

Evaluation of genetic diversity of sesame (*Sesamum indicum* L.) genotypes, using agro morphological and molecular markers (RAPD)

Abstract:

The purpose of this study was to look at the genetic variation in seventeen genotypes of sesame (*Sesamum indicum* L.) from different agro-climatic regions of Sudan, using both agro-morphological traits and RAPD markers. From July 13 to November 2013, the field experiment was conducted on the experimental farm of the College of Agricultural Studies, Sudan University of Science and Technology, Shambat. A randomized complete block design (RCBD) with three replications was employed in this investigation. The seventeen sesame genotypes had their nine growths and yield parameters assessed; the number of branches, the height of the first capsules, the number of capsules per plant, and the weight of 1000 seeds all showed a highly significant difference. There were no statistically significant differences between the two groups ($p \geq 0.05$). The plant's height and days to 50% flowering were counted. The number of capsules per plant and seed weight showed the largest genotypic and phenotypic variance. The heritability value was greater when 1000 seeds were used. On the other hand, plant height had the lowest rating. The Highland genotype had the maximum yield (0.2506 ton/ha). Seed yield (ton/ha) was found to be highly associated with seed output per plant, capsule number per plant, and stem diameter. However, there was a non-significant, inverse relationship between height to first capsule and days to flowering. Molecular DNA marker (RAPD) analysis revealed that three RAPD primers chosen for molecular analysis had 170 bands, 130 of which were polymorphic (76.47%). The results based on high genetic variation for agro-morphological traits and polymorphism at DNA level indicating that, the techniques was efficient in determining diversity

among sesame genotypes and this information will be useful for collection, conservation and breeding program in the future.

Keywords: sesame, genetic diversity, morphological and RAPD markers.

Introduction:

“Sesame (*Sesamum indicum* L.) is an annual plant in the Pedaliaceae family. It is the oldest of the oilseed crops, having been cultivated in Asia for over 5000 years” [1]. “It is now widely cultivated as an oil crop in tropical and subtropical climates. Sesame is the most important rotation crop in Sudan's rainfed cropping systems. Rainfed conditions are ideal for growing the crop, either as a stand-alone crop or in combination with other crops including sorghum, watermelon, Roselle, cowpea, and maize. Sudan has a very low average yield (0.21 t/ha), compared to the world average of 0.47 t/ha and China's 1.15 t/ha. The level of production is likewise highly changeable. Low productivity and inconsistent total output can be due to several biotic and abiotic issues, the most significant of which is a lack of adequate high-yielding cultivars” [2]. “A thorough understanding of the genetic diversity within and among the genetic resources of accessible sesame germplasm is required for a successful breeding program. Plant breeders can now select parental sources for hybrid creation or distinct populations for selection”. [3].

Crop genetic diversity is important for development that is long term and food security [4], as it allows crops to be grown under a variety of environmental stress conditions (including biotic and abiotic). “It is also necessary for the selection of parents for use in plant molecular breeding. Genetic diversity data is available. When it comes to improving plant varieties, this is crucial. (Various methods, such as morphological, biochemical, and molecular markers, are used to study genetic diversity. The most important tool for estimating genetic differences among sesame genotypes is morphology. Several morphological marker-based studies have discovered high genetic diversity in sesame populations” [5-6-1-7]. “Morphological markers, on the other hand, have a limited ability to estimate genetic diversity because they are strongly influenced by environmental factors and thus highly dependent on growing conditions. (Molecular markers get around this limitation.) Molecular markers such as amplified fragment length polymorphism

(AFLP), random amplified polymorphic DNA (RAPD), Inter Simple Sequence Repeats (ISSR), and Simple Sequence Repeats (SSR) have been developed, widely used in studies of sesame genetic diversity. However, the goals of this study are to assess the genetic diversity of sesame genotypes using geomorphological and molecular markers (RAPD), to estimate the values of heritability and phenotypic correlation among different sesame genotype traits, and to identify the most promising sesame genotypes for higher-yielding production”. [1]

Material and method

Plant material:

The plant material consisted of seventeen sesame genotypes obtained from different agro-climatic regions of Sudan and used for both agro morphological and molecular marker characterization (Table 1).

Table (1) lists the name's of seventeen sesame (*Sesamum indicum* L) genotypes used in this study

Genotype	Origin
Bash	Local variety collected by ARC
High Land	Ethiopian variety introduced by ARC
Caraway	Local variety collected by ARC
DanabAlgamal	Local variety collected by ARC
Soliamani	Local variety collected by ARC
Om Shagara	Local variety collected by ARC
Aldana	Local variety collected by ARC
Abraway	Local variety collected by ARC
Alradom	Local variety collected by ARC
5₍₃₎	Inbred line by lob of CAS(SUST)
Harba, 15	Local variety collected by ARC
Thailand	Introduced variety by ARC
J4	Introduced variety by ARC
17	Inbred line by lob of CAS(SUST)

13₍₃₎	Inbred line by job of CAS(SUST)
kenanna	Released variety by ARC Variety
Zagreb	Inbred line by ARC

ARC: Agricultural Research Corporation.

CAS: Sudan University of Science and Technology College of Agricultural Studies

Field trials:

The field experiments were carried out at the Sudan University of Science and Technology research farm (32°- 35° E and 15° N, 1650 m above sea level) during the summer season of 2008. All genotypes were evaluated geomorphologically in a randomized block trial with three replicates. Each plot consisted of four rows with a length of 4 m and a row spacing of 70 cm with a plant spacing of 7 cm between rows. Before sowing, 80 kg N/ha and 100 kg P/ha were fertilized and four weeks after sowing, 40 kg N/ha were re-fertilized. Days to flowering were recorded visually for each plot. (Plant height, first capsule height, stem diameter per plant, capsules per plant, 1000_seed weight, and seed yield per plant were measured on ten randomly selected plants per plot and their average was used. Two middle rows of each plot were harvested to determine seed yield (ton/ha)).

Data statistical analysis

Measuring data for growth and yield were subjected to an analysis of variance for randomized complete block design (RCBD) using (the computer package Statistics-8).

Coefficient of Variation (C.V)

The coefficient of variation (C.V) was calculated for each trait using the formula below.

$$CV \text{ percent} = (MSE) / \text{grand mean} \times 100$$

Where:

MSE is an abbreviation for mean square error, and G is an abbreviation for **grand mean**

Phenotypic (σ^2_{ph}) and genotypic (σ^2_g) variances.

For separate analysis of variance. They were estimated as follows:

$$\sigma^2g = (M2 - M1) / r$$

$$\sigma^2ph = \sigma^2g + \sigma^2e$$

Where:

r = number of replicates = 16

σ^2e = errors or environments

M1, M2 = errors and mean squares of the genotypes

Estimation of heritability (h^2):

Estimation of heritability (h^2): Heritability was estimated in the broad sense separately for both seasons using the formula proposed by [8] as follows:

Based on the separate ANOVA:

$h^2 = \sigma^2g / \sigma^2ph$ where σ^2g denotes genotypic variance and σ^2ph denotes phenotypic variance.

The phenotypic and genotypic coefficients of variation were calculated using [1] formula

PCV (phenotypic coefficient of variation) = $\sigma^2Ph / \text{Grand mean} \times 100$

GCV (genotypic coefficient of variation) = $\sigma^2g / \text{Grand mean} \times 100$

Correlation coefficients:

They were used to calculate phenotypic covariance. It was then used to calculate the phenotypic correlation between various traits using [10] formula

The phenotypic correlation coefficient (r_p) is equal $\text{cov}_p(xy) / \sqrt{(\sigma^2px \times \sigma^2py)}$

$r_p(xy)$ phenotypic correlation coefficient

$\text{cov}_p(xy)$ = phenotypic covariance of traits x, y

σ^2_{px} = phenotypic covariance of trait x

σ^2_{py} = phenotypic covariance of trait y

DNA molecular analysis:

DNA extraction

“DNA was extracted from young leaves of 3- to 4-week-old seedlings following a modified protocol described in” [11]. “The DNA pellet was washed twice in ethanol (75%) and allowed to dry for 20-30 min. After dissolving the DNA pellet in 30 μ l TE (10 mM Tris pH 8.0, 1 mM EDTA pH 8.0) buffer containing RNase (2 μ l 20 mg/ml RNase in 1 ml TE), Concentration of DNA obtained were determine through 260/280 absorbance measure using nm the NanoDrop spectrophotometer 2000” [12]. DNA samples were stored at -20°C until further use).

RAPD assay

“The PCR-RAPD procedure for sesame was performed” as described by [14]. “The amplification reaction was performed in a 25 μ l volume containing 1X PCR reaction buffer (10 mM Tris-HCl, pH 8.3, and 50 mM KCl), 0.2 mM dNTP. Respectively”. [14] “The PCR reaction was conducted in 50 μ l reaction volume containing 1x PCR buffer, 1.5 mM MgCl₂, 0.2 mM of each dNTPs, 1 mM of primer, 1 U Taq DNA (promega) polymerase and 10 ng genomic DNA. DNA amplification was performed using a thermal cycler programmed for first cycle of 5 min at 94°C (initial strand separation); followed by 40 cycles of 1 min at 94°C (denaturation), 1 min at 60°C (annealing) and 2 min at 72°C and a final cycle at 72°C for 10 min. The PCR product were mixed with 2.5 μ l of 10 X loading dye (0.25% bromophenol blue, 0.25% xylene cyanol and 40% sucrose, w/v) and spun briefly in a microfuge before loading. The PCR products and 1 kb DNA ladder were electrophoresed on 2% agarose gel at 100 V followed by staining with ethidium bromide and photographed on Polaroid 667 film under ultra-violet light”. [26]

Data analysis

“The experiments were repeated for a minimum of three times to confirm the banding patterns and only those consistent bands on the gels were scored for data analysis. For each primer, the number of polymorphic and monomorphic bands was determined. Bands clearly visible in at least one genotype were scored (1) for present and (0) for absent, and entered into a data matrix. Fragment size was estimated by interpolation from the migration distance of marker fragments. Percentage of polymorphism was calculated as the proportion of polymorphic bands over the total number of bands. The genetic dissimilarity (D) matrix among genotypes was estimated”

according to [14]. “The similarity coefficient was used to construct a dendrogram by the unweighted pair group method with arithmetic averages (UPGMA)” according [15]

Results and Discussion

Morphological characterization:

Analysis of the variance of this study revealed that highly significant differences were observed among genotypes for most of the traits studied (Table 2 and Table 3). A wide range of the genetic variability in most of the traits indicates potential genetic variability in the sesame genotypes studied. Similarly, a significant difference among a large number of Sudanese sesame genotypes was observed [16].

The highest yielding genotypes were High land, Harba15, and Alradom with seed yields of 43.86, 42.53, and 41.33 kg/plant, respectively (Table 3). The high genetic variability among genotypes observed in seed yield offers great potential for future sesame breeding programs. The estimation of genotypic (σ^2_g), phenotypic (σ^2_{ph}), phenotypic coefficient of variation (PCV), and genotypic coefficient of variation (GCV) are given in Table 4). (The phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV) for all traits studied). The highest values of the phenotypic coefficient of variation (170.229%-340.582%) were obtained by first capsule height and grain yield per plant (g), and the lowest values (43.714-6.5109) were obtained by stem diameter and seed per plant (t/ha), respectively (Table 4). These results indicate the low level of selection for improvement based on these traits. Similar results were reported by [16-17]. High broad-based heritability was estimated for the traits studied, ranging from 12.38% for seed yield/plant (g) to 90.63% for thousand weight (Table 2). A significant correlation coefficient was observed between each seed weight, capsules/plant, and stem diameter with seed yield (ton/ha) (Table 5). There was a significant and positive correlation between the height of the first capsule, stem diameter, number of branches, and number of capsules with plant height (Table 5). These results are in agreement with the findings of [18-19-20-21].

Molecular genetic diversity of sesame

Two RAPD primers were used for the analysis of the seventeen sesame genotypes studied. These primers were used to generate 22 polymorphic bands out of a total of 22 amplified bands, 22

being polymorphic. The RAPD primer OPL18 had the highest percentage of polymorphic bands at 100% (Table 6). This was also confirmed by previous RAPD marker results from other sesame studies using the OPM-06 primers (100% polymorphism). The high level of polymorphism observed in our study (75%) is consistent with the 78% polymorphism found in the genetic diversity assessment of Turkish sesame [22-23]. also observed a polymorphism of 86.75% in a study on the genetic diversity of Indian and exotic sesame germplasm. The similarity coefficient of seventeen sesame genotypes based on the RAPD marker ranges from 0.00 to 100 (Table 6). Among the genotypes, Soliamani and Alsodana showed the highest similarity index (100%), while genotype 17 with Soliananai, Omshagara, and Alsodana had the lowest index (Table 6). Cluster analysis was carried out using an RAPD marker, which produced a dendrogram that divided the genotypes into two distinct clusters. The first cluster was further subdivided into subgroups. The first cluster contained eight genotypes as sisters, namely the genotypes (Kenana and Tagrib) and the genotypes (Soliamani and Alsodana) as second sisters. Also, the genotypes (Bash and Highland) as third sisters and (Caraway and Alradom) (Figure 1). The second cluster contained only one genotype (17). “The results of this study are in agreement with previous studies based on morphological, agronomic traits, and molecular markers which showed high genetic diversity in sesame germplasm” [24-23-22-25].

CONCLUSION

It concluded that high genotypic variability was detected among the seventeen sesame genotypes from different geographical regions and localities which would be useful for plant breeding and conservation. The agro morphological and molecular markers complemented each other in assessing the extent of genetic variation in sesame and the combined application of these methods helps to better understand the genetic diversity and relationships within and among sesame genotypes.

REFERENCES

1. I.S. Bisht, R. K. Mahajan, and T.R. Loknathan (1998). Diversity Indian sesame collection and germplasm accession in various diversity groups. 325-335 in Genet. Res. Crop. vol.45.

2. M.O. Khidir (2007). Oil Seed Crops in Sudan (In Arabic). 2nd Edition, Khartoum University Press, Khartoum, Sudan.
3. Ibrahim, S.E (2010). Variability of seed Yield, Yield Components, and some Quality parameters in some Sesame (*Sesamum indicum*.) Genotypes. Ph.D. Thesis Faculty of Agriculture, University of Khartoum.
4. J. Esquinas-Alcázar, J. Esquinas-Alcázar, J. Esquinas-Alcázar, J. Esquinas-Alcázar, J. Esquinas-Alcázar, J. Esquinas-A (2005). 946-953 in Nature Reviews Genetics. <http://dx.doi.org/10.1038/nrg1729>.
5. D. Bedigian, D.S. Seigler, and J.R. Harlan (1985). Sesamin, sesamol, and the sesame's origin. *Biochemical Systematics and Ecology*, vol. 13, no. 2, pp. 133-139.
6. Ganesh, S. K. and Thangavelu, S. 1995. Genetic divergence in sesame (*Sesamum indicum*). – *Mad. Agric. J.* 82: 263 – 265.
7. N.H.C. Arriel, A.O.D. Mauro, E.F. Arriel, S.H. Unêda-Trevisoli, M.M. Costa, I.M. Bárbaro, and F.R.S. Muniz (2007) Genetic Divergence in Sesame Based on Morphological and Agronomic Traits. *Crop Breeding and Applied Biotechnology*, vol. 7, pp. 253-261. <http://dx.doi.org/10.12702>
8. H.W. Johnson, H.F. Robinson, and R.E. Comstock (1955). Soybean genetic and environmental variability was estimated. *Journal in agronomy*, 47, 314-318.
9. Burton, W.G. and E.H. Devane, 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agron. J.*, 45: 478.
10. Miller, P. A., C. Williams, H. F. Robiwsen and R. E. Comstock. 1958. Estimates of genotypic and environmental variance and covariance and their implication in section. *Agron. J.* 50: 126-131.
11. Warwick, S. I. and Gugel, R. K. 2003. Genetic variation in the *Crambe abyssinica* - *C. hispanica* - *C. glabrata* complex. – *Genet. Resour. Crop Evol.* 50: 291 – 30
12. User Manual Nano Drop 2000/2000c, *Spectrophotometer VI.0*, Thermo Scientific, Wilmington, DE, USA, 2009.
13. Williams, J.G.K.; Kubelik, A.R.; Leavk, K.J.; Rafaski, J.A. and Tingey, S.V. (1990). DNA polymorphism amplification by arbitrary primers is useful as genetic markers. *Nucleic Acid Research* 18: 6531-6535. <https://doi.org/10.1093/nar/18.22.6531>

14. Nei, M. and Li, W.H. (1979) Mathematical Model for Studying Genetic Variation in Terms of Restriction Endonucleases. *Proceedings of the National Academy of Sciences of the United States of America*, 76, 5269-5273.
15. F.J. Rohlf,(1993). Applied Biostatistics Inc., Exeter Software, NY, USA, NTSYSpc - Numerical Taxonomy and Multivariate Analysis System, Version 2.01.
16. B. K. Eye., A.E.S. Ibrahim, and K. A. Ali (2015). Sesame (*Sesamum indicum* L.) seed yield and component performance, genetic variability, and heritability in central Sudan Gezira *Journal of Agricultural Science*, 13(1), pp. 35-51. (2015).
17. S. G. Arameshwarappa, M. G. Palakshappa, P. M. Salimath, and K. G. Parameshwarappa. Arameshwarappa, S. G., M. G. Palakshappa, M. G. Palakshappa, M. G. Palakshappa, M. G. Palaks (2009). Studies on genetic variability and character association in a germplasm collection of sesame (*Sesamum indicum* L.). *Karnataka J. Agric. Sci.*, 22: 252-254.
18. Y. Engin, K. Emre, F. Eymus, and U. Bülent (2010). Correlation coefficients, route, and factor analyses were used to evaluate sesame selection criteria. 598-602. *Australian Journal of Crop Science*, vol. 4, no. 8, pp. 598-602.
19. M. Gnanasekaran, S. Jebaraj, and S. Muthuramu (2008). Analysis of correlation and path coefficients in sesame (*Sesamum indicum* L.). *Plant Archives*, vol. 8, no. 1, pp. 167-169.
20. Ogbonna, P. E., and S. I. Ukaan. "Yield evaluation of 13 sesame (*Sesamum indicum* L.) accessions in the derived savannah agro-ecology of south-eastern Nigeria." *African Journal of Agricultural Research* 7.43 (2012): 5772-5778.
21. Sandipan C, Animesh KD, Aditi S, Sonali S, Rita P, Susmita M, Ananya D (2010). Traits influencing yield in sesame (*Sesamum indicum*. L.) and multilocational trials of yield parameters in some desirable plant types. *Indian Journal of Science and Technology* 3 (2).
22. Ercan, A.G., Taskin, M., and Turgut, K. (2004). RAPD markers were used to examine genetic diversity in Turkish sesame (*Sesamum indicum* L.) populations. *Crop Evol.*, 51: 599-607. *Genet. Resources. Crop Evol.*, 51: 599-607.

23. K.V. Bhat, P.P. Babrekar, and S. Lakhanpaul (1999). Using random amplified polymorphic DNA (RAPD) markers, researchers investigated genetic diversity in Indian and exotic sesame (*Sesamum indicum* L.) germplasm. *Euphytica*, vol. 110, pp. 21-33.
24. Ashri A. 1988. Sesame breeding-objectives and approaches. In: Oil Crops-Sunflower, Linseed and Sesame. Proc. 4th Oil Crop Network Workshop. Njoro, Kenya, IDRC-MR20e, IDRC.
25. Salazar, Bertha, et al. "Reliability of the RAPD technique for germplasm analysis of sesame (*Sesamum indicum* L.) from Venezuela." *Interciencia* 31.6 (2006): 456-460.
26. Abuali AI, Abdelmula AA, Khalafalla MM. Assessment of genetic diversity in Sudanese maize (*Zea mays* L.) genotypes using random amplified polymorphic DNA (RAPD) markers. *African Journal of Biotechnology*. 2011;10(42):8245-50.

Table (2). Mean squares of individual analysis for growth and yield traits of seventeen genotypes of sesame (*Sesamum indicum* L.) evaluated at Shambat during the season (2013-2014)

Characters	Mean squares of blocks	Mean squares of genotypes	Mean squares of error
Flower 50%	0.41	85.37*	47.18
Plant height(cm)	160.80	307.73 ^{Ns}	183.52
Height first capsule (cm)	550.55	386.84**	129.124
Stem diameter(cm)	1.658	1.446*	0.567
No. of branches	3.90	8.35**	1.84
No. of capsules	223.46	1574.74**	550.65
Weight of 1000 seed (g)	9.35	0.733**	1.97
Seed yield per plant (g):	28.42	283.44 ^{Ns}	199.08
Seed yield (t/ha)	0.00102	0.00954 ^{Ns}	0.00646

N_s =not significant difference

**highly significant difference

*significant difference

Table (3) Means of different traits of seventeen sesame genotypes evaluated at shambat, during seasons (2013-2014)

Genotypes	Flower 50%	Plant height(cm)	Height. F.capsules(cm)	Stem diameter(cm)	No. of branches	No. of capsules	Seeds yield(g)	Seeds yield (t/ha)	Weight of 1000 seed
Abraway	48.33	130.43	73.43	5.87	4.7	78.03	38	0.2171	3.2
Om Shagara	61	141.53	85.39	5.32	7.44	123.53	29.63	0.1693	2.8
Alsodana	49	131.90	87.40	4.60	5.73	58.90	27.6	0.1577	2.6
DanabAlgamal	55.33	137.33	93.41	4.85	7.46	57.97	12.63	0.0721	2.9
Kenana()	44	135.50	81.35	4.13	4.56	73.60	20.20	0.1154	2.4
Alradom	45.33	141.27	82.05	5.57	6.73	131.27	41.33	0.2360	3
13₍₃₎	43	121.27	64.68	3.52	1.33	57.10	24.10	0.1377	3.4
Carawy	47.33	144.27	89.14	4.95	5.8	95.13	39.06	0.2232	2
Bash	40	123.57	62.16	4.06	2.3	73.63	38.46	0.2198	3.2
J4	51	131.23	67.91	5.17	4.6	89.83	38.40	0.2194	3.8
Harba15	42	119.50	53.63	4.29	4.43	86.33	42.53	0.2440	3.4
Highland	51	138.10	76.83	4.55	4.13	80.93	43.86	0.2506	3
Tailandi	42.66	111.63	61.16	3.89	3.76	59.10	25.53	0.1459	2.5
17	45	113.43	64.33	3.80	3.5	70.20	39.23	0.2242	3.4
Soliamani	46.66	116.28	66.03	3.85	3.66	62.03	19.80	0.1131	3
5₍₃₎	44.33	126.73	78.53	3.72	3.27	57.17	27.10	0.1549	2.8
Tagrib	52	129.53	73.96	4.80	5.08	52.53	19.66	0.1024	2
Grand Mean	47.52	129.03	74.20	4.52	4.61	76.9	31.01	0.1766	2.92
C.V	14.45	10.50	15.31	16.64	29.41	30.51	30.40	45.51	3.83
SE±	5.6085	11.061	9.2781	0.6152	1.1093	19.16	11.52	0.656	2.54
LSD	11.424	22.531	18.899	1.2532	2.2595	39.027	23.467	0.1337	1.32

Table (4) Phenotypic (PCV %) and Genotypic coefficient of variation (GCV %), phenotypic and genotypic variance for the different characters studied on seventeen genotypes of sesame evaluated at Shambat during the season (2013-2014)

Traits	Phenotypic variance (σ^2_{ph})	Genotypic variance (σ^2_g)	Genotypic coefficient of variation (GCV %)	Phenotypic coefficient of variation (PCV %)	Heritability(h) ² %
Flowering	59.914	12.731	51.754	112.27	21.248
Plant height	224.926	41.399	56.64	132.03	18.405
Height. F.capsules	215.029	85.905	107.59	170.229	39.950
Stem diameter	0.86550	0.29777	25.637	43.714	34.404
No. of branches	4.0152	2.169	68.541	93.229	54.019
No. of capsules	892.0133	341.36	210.68	340.582	38.268
Seed yield(g)	227.2063	28.119	95.224	270.681	12.375
Grain yield (t/ha)	0.00074866	0.00010266	2.4110	6.5109	13.71
Weight of 1000 seed	4.294	3.892	115.419	121.233	90.63

Table (5). Estimate of phenotypic correlation (above the diagonal) and phenotypic correlation (bellow the diagonal) of seventeen sesame genotypes

Traits	Flowering	Plant height	Height. F.capsules	Stem diameter	No. branches	No. capsules	Seed yield(g)	Grain yield (t/ha)	Weight of 1000 seed
Flowering	-	0.1636 ^{Ns}	0.3919 ^{**}	0.1700 ^{Ns}	0.4456 ^{**}	-0.0056 ^{Ns}	-0.2667 [*]	-0.2693 [*]	-0.1103 ^{**}
Plant height	0.1636 ^{Ns}	-	0.7661 ^{**}	0.5084 ^{**}	0.5095 ^{**}	0.4978 ^{**}	0.1800 ^{Ns}	0.1797 ^{Ns}	-0.2255 ^{Ns}
Height. F.capsules	0.3919 ^{**}	0.7661 ^{**}	-	0.3947 ^{**}	0.4824 ^{**}	0.2052 ^{Ns}	-0.1356 ^{Ns}	-0.1365 ^{Ns}	-0.3800 ^{**}
Stem diameter	0.1700 ^{Ns}	0.5084 ^{**}	0.3947 ^{**}	-	0.5399 ^{**}	0.5791 ^{**}	0.3256 [*]	0.3246 [*]	-0.3892 ^{Ns}
No. branches	0.4456 ^{**}	0.5095 ^{**}	0.4824 ^{**}	0.5399 ^{**}	-	0.5297 ^{**}	0.0594 ^{Ns}	0.0635 ^{Ns}	-0.2791 [*]
No. capsules	-0.0056 ^{Ns}	0.4978 ^{**}	0.2052 ^{Ns}	0.5791 ^{**}	0.5297 ^{**}	-	0.5134 ^{**}	0.5160 ^{**}	0.1003 ^{Ns}
Seed yield(g)	-0.2667 [*]	0.1800 ^{Ns}	-0.1356 ^{Ns}	0.3256 [*]	0.0594 ^{Ns}	0.5134 ^{**}	-	0.9991 ^{**}	0.2569 [*]
Grain yield (t/ha)	-0.2693 [*]	0.1797 ^{Ns}	-0.1365 ^{Ns}	0.3246 [*]	0.0635 ^{Ns}	0.5160 ^{**}	0.9991 ^{**}	-	0.2695 ^{**}
Weight of 1000 seed	-0.1103 ^{**}	-0.2255 ^{Ns}	-0.3800 ^{**}	-0.3892 ^{Ns}	-0.2791 [*]	0.1003 ^{Ns}	0.2569 [*]	0.2695 ^{**}	-

Table 6: Matrix of RAPD dissimilarity among eighteen *sesame* genotypes based on coefficient was used to construct a dendrogram by unweighted pair group method with arithmetic average (UPGMA) according to Rohlf (1993)

	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	S11	S12	S13	S14	S15	S16	S17	S18	
S1	1.00																		
S2	0.92	1.00																	
S3	0.50	0.52	1.00																
S4	0.73	0.79	0.59	1.00															
S5	0.67	0.71	0.55	0.93	1.00														
S6	0.71	0.77	0.50	0.86	0.92	1.00													
S7	0.67	0.71	0.55	0.93	1.00	0.92	1.00												
S8	0.50	0.53	0.56	0.60	0.63	0.67	0.63	1.00											
S9	0.43	0.45	0.68	0.52	0.55	0.57	0.55	0.56	1.00										
S10	0.14	0.14	0.26	0.17	0.18	0.19	0.18	0.24	0.21	1.00									
S11	0.44	0.46	0.61	0.52	0.48	0.44	0.48	0.40	0.45	0.42	1.00								
S12	0.23	0.24	0.46	0.26	0.27	0.28	0.27	0.31	0.41	0.43	0.57	1.00							
S13	0.33	0.35	0.41	0.42	0.38	0.39	0.38	0.36	0.41	0.57	0.63	0.48	1.00						
S14	0.04	0.05	0.14	0.04	0.00	0.00	0.00	0.07	0.10	0.39	0.33	0.28	0.28	1.00					
S15	0.31	0.32	0.54	0.38	0.35	0.36	0.35	0.38	0.54	0.40	0.64	0.62	0.68	0.26	1.00				
S16	0.30	0.31	0.52	0.37	0.33	0.35	0.33	0.37	0.52	0.38	0.62	0.65	0.72	0.25	0.80	1.00			
S17	0.50	0.53	0.43	0.63	0.56	0.60	0.56	0.43	0.50	0.25	0.38	0.33	0.52	0.09	0.55	0.52	1.00		
S18	0.11	0.12	0.26	0.10	0.11	0.11	0.11	0.13	0.26	0.17	0.23	0.33	0.17	0.18	0.30	0.29	0.18	1.00	

OPR10: CCATTCCCCA

OPL18: ACCACCCACC

Primers= OPL18; OPR10

Jaccard's similarity dendrogram:

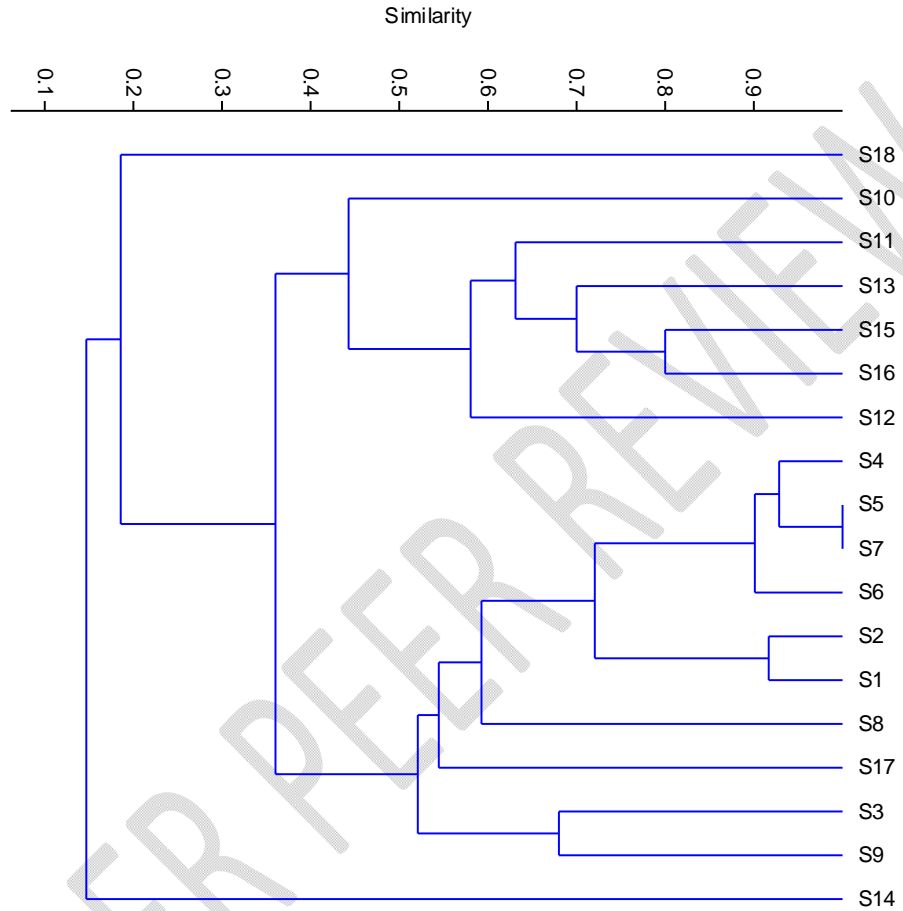


Figure:1 Dendrogram constructed for eighteen sesame genotypes based on genetic distances using three RAPD Primers