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Genetic Diversity in Some Sesame (*Sesamum indicum* L.) Accessions Detected by Agro-morphological Characters and RAPD Markers*

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Abstract: Agro-morphological and Randomly Amplified Polymorphic DNA (RAPD) markers were used to determine the diversity and relationships among 25 accessions of sesame from Sudan. Data on 16 agro-morphological characters were collected from a field experiment, carried out at Shambat for three consecutive seasons (2006-2008) and subjected to the procedure of cluster analysis. The results showed that cluster analysis, based on Euclidean distance, of the agro-morphological characters grouped the 25 sesame accessions into seven clusters. Application of RAPD markers generated 48 bands with a 97.9% polymorphism. A dendrogram constructed from the RAPD data classified the 25 sesame accessions into eight major clusters. It was concluded that for efficient estimation of genetic diversity and interrelationships among sesame accessions, information obtained from both agro-morphological characters and RAPD should be combined.

Key words: Sesame; genetic diversity; agro-morphological characters; RAPD

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INTRODUCTION

Sesame (*Sesamum indicum* L.) belongs to the family Pedaliaceae. It is one of the important oil seed crops in the Sudan. A substantial proportion of sesame under cultivation in the country is made up of a large number of landraces or traditional cultivars. These are locally adapted diverse populations, which are the result of natural and farmers' selection. Landraces have contributed genetic materials to many breeding programmes and constitute an important plant genetic resource. Estimation of genetic diversity of landraces is necessary, because it determines the gene pool and the manner by which it can be used.

Development of high-yielding cultivars is achieved via identification of genetic resources and characterization of genetic diversity present in plant populations and genotypes with desirable traits. Plant breeders use the present diversity in plant populations to develop new genotypes or to transfer the desirable traits into undesirable genotypes (De *et al*. 1992).

The estimates of genetic relationship can be helpful for organizing germplasm, for conservation of genetic resources, for the identification of cultivars, for selection of parents, for hybridization, for predicting favorable heterotic combinations. This also helps to reduce the number of samples required for sampling of genetically variable broad range of accessions in breeding programs (Ozkaya *et al.* 2006). However, there are many methods for estimating genetic diversity.

Measurements of diversity rely upon the ability to resolve differences in characters. Thus diversity could be estimated through data collected from electron microscope, biochemical and phytochemical assays, field performance (agro-morphological traits), morphological descriptors and molecular markers.

Morphological traits (syn. phenotypic traits) are commonly used to analyze genetic diversity since they provide a simple way of quantifying genetic variation. However, morphological traits are limited in number, modified by the environment and may be controlled by epistatic and pleiotropic gene effects (van Beuningen and Busch 1997), also several studies showed that morphological markers are not suitable for traits with

low heritability and are highly affected by environment (Smith and Smith 1992; Redfearn *et al*. 1999; Cadee 2000). Despite these limitations, morphological traits have been successfully used for genetic diversity analyses and cultivar development (Fufa *et al*. 2005).

In contrast, molecular markers are not directly influenced by environmental effects or epistatic interactions and can provide large numbers of loci (Shahnejat-Bushehri *et al.* 2005). Methods that detect variation at the level of the DNA sequence have proved to be an extremely effective tool for distinguishing between closely related genotypes (Hartl and Seefelder 1998). Molecular markers are useful in reducing the size of populations by evaluating the materials at early stages.

There are various studies that combined morphological and molecular markers to study diversity in plant species, e.g. barley (Vanhala *et al.* 2004), wheat (Fufa *et al*. 2005), cotton (Zhang *et al*. 2005) and rapeseed (Mahasi and Kamundia 2007), and reached reliable and useful information for breeders.

Several methods have been used to estimate the genetic variability in sesame. These include morphological characters (Osman and Khidir 1974; Bedigian *et al*.1986; Patil and Sheriff 1994; Ercan *et al*. 2002; Furat and Uzun 2010), phytochemical assays (Laurentin *et al.* 2003), isozymes (Isshiki and Umezake 1997), RAPD (Bhat *et al*. 1999), ISSR (Kim *et al*. 2002) and AFLP (Laurentin and Karlovsky 2006).

Karp *et al*. (1996) reported that molecular techniques vary in the way they resolve genetic differences, in the type of data they generate and in taxonomic level at which they can be most appropriately applied.
Randomly amplified polymorphic DNA (RAPD), has been widely employed because of its simplicity and ability to detect genetic variation among very closely related genotypes in a number of genera such as *Brassica* (Jain *et al.* 1994). Furthermore, RAPDs have been widely used to study the population genetic structure, genetic diversity and relationships and phylogenetic relationships (Baker *et al.* 1999).

Although several studies have reported poor reproducibility for RAPD markers, other studies have shown the importance of using optimized conditions and protocols to achieve consistent and reproducible RAPD results (Yu *et al*. 2004; Salem *et al*. 2007). Zhang *et al.* (2005) concluded that pedigree information or geographic origins of cultivars may not accurately reflect genetic relatedness among genotypes, whereas DNA markers could better reveal the genotypic relationships when there are sufficient markers and they are distributed across all chromosomes. Bucheyeki *et al*. (2009), in sorghum, reported that RAPD markers clearly separated landraces within and between groups than morphological markers. Pham *et al*. (2009), using RAPD, found close relations between sesame accessions and geographical origin, interestingly, some geographically distant accessions clustered in the same group. Salazar *et al*. (2006) reported that RAPD-based fingerprinting was a useful tool to identify unequivocally the sesame genotypes and assess the genetic variability of breeding stocks.

For plant improvement purposes, morphological and biochemical features are sensitive to environmental factors and can be observed only in mature plants. Hence, DNA markers will be a reliable tool to assure the results of morphological and biochemical features. Only a single study have been conducted to study sesame variability using molecular markers in the Sudan (Abdellatef *et al.* 2008). A successful breeding programme depends on the complete knowledge and understanding of the genetic diversity within and among genetic resources of the available germplasm. This enables plant breeders to choose parental sources for hybrid production or for generation of diverse populations for selection.
This study aimed to assess the amount of variation among some sesame genotypes of Sudanese origin, using cluster analysis, based on agro-morphological characters, quality traits as well as molecular markers.

MATERIALS AND METHODS

Plant material: Sesame (*Sesamum indicum*) genotypes used in this study comprised five released cultivars and twenty landraces from different regions of Sudan (Table 1).

Table 1. Name, seed colour, type and origin of 25 sesame (*Sesamum indicum* L.) accessions

Serial number	Code*	Name	Seed colour	Type	Origin
1	ShSi1	Gabaroak	Brown	Landrace	Kazgail
2	ShSi2	Kenana 2	White	Released cultivar	Seed admin
3	ShSi3	Abu Naama White	White	Landrace	Alabbassya
4	ShSi4	Shoshai	Brown	Landrace	Kazgail
5	ShSi5	Tigil Galabat	White	Landrace	Algadarif
6	ShSi6	Elobeid 1	White	Released cultivar	Seed admin
7	ShSi7	Um Shagara	Whit	Released cultivar	Seed admin
8	ShSi8	Promo	White	Released cultivar	Seed admin
9	ShSi9	Khidir	White	Released cultivar	Seed admin
10	ShSi10	Abbassya White	White	Landrace	Alabbassya
11	ShSi11	Abbssya Brown	Brown	Landrace	Alabbassya
12	ShSi12	Country Ivory	White	Landrace	Elobeid
13	ShSi13	Abu Sitta	White	Landrace	Kazgail
14	ShSi14	Abu Kashawa	White	Landrace	Abukarshola
15	ShSi15	Abu Sandoog	White	Landrace	Abukarshola
16	ShSi16	Ali Mahdi	White	Landrace	Abukarshola
17	ShSi17	Keiga	White	Landrace	Elddalang
18	ShSi18	Kabai	White	Landrace	Alabassya
19	ShSi19	Sinnar	Black	Landrace	Seed admin.
20	ShSi20	Babanosa	Brown	Landrace	Babanosa
21	ShSi21	Gagama	Brown	Landrace	Elobeid
22	ShSi22	Abu Naama Brown	Brown	Landrace	Alabbassya
23	ShSi23	Um Fakareen	Brown	Landrace	Umrowaba
24	ShSi24	Blwa	Brown	Landrace	Elrahad
25	ShSi25	Eltoboon	Brown	Landrace	Eltoboon

* ShSi stands for the accession number at Shambat

Field evaluation: The experiment was conducted for three seasons; namely, 2006/2007, 2007/2008 and 2008/2009, in the Experimental Farm of the Faculty of Agriculture, University of Khartoum at Shambat, using a 5 x 5 triple lattice design. Each genotype was grown in a plot consisting of four ridges each three metres long and spaced 70 cm apart. During the second week of July in the three seasons, five seeds, at least, were sown in holes at a distance of 20 cm along the ridge. Three weeks after sowing, the plants were thinned to two plants/hole. Other cultural practices were carried out following the recommended cultural practices for irrigated sesame.

Cluster analysis based on morphological data

Data were recorded for days to 50% flowering, days to maturity, plant height (cm), height to first capsule (cm), stem diameter (cm), number of branches/plant, number of capsules/branch, number of capsules/main stem, number of capsules/plant, number of seeds/capsule, 1000-seed weight, seed yield/plant and seed yield/ha. The traits used for determining end use quality were seed colour, oil content and protein content.

The statistical package for social sciences version 16 (SPSS 2008), statistical software for cluster analysis, was used for data analysis. Euclidean distance as similarity measure and Average Linkage (Between Groups) method were used to analyze the relationships among landraces.

RAPD fingerprinting

RAPD-PCR protocol: DNA was isolated from seven-day old seedlings of each genotype using the CTAB method of Doyle and Doyle (1990). RAPD assay was performed as described by Williams *et al.* (1990) with minor modifications. Briefly, PCR amplification was performed in 25 µl reaction mix containing 20.40 ng genomic DNA, 0.5 unit Taq polymerase (Sigma), 0.2 mM each of dATP, dCTP, dGTP, dTTP, 5 Pico mole random primer and appropriate amplification buffer. The reaction was assembled on ice, overlaid with a drop of mineral oil. Amplification was performed for 45 cycles, using Biometera Uno thermal cycler, as follows: One cycle at 95°C for 3 minutes and then 44 cycles at 92°C for 2 minutes, 37°C for 1 minute and 72°C for 2 minutes (for denaturation, annealing and extension, respectively). Reaction was finally incubated at 72°C for 10 minutes and further incubated at 4°C. Four primers coded as A1, A2,

B1 and B2 with the nucleotide sequences (5` - 3`): CAGGCCCTTC, TGCCGAGCTG. GTTTCGCTCC and TGATCCCTGG, respectively, were used for RAPD analysis based on their ability to amplify *Amaransis* genome and producing reproducible amplification patterns. The amplification products were analyzed by electrophoresis in 2% agarose in TAE buffer stained with 0.2 µg/ml ethidium bromide and photographed under UV light. A 100 bp DNA ladder was used as DNA size marker (Axygen).

Scoring and data analysis

Each amplification product was considered as an independent character (locus). The amplified fragments in each of the 25 accessions were scored manually for their presence (denoted as 1) or absence (denoted as 0) for each primer. The binary data then processed with the SPSS v.16.0 for windows software. A dendogram of 25 sesame genotypes was constructed using Average Linkage method based on Euclidean distance.

RESULTS

Polymorphism analysis based on agro-morphological characters

The hierarchical cluster analysis, based on Euclidean distance, of the agro-morphological characters of the 25 sesame entries is presented in Table 2 and Figure 1. The highest similarity was scored between ShSi1 and ShSi21. On the other hand, the minimum similarity was detected between ShSi19 and ShSi22.

The agglomeration of the 25 sesame genotypes at 10 Euclidean distance generated seven main clusters. The first cluster (I) comprised 11 accessions and was divided into five sub-clusters, the second one (II) consisted of four accessions and divided into three sub-clusters, the third cluster (III) contained only one accession, the fourth one (IV) had two accessions, the fifth cluster (V) comprised three accessions, the sixth one (VI) contained three accessions divided into two sub-clusters and the seventh one (VII) consisted of only one accession as the most divergent genotype.

Table 2. Similarity matrix of 25 sesame (*Sesamum indicum* L.) genotypes based on 16 morphological characters measured in three consecutive seasons (2006-2008) at Shambat, using Euclidean distance

Genotype	ShSi1	ShSi2	ShSi3	ShSi4	ShSi5	ShSi6	ShSi7	ShSi8	ShSi9	ShSi10	ShSi11	ShSi12	ShSi13
ShSi1	1.00												
ShSi2	0.77	1.00											
ShSi3	0.77	0.73	1.00										
ShSi4	0.56	0.48	0.68	1.00									
ShSi5	0.68	0.92	0.80	0.53	1.00								
ShSi6	0.76	0.93	0.82	0.48	0.93	1.00							
ShSi7	0.80	0.86	0.74	0.50	0.71	0.82	1.00						
ShSi8	0.83	0.94	0.92	0.58	0.95	0.98	0.84	1.00					
ShSi9	0.84	0.81	1.00	0.65	0.85	0.88	0.79	0.98	1.00				
ShSi10	0.51	0.54	0.71	0.61	0.57	0.56	0.66	0.65	0.65	1.00			
ShSi11	0.45	0.42	0.66	0.63	0.49	0.48	0.51	0.56	0.59	0.87	1.00		
ShSi12	0.73	0.86	0.91	0.71	0.86	0.84	0.83	0.92	0.90	0.75	0.63	1.00	
ShSi13	0.64	0.67	0.66	0.36	0.63	0.77	0.64	0.69	0.68	0.36	0.31	0.64	1.00
ShSi14	0.56	0.44	0.83	0.61	0.51	0.56	0.50	0.62	0.73	0.59	0.64	0.65	0.51
ShSi15	0.60	0.52	0.80	0.68	0.53	0.57	0.67	0.66	0.73	0.87	0.81	0.74	0.48
ShSi16	0.82	0.95	0.74	0.48	0.77	0.88	0.93	0.89	0.80	0.55	0.42	0.83	0.70
ShSi17	0.83	0.90	0.76	0.42	0.82	0.90	0.82	0.94	0.85	0.49	0.41	0.74	0.67
ShSi18	0.74	0.64	0.89	0.57	0.63	0.71	0.77	0.79	0.86	0.76	0.69	0.78	0.58
ShSi19	0.39	0.31	0.39	0.05	0.22	0.38	0.38	0.37	0.39	0.14	0.09	0.29	0.56
ShSi20	0.81	0.82	0.86	0.60	0.83	0.85	0.78	0.93	0.87	0.68	0.66	0.86	0.62
ShSi21	1.00	0.71	0.74	0.57	0.64	0.69	0.72	0.76	0.80	0.47	0.41	0.70	0.64
ShSi22	0.46	0.47	0.59	0.67	0.51	0.46	0.55	0.56	0.57	0.87	0.87	0.64	0.26
ShSi23	0.91	0.64	0.67	0.40	0.58	0.65	0.64	0.72	0.74	0.37	0.33	0.58	0.53
ShSi24	0.84	0.58	0.79	0.67	0.58	0.61	0.60	0.72	0.82	0.50	0.52	0.66	0.50
ShSi25	0.67	0.61	0.76	0.97	0.63	0.57	0.60	0.69	0.73	0.66	0.63	0.81	0.43

Table 2. Cont.

Genotype	ShSi14	ShSi15	ShSi16	ShSi17	ShSi18	ShSi19	ShSi20	ShSi21	ShSi22	ShSi23	ShSi24	ShSi25
ShSi1												
ShSi2												
ShSi3												
ShSi4												
ShSi5												
ShSi6												
ShSi7												
ShSi8												
ShSi9												
ShSi10												
ShSi11												
ShSi12												
ShSi13												
ShSi14	1.00											
ShSi15	0.76	1.00										
ShSi16	0.49	0.57	1.00									
ShSi17	0.50	0.52	0.89	1.00								
ShSi18	0.79	0.88	0.71	0.71	1.00							
ShSi19	0.38	0.32	0.44	0.43	0.46	1.00						
ShSi20	0.63	0.68	0.81	0.82	0.80	0.34	1.00					
ShSi21	0.56	0.59	0.75	0.75	0.71	0.40	0.76	1.00				
ShSi22	0.48	0.75	0.44	0.41	0.60	0.00	0.64	0.43	1.00			
ShSi23	0.48	0.47	0.69	0.80	0.67	0.41	0.69	0.86	0.31	1.00		
ShSi24	0.69	0.63	0.61	0.68	0.72	0.32	0.72	0.83	0.49	0.79	1.00	
ShSi25	0.61	0.70	0.60	0.53	0.63	0.13	0.72	0.67	0.69	0.51	0.73	1.00

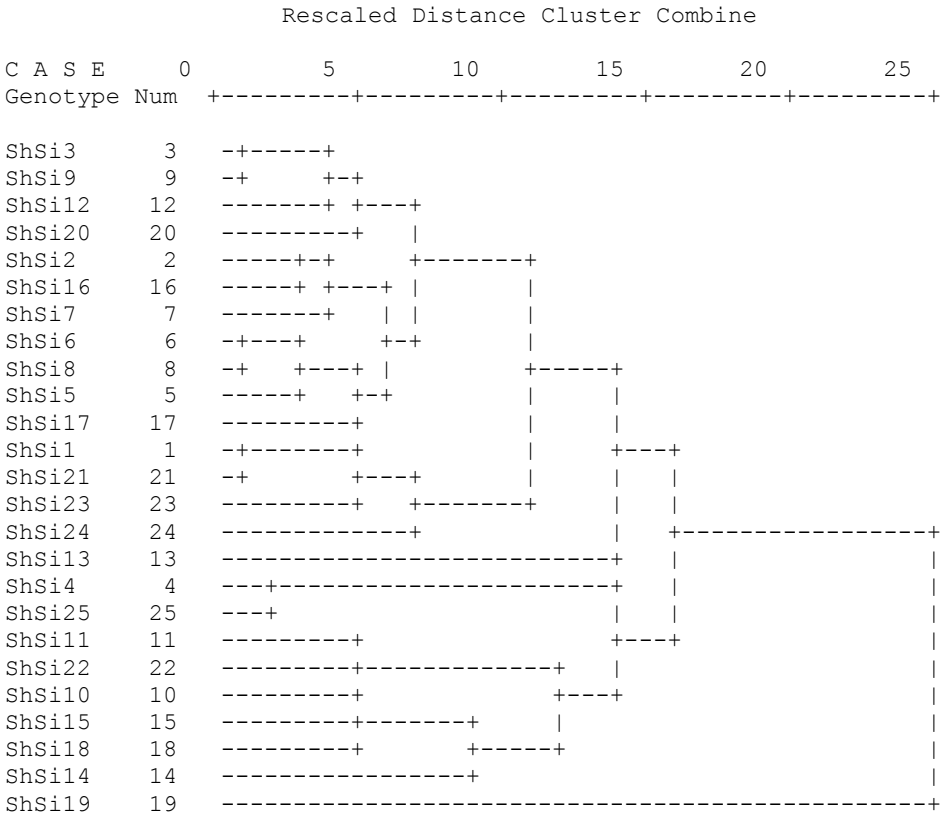

Figure 1. Dendrogram of 25 sesame (*Sesamum indicum* L.) genotypes based on 16 morphological characters measured in three consecutive seasons (2006-2008) at Shambat using Average Linkage (Between Groups) based on Euclidean distance

Profile description of the seven clusters

The mean of traits of each of the seven groups are presented in Table 3. The ranking of variable means of the seven clusters (Table 4) can be described as follows:

Cluster I: Medium flowering and maturing plants, bearing numerous capsules in a branch. They had high yield, high oil content and low seed protein.

Cluster II: Early flowering and medium maturing genotypes, with low number of capsules/plant and a few seeds/capsule. But they had heavy white seeds and very high oil percent.

Cluster III: Medium flowering and early maturing plants, bearing few branches and capsules. The plants had numerous capsules in the main stem, numerous seeds, heavy brown seeds and high yield. But they had low oil content.

Cluster IV: The genotypes of this group flowered and matured late and had high yield. They were tall with thick stems and numerous branches. The seeds were white, few, heavy and had low oil content.

Cluster V: Late flowering and maturing entries. It had long and thick stem, the capsules set at high nodes on the main stem. Furthermore, the plant had numerous branches and capsules, brown light weight seeds, low yield /unit area and high oil content.

Cluster VI: Late flowering and medium scores for morphological and yield components traits, but it had white light weight seeds and low yield. This group had the highest protein content.

Polymorphism analysis based on RAPD molecular markers

Application of the four RAPD markers to the 25 sesame accessions (Plates 1, 2, 3 and 4) revealed that the four primers exhibited informative amplification of sesame DNA. Forty–eight amplified bands were obtained (average 12 fragments/primer). The 48 bands exhibited a 97.9% polymorphism (Table 5). The size of the amplified fragments ranged from 100 to 3000 bp.

Table 3. Means of the 16 traits of sesame (*Sesamum indicum* L.) genotypes for each of the seven clusters produced at 10 Euclidean distance

Character	Cluster							Mean	STD
	I	II	III	IV	V	VI	VII		
Days to 50% flowering	47.50	39.70	45.10	58.90	66.70	56.50	32.20	49.50	11.90
Days to maturity	105.10	103.60	99.20	136.70	135.20	115.70	79.70	110.70	20.30
Plant height (cm)	135.30	112.50	132.50	146.40	150.30	137.00	77.60	127.40	25.10
Height to first capsule (cm)	79.00	55.20	61.50	103.40	100.10	82.20	28.10	72.80	26.60
Stem diameter (cm)	1.13	1.11	1.14	1.36	1.27	1.15	1.01	1.17	0.11
Number of branches/plant	3.00	3.10	0.40	4.60	5.30	3.80	0.30	2.90	1.90
Number of capsules /branch	10.70	8.70	9.10	9.80	12.30	9.30	7.20	9.60	1.60
Number of capsules/main stem	24.60	21.90	47.90	15.10	14.60	20.30	47.20	27.40	14.20
Number of capsules/plant	57.20	50.30	49.70	57.60	75.90	57.90	49.90	56.90	9.20
Number of seeds/capsule	55.70	49.50	63.60	47.20	53.20	52.30	58.20	54.20	5.50
1000-seed weight (g)	3.36	4.30	3.77	4.22	2.31	2.80	2.45	3.32	0.82
Seed yield/plant (g)	9.29	8.59	9.06	8.93	7.19	6.43	5.80	7.90	1.41
Seed yield (t/ha)	1.45	1.28	1.41	1.30	1.06	1.02	0.89	1.20	0.21
Oil content (%)	48.00	48.30	44.50	44.00	48.10	45.60	42.40	45.80	2.30
Protein content (%)	23.90	25.30	25.80	25.30	26.30	27.70	25.60	25.70	1.20
Seed colour	White	Brown	White	Brown	Brown	White	Black		

Table 4. Ranking the variable means of the seven clusters

Character	Cluster						
	I	II	III	IV	V	VI	VII
Days to 50% flowering	M	L	M	H	VH	H	VL
Days to maturity	M	M	L	VH	VH	M	VL
Plant height (cm)	M	L	M	H	H	M	VL
Height to first capsule (cm)	M	L	M	VH	VH	M	VL
Stem diameter (cm)	M	M	M	VH	H	M	VL
Number of branches/plant	M	M	VL	H	VH	M	VL
Number of capsules /branch	H	M	M	M	VH	M	VL
Number of capsules/main stem	M	M	VH	L	L	M	VH
Number of capsules/plant	M	L	L	M	VH	M	L
Number of seeds/capsule	M	L	VH	VL	M	M	H
1000-seed weight (g)	M	VH	H	VH	VL	L	VL
Seed yield/plant (g)	H	M	H	H	M	VL	VL
Seed yield (t/ha)	VH	M	H	M	L	L	VL
Oil content (%)	H	VH	L	L	H	M	VL
Protein content (%)	VL	M	M	M	M	VH	M

Very high (VH) > Mean+1STD; Mean+0.5STD < High (H) ≤ Mean+1STD; Mean-0.5STD ≤ Moderate (M) ≤ Mean+0.5STD; Mean-1STD ≤ Low (L) < Mean-0.5STD; Very Low (VL) < Mean-1STD

Table 5. Primers used for RAPD analysis and polymorphism detected on 25 sesame (*Sesamum indicum* L.) genotypes

Primer code	Nucleotide sequences (5`- 3`)	Total number of amplified bands	Number of polymorphic bands	Percentage of polymorphic bands
A1	CAGGCCCTTC	12	12	100
A2	TGCCGAGCTG	12	12	100
B1	GTTTCGCTCC	12	11	91.7
B2	TGATCCCTGG	12	12	100
Total		48	47	391.7
Average		12	11.75	97.9

The similarity coefficient values, based on RAPD analysis, are presented in Table 6. The most similar accessions were ShSi20 and ShSi21. On the other hand, ShSi11 and ShSi22 were the most dissimilar accessions.

A dendrogram, constructed from the RAPD data (Figure 2), classified the 25 sesame accessions, at 15 Euclidean distances, into eight major clusters. The first cluster (I) comprised seven accessions and was divided into two sub-groups, the second one (II) had one accession, the third one (III) consisted of three accessions and divided into two sub-groups, the fourth cluster (IV) had only one accession, the fifth one (V) contained two accessions, the sixth cluster (VI) comprised 11 accessions and divided into six sub-groups, the seventh one (VII) had of only one accession and the eighth one (VIII) contained only one accession as the most divergent genotype. The RAPD markers separated sesame genotypes in more groups than morphological markers. Interestingly, some genotypes have been grouped together in both morphological and RAPD-based clustering. These were ShSi21 and ShSi23; ShSi2, ShSi5, ShSi6, ShSi7, ShSi9 and ShSi12; ShSi14 and ShSi18.

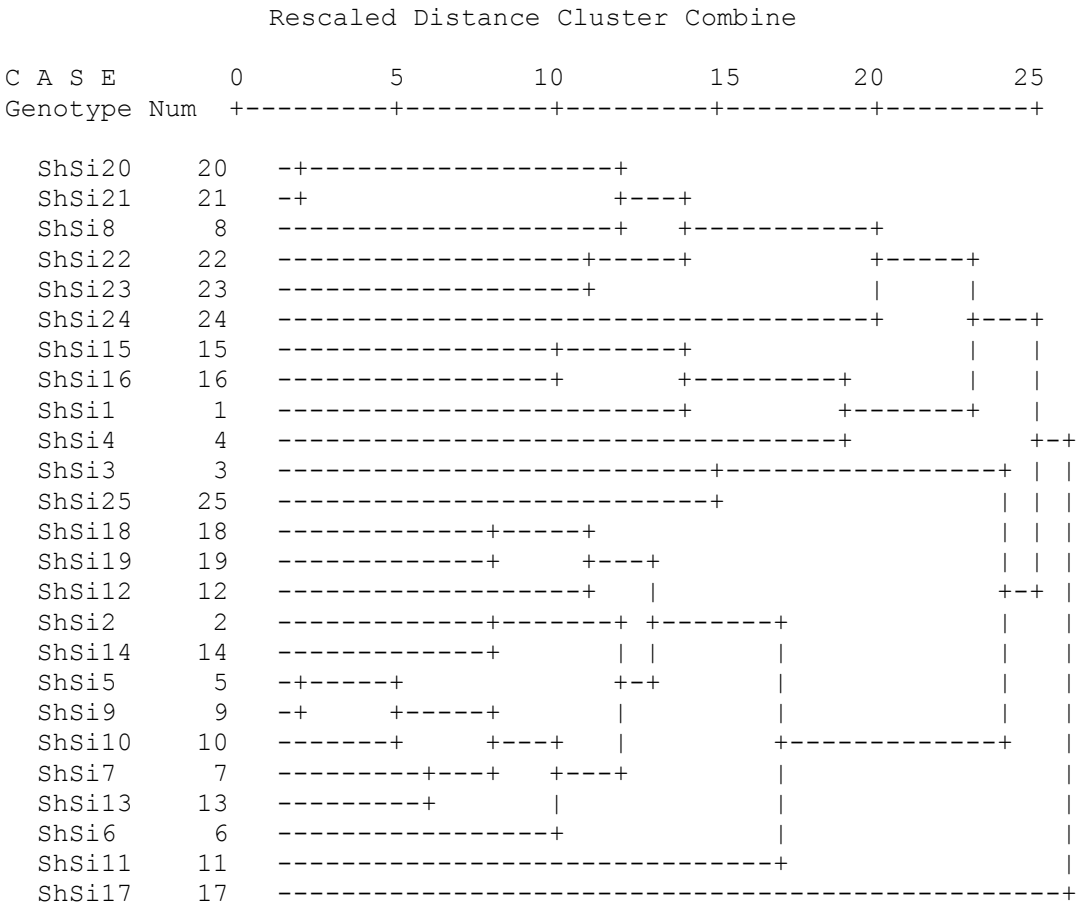

Figure. 2. A dendrogram of 25 sesame (*Sesamum indicum* L.) genotypes developed from four RAPD markers using Average Linkage (Between Groups) based on Euclidean distance

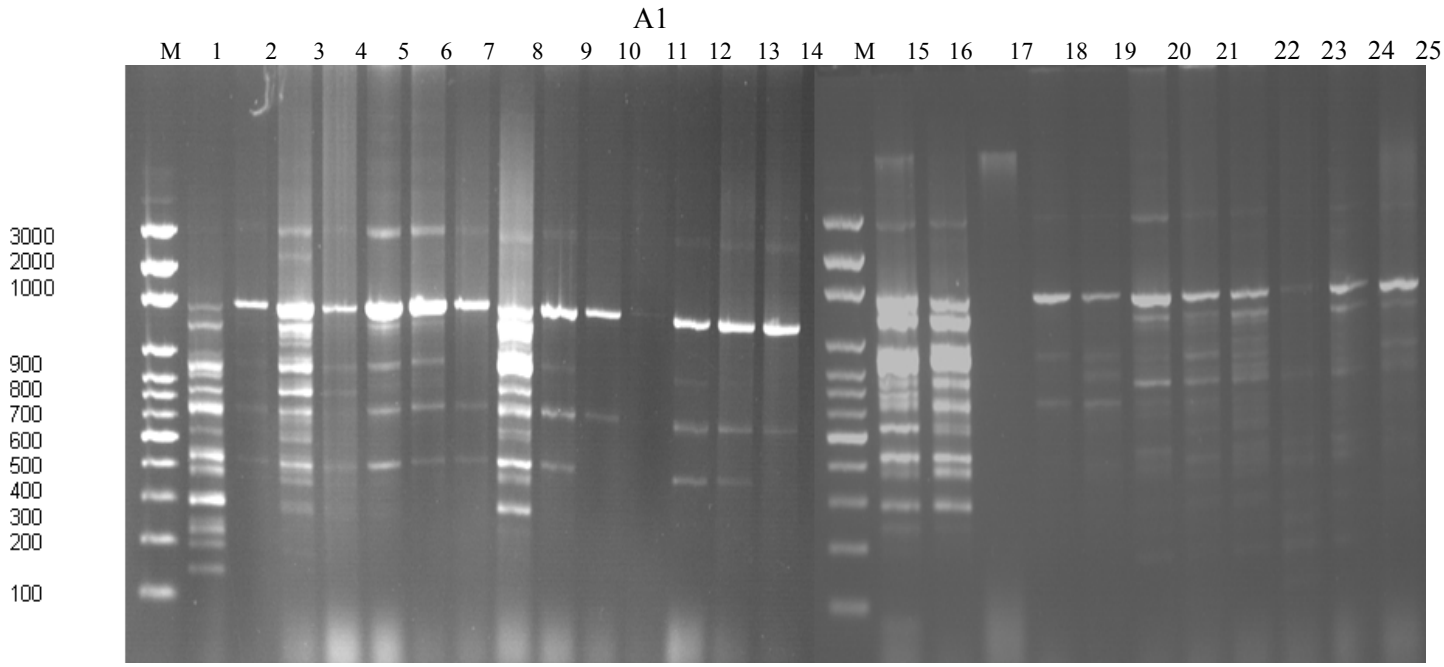

Plate 1. Detection of diversity in sesame accessions ShSi 1-25 (Lanes: 1-25) using primer A1
M= 100 bp DNA ladder

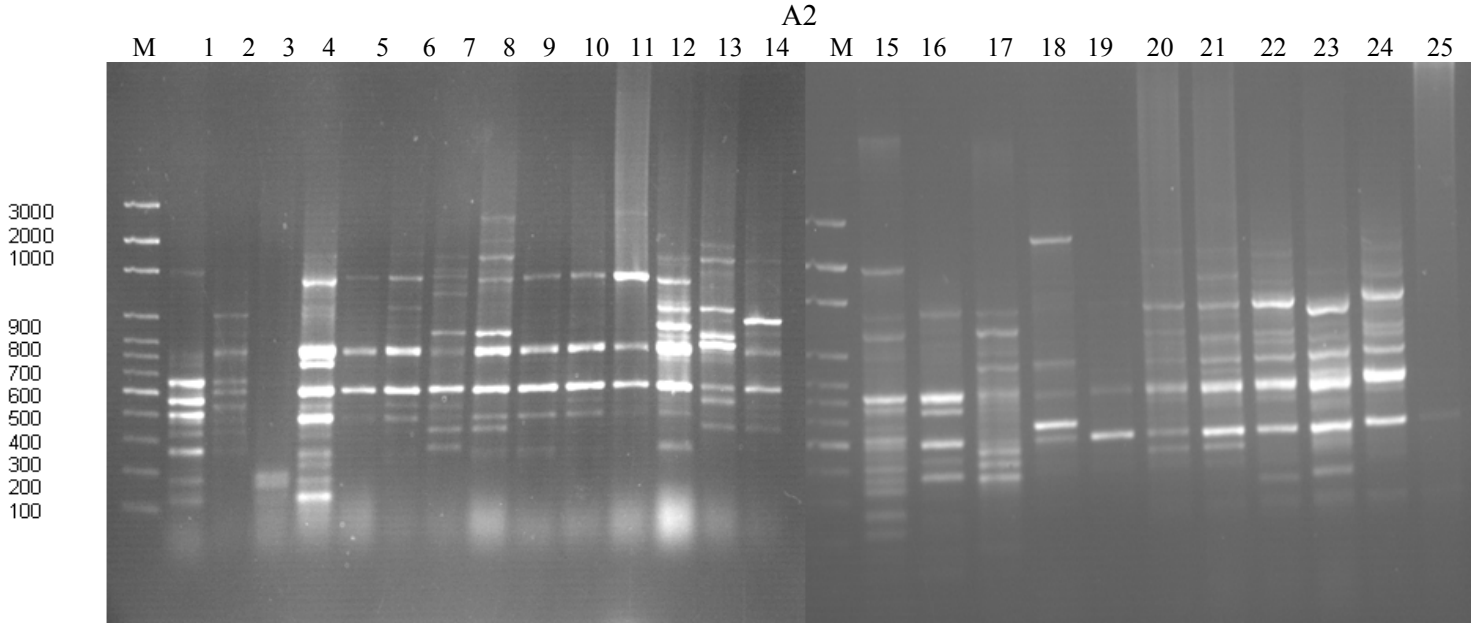

Plate 2. Detection of diversity in sesame accessions ShSi 1-25 (Lanes: 1-25) using primer A2;
M= 100 bp DNA ladder

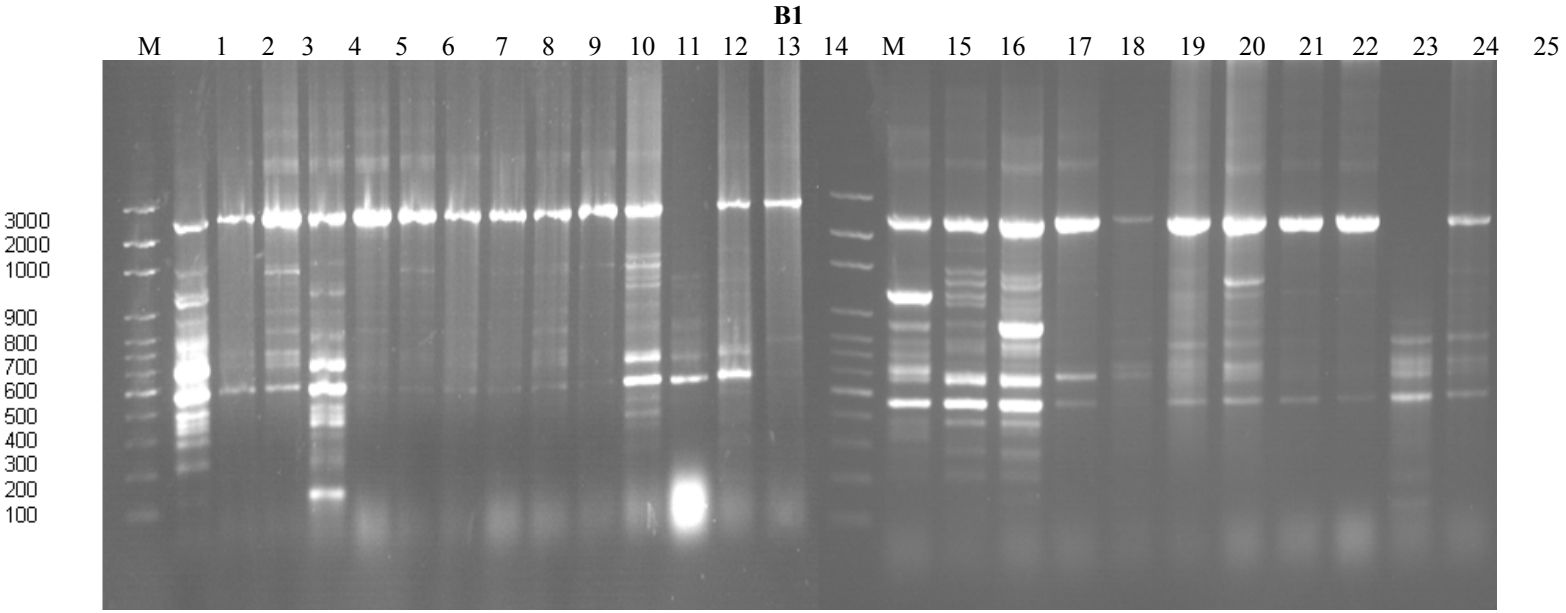

Plate 3. Detection of diversity in sesame accessions ShSi 1-25 (Lanes: 1-25) using primer B1; M= 100 bp DNA ladder

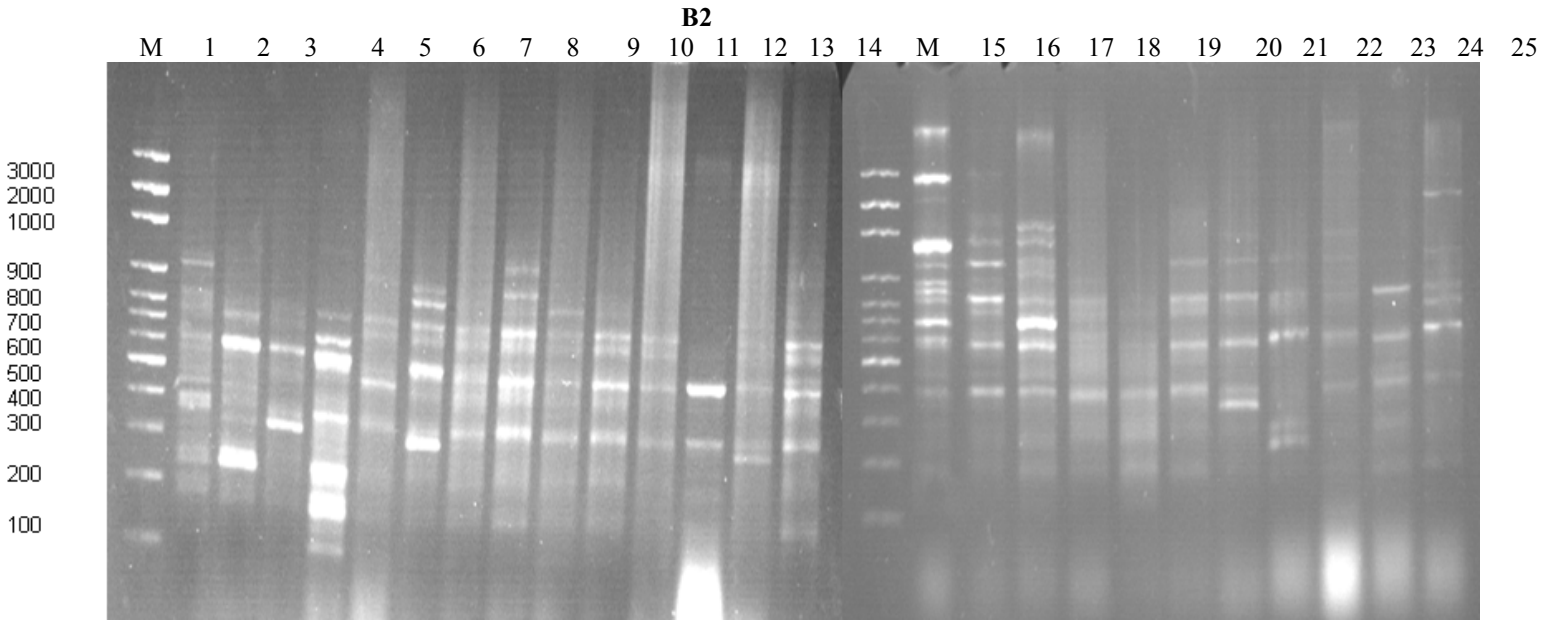

Plate 4. Detection of diversity in sesame accessions ShSi 1-25 (Lanes: 1-25) using primer B2; M = 100 bp DNA ladder

Table 6. Similarity matrix of 25 sesame (*Sesamum indicum* L.) genotypes based on four RAPD markers using Euclidean distance

Genotype	ShSi1	ShSi2	ShSi3	ShSi4	ShSi5	ShSi6	ShSi7	ShSi8	ShSi9	ShSi10	ShSi11	ShSi12	ShSi13
ShSi1	1.00												
ShSi2	0.33	1.00											
ShSi3	0.33	0.26	1.00										
ShSi4	0.55	0.33	0.26	1.00									
ShSi5	0.20	0.72	0.47	0.33	1.00								
ShSi6	0.20	0.63	0.33	0.47	0.82	1.00							
ShSi7	0.14	0.72	0.26	0.40	0.82	0.82	1.00						
ShSi8	0.40	0.40	0.33	0.33	0.55	0.72	0.63	1.00					
ShSi9	0.36	0.68	0.51	0.43	1.00	0.77	0.77	0.59	1.00				
ShSi10	0.20	0.72	0.33	0.33	0.94	0.72	0.82	0.55	0.88	1.00			
ShSi11	0.30	0.43	0.36	0.30	0.68	0.43	0.43	0.30	0.72	0.77	1.00		
ShSi12	0.17	0.59	0.23	0.30	0.68	0.59	0.68	0.36	0.72	0.51	0.47	1.00	
ShSi13	0.30	0.68	0.36	0.43	0.77	0.68	0.88	0.51	0.94	0.77	0.63	0.72	1.00
ShSi14	0.20	0.82	0.33	0.26	0.63	0.55	0.72	0.33	0.68	0.82	0.59	0.59	0.77
ShSi15	0.63	0.14	0.20	0.47	0.08	0.20	0.14	0.33	0.23	0.08	0.11	0.11	0.17
ShSi16	0.68	0.17	0.30	0.51	0.23	0.17	0.11	0.30	0.26	0.23	0.20	0.08	0.20
ShSi17	0.33	0.20	0.08	0.33	0.20	0.20	0.26	0.08	0.30	0.33	0.51	0.17	0.36
ShSi18	0.23	0.77	0.30	0.36	0.77	0.68	0.68	0.43	0.72	0.88	0.55	0.63	0.63
ShSi19	0.36	0.68	0.43	0.30	0.77	0.43	0.51	0.36	0.82	0.68	0.55	0.82	0.63

Table. 6. cont.

Genotype	ShSi1	ShSi2	ShSi3	ShSi4	ShSi5	ShSi6	ShSi7	ShSi8	ShSi9	ShSi10	ShSi11	ShSi12	ShSi13
ShSi20	0.59	0.36	0.43	0.51	0.36	0.51	0.51	0.68	0.55	0.36	0.33	0.47	0.55
ShSi21	0.55	0.33	0.40	0.40	0.33	0.47	0.40	0.72	0.51	0.33	0.30	0.51	0.51
ShSi22	0.26	0.33	0.33	0.26	0.26	0.47	0.47	0.63	0.23	0.26	0.00	0.30	0.23
ShSi23	0.33	0.47	0.08	0.26	0.33	0.47	0.63	0.55	0.30	0.40	0.23	0.36	0.36
ShSi24	0.40	0.20	0.26	0.40	0.14	0.14	0.33	0.26	0.23	0.14	0.17	0.43	0.36
ShSi25	0.40	0.33	0.63	0.26	0.40	0.33	0.26	0.33	0.51	0.40	0.43	0.23	0.36

Table 6 cont.

Genotype	ShSi14	ShSi15	ShSi16	ShSi17	ShSi18	ShSi19	ShSi20	ShSi21	ShSi22	ShSi23	ShSi24	ShSi25
ShSi14	1.00											
ShSi15	0.08	1.00										
ShSi16	0.05	0.77	1.00									
ShSi17	0.26	0.40	0.43	1.00								
ShSi18	0.68	0.17	0.26	0.36	1.00							
ShSi19	0.59	0.17	0.33	0.23	0.82	1.00						
ShSi20	0.36	0.68	0.47	0.43	0.47	0.47	1.00					
ShSi21	0.33	0.63	0.51	0.33	0.43	0.51	1.00	1.00				
ShSi22	0.26	0.40	0.36	0.14	0.36	0.30	0.68	0.72	1.00			
ShSi23	0.33	0.26	0.23	0.33	0.43	0.36	0.59	0.63	0.72	1.00		
ShSi24	0.33	0.33	0.23	0.33	0.23	0.36	0.59	0.55	0.47	0.47	1.00	
ShSi25	0.40	0.40	0.43	0.40	0.43	0.51	0.59	0.47	0.26	0.26	0.33	1.00

DISCUSSION

The average polymorphism of 97.9% detected on the 25 sesame genotypes, using four RAPD markers, is comparable to the 86.75% found by Bhat *et al.* (1999) in some Indian and non Indian genotypes, 78% reported by Ercan *et al.* 2004 in some Turkish accessions, 100% of Salazar *et al.* (2006) in some Venzuelian genotypes, 84.74% recorded by Abdellatef *et al.* (2008) in some Sudanese entries and 82.99% of Pham *et al.* 2009 in some Vietnamian and Combodian entries. Li and Midmore (1999) reported that when the variation between genotypes is high, the use of a few primers will be sufficient.

Based on square Euclidean distance, cluster analysis of the agro-morphological characters grouped the 25 sesame accessions into seven clusters, whereas the dendrogram constructed from the RAPD data classified them into eight major clusters. These results indicated that both the evaluation of agro-morphological characters and RAPD analysis are useful for estimating genetic diversity and relationships among sesame accessions. Furthermore, the four RAPD markers separated the 25 sesame genotypes in more groups than do agro-morphological traits. This result is in agreement with the findings of Fufa *et al.* (2005) in wheat, Beyene *et al.* (2005) in maize and Bucheyeki *et al.* (2009) in sorghum.

The genotypes, ShSi21 and ShSi23; ShSi2, ShSi5, ShSi6, ShSi7, ShSi9 and ShSi12; ShSi14 and ShSi18 were grouped together in both agro-morphological and RAPD based clustering. This result denotes that each group of such genotypes could have a common genetic background. In addition, some genotypes from different ecological zones were grouped together in the same cluster. The lack of relationship between ecological distribution and clustering, for these genotypes, may be attributed to the fact that most sesame growers in Sudan get their seeds from local markets or from the former crop. Kim *et al.* (2002) and Pham *et al.* (2009) reported that human factor could be responsible for such results.

CONCLUSION

Both the evaluation of agro-morphological characters and RAPD analysis are useful for estimating genetic diversity and relationships among sesame accessions, and RAPD markers can separate genotypes in more groups than do agro-morphological traits.

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التباين الوراثى فى بعض مدخلات السمسم بإستخدام الصفات الزراعية المظهرية وموسمات الحمض النووى المتباين المتضاعف عشوائيا (RAPD)*

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المستخلص: أستخدمت الصفات الزراعية المظهرية وموسمات الحمض النووى المتباين المتضاعف عشوائياً (RAPD) لتحديد التباين والعلاقات بين 25 مدخلاً من محصول السمسم من السودان . جُمعت بيانات عن 16 صفة زراعية من تجربة حقلية ، أُجريت بشمبات لثلاثة مواسم متتالية (2006-2008م) ، وأُخضعت للتحليل العنقودى . دلت النتائج على أن التحليل العنقودى ، على أساس مسافة إقليدس للصفات الزراعية المظهرية ، جمَّع مدخلات السمسم الـ 25 في سبع مجموعات . تطبيق الموسمات الجزيئية للحمض النووى المتباين المتضاعف عشوائياً (RAPD) أنتج 48 قطعة دنا بتنوع قدره 97.9%. مخطط الشجرة الذى تم تكوينه من بيانات الصفات الجزيئية RAPD قسَّم الـ 25 مُدخل من السمسم إلى ثمانِ مجموعات رئيسية . خلصت الدراسة إلى أن الجمع بين كل من الصفات الزراعية المظهرية وموسمات الحمض النووى المتباين المتضاعف عشوائيا (RAPD) يعطى تقديراً كفؤاً لكلٍ من التباين الوراثى والعلاقات بين المصادر الوراثية لمحصول السمسم .

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