EVALUATION AND GENETIC DIVERSITY OF ELEVEN SESAME LINES

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Sesame (*Sesamum indicum* L) is one of the most essential oil crops in Egypt as well as in many parts of the world. It plays an important role as an industrial food crop because of its high nutritional value. The seeds contain 50 to 60% oil and 35 to 50% protein Ram *et al*. (1990). The seed is consumed as a source of calcium and potassium. The oil contains high content of antioxidants, such as sesamin and sesamoiln. It also, provides mono-unsaturated fatty acid (oleic acid) and polyunsaturated fatty acid (linoleic acid). It is used in pharmaceutical and cosmetic industries, Pornparn *et al.* (2009).

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 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. El-Shakhess *et al.* (2003 and 2008), 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.

Information on genetic diversity and relationships among populations is important for plant breeding programs as

it helps to select the right genetic material to be used Ganesh and Thangavelu (1995). Genetic diversity in crop species can be determined by using the agro-morphological as well as biochemical and molecular markers Geleta *et al*. (2008). PCR-based techniques such as amplified fragment length polymorphism (AFLP), simple sequence repeats (SSR), inter simple sequence repeats (ISSR) and random amplified polymorphic DNA (RAPD) also have been widely used in genetic diversity studies in sesame Pham *et al*. (2009). Some of these techniques, such as RAPD do not require prior knowledge of DNA sequence and therefore arbitrary primers can be used.

RAPD can be quickly and effectively applied to distinguish useful polymorphisms Ko *et al*. (1998). The resolving influence of this tool is numerous folds superior than morphological or biochemical markers and is much simpler and technically less demanding than RFLP and other new generation markers. RAPD markers have proved their significance for assortment analysis in a number of field crops such as rice Pervaiz *et al*. (2010) and particularly in sesame Ercan *et al*. (2004).

The main objectives of this work were to study sesame seed quality by using some vigor, viability test and to determine the major chemical composition, the performance, heritability, genotypic and phenotypic variability and determine the genetic diversity among the different sesame genotypes by RAPD-PCR.

MATERIALS AND METHODS

Field trial

Ten sesame lines and one commercial cultivars (Shandweel3), namely: line 108-6, line 109-9, line 111-4, line111-6, line112-1, line 112-5, line 112-8, line 115-8, line117-1 and line 117-7. The pedigree of these lines is shown in Table (1). The lines were planted during the summer seasons in 2011 and 2012 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 (cm), length of fruiting zone (cm), number of branches/pl. and number of capsules/pl.)

2. Yield parameters: seed yield/pl (g), weigth of 1000 seed (g), Seed yield/fed (ard.) and oil yield/fed. (Kg) were determined.

Laboratory tests

1. **Germination test:** Normal seedlings were counted according to the international rules of ISTA (1993). Germination percentage was calculated using the formula by Krishnasamy and Seshu (1990).

2. **Seedlings evaluation:** Normal seedlings 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 six days of germination test. The shoots and roots were also dried at 70°C for 72 h. seedling vigor index was calculated according to formula describe by ISTA (1985).

3. **Electrical conductivity test:** The electrical conductivity of the leachate was determined according to procedures described by AOSA (1983). The electrical conductivity of the leachates was determined using Ec meter.

4. **Accelerated ageing:** The seeds were kept in an aging chamber at 45°C and 100% relative humidity for three days. After aging, the seeds were dried up in the sun and percentage survival of the seeds was determined by standard germination test at 25°C and the mean normal seedling percentage was calculated according to AOSA (1983).

5. **Chemical composition:** Samples of about 50 g of air dried seeds of each genotype were randomly chosen from two replications and fine ground for estimating chemical composition. 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). The methyl esters of fatty acids were analyzed using Hewlett Packard gas chromatograph model 5890 provided with cabowa x Hp 20 M column.

Analysis of variance was calculated for each season separately according to Mather and Jinks (1982). According to homogeneity test, the results of 2011 and 2012 did not differ significantly, so the combined analyses of the two seasons were conducted.

Molecular markers

Genomic DNA extraction: DNAeasy plant minikit (Quigen Inc., Cat.no.69104, USA) was used for DNA extraction.

RAPD-PCR analysis: For testing the genetic diversity, RAPD-PCR reactions were conducted using 5 arbitraty 10-mer primers with the 5′→3′ sequences as shown in Table (2). The reaction conditions were optimized and mixtures were prepared (30 µl total volume) consisting of the following: dNTPs 2.4 µl, $MgCl_2$ 3.0 µl, 10 x buffer 3.0 µl, primer (10 um) 2.0 µl, Taq (5u/µl) 0.2 µl, template DNA (50 ng/µl) 2.0 ul, H_2O (dd) 17.4 ul. Amplification was carried out in a PTC- 200 thermal cycler (MJ Research, Watertown, USA) programmed as follows: denaturation, 94°C for 2 minutes, then for 40 cycles. Each cycle consisted of 1 minute at 94°C, 1 minute at 37°C, 2 minutes and 30 second at 72°C, followed by a final exten-

sion time of 12 minutes at 72°C and 4°C (infinitive).

Gel electrophoresis: Gel electrophoresis was applied according to Sambrook *et al.* (1989). Agarose (1.2%) was used for resolving the PCR products. Bands were detected on UV-transilluminator and photographed by Gel documentation 2000, Bio-RAD.

Similarity and dendrogram tree was performed using the SPSS program version 10.

RESULTS AND DISCUSSION

Agronomic characters

Wide range of variability was recorded for some morphological characters in Table (3). The differences among genotypes were significant for plant height; length of fruiting zone; number of branches/pl. and number of capsules/pl. Range for plant height were from 163.67 for Shandweel3 to 262.5 for line 117-7. Length of fruiting zone ranged from 124.17 for line 117-1 to 213.3 for line 117-7. With respect to number of branches/pl. ranged from 1.5 for Shandweel3 to 12.83 for line 112-5. Ranges for number of capsules/pl., were 97.52 for Shandweel3 to 665.02 for line 117-7.

Yield

Mean performances and range for seed yield / fed., seed yield/ pl., weight of 1000 seed and oil yield/ fed. of eleven sesame genotypes over the two seasons are presented in Table (4). It was obvious that the range for seed yield/fed. was 4.5-9.04. Line 111-6 was significantly higher yielding than check variety shandweel3 by 54.3%. On the average over the two seasons, Line 111-6 recorded the highest seed yield / fed. (9.04 ardb). This was followed by line 117-7 (8.83 ardb).

With respect to seed yield/pl. line 117-7 recorded the highest mean performance (56.02 g), followed by line 117-1 (50.35 g). They were higher than check variety Shandweel3, by 67.8% and 64.21 %, respectively. Ranges of seed yield/ pl. among eleven lines were 18.02 (Shandweel3) - 56.02 (line 117-7). Line 117-7 gave the greatest seed yield/ pl. followed by line 117-1. Table (4) showed the weight of 1000 seed. It was obvious that the range was 3.51 for Shandweel3 to 5.29 for line 112-1. Significant difference in oil yield/ fed. were detected among sesame entries over two seasons. The greatest value of oil yield /fed. (609.74) was recorded for line 117-7, while line 112-8 recorded the lowest oil yield/fed. (304.5).

Germination characters

Mean values of standard germination percentage, seed vigor index, accelerated aging germination and electrical conductivity are presented in Table (5). Standard germination percentage of seeds was differed due to the differences between the genotypes. It was ranged from 93% to 99.5%. The highest germination percentage was 99.5% in line 117-1 with no significant differences with line 111-6,

line 112-5, line 112-8 and line 117-7, while the lowest germination percentage was 93% in Shandweel3 without any significant differences with line 111-4.

With respect to seed vigor index, line 117-1 recorded the highest seed vigor index (24.42) without significant differences with line 112-1. While, line 111-6 gave the lowest seed vigor index (21.57) followed by line 111-4.

Accelerated aging germination ranged from 96.50% for line 117-7 followed by line 117-1 (95.75%) to 79% for Shandweel3. Electrical conductivity after 24 hours varied among different genotypes. 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 line 108- 7 was the highest electrical conductivity (74.5). Meanwhile, line 111-6 recorded the lowest value (39.27). Higher electrical conductivity of deteriorated seeds was also observed by Schuttle and Leopold (1984) in soybean. There is negative relationship between electrical conductivity and seed germination which indicated that more cell leachates escaped from deteriorated seed lowered the germination percentage of seed.

Seedling characters

Data in Table (6) revealed that line 117-1 was the longest Shoot length (3.36). In contrast, line 112-1 was the shortest shoot length. The longest radical length was 6.40 cm for line109-6 followed by line117-1. On the other hand, line112-1 was the shortest radical length. The highest seedling fresh weight was 43.05 for line112-1. While, line 108-6 was the lowest seedling fresh weight (26.36). The line111-6 recorded the highest seedling dry weight (4.43) followed by line112-1 with no significant differences. Meanwhile, line112-8 had the lowest seedling dry weight (3.51). Line 117-1 followed by line 109-6 had significantly the highest seed vigor index over two seasons. In contrast line 112-1 recorded the lowest vigor index.

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 55.35 for line 111-6 to 58.8 for line 112-5. The line 112-5 recorded the highest crude oil in both seasons. Meanwhile, the line 111-6 had lowest crude oil in both seasons. These results are in agreement with those obtained by El-Shakhess *et al*. (2003 and 2008) and Hiremath *et al*. (2007).

It was also obvious from results in Table (7) that the ranges of crude protein were 22.74 for line 108-6 to 26.9% for line 117-7. Total carbohydrates ranged from 10.34 for line 117-1 to 13.05 % for line 112-8. These results are in accordance

with obtained by El-Emery *et al*. (1997) and El- Shakhess *et al*. (2003 and 2008)

Fatty acid compositions%

A low level of saturated fatty acids, a relatively high level of the monounsaturated fatty acids, oleic acid, and polyunsaturated fatty acid; linoleic acid, characterizes sesame oil. Table (8) showed that the fatty acids were predominant in the eleven sesame genotype, palamitic, stearic oleic, linoleic, lenolenic and arachidic. The total unsaturated fatty acids ranged from 85.02% to 87.31%. Meanwhile, total saturated fatty acids ranged from 13.41% to 15.46%. Results in Table (8) indicated that the greatest value of oleic acid (45.2%) was obtained for check cultivar followed by line 117-7 (44.67%). Whereas, the line 112-8 gave the lowest value (42.50%) of oleic acid predominate fatty acids comprised palmitic, static, oleic, linoleic and linolemic ranged from (8.46-10.26%), (4.38-5.95%), (42.5-45.2%), (40.83-44.67%) and (0.42-0.73%), respectively . These results are in good agreement with those obtained by Uzun *et al*. (2002), El- Shakhess *et al*. (2003 and 2008), Mosjidis and Yermanos (2004), Were *et al*. (2006) and Hiremath *et al*. (2007).

Genetic analysis

The estimates of genetic variance (σ^2g), phenotypic (σ^2ph) and environment (σ^2e) variance, genotypic (GCV) and phenotypic (PCV) coefficient of variability. broad sense heritability and expected genetic advance (GS) under 5% selection on intensity and as percentage of the general mean (GS%) are presented in Table (9). The genotypic variance was greater then the environmental variance for all studied traits. The phenotypic variance (σ^2ph) and genotypic variance (σ^2g) values for number of capsules pl^{-1} and oil fad^{-1} were high over the two seasons. These results are in confirmatory with these of Laurentin and Montilla (2002), Babu *et al*. (2005), Ganesan (2005), Kumar Sasivannan (2006) and El-Shakhess *et al*. (2008). The extant of coefficient of variation indicated that high estimates of (PCV) and (GCV) were exhibited for number of branches pl^{-1}, number of capsules pl^{-1} and seed yield pl^{-1}. The GCV for number of branches/pl^{-1}., number of capsules/ pl. and seed yield/ pl^{-1} were 51.03, 47.79 and 36.02 respectively, suggesting wide spectrum of genotypic variation for these trait. Similar results were obtained by Senthil *et al*. (2002), Raghuwanshi (2005), Banerjee and Kole (2006), Prasad *et al*. (2007), Iwo *et al*. (2007) and El-Shakhess *et al*. (2008). Low magnitude GCV and PCV were observed for plant height, length of fruiting zone, weight 1000 seed and oil yield fad^{-1}. These results are in harmony with those obtained by Velu and Shunmugavalli (2005), Mothilal (2006), Banerjee and Kole (2006), Prasad *et al*. (2007), Iwo *et al*. (2007) and El-Shakhess *et al*. (2008). The high broad sense heritability was exhibited for number of capsules pl-^{1} and weight of 1000 seeds. These results are in harmony with those obtained by Velu and Shunmugavalli (2005), Mothilal (2006), Prasad *et al*. (2007) and El-Shakhess *et al*. (2008).

Mean while, the heritability was moderates for number of branches pl^{-1}, seed yield pl^{-1}, seed yield fad-1. and oil yield fad^{-1}. Similar results were obtained by 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).

Number of capsules pl^{-1} had the highest estimated of genetic advance coupled with high broad- sense heritability thus, these character 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. Length of fruiting zone, seed yield/fed and oil field/fed expressed moderate heritability and low genetic advance, indicating the role of non-fixable genetic variance in the expression of these traits. The moderate values of heritability as well as genetic advance were observed for seed yield pl^{-1}. The magnitude of heritability in broad sense was low coupled with low genetic advance for plant height. These results were in harmony with that obtained by Singh and Singh (2004), Banerjee and Kole (2006), Kumar and Saivannan (2006) and Iwo *et al.* (2007).

The genotypic variance was greater than that of environmental variance for all studied germination characters except standard germination% (Table 10). These results are in agreement with those obtained by Ganesan (2005) and Kumar and Sasivannan (2006). There were few differences between PCV and GCV, thus, these characters showing to be highly heritable so it can be good characters for effective selection. The value of GCV and PCV were approximately equivalent for all of studied characters indicating that environmental effects on these characters can be neglected. Broad sense heritability (h^2_b%) was high for electrical conductivity µScm-1g-1, seedling fresh weight and seedling dry weight. Accordingly, the selection would be relatively effective for these characters. The expected genetic advance were in the favorable direction of the seed vigor, electrical conductivity $\mu Scm^{-1}g^{-1}$, Accelerated ageing germination, seedling fresh weight and seedling vigor index than other traits. These finding indicated that considerable level of improvement can be achieved in these traits by selection from population. Similar results were reported by 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 GS% for chemical characteristics (over two seasons) for crude oil%, crude protein % and total carbohydrate% 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 over two seasons, indicating that these traits were not affected by environmental conditions. Heritability h^2_b was 70% at crude oil, 75% for crude protein and 87.51 % for total carbohydrate. The expected genetic advance ranged from 1.76 to 2.73.

Crude protein expressed the highest estimates value of genetic advance followed by crude oil and total carbohydrate over two seasons. According to previous results, the selection would be relatively effective for crude protein, crude oil and total carbohydrate. These results are confirmatory with those of Pathak and Dixit (1992), Tamina and Dasgupta (2003) and El-Shakhess *et al*. (2008).

RAPD-PCR analysis

Randomly amplified polymorphic DNA (RAPD) analysis would be useful in describing any genotype in the genetic basis. Out of twelve random decamer primers screened for their capability of amplifying DNA via the polymerase chain reaction (PCR), five primers were used to test the genetic diversity which generated a total of 52 DNA fragments, out of them 43 bands (82.7%) were polymorphic and 9 bands were monomorphic for all genotypes. The highest levels of polymorphism (91.7%) were observed in primers OP-A11, while, the lowest level of polymorphism was 60% in primer OP-A06 as shown in Table (12). In this study a high level of polymorphism was detected among sesame genotypes. This result was in agreement with Akbar *et al.* (2011). This high level of genetic diversity among the sesame genotypes proposed that the RAPD technique can be fruitful for the sesame systematics and selection of parents for breeding programs.

Genotypes specific markers generated from RAPD-PCR analysis are shown in Table (12) and Fig (1). RAPD-PCR primers were found to be useful as genotypes unique markers. The highest number of RAPD–PCR markers was scored for genotypes Line112-1, Line112-5 (two markers) while, the lowest number of RAPD-PCR markers was scored for genotypes Shandweel3, Line111-6, Line115-8 (one marker). In conclusion, the RAPD-PCR analysis can successfully detect the genetic diversity among the different genotypes in this study.

Genetic distances

Genetic similarities among the eleven genotypes based on RAPD data are shown in Table (13) and dendrogram (Fig. 2). The highest similarity was 88% between line108-6 and line111-4, While, line111-6 was genetically distant from line117-1 (similarity index 56%). The dendrogram utilizing RAPD analysis (Fig. 2), divided the eleven genotypes into two main clusters. The first cluster included Shandweel3, line108-6, line109-6, line111-4, line112-8, line115-8, line117-1, and line117-7 whereas, the second cluster was composed of line111-6, line112-1 and line112-5.

SUMMARY

This investigation was carried out to identify eleven sesame lines during two successive seasons, 2011 and 2012. Results revealed that line 117-7 surpassed the other genotypes in plant height, length of fruiting zone, number of capsules/pl., seed yield/pl., oil yield /fed., accelerated ageing germination and crude protein, while, line 112-5 gave the maximum estimates for number of branches/pl. and

crude oil. Line 111-6 recorded high seed yield/fed. and seedling dry weight. Line 117-1 has the highest germination percentage, seed vigor index, shoot length and seedling vigor index. The total unsaturated fatty acids ranged from 85.02% to 87.31%. Meanwhile, total saturated fatty acids ranged from 13.41% to 15.46%. High estimates of (PCV) and (GCV) were exhibited for number of branches pl-1, number of capsules pl-1 and seed yield pl-1. The high heritability was exhibited for number of capsules pl-1, weight of 1000 seeds, seed vigor index, accelerated ageing germination, electrical conductivity µScm-1g-1, Seedling fresh weight and Seedling dry weight, so, selection could be effective for these characters. Heritability h^2_b was 70% at crude oil, 75% in crude protein and 87.51 % in total carbohydrate so; selection would be relatively effective for these traits. Randomly amplified polymorphic DNA (RAPD) analysis used to test the genetic diversity which generated a total of 52 DNA fragments, out of them 43 bands (82.7%) were polymorphic and high level of polymorphism was detected among sesame genotypes. RAPD-PCR was found to be useful as genotypes unique markers. The highest similarity was 88% between line108-6 and line111-4, While, line111-6 was genetically distant from line117-1 (similarity index 56%).

REFERENCES

Akbar, F., M. A. Rabbani, M. S. Masood and Z. K. Shinwari (2011). Genetic diversity of sesame (*sesamum indicum* l.) germplasm from pakistan using rapd markers. Pak. J. Bot., 43: 2153-2160.

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

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

Babu, D. R., P. V. R. Kumar and C. V. D. 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: 307-308.

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

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

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

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. Appl. Sci., 12: 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: 41-53.

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.

Ercan, A. G., M. Taskin and K. Turgut (2004). Analysis of genetic diversity in Turkish sesame (*Sesamum indicum* L.) populations using RAPD markers. Genet. Resource Crop Evol., 51: 599-607.

Ganesan, K. N. (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: 176-177.

Ganesh, S. K. and S. Thangavelu (1995). Genetic divergence in sesame (*Sesamum indicum*). Mad. Agric. J., 82*:* 263-265.

Geleta, M., T. Bryngelsson and E. Bekele (2008). Assessment of genetic diversity of *Guizotia abyssinica* (L. f.) Cass. (*Asteraceae*) from Ethiopia using amplified fragment length polymorphism. Plant Genet. Resoure Characterization Utilization 6*:* 41-51.

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.

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: 539-543.

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

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

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. Bachudo Science Co. Ltd., Calabar, Nigeria, 13: 35-38.

Ko, M. K., J. Yang, Y. H. Jin, C. H. Lee and B. J. Oh. (1998). Genetic relationships of *Viola* species evaluat-

ed by random amplified polymorphic DNA analysis. J. Hort. Sci. Biotech., 74: 601-605.

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: 258 -260.

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. (3rd 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: 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: 117-120.

Pathak, H. C. and S. K. Dixit (1992). Genetic variability and inter- relationship studies in black seeded sesame. Madras Agric. J., 79: 94-100.

Pervaiz, Z. H., M. A. Rabbani, Z. K. Shinwari, M. S. Masood and S. A. Malik (2010). Assessment of genetic variability in rice (*Oryza sativa* L.) germplasm from Pakistan using RAPD markers. Pak. J. Bot., 42: 3369-3376.

Pham, D. T., M. T. Bui and G. Werlemark (2009). A study of genetic diversity of sesame (*Sesamum indicum* L.) in Vietnam and Cambodia estimated by RAPD markers. Genet. Resoure Crop Evol., 56*:* 679-690.

Pornparn, S., S. Suwannaketnikom, W. Dumkhum and N. Duadao (2009). Fertilizers for organic sesame. J. Food Ag-Ind., 197-S204.

Prasad, Y. V. N. S., N. D. Bangar and P. A. 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: 59-61.

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

Ram, R., D. Catlin, J. Romero and C. Cowley (1990). Sesame: New approaches for crop improvement. Advances in new crops. Timber

Pres, Portland, OR., p. 225-228

Sambrook, J., E. F. Fritsch and T. Maniatis (1989). Molecular cloning. A Laboratory manual, second edition. Volume 1. Cold Spring Harbor, New York.

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

Senthil, K. 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 Sunflower Newsletter, 17: 36-39.

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

Singh, S. B. and S. D. Singh (2004). Estimation of variability parameters for some quantitative characters in sesame (*Sesamum indicum* L.). Annalas of Agric. Research, 25: 43-45.

Tamina, B. and T. Dasgupta (2003). Character association in sesame (*Sesamum indicum* L.). Indian Agric., 47: 253-258.

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: 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.

Table (1): Pedigree of sesame lines studied.

Liens	Origin	Pedigree
Shandweel3	Egypt	A line selected from Giza 32x NA 130
Line 108-6	Egypt	A line selected from NA 130x NA 217
Line109-6	Egypt	A line selected from NA 114 x line217
Line 111-4	Egypt	A line selected from B32 x NA 432
Line 111-6	Egypt	A line selected from B32 x NA 432
Line 112-1	Egypt	A line selected from B24 x NA 32
Line 112-5	Egypt	A line selected from B24 x NA 32
Line 112-8	Egypt	A line selected from B24 x NA 32
Line115-8	Egypt	A line selected from NA 32 x Giza25
Line 117-1	Egypt	A line selected from NA 413 x Giza25
Line 117-7	Egypt	A line selected from NA 413 x Giza25

Table (2): Names and sequences of primers that gave bands for RAPD-PCR analysis**.**

Primer name	Sequence
0P-A06	5′ GGTCCCTGAC 3′
0P-A11	5′ CAATCGCCGT 3′
0P-A13	5′ CAGCACCCAC 3′
0P-B15	5′ GGAGGGTGTT 3′
0P-B18	5′ CCACAGCAGT 3′

Table (3): Mean performance, Range for some morphological characters of eleven genotypes (over two seasons).

Genotypes	Plant height (cm)	Length of fruiting zone (cm)	Number of branches/pl.	Number of capsules/pl
Shandweel3	163.67	132.50	1.50	97.52
Line 108-6	184.17	145.00	10.67	221.73
Line109-6	225.83	182.50	5.33	225.47
Line 111-4	201.67	159.17	8.00	311.97
Line 111-6	211.67	167.50	1.67	367.22
Line 112-1	205.00	167.50	5.00	411.85
Line 112-5	213.33	169.17	12.83	400.88
Line 112-8	220.00	187.50	9.67	199.30
Line115-8	187.50	142.50	4.83	265.15
Line 117-1	199.17	124.17	11.67	541.07
Line 117-7	262.50	213.33	8.00	665.02
LSD	34.24	27.72	3.28	82.15
Mean	206.77	162.80	7.197	337.02
Range	163.67-262.50	124.17-213.30	1.50-12.83	97.52-665.02

Table (4): Mean performance and range for seed yield/fed., 1000 seed weight, seed yield/pl and oil yield/fed. for eleven sesame genotypes (over two seasons).

Genotypes	Seed yield/fed (ardb)	Seed yield/plant (g)	1000 seed weight (g)	Oil yield/fed. (kg)
Shandweel3	5.86	18.02	3.51	404.09
Line 108-6	6.72	29.10	3.88	469.57
Line109-6	6.94	25.68	4.04	467.70
Line 111-4	5.71	37.12	3.82	397.84
Line 111-6	9.04	25.50	5.13	550.47
Line 112-1	6.96	46.72	5.29	462.26
Line 112-5	8.02	36.28	3.92	566.14
Line 112-8	4.50	22.02	3.96	304.54
Line115-8	4.77	25.92	3.94	316.19
Line 117-1	7.50	50.35	3.86	512.02
Line 117-7	8.83	56.02	3.94	609.74
LSD	1.250	7.45	0.23	39.79
Mean	6.804	33.88	4.12	460.05
Range	4.5 - 9.04	18.02 - 56.02	3.51 - 5.29	304.50 - 609.74

Table (5): Mean performance and range for standard germination percentage, seed vigor index, accelerated aging germination and electrical conductivity for eleven sesame genotypes (over two seasons).

Genotypes	Standard germination %	Seed vigor index	Accelerated ageing germination%	Electrical conductivity $\mu Scm^{-1}g^{-1}$
Shandweel3	93.00	23.64	79.00	52.77
Line 108-6	97.00	22.65	95.50	74.95
Line 109-6	96.00	22.99	95.00	58.17
Line 111-4	93.50	21.89	92.50	47.63
Line 111-6	97.00	21.57	95.00	39.27
Line 112-1	96.50	24.28	95.50	56.70
Line 112-5	98.00	23.30	95.00	47.31
Line 112-8	98.00	23.62	94.50	41.59
Line 115-8	96.50	23.83	94.00	63.82
Line 117-1	99.50	24.42	95.75	42.27
Line 117-7	98.00	22.21	96.50	44.06
LSD	2.32	0.72	2.83	5.14
Mean	96.73	23.13	93.48	51.69
Range	93.00-99.50	21.57-24.42	79.00-96.50	39.27-74.95

Table (6): Mean performance and range of radical length, shoot length, seedling fresh weight, seedling dry weight and seedling vigor index for eleven sesame genotypes (over two seasons).

Genotypes	Radical length (cm)	Shoot length (cm)	Seedling fresh weight (mg)	Seedling dry weight (mg)	Seedling vigor index
Shandweel3	4.94	2.83	31.14	4.14	724.14
Line 108-6	5.71	2.74	26.36	3.57	816.53
Line 109-6	6.40	3.09	37.10	3.96	917.02
Line 111-4	6.02	2.85	26.89	3.67	832.03
Line 111-6	5.22	2.88	33.94	4.43	789.90
Line 112-1	4.70	2.62	43.05	4.42	703.32
Line 112-5	5.33	2.98	32.23	3.57	814.18
Line 112-8	5.47	3.10	30.44	3.51	840.58
Line 115-8	5.09	2.87	37.28	4.09	766.80
Line 117-1	6.29	3.36	38.74	3.70	959.70
Line 117-7	4.66	2.72	41.30	3.85	860.65
LSD	0.56	0.20	2.83	0.18	72.33
Mean	5.44	2.91	34.41	3.90	820.44
Range	4.66-6.40	2.62-3.36	26.36-43.05	3.51-4.43	703.32-959.70

Table (7): Chemical composition of eleven sesame genotypes (over two seasons).

Genotypes	Crude oil %	Crude protein %	Total carbohydrates %
Shandweel3	57.38	23.57	11.63
Line 108-6	57.94	22.74	12.09
Line109-6	56.14	24.07	11.79
Line 111-4	58.11	23.58	11.66
Line 111-6	55.35	26.62	10.43
Line 112-1	56.12	24.14	12.28
Line 112-5	58.88	26.60	11.48
Line 112-8	56.18	23.44	13.05
Line115-8	55.76	23.04	12.90
Line 117-1	56.90	25.75	10.34
Line 117-7	57.56	26.90	10.52
LSD	0.827	0.433	0.172
Mean	56.93	24.58	11.65
Range	55.35 - 58.8	22.74 - 26.90	10.34 - 13.05

Table (8): Fatty acid composition of eleven sesame genotypes.

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 $C_{18:3}$			
Shandweel3	8.46	4.95	45.2	40.83	0.60	13.41	86.63	6.46
Line 108-6	10.26	4.38	43.15	41.28	0.59	14.64	85.02	5.80
Line109-6	9.38	4.95	44.15	41.35	0.73	14.33	86.23	6.01
Line 111-4	9.44	5.15	44.25	42.35	0.42	14.59	87.02	5.96
Line 111-6	9.86	5.46	43.75	41.10	0.55	15.32	85.40	5.57
Line 112-1	10.25	5.21	43.55	42.70	0.38	15.46	86.63	5.60
Line 112-5	8.77	5.11	42.81	43.04	0.44	13.88	85.85	6.18
Line 112-8	7.95	5.95	42.50	43.22	0.48	13.90	86.20	6.20
Line115-8	9.40	4.80	44.60	41.23	0.56	14.20	86.39	6.08
Line 117-1	10.22	4.39	43.96	41.56	0.61	14.61	86.14	5.89
Line 117-7	8.95	5.32	44.67	44.67	0.53	14.27	87.31	6.11

TS = Total saturated fatty acids. TU = Total unsaturated fatty acids.

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 for yield and some agronomic characters of eleven sesame genotypes (over two seasons).

Characters	Component of variance			Genetic variability		$h^2_b\%$	Genetic advance	
	σ^2_g	σ^2_{ph}	σ^2_e	GCV	PCV		GS	GS%
Plant height	810.33	1371.38	564.05	10.92	17.90	37.21	28.38	13.72
Length of fruiting zone	584.85	1149.2	564.41	14.85	20.82	50.88	35.53	21.82
Number of branches/pl.	13.48	21.41	7.92	51.03	64.29	62.99	6.005	83.43
Number of capsules/pl.	25940.00	308.96	4956	47.79	52.15	83.95	30.14	90.20
Seed yield/fad.	2.07	3.22	1.14	21.15	26.37	64.33	2.37	34.95
1000 seed weight	0.3044	0.3454	0.0410	13.40	14.27	88.12	1.067	25.91
Seed yield/plant.	149.02	189.88	40.85	36.02	40.66	78.48	22.27	65.75
Oil yield/fad.	8591.20	14988.3	6397.07	20.14	26.61	57.31	144.55	31.42

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

Table (10): Estimates of component of variance, genotypic (GCV) and phenotypic (PCV) coefficients of variation, broad sense Heritability estimates ($h^2_b\%$) and genetic advance for germination characters of sesame genotypes (over two seasons).

Characters	Component of variance			variability		$h^2_b\%$	Genetic advance	
	σ^2_g	σ^2_{ph}	σ^2_e	GCV	PCV		G.s	G.s %
Standard germination%	3.31	7.27	3.97	1.88	2.79	45.48	2.53	2.61
Seed vigor index	0.84	1.22	0.38	3.97	4.78	68.84	1.57	6.78
Accelerated ageing germin.	23.15	29.06	5.91	5.15	5.77	79.65	8.85	9.46
Electrical conductivity.	116.29	135.75	19.46	20.86	22.54	85.66	20.56	39.77
Radical length	0.33	0.56	0.24	10.50	13.82	57.77	0.89	16.44
Shoot length	0.04	0.07	0.03	6.73	9.01	55.80	0.30	10.36
Seedling fresh weight	29.91	35.83	5.92	15.89	17.39	83.48	10.29	29.92
Seedling dry weight	0.11	0.13	0.03	8.41	9.35	80.85	0.61	15.58
Seedling vigor index	5132.62	8975.49	3842.88	8.73	11.55	57.19	11.60	13.60

σ^2_g = Genetic variance σ^2_{ph} = phenotypic variance σ^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 for chemical characteristics of eleven sesame genotype (over two seasons).

Characters	Component of variance			variability		h^2_b%	Genetic advance	
	σ^2_g	σ^2_{ph}	σ^2_e	GCV	PCV		GA	GA%
Crude oil %	1.16	1.67	0.50	1.89	2.27	70.00	1.86	3.27
Crude protein %	2.33	3.09	0.75	6.21	7.15	75.45	2.73	11.12
Total carbohydrate %	0.84	0.96	0.12	7.88	8.42	87.51	1.76	15.18

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

Table (12): Levels of polymorphism based on RAPD analysis**.**

Primer	TB	PB	MB	P%	Unique bands	
					Cultivar	(bp) MS
OP-A06	10	6	4	60	line 112-1	176
OP-A11	12	11	1	91.7	Shandweel3 line 115-8	275 104
OP-A13	12	10	2	83.3	line 111-6	299, 370,328
OP-B15	10	9	1	90	line 112-5	126
OPB18	8	7	1	87.5	line 112-1 line 112-5	200 353
Total	52	43	9	82.7		

TB: Total bands, PB: Polymorphic bands, MB: Monomorphic bands
P%: Polymorphism% and MS: molecular size

Table (12): Similarity matrix among the eleven sesame genotypes based on RAPD analysis.

Lines	Shandweel 3	Line 108-6	Line 109-6	Line 111-4	Line 111-6	Line 112-1	Line 112-5	Line 112-8	Line 115-8	Line 117-1
Shandweel3										
Line 108-6	0.83									
Line 109-6	0.82	0.78								
Line 111-4	0.79	0.88	0.74							
Line 111-6	0.69	0.64	0.65	0.62						
Line 112-1	0.73	0.72	0.69	0.72	0.76					
Line 112-5	0.71	0.70	0.71	0.69	0.74	0.82				
Line 112-8	0.79	0.79	0.78	0.74	0.60	0.72	0.74			
Line 115-8	0.76	0.76	0.79	0.71	0.58	0.63	0.57	0.68		
Line 117-1	0.75	0.75	0.75	0.69	0.56	0.65	0.59	0.75	0.84	
Line 117-7	0.67	0.66	0.74	0.65	0.60	0.69	0.59	0.70	0.79	0.86

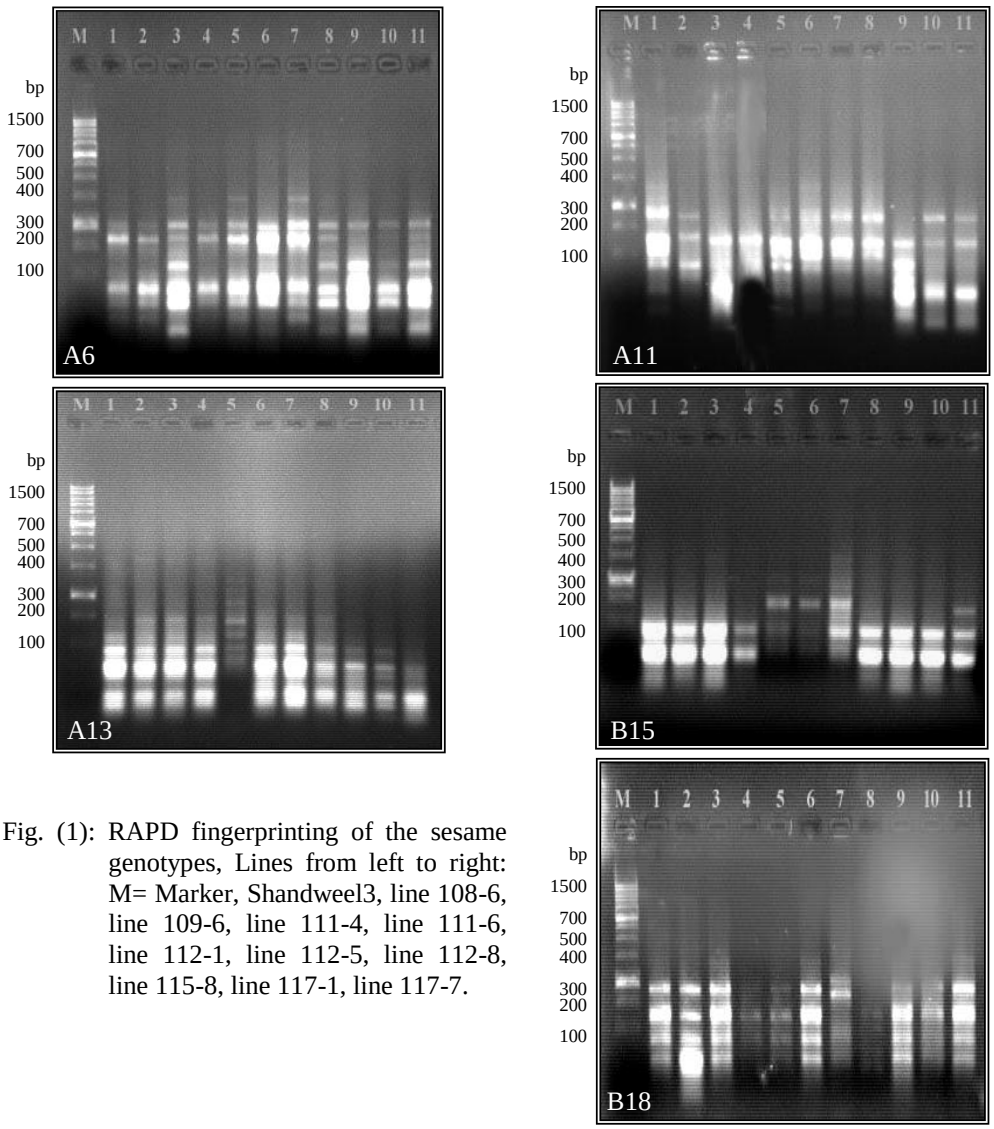

Fig. (1): RAPD fingerprinting of the sesame genotypes, Lines from left to right: M= Marker, Shandweel3, line 108-6, line 109-6, line 111-4, line 111-6, line 112-1, line 112-5, line 112-8, line 115-8, line 117-1, line 117-7.

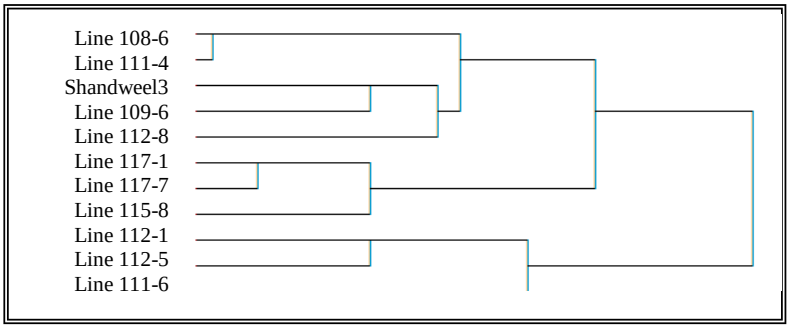

Fig. (2): Dendrogram of the genetic distances among the eleven sesame genotypes based on RAPD analysis.