (7) that the ranges of crude protein were 21.94 for S_{15} to 25.45% for S_{28} in 2006 and from 22.67 for S_{15} to 25.39% for S_{28} in 2007. The variation in total carbohydrates content was not as large as that of crude oil or crude protein. Total carbohydrates ranged

from 10.24 for line S_{11} to 12.75% for line S_{13} in 2006 and from 10.07 forlinS_{11} to 11.74% for line S_{13} in 2007, while most lines had close value that did not differ significantly from each other. These results are in accordance with obtained byEl-Emery *et al* (1997) and El- Shakhess *et al* (2003).

Table 7. Chemical characteristics of various sesame genotypes and sesame seeds in 2006 and 2007 seasons.

Genotypes	Crude oil%		Crude protein%		Total carbohydrate%	
	2006	2007	2006	2007	2006	2007
lineS_4	52.67	52.86	22.24	22.84	11.79	11.56
lineS_5	51.63	51.92	23.25	23.62	11.70	11.73
lineS_8	63.61	53.99	23.02	22.81	11.23	10.49
lineS_{11}	54.54	54.58	23.40	23.87	10.24	10.07
lineS_{13}	51.62	52.65	22.97	23.18	12.75	11.74
lineS_{15}	54.12	54.22	21.94	22.67	10.94	10.32
lineS_{27}	53.59	53.28	23.60	23.68	10.78	10.14
lineS_{28}	50.36	50.71	25.45	25.39	11.53	10.87
lineS_{33}	53.61	53.69	23.52	23.59	10.32	10.09
lineS_{34}	50.57	50.85	25.24	25.16	11.46	10.83
Shandweel$_3$	52.55	52.66	23.76	24.53	10.92	10.39
L.S.D	0.71	0.72	0.44	0.52	0.58	0.73
Mean	52.63	52.86	23.49	23.75	11.24	10.72
Range	50.36-54.54	50.71-54.58	21.94-25.45	22.67-25.39	10.24-12.75	10.07-11.74

Fatty acid composition of the eleven sesame genotypes are presented in Table (8). The quantities of plamitic, stearic,oleic,linoleic and linolenic acids varied among lines. The results confirmed that oleic acid was the major component, comprising 39.08-46.89% of total fatty acids, followed by linoleic acid, (35.15-45-13%). It is of great importance to obtain high oleic/ low linoleic and high linoleic/ low oleic acid genotypes for different needs. The percentages of oleic and linoleic acids are very close to each

Table 8. Fatty acid composition of various sesame lines.

Genotypes	Fatty acid composition %					TS%	TU%	Ts/TU ratio
	Saturated fatty acids		Unsaturated fatty acid					
	Palamitic $C_{16:0}$	Stearic $C_{18:0}$	Oleic $C_{18:1}$	Linoleic $C_{18:2}$	Linolenic $C_{18:3}$			
Line S_4	14.54	7.51	39.08	35.15	1.17	21.64	75.40	3.48
Line S_5	9.00	7.52	42.05	43.64	0.00	14.27	85.69	6.00
Line S_8	8.44	4.51	41.87	44.66	0.49	12.39	86.95	6.71
Line S_{11}	10.00	5.18	41.45	42.97	0.00	15.18	84.42	5.56
Line S_{13}	8.53	4.68	41.54	44.63	0.58	13.21	86.75	6.57
Line S_{15}	9.17	4.80	41.82	43.56	0.30	13.97	85.68	6.13
Line S_{27}	8.65	5.06	43.04	42.81	0.41	13.71	86.26	6.29
Line S_{28}	8.92	4.01	41.54	44.28	0.71	12.95	86.53	6.69
Line S_{33}	8.49	5.29	46.89	38.77	0.53	13.78	86.19	6.25
Line S_{34}	7.69	5.36	45.72	40.74	0.45	13.05	86.91	6.66
Shandweel$_3$	8.84	4.55	41.07	45.13	0.39	13.39	86.59	6.47

TS = Total saturated fatty acids.

TU = Total unsaturated fatty acids.

other in sesame oil (Baydar *et al* 1999). The predominant saturated fatty acid in all genotypes were plamitic and stearic, which ranged from 7.69 (S_{34}) to a4.54 (S_4) and from 4.01 (S_{28}) to 7.51(S_4). The total saturated fatty acids ranged from 12.93-21.64%.Meanwhile, the total unsaturated fatty acids contributed 75.40 to 86.95%. The genotypes displayed variation amongst them for individual fatty acids. Three genotypes (S_{33},S_{34} and S_{27}) showed high level of oleic acid, while three genotypes (S_8 ,S_{13} and S_{28}) had high level of linoleic acid. In contrast, S_4 had the lowest value of oleic and S_4 and S_4 and S_{33} had the lowest values of lionleic acid. Such variation in the seed fatty acids point to an inheritable capacity that makes these genotypes valuable in breeding program for high oleic or linoleic sesame lines. These results are compatible with those obtained by Uzun *et al* (2002), El-Shakhess *et al* (2003), Mosjidis and Yermanos (2004), Were *et al* (2006) and Hiremat *et al* (2007).

Genetic analysis

Table(9) shows estimates of component of variance, genotypic (δ^2_g), phenotypic (δ^2_{ph}) and environmental (δ^2_e) variance, genotypic (GCV) and phenotypic (PCV) coefficient of variability, broad sense heritability and expected genetic advance(G.A) under 5% selection on intensity and as a mean% (G.A%). The magnitude of genotypic variance was greater than that of environmental variance for all studied characters. The phenotypic (δ^2ph) and genotypic (δ^2g) for number of capsules/pl. and oil yield/fed. were high in both seasonl. These results are in harmony with those obtained by Laurentin and Montilla (2002), Babu *et al* (2005), Ganesan (2005) and Kumar and Sasivannan (2006). The extent of coefficient of variation indicated that high estimates of (PCV) and (GCV) were exhibited for number of branches/pl., number of capsules/pl. and seed yield/pl. in the two seasons. The GCV for number of branches/pl., number of capsules/pl. and seed yield/pl. were (34.95 and 37.56), (26.23 and 27.86) and (20.96 and 21.33) in 2006 and 2007, respectively. These results are in confirmatory with those of Senthil Kumar *et al* (2002), Raghuwanshi (2005), Banerjee and Kole (2006), Prasad *et al* (2007) and Iwo *et al* (2007). The broad sense heritability was relatively high (more than 80%)for plant high, length of fruiting zone, number of branches/pl., number of capsules/pl. and seed yield/pl. Similar results in sesame were obtained by Kokane and Sakhare (2004), Sonali Sengupta and Datta (2004), Velu and Shunmugavalli (2005), Mothilal (2006), Banerjee and Kole (2006), Prasad *et al* (2007) and Iwo *et al* (2007). On other hand, seed yield/fed and oil yield/fed had moderately high estimates of heritability (more than 50%).

It is known that expected genetic advance from selection is commonly predicted as the product of heritability ratio and the selection differential. Length of fruiting zone, number of branches/pl., number of capsules/pl. and seed yield/pl. had the highest estimates of genetic advance coupled with high broad- sense heritability. Meanwhile, there were not much differences between PCV and GCV, thus, these characters showing to be highly heritable, points to the predominance of additive gene effect, easily fixable and can be taken as unit characters for effective selection. Plant height had medium genetic advance values in two seasons with high heritability. Thus, a high heritability can not be considered as criteria for high genetic gain. Seed yield/fed and oil yield/fed had moderate estimates of GCV and PCV value with moderate heritability. The results are in confirmatory with those of Singh and Singh (2004),Velu and Shumugavalli (2005), Singh (2005), Ganesan (2005), Kumar and Saivannan (2006), Banerjee and Kole (2006) and Iwo *et al* (2007).

Table 10) shows that genotypic variance was prominent than that of environmental variance for standard germination%, seed vigor index,

accelerated ageing germination, electrical conductivity $\mu Scm^{-1}g^{-1}$, seed index and seed coat/ whole seed ratio in 2006 and 2007. The magnitude of environmental variance was greater than that of genotypic variance for radical length, shoot length, seedling length, seedling dry weight and seedling vigor index, in 2006 and 2007, indicating that those variability influenced mainly by environments. PCV estimates were larger than the GCV for standard germination %, accelerated ageing germination, radical length, shoot length, seedling length, seedling dry weight and seedling vigor index, in both two seasons. Meanwhile, the value of GCV and PCV were near equal for seed vigor index, electrical conductivity $\mu Scm^{-1}g^{-1}$, seed index and seed coat/ whole seed ratio in 2006 and 2007, indicating that environmental effects on these characters can be neglected. Whereas, the effectiveness of selection according to quantitative traits is largely dependent on the ratio between the levels of their genotypic and phenotypic variability within the population (Guzhov,1984).Thereby each of those characters that appeared equal or approximate ratio for GCV value and PCV value, selection according to such characters will be effective. Broad sense heritability (h^2_b) was high for seed vigor index, electrical conductivity $\mu Scm^{-1}g^{-1}$, seed index and seed coat/ whole seed ratio in both two seasons. Accordingly, the selection would be relatively effective for these characters. On the other hand the other characters exhibited lower magnitude of heritability in both seasons. The expected genetic advance were in the favorable direction of the seed vigor, electrical conductivity $\mu Scm^{-1}g^{-1}$, seed index and seed coat/ whole seed ratio than other traits in both seasons. These finding illustrated that considerable level of improvement can be achieved in these traits by selection from population. Similar results were reported, previously by Sing and Singh (2004), Adebisi *et al* (2005), Banerjee and Kole (2006), Kumar and Saivannan (2006) and Iwo *et al* (2007).

Estimates of component of variance, GCV) and PCV, h^2_b and G.A% for chemical characteristics in 2006 and 2007 are presented in Table (11). The data exhibited that the genotypic variance was higher than that of environmental variance in all characters. The values of GCV and PCV were approximately equivalent for all studied characters in both seasons, indicating that these traits were not affected by environmental conditions. H^2 accessed 90% at crude oil in 2006 and 2007 and crude protein in 2007. The expected genetic advance ranged from 4.7 to 8.5 and from 5.3 to 11.4 in 2006 and 2007, respectively. Total carbohydrates expressed the highest estimates value of genetic advance by crude protein and crude oil in both seasons. According to previous results, the selection would be relatively effective for crude oil, crude protein and total carbohydrate. These results are confirmatory with those of Pathak and Dixit (1992), Tamina Begum and Dasgupta (2003) and Babu *et al* (2004).

Table 9. Estimates of component of variance, genotypic (GCV) and phenotypic (PCV) coefficients of variation, broad sense heritability estimates (h^2_b) and genetic advance as percentage of mean (G.s %) for yield and some agronomic characters of eleven sesame genotypes in 2006 and 2007 seasons.

Characters	Component of variance						Genetic variability				h^2_b		Genetic advance			
	δ^2_g		δ^2_{ph}		δ^2_e		GCV		PCV				G.s		G.s %	
	2006	2007	2006	2007	2006	2007	2006	2007	2006	2007	2006	2007	2006	2007	2006	2007
Plant height	336.8	428.9	430.3	482.4	63.6	53.5	8.6	9.3	9.3	9.3	85.2	88.9	36.4	40.2	16.4	18.0
Length of fruiting zone	664.4	694.8	747.9	741.1	98.1	76.7	16.2	16.6	17.8	17.1	86.9	89.7	49.0	50.3	31.9	31.6
Branches/pl.	3.9	3.4	4.3	4.9	0.9	0.9	35.0	37.6	42.2	38.9	79.3	80.6	3.4	3.7	68.9	64.7
Capsules/pl.	7688.5	8300.5	9355.5	8299.6	1055.1	611.11	26.2	27.9	29.6	25.3	82.7	88.6	176.8	173.9	54.1	52.0
Seed yield/pl.	129.9	142.9	164.0	160.3	21.3	30.26	21.0	21.3	22.9	22.9	87.0	81.1	23.0	21.2	41.0	38.9
Seed yield/fed.	0.57	1.01	1.3	1.01	0.29	0.37	8.1	12.2	13.8	12.2	66.1	77.8	1.8	0.91	22.1	11.0
Oil yield/fed.	2208.0	3355.3	4622.9	4616.2	126.69	2408.2	9.0	11.1	13.0	12.9	72.58	74.8	101.7	67.0	19.5	12.8

Table10. Estimates of component of variance, genotypic (GCV) and phenotypic (PCV) coefficients of variation, broad sense heritability estimates (h^2_b) and genetic advance as percentage of mean (G.s %) for germination, seedling and seed characters of eleven sesame genotypes in 2006 and 2007 seasons.

characters	Component of variance						Genetic variability				h^2_b		Genetic advance					
	δ^2_g		δ^2_{ph}		δ^2_e		GCV		PCV				G.s		G.s %)			
	2006	2007	2006	2007	2006	2007	2007	2006	2007	2006	2007	2006	2007	2006	2007	2006	2007	
Standard germination%	1.26	4.2	18.2	5.7	14.04	4.4	1.2	2.2	2.5	4.5	22.3	23.0	1.1	2.0	1.1	2.1		
Seed vigor index	4.0	6.6	5.1	8.9	2.3	1.1	4.6	5.8	5.2	6.76	74.4	78.2	3.6	4.6	8.4	10.4		
Accelerated ageing germination	9.3	9.5	12.1	14.3	8.7	4.7	2.3	3.8	4.3	4.7	27.6	66.9	2.0	5.2	2.5	6.5		
Electrical conductivity.	22.4	25.9	22.9	29.8	3.9	0.56	11.8	12.9	12.0	13.8	87.0	97.6	9.8	9.6	24.7	24.1		
Radical length	0.01	0.03	0.30	0.27	0.31	0.24	0.0	5.1	15.9	14.5	0.0	12.3	0.0	0.13	0.0	3.7		
Shoot length	0.04	0.05	0.14	0.23	0.18	0.10	6.0	8.0	11.5	17.1	22.2	27.3	0.21	0.22	6.5	7.8		
Seedling length	-0.03	0.04	0.47	0.43	0.50	0.39	0.0	3.2	10.7	9.8	0.0	10.3	0.0	0.14	0.0	2.1		
Seedling dry weight	0.05	0.08	0.26	0.19	0.21	0.08	6.2	8.0	14.6	12.0	17.9	43.9	0.19	0.39	5.4	10.9		
Seedling vigor index	-71.5	108.3	4261.62	4571.8	4333.1	3488.4	0.0	5.1	10.8	10.5	0.0	23.7	0.0	33.0	0.0	5.1		
Seed index	0.04	0.06	0.06	0.06	0.01	0.01	5.1	6.1	5.9	6.4	75.1	92.1	0.37	0.48	9.2	12.1		
Seed coat/whole seed	1.4	1.5	1.5	1.6	0.05	0.03	7.2	7.7	7.4	7.8	96.3	97.5	2.4	2.5	14.6	15.6		

Genetic variance
δ^2_g = Genetic variance
δ^2_{ph} = phenotypic variance
δ^2_e = environmental variance

Table 11. Estimates of component of variance, genotypic (GCV) and phenotypic (PCV) coefficients of variation, broad sense Heritability estimates (h^2_b) and genetic advance as percentage of mean (G.s %) for chemical characteristics of eleven sesame genotypes in 2006 and 2007 seasons.

characters	Component of variance						Genetic variability		h^2_b		Genetic advance					
	δ^2_g		δ^2_{ph}		δ^2_e		GCV	PCV			G.s		G.s %)			
	2006	2007	2006	2007	2006	2007	2006	2007	2006	2007	2006	2007	2006	2007	2006	2007
Crude oil	1.6	2.0	1.8	2.1	0.18	0.17	2.4	2.7	2.5	2.8	90.0	91.9	2.5	2.8	4.7	5.3
Crude protein	0.82	1.1	0.92	1.2	1.1	0.07	3.8	4.5	4.0	4.7	89.6	94.5	1.8	2.1	7.4	9.1
Total carbohydrate	0.32	0.48	0.50	0.59	0.18	0.12	5.3	6.2	6.6	6.9	63.6	80.5	0.93	1.3	8.6	11.4

Genetic variance
δ^2_g = Genetic variance
δ^2_{ph} = phenotypic variance
δ^2_e = environmental variance

Protein banding pattern

The SDS-PAGE for total proteins of the eleven genotypes is illustrated in Table (12) and Fig. (4). A maximum of 12 bands were detected with molecular weight ranging from 233.5 to 74.5 kDa. Two common (monomorphic) bands were detected, while 10 polymorphic bands (83.3%) were observed. Three negative specific markers were scored for the absence of a common band. These are 202.9, 90.6, and 82.6 kDa for genotypes line S_{13}, Shandaweel$_3$, and line S_{28}, respectively. One positive specific marker was observed for the presence of unique bands at 101.3 kDa for the line S_4. The results indicate that the eleven genotypes could be identified by their protein banding patterns. The usefulness of seed protein variability for discriminating among genotypes as well as for studying the genetic relationships has been reported by many investigators Abdel Salam *et al* (1998), Hassan *et al* (2002) and Barakat and Elham (2004).

Table 12. SDS-PAGE of total proteins extracted from the seeds of the eleven Sesame genotypes.

Band No.	MW (kDa)	Genotypes										
		LS1	LS 2	LS 3	LS 4	LS 5	LS 6	LS 7	LS 8	LS 9	LS 10	LS 11
1	233.5	+	+	+	+	+	+	+	+	+	+	+
2	216.5	+	+	+	+	+	+	+	-	-	-	-
3	202.9	+	+	+	+	+	+	-	+	+	+	+
4	180.3	+	+	+	+	+	-	-	+	-	-	+
5	159.4	-	+	-	+	+	-	-	-	+	+	-
6	137.6	+	-	-	-	+	+	+	-	+	+	-
7	110.4	+	+	+	+	+	+	+	+	+	+	+
8	101.3	-	+	-	-	-	-	-	-	-	-	-
9	90.6	+	+	+	+	+	+	+	+	+	+	-
10	82.6	+	+	+	+	+	+	+	-	+	+	+
11	78.5	-	-	-	-	-	-	-	+	+	+	+
12	74.5	+	+	+	+	+	+	+	-	-	+	+

+ = Band presence - = Band absence

RAPD-PCR analysis

Many random primers were pre-selected for the ability to detect polymorphism in the eleven sesame genotypes. Five primers, which displayed marked amplification with distinct bands and succeeded to anneal with all genotypes, were chosen. The results of these five primers are shown in Table (12) and Fig. (5). A total of 44 DNA bands were detected as generated by the 5 primers for the 11 genotypes used in the present study, in which 33 (75%) were polymorphic bands. The lowest number of polymorphic bands was detected for primer B18 (4 out of 7 amplified bands), while the largest number of polymorphic bands was detected for primer B15 (9 out of 10 amplified bands). Nine out of 33 bands were found to be useful as genotype-specific markers. The largest number of RAPD-PCR markers was scored for the line S27 (5 markers), while the lowest (1 marker) was scored for the genotype H34. In the meantime, the largest number of RAPD-PCR genotype-specific markers was generated by primer

B05 (4 markers), while the lowest number of RAPD-PCR genotype-specific markers was generated by primer A11 (one marker). On the other hand, primer A09 did not show any specification. Six positive specific markers were scored for the presence of unique bands for a given genotype, while 3 negative specific markers were scored for the absence of a common band. These genotype-specific markers can be used in subsequent experiments to detect molecular markers for polymorphic genes with economic importance among these and other genotypes. The five primers used in this study allowed enough distinction among the genotypes.

Genetic distance among genotypes

The similarity indices and the dendrogram tree among genotypes utilizing SDS-PAGE and RAPD markers are shown in Table (13) and Fig. 6, respectively. A strong relationship was scored between line S_8 and line S_{11} genotypes (similarity index 91%), while a weak relationship was scored between (line S_{34} and line S_{27}) and (line S_{34} and line S_{15}) genotypes (similarity index (64%). The dendrogram tree resulted in two main clusters. One of them involved the line S_{27}, while the second cluster involved into two sub-clusters. One of them included the line S_4, while the other sub-cluster involved the lines S8, S_{34}, S_{11}, S_{33}, S_{28}, S15, Shandaweel$_3$, S_5, and S_{13}. In conclusion, the SDS-PAGE and RAPD-PCR analysis can successfully be used to identify and discriminate among the different genotypes in this study.

Table 13. Similarity matrix among the eleven sesame genotypes based on combined analysis of SDS-PAGE and RAPD analysis.

Lines	1	2	3	4	5	6	7	8	9	10
Line S_1										
Line S_2	0.81									
Line S_3	0.91	0.80								
Line S_4	0.78	0.81	0.83							
Line S_5	0.76	0.70	0.78	0.81						
Line S_6	0.86	0.71	0.82	0.80	0.83					
Line S_7	0.72	0.64	0.68	0.69	0.73	0.81				
Line S_8	0.74	0.64	0.73	0.71	0.77	0.85	0.67			
Line S_9	0.78	0.68	0.74	0.72	0.73	0.86	0.68	0.83		
LineS_{10}	0.82	0.73	0.75	0.79	0.77	0.81	0.70	0.75	0.85	
LineS_{11}	0.87	0.77	0.83	0.75	0.73	0.83	0.71	0.79	0.81	0.82

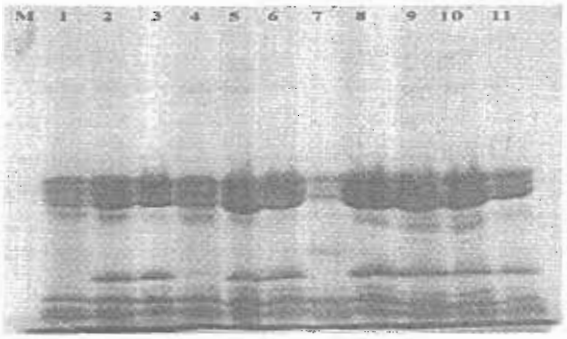
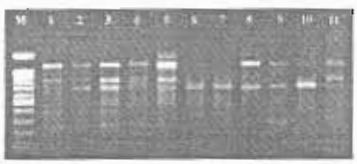
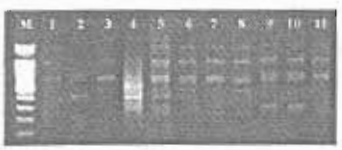


Figure 4. SDS-PAGE of total proteins of the eleven sesame genotypes (Lanes 1-11, H15, H4, H5, H27, H11, H34, H13, H28, H33, H8 and Shandaweel$_3$, respectively). M refers to high molecular weight (HMW)protein marker.


A11


A09


B15


B18

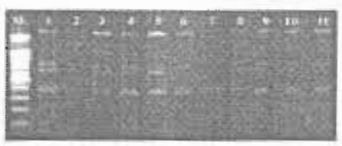

B05

Figure 5. Agarose gel (1.2%) in TAE buffer stained with ethidium bromide showing RAPD-PCR polymorphism of DNA for eleven sesame genotypes (Lanes 1-11, S_8, S_{34}, S_{11}, S_{33}, S_4, S_{28}, S_{27}, S_{15}, Shandaweel$_3$, S_5 and S_{13}, respectively) using random primers. M refers to 100 bp DNA Ladder plus.

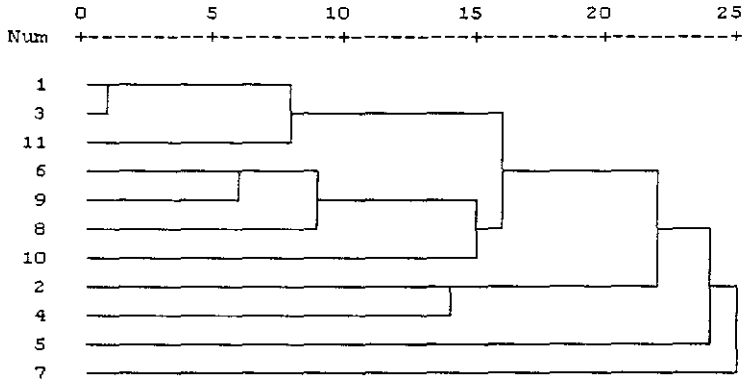


Figure 6. Dendrogram (Nei and Li 1979) of the genetic distances among the eleven sesame lines based on combination of SDS-protein and RAPD analysis.

REFERENCES

Abdel-Salam, A.Z.E., S.A. Ibrahim, F.M. Eldomyati and H. El-Nady, Ghada (1998). Biochemical and molecular genetic characterization of Egyptian barley cultivars and a trial for their micropropagation. 3rd Arab Conference. Modern Biotech. & Areas of Application in the Arab World, 14-17 December, Cairo, Egypt, Pp 582-605.

Adebisi, M.A.,M.O.Ajala,O.J.Ariyo and T.O.AdeniJi .(2005). Genetic studies on seed quality in sesame (*Sesamum indicum* L). J. of Genetic and Breeding 59. 3-4;199-204.

AOAC (2000). Official Methods of Analysis of the Association of Official Analytical Agricultural Chemists, 17th ed. Published by A. O. A. C.

AOSA (1983). Seed vigor testing handbook. Contribution No. 32 to handbook on seed testing. Association of official seed analysis, 88-93.

Ashri,A. (1998). Sesame breeding. Plant breed. Rev. 16.179-228.

Babu, DR., P.VR.Kumar and C.VD.Rani (2005). Genetic variability, heritability and genetic advance of seed yield and its components in sesame (*Sesamum indicum* L.). Research on crops- Gaurav Society of Agricultural Research Information Center, Hisar, Indias. 6 (2) 307-308.

Banerjee, P.P. and P.C.Kole (2006). Genetic variability and yield analysis is sesame (*Sesamum indicum* L) . Crop research 32(3)430 – 433.

Barakat, H.M. and A.A. Elham (2004). Genetic characterization of two cotton species as revealed by SDS-protein, isozymes and RAPD-PCR. Egypt, J. Genet. Cytol., 33: 63-83.

Baydar, H,R.Marquard and I.Turgut (1999a). Pure line selection for improving of yield, oil contant and different fatty acids composition of sesame (*Sesamum indicum* L). Plant Breed. 118: 462 -464.

Baydar,H.,I. Turgut and K.Turgut (1999b). Variation of certain characters and line selection for yield, oil, oleic and linoleic acids in the Turkish sesame (*Sesamum indicum* L.). Tr.J. Agric. For. 23. 431-441.

Copeland. L.O. (1976). Principles of Seed Science and Technology. Burgess Pub.Com., Minneapolis, Minnesota 164-165.

Das, A. and SK. Samanta (1998). Genetic analysis of oil content and fatty acids in sesame (*Sesamum indicum* L.). Crop Research (Hisar) 15 (2-3) 199-205.

Dornbos, D.I.(1995). Seed Vigor. In: Seed Quality: Basic Mechanisms and Agricultural implications. (Ed. A.S.Basra) Food Product Press, New York, 45-80.

Ellis, R. H.(1992). Seed and seedling vigor in relation of crop growth and yield. Plant Growth Regul.,11: 249-255.

El-Emery,M.I.,S.T.El-Serogy and H.G.El-Rabia (1997). Effects of irrigation and harvesting treatment on yield and quality of some sesame (*Sesamum indicum* L) genotypes. Egypt.J.App.Sci. 12 (11) 168 – 187.

El-Shakhess, Samar. A. M., Nemat, A. Nagib and M.A.Madkour(2003). Performance and chemical composition some promising sesame lines (*Sesamum indicum* L). Egypt. J. Plant Breed.7 (1) 41-53.

Ganesan, KN. (2005). Variability studies in determinate type sesame, *Sesamum indicum* L., germplasm lines for yield and its component traits. J. of Oilseeds Research. Indian Society of Oilseeds Research, Rajendranagar, India. 22(1) 176-177.

Gupta, S.K.,I.P.Yadava,K.Farksh, N.K.Thakral and P.Kumar (1998). Influence of date of sowing on oil and fatty acid composition in sesame (*Sesamum indicum* L.). Euphytica. 93: 375-377.

Guzhov, Y.U. (1984). Genetic and plant breeding for agri. Mir. Publisher.

Hassan, H.Z.; M. Mervat and S.L. Maximous (2002). Geographical effect on the genetic fingerprint of some *Populus* species based on isozymes and DNA polymorphism. Egypt. J. Genet. Cytol., 31: 47-66.

Hiremath, S.C.,C.G.Patil,K.B.Patil and M.H.Nagasamping(2007). Genetic diversity of seed lipid content and fatty acid composition in some species of sesame (pedaliaceae). African J. of Biotechnology 6 (5) 539-543.

ISTA (1985). International seed testing association. International rules for seed testing proc. Int.seed test. Assoc. 31:1- 52.

ISTA (1987). International Seed Testing Association.Handbook of Vigor Test Methods. 2nd Ed., Zurich, Switzerland.

ISTA (1993). International Seed Testing Association. International rules for seed testing – Seed Sci. and Technol., 21: 187-209.

Iwo, GA., AA. Idowu and S. Misari (2007). Genetic variability and correlation studies in sesame (*Sesamum indicum* L.) Global J. of Pure and Applied Sciences. Bachudo Science co. Ltd., Calabar, Nigeria. 13 (1) 35-38.

Kokane, G.M. and S.B.Sakhare (2004). Studies on genetic variability in sesamum. Annals of Plant Physiology. 18 (1) 61-63.

Krishnasamy. V. and D.V.Seshu (1990). Germination after accelerated ageing and associated characters in rice varieties. Seed Sci. Technol. 18:147-156.

Kumar,P.S. and S.Sasivannan (2006). Variability, heritability and genetic advance in sesame (*Sesamum indicum* L). Crop Research. 31.2:258 - 260.

Laemmli, U.K. (1970). Cleavage of structural proteins during assembly of head Bacteriophage T4. Nature 227: 680-685.

Laurentin,H.and D.Montilla(2002). Variability studies for yield and yield components in white- grain in sesame. Sesame and Safflower Newsletter 17:26-28.

Mather, K. and J.L.Jinks (1982).Biometrical Genetics. (3 rd Edition) Champman and Hall, London.

Mosjidis, J.A. and D.M.Yermanos (2004). Plant position effect on seed weight, oil content and oil composition in sesame. Euphytica, 34(1) 193-199.

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(2)117-120.

Nei, M. and W.H. Li (1979). Mathematical model of studying genetic variation in terms of restriction endonucleases. Proc. Natl. Acad. Sci. USA, 76: 5269-5273.

Pathak, H.C. and S.K. Dixit (1992). Genetic variability and inter- relationship studies in black seeded sesame. Madras Agric. J. 79.2:94-100.

Perry, D. A. (1989). Handbook of Vigor Test Methods 2nd Ed. ISTA, Zurich, Switzerland.

Prasad, Y.V.NS, ND.Bangar and PA. Navale (2007). Genetic variability, correlation and Path analysis in F_2 and F_3 populations of cross JLSV X Hawari in *Sesamum*. J.of.Maharashtra Agric. 32.1:59 -61.

Raghuwanshi, K. Ms. (2005). Study of genetic variability in sesame (*Sesamum indicum* L). J.of Maharashtra Agric. 30(3) 264-265.

Schuttie, A.W. and A.C.Leopold (1984). Solute leakage from artificially aged soybean seed after imbibitions. Crop Sci. 24:835-838.

Senthil Kumar, P., R.Sndararajan, P.Thangavel, P.Karuppia and J.Ganesan (2002). Variability studies in the second generation of inter varietals crosses in sesame (*Sesamum indicum* L). Sesame and Safflower Newsletter. 17:36 -39.

Sing, S.B.(2005). Genetic variability and relative contribution of component characters on yield of sesame. Farm Sci. J. 14. 1: 1 -3.

Sing, S.B.and S.D.Sing(2004). Estimation of variability parameters for some quantitative characters in sesame (*Sesamum indicum* L). Annalas of Agric. Research.25.1:43 -45.

Sonali Sengupta and AK.Datta (2004). Genetic studies to selection criteria for yieled improvement in sesame. J.of Phytological Research. 17(2)163-166.

Tamina, Begum and T.Dasgupta (2003). Character association in sesame (*Sesamum indicum* L.). Indian Agric. Agrc. 47(3-4) 253-258.

Turkey, J.W. (1977). Exploratory Data Analysis. "Adision Wesely, Reading, Massachusetts.

Uzun, B.,S.Lger and M.I. ÇAĞrgan (2002). Comparison of determinate and indeterminate types of sesame for oil content and fatty acid composition. Turk J. Agric. For .26.269-274.

Velu, G.and N.Shunmugavalli (2005). Genetic variation and genotype X environment interaction in sesame. J.of Oilseeds. Research 22(1)178 - 179.

Were,B.A., A.O.Onkwar, S.Gudu, M.Welander and A.S. Carlsson (2006). Seed oil content and fatty acid composition in East African sesame (*Sesamum indicum* L) accessions evaluated over 3 years. Field Crops Research 97:254 -260.

Williams, J.G.K., A.R. Kubelk, K.J. Livak, J.A. Rafalski and S.V. Tingey (1990). DNA polymorphism amplified by arbitrary primers are useful as genetic markers. Nucl. Acid Res., 18: 6231-6235.

تقييم وتمييز أحدى عشر سلاله من السمسم

سمر أحمد منير الشخص[1] – يار محمد عبد التواب[2] – نعمت عدلي نجيب[2]

١- معهد بحوث المحاصيل الزيتية ٢- قسم بحوث تكنولوجيا البذور
معهد بحوث المحاصيل الحقليه – مركز البحوث الزراعيه - الجيزه

أجريت هذه الدراسه بمحطه بحوث الجيزه – مركز البحوث الزراعيه خلال موسمى 2006و 2007 وذلك بهدف دراسه تقدير الثوابت الوراثيه لبعض الصفات الانتاجيه و المحصول و أختبارات الانبات وكذلك الصفات الكيميائيه و بصمة الاصبع والعلاقه الوراثيه لأحدى عشر تركيبيا وراثيا من السمسم أشتملت الصنف التجارى شندويل3.

أوضحت النتائج أن التركيب الوراثى س5 أظهر تفوقا فى طول المنطقه الثمريه وعدد الكبسولات/ نبات و محصول البذور/نبات و محصول البذور/ فدان ومحصول الزيت/فدان. وقد أظهر التركيب س33 أعلى نسبه أنبات و دليل قوة البذور و اعلى قيمة من التوصيل الكهربى، فى حين تراوحت نسب الاسراع بالشيخوخه من 74.0% إلى 84.33%. وقد أظهرت النتائج وجود إختلاف

التراكيب الوراثيه التى شملتها الدراسه فى جودة البادره و البذور. وقد تراوحت متوسطات نسبة الزيت ما بين 50.3% الى 54.58% وتراوحت متوسطات نسبة البروتين مابين 21.94% الى 25.45%وتراوحت متوسطات نسبه الكربوهيدرات من 10.07% الى 12.75%. كما أشارت النتائج أن نسبه حامضى الاوليك و اللينوليك هى المكون الاكبر للاحماض الدهنيه غير المشبعه فى زيت السمسم.

كما أشارت النتائج أن الصفات: عدد الافرع /نبات و عدد الكبسولات/نبات ومحصول البذور/ نبات سجلت أعلى قيم لكل من معامل الاختلاف الوراثى ومعامل الاختلاف الظاهرى. وقد كانت قيم معامل الاختلاف الوراثى و المظهرى تقريبا متساوية لصفات دليل قوة البذره والتوصيل الكهربى ودليل البذره ونسبه غلاف البذره/ الوزن الكلى للبذره و نسبة الزيت و نسبة البروتين و نسبه الكربوهيدرات. و أظهرت كفاءة التوريث فى معناها الواسع قيم مرتفعه و كذلك النسبه المئويه للتحسين الوراثى المتوقع لصفات طول المنطقه الثمريه و عدد الافرع /نبات و عدد الكبسولات/نبات ومحصول البذور/ نبات و عدد الافرع /نبات و عدد الكبسولات/نبات ومحصول البذور/ نبات مما يشير انه يمكن تحسين هذه الصفات بواسطة الانتخاب.

كما أشارت نتائج بصمة الاصبع و العلاقه الوراثيه بواسطة التفريد الكهربى للبروتينات بطريقة SDS-PAGEعدد 12 حزمه منها 10 حزمه متباينه وكذلك 4حزمه يمكن أستخدامها كدلائل خاصه. وأظهرت النتائج بطريقه ال RAPDبأستخدام 5 بادئات عشوائيه44 حزمه منها 33 حزمه متباينه، وكذلك 9 حزمه يمكن الاستفادة منها كدلائل خاصه للتراكيب الوراثيه. قسمت الشجره التطوريه السلالات الى مجموعتين رئيسيتين.