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EVALUATION OF SOME EGYPTIAN COTTON GENOTYPES UNDER DIFFERENT ENVIRONMENTS AND MOLECULAR GENETICS OF SOME PROMISING STRAINS

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ABSTRACT

Comparison among thirty-eight long staple Egyptian cotton genotypes descending from eighteen crosses were included in trail (A) at Sids Agricultural Experiment Station in 2008 season, and among eighteen genotypes descending from thirteen crosses in trail (B) along with the check cultivars Giza 90 and Giza 80. Trial (B) was raised at five different locations in Middle and Upper Egypt (Sids, El-Fayoum, EL-Minia, Assiut and Sohag).The results obtained from trial (A) showed that only families derived from two crosses exceeded the check cultivars Giza 90 and Giza 80 in yield and its contributing variables. These crosses were [Giza 90 x Pima S_{62} (24240)] and [{Giza 83 x (Giza 75 x 5844)} x Giza 85], while families resulting from three crosses were promising as regard to their performance for yield and its contributing variables in trial (B). These three crosses were [{Giza 83 x (Giza 75 x 5844)} x Giza 80], [Giza 91 x Giza 90] and [{Giza 83 x (Giza 75 x 5844)} x {Giza 83 x (Giza 72 x Dendera)}]. High heritability estimates in broad sense were recorded for most traits in trail (A), indicating that phenotypic selection for these traits could be highly effective. The relatively low and moderate heritability values in broad sense were recorded for seed cotton yield and lint yield in trail (A), and for boll weight in trail (B). These values were verified by the presence of significant, genotypes x locations interaction. In general, it could be concluded from the results in trials (A and B) that the crosses [{Giza 83 x (Giza 75 x 5844)} x Giza 80], [Giza 91 x Giza 90] and [{Giza 83 x (Giza 75 x 5844)} x {Giza 83 x (Giza 72 x Dendera)}] have shown to be promising ones due to their performance for yield components and fiber quality than others. These promising crosses were characterized on the molecular level, using RAPD-PCR. Ten out of the tested eighteen primers succeeded to amplify high polymorphic DNA. Based on the obtained RAPD data a dendrogram was constructed for the studied genotypes. From this phylogenetic tree, it has been noticed that the most related crosses genotypes were the family from (Giza 91 x Giza 90) and the cultivar which Giza 90 exhibited 80 % genetic similarity. While, the least related genotypes were Giza 80 and Giza 90 which showed 65.7 % similarity. Meanwhile, there were some specific RAPD markers, which could differentiate between the different genotypes.

Key words: ***Egyptian cotton, Gossypium barbadense , Yield components and fiber traits, RAPD, Dendrogram.***

INTRODUCTION

The fiber quality of the Egyptian cotton (*Gossypium barbadense* L.) is the best all over the world where it combines the high length, fineness and

high yarn strength. The main objective of the cotton breeding program implemented by the Cotton Research Institute is to produce new cotton varieties with superior fiber quality characters over the commercial ones. To achieve this goal, the breeder uses artificial hybridization between the desired genotypes, followed by the pedigree method of selection.

The obtained hybrids are selected until the fifth segregating generation. The promising and desired families from different crosses are tested in the preliminary strain test (Trail A), in comparison with the commercial varieties.

Families selected in (Trail A) are tested through the advanced strain test (Trail B), beside the cultivated varieties for comparison at different locations to study the interaction between the new genotypes and the environments.

The superior crosses over commercial varieties will be grown for increasing enough seeds to produce the breeder seed. Performance of cotton genotypes under different environments were studied by several workers, El-Moghazy *et al* 1982, Abo-Zahra *et al* 1986, El-Marakby *et al* 1986, Shafshak *et al* 1987, Sallam *et al* 1987, Ismail *et al* 1989, Mohamed 1991, Awaad *et al* 1996, Hassan *et al* 2001 and Mohamed *et al* 2003.

Biochemical and molecular genetic fingerprinting are useful tools for phylogenetic studies among different genetic resources (Suiter 1988, Percy and Wendel 1990, Wendel *et al* 1991 , Zhang *et al* 1998 and Jinggao *et al* 1999).

The randomly amplified polymorphic (RAPD) DNA (Williams *et al* 1990 and Welsh and Mc Clelland 1990) is used to identify genotypes and to detect molecular linkage to certain gene (S) of interest. This PCR-based technology also has important applications in plant breeding and seed testing programs.

The major purpose of this study was to evaluate genotypes derived from 18 crosses in Trial (A) and from 13 crosses in Trial (B), to recognize the promising cross which surpassed the commercial varieties for some major characters i.e., earliness, yield components and fiber quality and to detect biochemical and molecular markers of some promising genotypes that proved superiority in the yield evaluation under different environments.

MATERIALS AND METHODS

The present investigation was carried out at the Department of Cotton Breeding, Cytology and Genetics Unit, Cotton Research institute, Agricultural Research Center, Giza, Egypt. In 2008 season, two field experiments were carried out, i.e. Trial (A) and the advanced Trial (B). Trial (A) consisted of 40 genotypes of Egyptian cotton, 38 lines descending from 18 crosses and the two check cultivars, Giza 90 and Giza 80. Trial A was cultivated at sids Experimental Station, Agriculture of Research Center.

While Trial was (B) cultivated at five locations in the Middle and Upper Egypt i.e., Sids, El-Fayoum, El-Minia, Assiut and Sohag. Trial B consisted of 20 genotypes, 18 lines descending from 13 crosses and the two commercial cultivars Giza 90 and Giza 80.

The experimental design in Trial (A) and Trial (B) AT all locations was a randomized complete blocks design with six replications. Each plot consisted of five rows; each row was four meters long, 60 cm apart and 20 cm between hills. Hills were thinned after three weeks from planting to two plants per hill. The middle three rows of each plot were hand harvested to determine the following traits.

A. **Yield components**

1. Seed cotton yield (SCY/fed): estimated as weight of seed cotton yield in kentar / feddan (kentar = 157.5 kg).
2. Lint yield (LY/fed): measured as average weight of lint yield in kentar / feddan.
3. Boll weight (BW): as the mean weight of 50 bolls picked at random from the first and fifth row of each plot.
4. Lint percentage (L %): calculated as the relative amount of lint in the seed cotton sample, expressed in percentage.

$$\text{Lint percentage (L \%)} = \frac{\text{weight of lint cotton in sample}}{\text{weight of seed cotton}} \text{X } 100$$

5. Earliness index (E %): Earliness percentage was calculated from the following equation:

$$\text{Earliness percentage} = \frac{\text{Yield of first pick}}{\text{Total seed cotton yield}} \text{X } 100$$

6. Seed index (SI): estimated as average weight of 100 seeds in grams.
7. Lint index (LI): estimated as average weight in grams of lint born by 100 seeds.

$$\text{LI} = \frac{\text{SI x LP \%}}{100 - \text{LP \%}} = \frac{\text{(seed index x lint percentage)}}{\text{(100 – lint percentage)}}$$

B. **Fiber properties**

1. Fiber fineness and maturity (Mic): measured by micronaire apparatus in micronaire units.
2. Hair weight (HW): expressed as millitex (10^{-8} g/cm).
3. 2.5 % span length (2.5 % SL): determined by the digital fibro-graph.
4. Yarn strength (Y.St): is the product of "Lea strength x yarn count" (60_s carded and 3.6 twist multiplier) measured by the Good Brand Tester.

All fiber properties tests were performed in the laboratory of the Cotton Technology Research Division, Cotton Research Institute at Giza according

to ASTM (1961), under the standard conditions of tests (65 ± 2 % relative humidity and 70 ± 20° F temperature).

The analysis of variance was calculated according to Le Clerge *et al* (1962) and Snedecor and Cochran (1981).

Heritability estimates in broad sense (h^2_{bs} %) were calculated by using the following formula as follows (Sakai 1960):

$h^2_{bs}\ \% = [\grave{o}^2\ g / (\grave{o}^2\ g + \grave{o}^2\ ge + \grave{o}^2\ e)] \times 100$

Where: $\grave{o}^2$ g : genotypic variance component.

$\grave{o}^2$ ge : variance component due to genotype x environment.

$\grave{o}^2$ e : error variance component.

Genetic advance under selection was calculated according to Allard (1960) as follows:

$$G.S. = K.\ \grave{o}^2{}_P \cdot h^2_{bs}$$

Where: K = selection differential and its value in this study is 2.06 at 5 % selection intensity.

$\grave{o}^2$ P = phenotypic standard deviation.

h^2_{bs} = heritability value in broad sense.

C. Molecular genetic analysis

1. Extraction and purification of genomic DNA

Genomic DNA was isolated according to Dellaporta *et al* (1983), as modified by Porebski *et al* (1997) and purified by the cesium chloride density gradient centrifugation method (Sambrook *et al* 1989).

2. Quantization of DNA

Two different methods were used to measure the amount of DNA:

2.1. Using spectrophotometer

2.2. Visual quantitation of DNA by ethidium bromide fluorescence

3. Random amplified polymorphic DNA (RAPD)

RAPD (Williams *et al* 1990) is based on DNA amplification at random locations in the plant genome.

3.1. Primers

The sequences of eighteen primers used for RAPD analysis was shown as follows:

Primer Code	Sequence 5 - 3	% of GC	Primer Code	Sequence 5 - 3	% of GC
OPA-01	CAGGCCCTTC	70 %	OPA-11	CAATCGCCGT	60 %
OPA-02	TGCCGAGTG	70 %	OPA-12	TCGGCGATAG	60 %
OPA-03	AGTAGCCAC	60 %	OPA-13	CAGCACCCAC	70 %
OPA-04	AATCGGGCTG	60 %	OPA-14	GGATGAGACC	60 %
OPA-05	AGGGGTCTTG	60 %	OPB-09	TGGGGGACTC	70 %
OPA-06	GGTCCCTGAC	70 %	OPB-15	GGAGGGTGTT	60 %
OPA-08	GTGACGTAGG	60 %	OPG-14	GGATGAGACC	60 %
OPA-09	GGGTAACGCC	70 %	OPG-18	GGCTCATGTG	60 %
OPA-10	GTGATCGCAG	70 %	OPZ-02	CCTACGGGGA	70 %

Oligonucleotide sequences of the ten-mere random primers used in this study were selected from a set of Operon Kits (A, B, C, D and Z) Operon Technologies Inc., Alameda, (A).

3.2. PCR reaction: Each reaction contained the following

Components	Amount for one reaction
10 reaction buffer	5.0 µl
$dNTP_5$ mix	5.0 µl
$Mgcl_2$	6.0 µl
Primer	4.0 µl
Tag DNA Polymerase	0.5 µl
Template	2.5 µl
H_2O	27.0 µl
Total volume	50.0 µl

3.3. Thermo cycling profile and detection of PCR products

PCR amplification was performed in thermal circler Perkin Elmer Gene Amp PCR system (2400) with a heated lid to reduce evaporation and the reaction mixture was overlaid with a few drops of light mineral oil (Sigma, USA) programmed to fulfill 40 cycles after an initial denaturation cycle for 4 min at 94° C. Each cycle consisted of a denaturation step at 94° C for 1 min, an annealing step at 37° C for 2 min and an elongation step at 72° C for 2 min.

The primer extension segment was extended to 7 min at 72° C in the final cycle.

3.4. Electrophoresis of PCR products

The amplicons were resolved by electrophoresis in 1.5 % agaroso gel containing ethidium bromide. The gels were run at 95 – 100 volts for two hours.

3.5. Visualization, scoring and photography

After electrophoresis, the amplicons were visualized with a UV Tran illuminator. Then, they were examined and the presence or absence of each size class was scored as 1 or 0, respectively. The gels were photographed using a Polaroid camera (MP4L camera) and Polaroid films (Types 57, ASA 3000).

RESULTS AND DISCUSSION

The preliminary strain test (Trial A)

Trial A included the evaluation of 40 cotton genotypes, 38 strains descending from 18 crosses and the two check varieties (Giza 90 and Giza 80) as control. The analysis of variance not presented showed that

significant mean squares due to genotypes were detected for yield, yield components and fiber properties.

A. Yield and its components

1. Seed cotton yield (SCY)

Table (1) showed that, 34 out of 38 genotypes exceeded the check variety Giza 90 in seed cotton yield. The increases ranged from 0.35 to 2.60 k/fed. These estimates were significant for11 genotypes belonging to 8 crosses i.e. [Giza 83 x (Giza 75 x 5844) x Giza 85], [Giza 90 x Pima S_{62} (24240)], [Giza 91 x Pima S_{62} (24202)], [{Giza 83 x (Giza 75 x 5844)} x Dendera)], [{Giza 83 x (Giza 75 x 5844)} x Giza 91], [{Giza 83 x Pima S_6} x Dendera], [Giza 91 x Giza 90] and [{Giza 83 x (Giza 75 x 5844)} x Giza 80].

The highest yield was achieved by families resulted from the crosses [Giza 83 x (Giza 75 x 5844) x Giza 85] , [Giza 90 x Pima S_{62} (24240)] and [Giza 91 x Pima S_{62} (24202)] which exceeded the control variety Giza 90 with 2.60 k/fed. (27.8 %), 2.59 k/fed (27.7 %) and 2.54 k/fed (27.1 %), respectively.

On the other hand, the families from the cross [{Giza 83 x (Giza 75 x 5844)} x Giza 90], were equal to Giza 90 variety in seed cotton yield. The commercial variety Giza 80 was lower in seed cotton yield compared with other genotypes. Heritability value was 55.63 %, which indicated that this character was moderately affected by the environmental fluctuation. Genetic gain at 5 % selection intensity for seed cotton yield was 0.01 k/fed per cycle.

2. Lint cotton yield (LY)

Results in Table (1) showed that, 36 out of 38 genotypes exceeded the check variety Giza 90 in character. The excess over Giza 90 in LY ranged from 0.07 to 3.96 k/fed. Only 15 genotypes belonging to 12 crosses showed significant increases over Giza 90 for lint yield. The highest lint yield was achieved by F_5 83/2007 strain that belonged to the cross [Giza 90 x Pima S_{62} (24240)]. It exceeded the control variety Giza 90 by 3.96 k /f (33.73 %). Then it was followed by genotypes F_6 126 / 2007, and F_6 127/2007 belonging to the cross [{Giza 83 x (Giza 75 x 5844)} x Giza 85], F_6 139/2007 belonging to the cross [{Giza 83 x (Giza 75 x 5844)} x Giza 90] and F_9 264/2007 that belonged of the cross [Giza 91 x Giza 90]. These crosses exceeded the control variety Giza 90 by 3.41 k/fed (29.04 %), 3.19 k/fed (27.17 %) and 3.16 k/fed (26.91 %), respectively. Giza 80 had the lowest lint yield (11.66 k/fed). Low estimates of heritability (10.71 %) and genetic gain at 5 % selection intensity (1.03 k/fed) were estimated for this trait, indicating the strong environmental effect on this trait.

3. Boll weight (BW)

Boll weight is one of the main components of high seed cotton yield. Therefore, selection for heavy bolls could help the cotton breeder to improve the yield.

Table (1) showed that, only six genotypes exceeded the check variety Giza 90 in the weight of 50 bolls. The increase ranged from 2.0 to 10.0 grams. The increase was significant for only one strain (F_7 185/2007) belonging to the cross [{Giza 83 x (Giza 72 x Dendera)} x Giza 85].

The heritability value for boll weight was 77.09 %, indicating that this trait was slightly affected by the environmental conditions. The present results somewhat varied with the finding of Mohamed *et al.* (2003). Expected genetic advance under selection was 6.49 g /cycle.

4. Lint percentage (L %)

Table (1) showed that means of this trait ranged from, 37.19 % to 42.25 %. Twenty five strains exceeded the check variety Giza 90 in lint percentage. The superiorities were significant for 13 strains belonging to 9 crosses. The highest lint percentage was achieved by F_8 235/2007 that belonged to the cross [{Giza 83 x (Giza 75 x 5844)} x Giza 80] which exceeded the control variety Giza 90 by 2.43 %. On the other hand, the commercial variety Giza 80 was higher than Giza 90 in this trait, which was 41.0 %.

Heritability estimate for lint percentage was 84.82 %, which indicated low environmental effect on this character. Genetic gain at 5 % intensity of selection (4.4) was observed, indicating that selection is effective for the improvement of this character.

5. Earliness index (E %)

Earliness is one of the most important characters for which the cotton breeder in Egypt aim to develop varieties that can escape from the boll worms and can be harvested early enough before sowing winter crops.

Table (1) showed that all studied strains were earlier than the check cultivar Giza 90 except the stains F_9 256/2007 descending from the cross [Giza 91 x Giza 90] which was equal to Giza 90 cultivar in earliness index. On the other hand, the commercial variety Giza 80 was higher earliness index than the check variety Giza 90 and the other cultivated varieties.

6. Seed index (SI)

Seed index values presented in Table (1) showed that means of this trait ranged from 8.82 to 11.1 grams. The highest seed index (11.1 g) was achieved by the strain F_5 116/2007 that descended from the cross Giza 91 x Pima S_{62} (24202)] followed by the strain $F_6$127/2007 descending from the cross [{Giza 83 x (Giza 75 x 5844)} x Giza 85]. These genotypes were significantly higher in this trait than Giza 90. While, the strain F_5 83/2007 descending from the cross [Giza 90 x Pima S_{62} (24240)] was higher in seed index but with insignificant value. High heritability value (67.97 %) was

Table 1. Mean performance of seed cotton yield and its contributing variables of 38 cotton strains and two check cultivated cultivars grown in trail (A) at Sids in 2008 season.

NO.	Strains	Parent	Origin	Yield (k/fed)		L %	BW (g)	Ear (%)	SI (g)	LI (g)	Mic	HW militex	2.5 % SL	Y.St
				SCY	LY									
1	F_5 82/2007	F_4 27/2006	[G. 90 x Pima S_{62} (24240)]	10.28	13.44	41.53	140	81	9.67	6.72	3.8	158	30.8	2035
2	F_5 83/2007	F_4 29/2006	" "	11.95	15.70	41.70	150	76	10.5	7.21	4.3	162	30.1	2030
3	F_5 87/2007	F_4 37/2006	G. 90 x [G. 83 x (G. 72 x Delcero) x Pima S_6]	9.82	12.21	39.45	144	82	9.63	6.60	3.9	156	29.9	1950
4	F_5 96/2007	F_4 43/2006	" "	8.61	10.45	38.55	152	79	9.63	6.55	3.9	159	30.6	2235
5	F_5 97/2007	"	" "	10.11	12.42	39.01	151	79	10.1	6.79	3.9	159	30.3	2230
6	F_5 100/2007	F_4 44/2006	[(G. 83 x Pima S6) x krashinky]	8.58	10.07	37.24	152	84	9.65	6.56	3.7	150	30.9	2105
7	F_5 101/2007	F_4 49/2006	" "	10.80	12.65	37.19	146	80	9.88	6.29	3.7	150	31.5	2350
8	F_5 102/2007	"	" "	10.97	13.36	38.68	146	79	9.58	6.09	3.9	160	31.2	2350
9	F_5 104/2007	F_4 52/2006	[(G. 83 x Pima S_6) x Dendera]	10.11	12.69	39.87	151	72	9.98	6.33	4.10	162	32.5	2465
10	F_5 111/2007	F_4 53/2006	" "	11.61	14.27	39.00	155	73	9.88	5.88	4.2	167	30.6	2305

Table 1. Cont.

11	F_5 116/2007	F_4 63/2006	[G. 91 x Pima S_{62} (24202)]	11.90	14.65	39.08	154	74	11.1	6.82	4.2	162	31.0	2580
12	F_5 118/2007	F_4 64/2006	„ „	11.63	14.07	38.43	146	75	10.0	5.85	4.1	160	32.5	2525
13	F_5 122/2007	F_4 74/2006	„ „	11.10	13.77	39.39	146	76	9.58	5.99	4.2	165	31.0	2670
14	F_6 126/2007	F_5 85/2006	[{G. 83 x (G. 75 x 5844)} x G. 85]	11.73	15.15	40.99	161	74	10.3	7.31	4.0	158	32.0	2525
15	F_6 127/2007	„	„ „ „	11.96	15.11	40.11	155	70	10.7	7.20	4.1	160	31.2	2620
16	F_6 133/2007	F_5 93/2006	„ „ „	11.78	14.24	38.37	150	78	10.4	6.53	4.1	161	30.4	2160
17	F_6 139/2007	F_5 101/2006	[{G. 83 x (G. 75 x 5844)} x G. 91]	11.77	14.93	40.27	145	75	8.98	6.02	4.2	162	31.1	2535
18	F_6 145/2007	F_5 110/2006	[G. 91 x G. 80]	10.94	13.98	40.57	164	71	10.0	6.69	4.2	161	31.7	2535
19	F_6 158/2007	F_5 138/2006	[{G. 83 x (G. 75 x 5844)} x G. 90]	9.36	11.96	40.55	144	75	9.90	6.32	3.9	159	29.6	2370
20	F_6 159/2007	„	„ „ „	10.79	13.77	40.52	146	77	10.3	6.55	4.2	161	32.4	2440
21	F_6 160/2007	F_5 138/2006	„ „ „	10.10	12.82	40.28	139	81	9.88	6.30	3.9	157	31.1	2640

Table 1. Cont.

NO.	Strains	Parent	Origin	Yield (k/fed)		L %	BW (g)	Ear %	SI (g)	LI (g)	Mic	HW	2.5 % SL	Y.St
				SCY	LY									
22	F_7 165/2007	F_5 140/2006	[{G. 83 x (G. 72 x Dendera)} x G. 80]	9.31	11.81	40.28	142	76	9.00	5.88	4.0	160	30.5	2580
23	F_7 167/2007	,,	,, ,, ,,	9.71	11.95	39.07	143	82	8.82	5.65	3.9	157	30.6	2500
24	F_7 168/2007	F_6 149/2006	[{G. 83 x (G. 72 x Dendera)} x G. 91]	10.29	12.81	39.53	155	79	10.0	6.95	4.1	163	31.3	2570
25	F_7 169/2007	,,	,, ,, ,,	9.95	12.48	39.84	153	76	10.1	6.65	4.2	161	29.7	2440
26	F_7 173/2007	F_6 152/2006	,, ,, ,,	10.78	13.92	41.01	161	82	10.5	6.85	4.1	162	29.2	2230
27	F_7 182/2007	F_6 165/2006	[{G. 83 x (G. 72 x Dendera)} x G. 85]	10.16	12.89	40.27	153	76	9.97	6.49	4.1	161	30.8	2565
28	F_7 184/2007	,,	,, ,, ,,	10.73	13.99	41.38	148	73	9.78	6.61	4.1	162	30.9	2430
29	F_7 185/2007	,,	,, ,, ,,	10.54	13.70	41.25	166	70	10.3	6.91	4.0	160	30.0	2310
30	F_7 187/2007	F_6 177/2006		9.74	12.49	40.72	149	71	10.1	6.39	4.1	163	30.0	2415
31	F_8 208/2007	F_7 193/2006	[{G. 83 x (G. 75 x 5844)} x {G. 83 x (G. 72 x Dendera)}]	10.01	13.04	41.34	150	74	9.97	7.10	4.1	161	31.5	2375
32	F_8 214/2007	F_7 195/2006	,, ,, ,,	10.47	13.52	41.00	158	77	9.85	7.13	4.1	161	30.6	2150
33	F_8 225/2007	Mixed of	[{G. 83 x (G. 75 x 5844)} x G. 80]	11.28	14.48	40.75	155	71	9.08	6.02	3.9	159	29.0	2250
34	F_8 229/2007	,,	,, ,, ,,	10.91	14.06	40.93	155	79	9.27	6.45	3.9	159	30.5	2215
35	F_8 235/2007	,,	,, ,, ,,	9.95	13.24	42.25	160	72	9.47	6.83	3.6	140	28.2	1950
36	F_9 256/2007	F_8 233/2006	[G. 91 x G. 90]	10.33	13.41	41.22	155	83	9.88	6.68	4.0	159	29.0	2110
37	F_9 264/2007	F_8 237/2006	,, ,,	11.53	14.90	41.00	159	76	10.0	6.71	4.0	159	29.0	2225
38	Mixed families of G. 90 x Aut.			10.94	14.30	41.51	154	77	9.37	6.38	4.1	162	30.5	2525
39	Giza 90			9.36	11.74	39.82	156	83	9.88	6.52	3.9	159	30.1	2625
40	Giza 80			9.03	11.66	41.00	149	63	9.52	6.49	3.9	159	31.2	2510
Mean				**10.52**	**13.30**	**40.12**	**151.5**	**76**	**10.0**	**7.00**	**4.0**	**159**	**30.6**	**2365**
L.S.D. at 5 %				1.70	2.17	1.08	8.20	---	0.74	0.50	---	---	---	---
L.S.D. at 1 %				2.24	2.85	1.42	10.77	---	0.98	0.66	---	---	---	---
Heritability in broad sense				55.6	10.7	84.80	77.10	---	67.9	79.39	---	---	---	---
Genetic gain at 5 % selection intensity				0.01	0.01	4.39	6.49	---	6.72	9.97	---	---	---	---

estimated for this trait, indicating that the genotypes were slightly affected by environmental fluctuation.

7. Lint index (LI)

It appeared from Table (1) that lint index ranged from 5.65 to 7.31 for F_7 167/2007 that belonged to the cross [{Giza 83 x (Giza 72 x Dedera)} x Giza 80] and F_6 126/2007 that belonged to the cross [{Giza 83 x (Giza 75 x 5844)} x Giza 85], respectively. Lint index showed that 22 out of 38 strains exceeded the check variety Giza 90. The increases were significant for 5 strains belonging to three crosses [Giza 90 x Pima S_{62} (24240)], [{Giza 83 x (Giza 75 x 5844)} x Giza 85] and [{Giza 83 x (Giza 75 x 5844)} x {Giza 83 x (Giza 72 x Dedera)}].

The broad sense heritability estimate was 79.39 % for this trait. High expected genetic advance (9.97 g) was observed for this trait. This high value indicated that the improvement of lint index is possible through selec

B. Fiber properties

1. Fiber fineness and maturity (Mic)

Results presented in Table (1) showed that 25 out of 38 strains had micronaire reading which exceeded that of the check varieties Giza 90 and Giza 80, which gave good micronaire values ranged from 4.0 to 4.2 micronaire unit. The desired micronaire reading for the genotypes of Middle and Upper Egypt (above 4.0) could be achieved through selection.

2. Hair weight (HW)

Hair weight measures fiber fineness in terms of millitex. The results in Table (1) revealed that this trait was nearly in the same line with that of micronaire reading.

3. Fiber length at 2.5 % span length (2.5 % SL)

All the strains could be considered in the long staple category (Table, 1). The longest fiber (32.5 mm) was achieved by F_5 104/2007 and F5 118/2007 while were belonging to two crosses [(Giza 83 x Pima S_6) x Dendera] and [Giza 91 x Pima S_{62} (24202)], while the shorter fiber (28.2 mm) was achieved by F_8 235/2007 which belonged to the cross [{Giza 83 x (Giza 75 x 5844)} x Giza 80]. On the other hand the commercial variety Giza 80 had higher fiber length (31.2 mm) than Giza 90 variety (30.1 mm).

4. Yarn strength (Y.St)

From Table (1), it is evident that the highest yarn strength was achieved by F_5 122/2007 belonging to cross [Giza 91 x Pima S_{62} (24202)] and F_6 160/2007 descending from the cross [{Giza 83 x (Giza 75 x 5844)} x Giza 90] which was 2670 and 2640, respectively. The remaining strains were lower in yarn strength than the check variety Giza 90. In the same time, the desired yarn strength measured for the strains of Middle and Upper Egypt could be achieved through selecting strains that exceed 2000(Y.St).

From the results obtained from Trial (A), it could be concluded that the strains F_5 83/2007 and F_6 126/2007 belonging to the crosses [Giza 90 x

Pima S_{62} (24240)] and [{Giza 83 x (Giza 75 x 5844)} x Giza 85], respectively exhibited increases for yield components than the check varieties Giza 90 and Giza 80. Meanwhile, these strains exhibited good fiber properties of Middle and Upper Egypt category. High and moderate estimates of heritability in broad sense (h^2_{bs}) and genetic advance under selection (G.S.) were computed for seed cotton, lint percentage, boll weight, seed index and lint index in trail (A); it could be stated that the environmental conditions slightly affected these characters.

The advanced strain test (Trial B)

Trial (B) included the evaluation of 20 genotypes that consisted of 18 strains descending from 13 crosses and two check cultivars, Giza 90 and Giza 80. All promising strains selected from trial (A) were tested one year later through. Trail (B) was carried out at five locations in Middle and Upper Egypt, i.e. Sids, El-Fayoum, El-Minia, Assiut and Sohag in order to study the performance of the promising genotypes under different environments.

A. Yield and its components

1. Seed cotton yield (SCY)

Table (2) showed that, 13 out of 18 genotypes exceeded the check cultivar Giza 90 and the commercial variety Giza 80 in seed cotton yield. The highest yield was achieved by the strain F_7 206/2006 belonged that to the cross [{Giza 83 x (Giza 75 x 5844)} x Giza 80], followed by F_7 193/2006 that belonged to the cross [{Giza 83 x (Giza 75 x 5844)} x{Giza 83 x (Giza 72 x Dendera)}, strain F_6 149/2006 that belonged to the cross [{Giza 83 x (Giza 72 x Dendera)} x Giza 91] and F_8 237/2006 that belonged to the cross [Giza 91 x Giza 90]; they exceeded the check variety Giza 90 by 1.74 k/f (16.0 %), 1.63 k/f (15.0 %), 1.54 k/f (14.0 %) and 1.54 k/f (14.0 %), respectively. On the other hand, the commercial variety Giza 80 gave the lowest seed cotton yield as compared with studied strains.

The interaction between genotypes and locations for seed cotton yield was significant. Therefore, these genotypes should be evaluated for their high yield ability under different environments for a number of years. **Bader *et al* (1999)** studied the two new Egyptian cotton cultivars and four commercial varieties at three locations and found that highly significant interaction between genotypes and locations was existed for seed cotton yield.

Heritability value of SCY for the combined data was 73.93 % indicating low environmental effects on this trait. **Ismail *et al* (1989)** found also, high heritability value of 76.0 % for seed cotton yield. However, a low expected genetic gain was estimated for this trait.

Table 2. The combined data across five locations of selected strains of cotton and cultivated varieties grown in trail (B) in 2008 season.

NO.	Strains	Parent	Origin	Yield (c/f)		L %	BW (g)	Ear (%)	SI (g)	LI (g)	Mic	HW	2.5 % SL	Y.St
				SCY	LY									
1	F_5 85/2006	F_4 56/2005	[{G. 83 x (G. 75 x 5844)} x G. 85]	11.74	14.59	39.5	151	82	10.53	6.87	4.0	160	30.6	2225
2	F_5 93/2006	F_4 61/2005	[{G. 83 x (G. 75 x 5844)} x Dendera]	11.71	14.11	38.2	148	86	10.58	6.39	4.3	168	30.5	2315
3	F_5 101/2006	F_4 70/2005	[{G. 83 x (G. 75 x 5844)} x G. 91]	11.75	14.49	39.2	148	86	9.79	6.20	4.4	170	28.7	2080
4	F_5 110/2006	F_4 76/2005	[G. 91 x G. 80]	11.79	14.77	39.8	152	83	10.49	6.89	4.4	172	31.6	2490
5	F_5 138/2006	F_4 90/2005	[{G. 83 x (G. 75 x 5844)} x G. 90]	11.76	14.43	39.0	146	90	10.18	6.47	4.1	162	30.6	2340
6	F_6 140/2006	F_5 95/2005	[{G. 83 x (G. 72 x Dendera)} x G. 80]	10.78	13.07	38.6	145	86	10.0	6.14	4.0	162	31.9	2510
7	F_5 149/2006	F_5 104/2005	[{G. 83 x (G. 72 x Dendera)} x G. 91]	12.23	14.89	38.7	144	87	10.32	6.54	4.3	170	30.6	2420
8	F_6 152/2006	„	„ „ „ „	11.76	14.52	39.3	145	90	10.13	6.43	4.3	172	29.7	2235
9	F_6 165/2006	F_5 124/2005	[{G. 83 x (G. 72 x Dendera)} x G. 85]	11.34	14.12	39.7	148	83	10.35	6.76	4.1	167	30.2	2240
10	F_6 177/2006	F_5 141/2005	[{(G.83xG.80)x G.75}x(G.83xPima S_6)]	11.20	13.89	39.4	147	84	10.19	6.39	4.2	166	30.9	2350
11	F_7 193/2006	F_6 161/2005	[{G. 83 x (G. 75 x 5844)} x {G. 83 x (G. 72 x Dendera)}]	12.32	15.31	39.5	151	86	10.87	6.04	4.3	170	29.9	2300
12	F_7 195/2006	F_6 162/2005	„ „ „	11.93	14.86	39.6	148	85	10.79	6.03	4.3	169	29.8	2220
13	F_7 202/2006	F_6 173/2005	[{G. 83 x (G. 75 x 5844)} x G. 80]	12.16	15.06	39.4	151	85	10.10	6.43	4.3	169	29.6	2165
14	F_7 204/2006	„	„ „ „	12.05	15.02	39.6	149	88	9.82	6.35	4.2	166	29.1	2100
15	F_7 206/2006	F_6 175/2005	„ „ „	12.43	15.88	40.6	147	87	9.96	6.67	4.0	157	29.9	2300
16	G. 90 x Aust	F_7 213/2005	[G. 90 x Aust]	11.25	14.15	40.0	148	86	9.72	6.36	4.2	163	30.7	2330
17	F_8 233/2006	F_7 226/2005	[G. 91 x G. 90]	11.70	14.30	38.8	152	89	9.87	6.23	4.2	163	30.0	2340
18	F_8 237/2006	F_7 227/2005	„ „	12.23	15.39	40.1	146	88	10.02	6.52	4.4	169	28.7	2210
19	Giza 90		[G. 83 x Dendera]	10.69	12.96	38.5	149	86	10.18	6.41	4.1	161	29.3	2210
20	Giza 80		[Giza 66 x Giza 73]	9.43	11.56	39.4	150	81	10.13	6.48	4.2	165	30.5	2375
Means				**11.61**	**14.37**	**39.4**	**149**	**86**	**10.2**	**6.53**	**4.2**	**166**	**30.1**	**2285**
L.S.D. at 5 %				1.97	3.46	0.67	7.82	---	0.27	0.23	---	---	---	---
L.S.D. at 1 %				N.S.	N.S.	0.88	10.27	---	0.36	0.30	---	---	---	---
Heritability in broad sense				73.93	77.77	76.47	30.68	---	75.37	78.93	---	---	---	---
Genetic gain at 5 % selection intensity				0.006	0.002	2.44	0.99	---	4.91	6.56	---	---	---	---

2. Lint cotton yield (LY)

Table (2) showed that mean lint cotton yield of all studied strains in trail (B) exceeded that of both control varieties Giza 90 and Giza 80. Mean lint yield ranged from 11.56 k/f for the commercial cultivar Giza 80 to 15.88 k/f for the strain F_7 206/2006 resulting from the cross [{Giza 83 x (Giza 75 x 5844)} x Giza 80]. The strain F_7 193/2006 that belonged to the cross [{Giza 83 x (Giza 75 x 5844)} x {Giza 83 x (Giza 72 x Dendera)], F_7 202/2006, F_7 204/2006 and 206/2006 that belonged to the cross [{Giza 83 x (Giza 75 x 5844)} x Giza 80] and strain F8 237/2006 that belonged to the cross [Giza 91 x Giza 90] showed significant increases for lint yield over the commercial variety Giza 80 ranging from 30 % to 37 %. Moreover, the genotype x environment interaction for this trait was significant.

High heritability value was computed for LY from combined data (77.77 %), indicatING high genetic variability for this trait. Similar findingS were recorded by Abou-Zahra *et al* (1986) and Mustafa *et al* (1995). Low expected genetic advance under selection was calculated for LY trait.

2. Boll weight (BW)

Results in Table (2) indicated that five strains, i.e. F_8 233/2006 from the cross [Giza 91 x Giza 90], F_5 110/2006 from the cross [Giza 91 x Giza 80], F_7 202/2006 from the cross [{Giza 83 x (Giza 75 x 5844)} x Giza 80], F_7 193/2006 from the cross [{Giza 83 x (Giza 75 x 5844)} x {Giza 83 x (Giza 72 x Dendera)}] and F_5 85/2006 from the cross [{Giza 83 x (Giza 75 x 5844)} x Giza 85] had heavier bolls than check cultivar Giza 90.

Highly significant interaction between genotype x location was recorded for BW character. In this respect, Hassan *et al* (2001), reported that boll weight for Giza 80 and Giza 83 WAS higher than the other genotypes under their study.

The broad sense heritability estimate of 30.68 % was obtained for this trait indicating that the environmental factors had higher effects on boll weight than seed cotton yield and lint yield in this study. The genetic gain from selection for BW trait was of low value (0.99 g /cycle).

3. Lint percentage (L %)

It appeared from Table (2) that all studied strains exceeded the check cultivar Giza 90 except the strain resulting from the cross [{Giza 83 x (Giza 75 x 5844)} x Dendera] for lint percentage. The increases in this trait were significant for 13 strains belonging to the 10 crosses. On the other hand, nine strains belonging to seven crosses revealed that lint percentage values exceeded that of the commercial cultivar Giza 80. Two strains exceeded significantly Giza 80 for lint percentage. These strains were F_7 206/2006 resulting from the cross [{Giza 83 x (Giza 75 x 5844)} x Giza 80] and F8 237/2006 from the cross [Giza 91 x Giza 90].

Significant interaction between genotypes and locations was shown for lint percentage. Mohamed (1991) and Mohamed *et al* (2003) reported that the Egyptian cotton varieties had a good material for lint percentage.

Heritability value estimated from combined analysis was 76.47 % for lint percentage trait, indicating that the environmental conditions affected slightly on this trait. The genetic gain from selection (2.44 %) was observed, indicating that selection is efficient for improvement of this character.

4. Earliness index (E %)

As shown in Table (2), six strains were earlier than the check cultivar Giza 90. It could be noted that all the earlier strains were derived from the crosses [{Giza 83 x (Giza 75 x 5844)} x Giza 85], [Giza 91 x Giza 80], [{Giza 83 x (Giza 72 x Dendera)} x Giza 85], [{(Giza 83 x Giza 80) x Giza 75} x (Giza 83 x pima s_6)], [{Giza 83 x (Giza 75 x 5844)} x {Giza 83 x (Giza 72 x Dendera)}] and [{Giza 83 x (Giza 75 x 5844)} x Giza 80]. Meanwhile, the mean earliness index of the commercial cultivar Giza 80 was higher than all the crosses.

5. Seed index (SI)

It is clear from Table (2) that means of SI trait ranged from 9.72 to 10.87 g. The highest values of seed index (10.87 and 10.87 g) were recorded by the two strains F_7 193/2006 and F_7 195/2006, respectively belonging to the cross [{Giza 83 x (Giza 75 x 5844)} x {Giza 83 x (Giza 72 x Dendera)}], followed by the F_5 93/2006 resulting from the cross [{Giza 83 x (Giza 75 x 5844)} x Dendera], F_5 85/2006 from the cross [{Giza 83 x (Giza 75 x 5844)} x Giza 85] and F5 110/2006 from the cross [Giza 91 x Giza 80]. While strain resulted from the cross [Giza 90 x Aust.] had the lowest SI value (9.72 g). On the other hand, the control cultivars Giza 90 and Giza 80 recorded means of 10.18 and 10.13 g for seed index, respectively.

Highly significant interaction between genotypes x locations was noticed for seed index. Heritability value of 75.37 % was computed for this trait, indicating that the genotypes were slightly affected by environmental fluctuation. A genetic gain from selection (4.91g per cycle) was observed, indicating that selection is possible for improvement of this character. These results are in agreement with those obtained by Mustafa *et al* (1995).

6. Lint index (LI)

Results in Table (2) indicated that means of lint index ranged from 6.14 to 7.04 g for the two strains F_6 140/2006 to F_7 193/2006, respectively. Six strains showed significantly higher values of lint index than the check cultivar Giza 90. These strains were F_5 110/2006 from the cross [Giza 91 x Giza 80], F_5 85/2006 from the cross [{Giza 83 x (Giza 75 x 5844)} x Giza 85], F_6 165/2006 from the cross [{Giza 83 x (Giza 72 x Dendera)} x Giza 85], F_7 206/2006 from the cross [{Giza 83 x (Giza 75 x 5844)} x Giza 80], F_7 193/2008 and F_7 195/2006 from the cross [{Giza 83 x (Giza 75 x 5844)} x {Giza 83 x (Giza 72 x Dendera)}]. Insignificant interaction between

genotypes x locations was noticed for this trait. High heritability value for lint index was computed (78.93 %), indicating that the environments slightly influenced this trait. Expected genetic gain from selection (6.56 g /cycle) was observed for lint index, indicating that selection is possible for the improvement of this character.

B. Fiber properties

1. **Fiber fineness and maturity (Mic)**

   Results in Table (2) showed that micronaire reading of all studied strains the all ranged from 4.0 to 4.4 mic. The strains F_5 85/2006 from the cross [{Giza 83 x (Giza 75 x 5844)} x Giza 85], F_6 140/2006 from the cross [{Giza 83 x (Giza 72 x Dendera)} x Giza 80] and F_7 206/2006 from the cross [{Giza 83 x (Giza 75 x 5844)} x Giza 80] had finest fiber (4.0 mic.), while the strains F_6 138/2006 from the cross [{Giza 83 x (Giza 75 x 5844)} x Giza 90] and F6 165/2006 from the cross [{Giza 83 x (Giza 72 x Dendera)} x Giza 85] had the same micronaire reading as check cultivar Giza 90 (4.1 mic). On the other hand, the remaining strains recorded the higher micronaire readings than the check variety Giza 90. Desirable micronaire reading for the strains of Middle and Upper Egypt were above 4.0 mic.

2. **Hair weight (HW)**

   Hair weight estimates (Table, 2) showed nearly the same trend as the micronaire reading.

3. **Fiber length at 2.5 % span length (2.5 % SL)**

   Table (2) showed that fiber length in all genotypes under this study ranged from 28.7 to 31.9 mm. In general, staple length of all genotypes could be considered belonging to the long staple category.

4. **Yarn strength (Y.St)**

   From Table (2), results showed that the highest yarn strength was achieved by the strain F_6 140/2006 from the cross [{Giza 83 x (Giza 72 x Dendera)} x Giza 80] followed by the strain F_5 110/2006 from the cross [Giza 91 x Giza 80] and the strain F6 149/2006 from the cross [{Giza 83 x (Giza 72 x Dendera)} x Giza 91]. These strains exceeded the check cultivars Giza 90 and Giza 80. It is evidently to notice that increases in these strains over check cultivars Giza 90 ranged from 210 units (F_6 149/2006) to 300 units (F_6 140/2006).

The results obtained in trial (B) indicated that the crosses [{Giza 83 x (Giza 75 x 5844)} x Giza 80], [Giza 91 x Giza 90] and [{Giza 83 x (Giza 75 x 5844)} x {Giza 83 x (Giza 72 x Dendera)}] have almost shown increases for yield, its components and fiber properties over the check cultivar Giza 90

Regarding the best three crosses comparing with the cultivar Giza 90 for combined data of trial (B) across different locations (Table, 2), it could be concluded that the promising strains belonging to the cross [{Giza 83 x

(Giza 75 x 5844)} x Giza 80] exceeded those belonging to the cross [{Giza 83 x (Giza 75 x 5844)} x {Giza 83 x (Giza 72 x Dendera)}], [Giza 91 x Giza 90] and the cultivar Giza 90 in seed cotton yield by 0.9 %, 1.6 % and 16.3 %, respectively. At the same time, these strains achieved increases in lint cotton yield by 3.7 %, 3.2 % and 22.5 %, respectively and showed desirable fiber characters.

High heritability values in broad sense were recorded from seed cotton yield and lint yield and low values for boll weigh, indicating that the environmental factors had more effect on boll weight than other traits in this study.

The interaction between genotype x locations for yield traits was significant, suggesting that the performance of these crosses varied from location to another. Therefore, such material should be evaluated for a number of years at different locations.

Results in trails (A and B) indicated that families resulting from the crosses [{Giza 83 x (Giza 75 x 5844)} x Giza 80], [Giza 91 x Giza 90] and [{Giza 83 x (Giza 75 x 5844)} x {Giza 83 x (Giza 72 x Dendera)}] are promising and therefore should be selected for further use in the breeding programs.

C. Molecular studies

Within the last few years restriction fragment length polymorphism (RFLP) technology has been applied to several cotton species to study evolution, population genetics, phylogenetic relationship and genome mapping (Shappley *et al* 1996 and Yu *et al* 1997), but was found to create low variation in cotton compared to other plant taxa (Brubaker and Wendel 1994).

Plant molecular geneticists currently use RAPD markers routinely to identify genetic variations (Keil and Griffin 1994, Perron *et al* 1995, Lashermes *et al* 1996, *Irwin et al* 1998 and Sun *et al* 1998).

D. Randomly amplified polymorphic DNA analysis (RAPD)

In the present study, the genetic variability among different genotypes of *Gossypium barbadense* based on RAPD analysis has been studied. Initial screening of 18 random primers with five genotypes of cotton resulted in ten primers that could produce informative and polymorphic products resolvable by agarose gel electrophoresis.

Table 3. Molecular weights (MW) in base pairs (bp) of amplified DNA fragments that were produced by A01 primer with five different cotton genotypes.

MW Approx band size in bp	Giza 80	[{G. 83 x (G.75 x 5844)} x G.80]	[{G.83 x (G.75 x 5844)} x {G.83 x (G.72 x Den.)}]	[G. 91 x G. 90]	Giza 90
1615	-	+	-	-	+
1205	+	+	+	+	+
1019	+	+	-	+	+
862	+	+	+	+	+
700	-	+	-	-	-
617	-	-	-	-	+
423	+	+	+	+	+
344	+	+	-	+	-
316	+	+	-	+	+
246	-	+	-	-	-

+ : present band.
- : absent band.

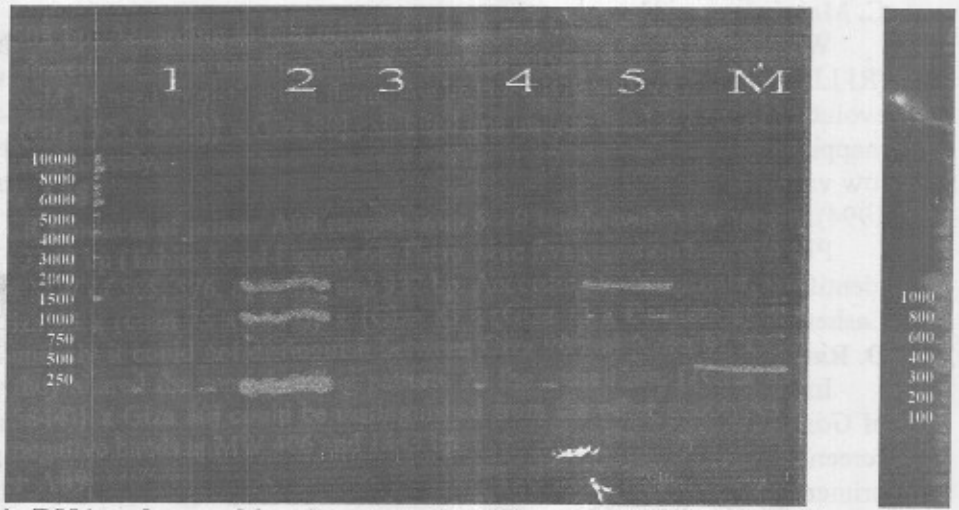

Fig. 1: DNA polymorphism based on RAPD analysis for five genotypes against primer A01

M : Marker
1 : Giza 80
2 : [{G. 83 x (G.75 x 5844)} x G.80]
3 : [{G.83 x (G.75 x 5844)} x {G.83 x (G.72 x Den.)}]
4 : [G. 91 x G. 90]
5 : Giza 90

Primer A01

The PCR products of this primer ranged from 3 bands in [{Giza 83 x (Giza 75 x 5844)} x {Giza 83 x (Giza 72 x Dendera)}] to 9 bands in [{Giza 83 x (Giza 75 x 5844)} x Giza 80] with a molecular weight (MW) ranging from 246 to 1615 bp (Table, 3 and Figure 1). This primer produced three common bands in all genotypes at MW of 423, 862, and 1205 bp. The other bands were polymorphic as they were present in some genotypes and absent in the others.

Some genotypes had some specific unique bands and could be used to distinguish them. For instance the genotypes [{Giza 83 x (Giza 75 x 5844)} x Giza 80] showed two unique bands of MW 246 and 700 bp. Also, Giza 90 exhibited one unique band at MW of 617 bp.

Meanwhile, the genotype resulting from the cross [{Giza 83 x (Giza 75 x 5844)} x {Giza 83 x (Giza 72 x Dendera)}] could be distinguished from the other genotypes by two unique negative molecular markers at MW 316 and 1019 bp.

Primer A02

The obtained results of primer A02 are illustrates in Table (4) and Figure (2). The total number of bands per genotype was variable, where the lowest number was 4 bands in Giza 80 and [{Giza 83 x (Giza 75 x 5844)} x {Giza 83 x (Giza 72 x Dendera)}], while the highest number was 12 bands in [Giza 91 x Giza 90]. Some genotypes exhibited some specific bands and could be used to distinguish among them. For instance in Giza 80, one band at MW of about 793 bp was absent, while was present in all other genotypes. The absence of this band can be considered as negative genetic marker. Otherwise, the cross [Giza 91 x Giza 90] could be distinguished from the other genotypes by the existence of one unique band at MW 291 bp. (a positive molecular marker). There were three common bands in all genotypes at MW of 1108, 1256 and 1424 bp.

Primer A03

The PCR products of primer A03 and analysis of these products are illustrated in Table (5) and Figure (3). This primer produced 5.9 bands for the studied genotypes with MW ranging from 358 to 1256 bp. The results indicated two common bands in all

Table 4. Molecular weights (MW) in base pairs (bp) of amplified DNA fragments that were produced by A02 primer with five different cotton genotypes.

MW Approx band size in bp	Giza 80	[{G. 83 x (G.75 x 5844)} x G.80]	[{G.83 x (G.75 x 5844)} x {G.83 x (G.72 x Den.)}]	[G. 91 x G. 90]	Giza 90
1615	-	+	-	+	+
1424	+	+	+	+	+
1256	+	+	+	+	+
1108	+	+	+	+	+
937	-	+	-	+	+
793	-	+	+	+	+
700	+	+	-	+	-
671	-	+	-	+	-
568	-	+	-	-	+
480	-	+	-	+	+
389	-	-	-	+	+
344	-	+	-	+	+
291	-	-	-	+	-

+ : present band.
- : absent band.

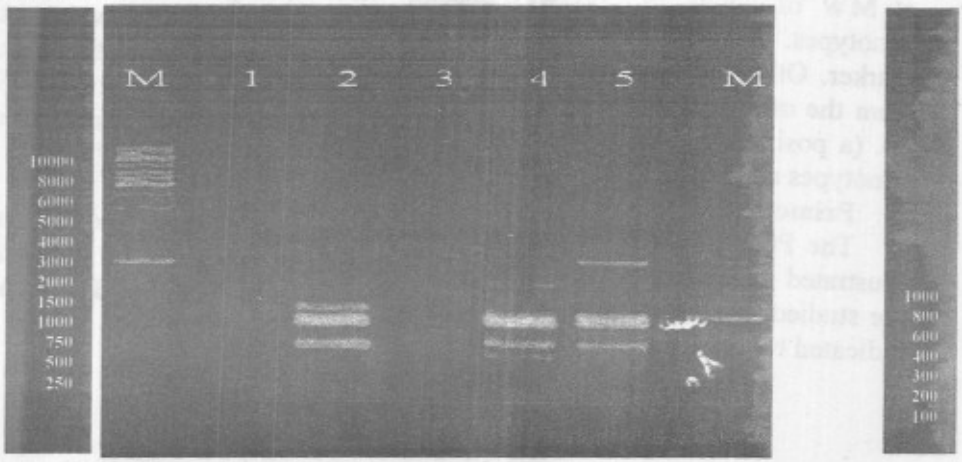

Fig. 2: DNA polymorphism based on RAPD analysis for five genotypes against primer A02

M : Marker
1 : Giza 80
2 : [{G. 83 x (G.75 x 5844)} x G.80]
3 : [{G.83 x (G.75 x 5844)} x {G.83 x (G.72 x Den.)}]
4 : [G. 91 x G. 90]
5 : Giza 90

Table 5. Molecular weights (MW) in base pairs (bp) of amplified DNA fragments that were produced by A03 primer with five different cotton genotypes.

MW Approx band size in bp	Giza 80	[{G. 83 x (G.75 x 5844)} x G.80]	[{G.83 x (G.75 x 5844)} x {G.83 x (G.72 x Den.)}]	[G. 91 x G. 90]	Giza 90
1256	-	+	+	+	+
1156	-	+	+	+	+
827	+	+	+	+	+
761	-	+	+	+	+
671	-	+	-	+	+
592	-	-	-	+	+
544	+	+	+	+	+
501	+	-	-	-	-
480	-	-	-	-	+
442	+	+	-	+	-
358	+	+	-	+	-

+ : present band.
- : absent band.

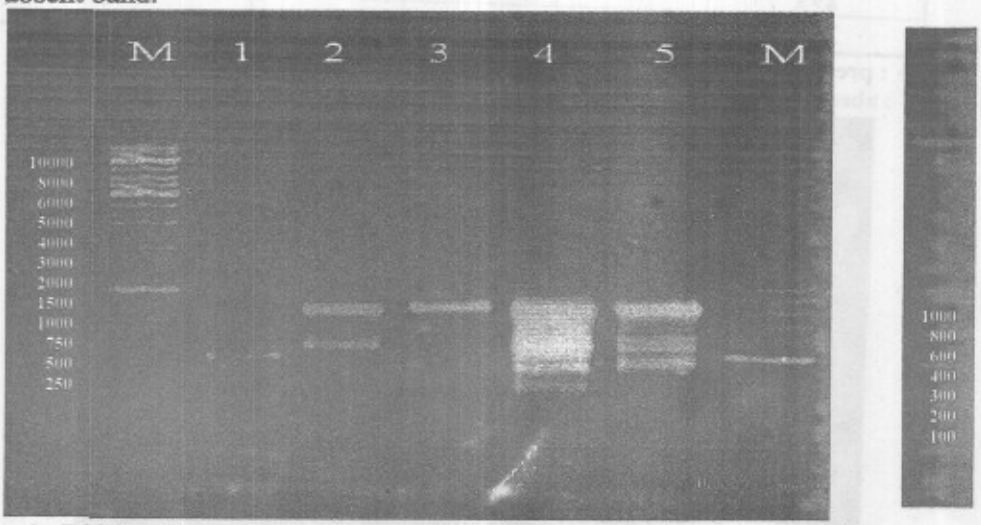

Fig. 3: DNA polymorphism based on RAPD analysis for five genotypes against primer A03

M : Marker
1 : Giza 80
2 : [{G. 83 x (G.75 x 5844)} x G.80]
3 : [{G.83 x (G.75 x 5844)} x {G.83 x (G.72 x Den.)}]
4 : [G. 91 x G. 90]
5 : Giza 90

Table 6. Molecular weights (MW) in base pairs (bp) of amplified DNA fragments that were produced by A04 primer with five different cotton genotypes.

MW Approx band size in bp	Giza 80	[{G. 83 x (G.75 x 5844)} x G.80]	[{G.83 x (G.75 x 5844)} x {G.83 x (G.72 x Den.)}]	[G. 91 x G. 90]	Giza 90
1615	+	+	+	+	+
1424	+	+	+	+	+
1256	+	+	+	+	+
899	+	+	+	+	+
793	+	+	+	-	+
700	+	+	+	+	+
671	+	+	+	+	+
592	+	+	+	+	+
522	+	+	+	-	-
460	+	+	+	+	+
423	+	-	+	-	-
406	-	-	-	+	-
374	-	+	+	+	+
344	+	+	+	+	+
291	+	+	+	+	+
256	-	-	-	-	+

+ : present band.
- : absent band.

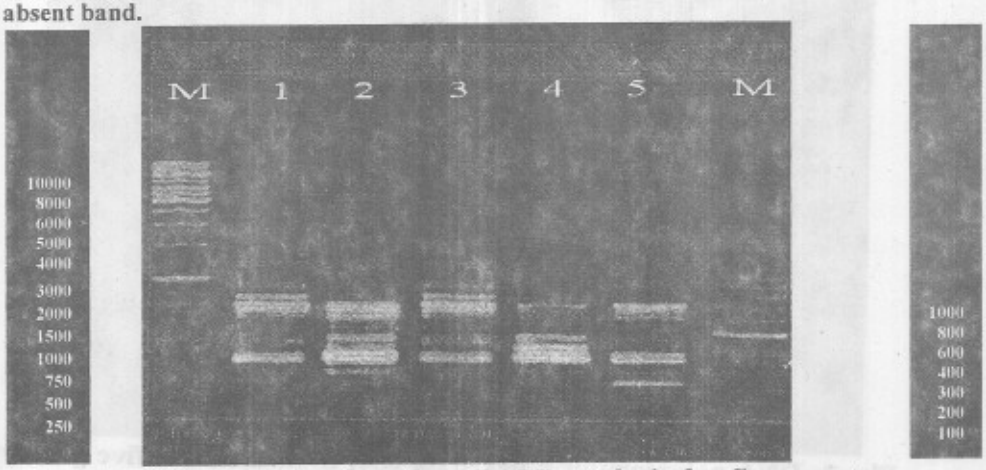

Fig. 4: DNA polymorphism based on RAPD analysis for five genotypes against primer A04

M : Marker
1 : Giza 80
2 : [{G. 83 x (G.75 x 5844)} x G.80]
3 : [{G.83 x (G.75 x 5844)} x {G.83 x (G.72 x Den.)}]
4 : [G. 91 x G. 90]
5 : Giza 90

genotypes with MW of 544 and 827 bp. One unique positive band was found in Giza 90 with MW of 480 bp.

Meanwhile, Giza 80 variety could be distinguished from the other genotypes by the four unique bands three of them were considered as negative markers at MW of 761, 1156 and 1256 bp and the other band was a positive one with MW of 501 bp.

Primer A04

The results of RAPD analysis using primer A04 were illustrated in Table (6) and Figure (4).This primer produced 12 -14 bands for the studied genotypes with MW ranging from 256 to 1615. There were ten common bands in all genotypes with MW of 291, 344, 460, 592, 671, 700, 899, 1256, 1424 and 1616 bp.Some genotypes had some specific bands which could be used to distinguish them. Giza 80 and the cross [Giza 91 x Giza 90] showed one negative unique band at MW of 374 and 793 bp, respectively. Meanwhile, Giza 90 and [Giza 91 x Giza 90] had one positive unique band at MW of 256 and 406 bp, respectively.

Primer A05

The obtained results of primer A05 are illustrated in Table (7) and Figure (5). This primer produced 4 – 7 bands for the studied genotypes with MW ranging from 326 to 1508 bp. There were three common bands in all genotypes at MW of 762, 1322 and 1508 bp. According to this primer Giza 80 and Giza 90 were identical, where they shared the same banding pattern. Some genotypes had some specific bands and could be used to distinguish them. For instance [Giza 91 x Giza 90] and [{Giza 83 x (Giza 75 x 5844)} x Giza 80] exhibited one unique band at MW of 326 and 892 bp, respectively.

Primer A08

The PCR products of primer A08 ranged from 5 - 9 bands with MW ranging from 286 to 2140 bp (Table, 8 and Figure, 6). There were five common bands in all genotypes at MW of 505, 576, 657, 817 and 932 bp. According to this primer, Giza 80 and [{Giza 83 x (Giza 75 x 5844)} x {Giza 83 x (Giza 72 x Dendera)}] were identical. Similarly it could not distinguish between Giza 90 and [Giza 91 x Giza 90], where they shared the same banding pattern. At the same time, [{Giza 83 x (Giza 75 x 5844)} x Giza 80] could be distinguished from the other genotypes by two unique negative bands at MW 406 and 1443 bp.

Primer A09

The results of RAPD analysis using primer A09 were illustrated in Table (9) and Figure (7). The total number of bands varied with the lowest number of 4 bands shown in Giza 80 and the highest number (12 bands) shown in the cross [{Giza 83 x (Giza 75 x 5844)} x {Giza 83 x (Giza 72 x Dendera)}]. There were three common bands in all genotypes at MW of 382, 462 and 560 bp. One unique positive band was found in the cross [{Giza 83 x (Giza 75 x 5844)} x {Giza 83 x (Giza 72 x Dendera)}], while there were three unique negative bands, two of them were found in Giza 80 at MW 315 and 646 bp and other one in [Giza 91 x Giza 90] at MW 782 bp.

Table 7. Molecular weights (MW) in base pairs (bp) of amplified DNA fragments that were produced by A05 primer with five different cotton genotypes.

MW Approx band size in bp	Giza 80	[{G. 83 x (G.75 x 5844)} x G.80]	[{G.83 x (G.75 x 5844)} x {G.83 x (G.72 x Den.)}]	[G. 91 x G. 90]	Giza 90
1508	+	+	+	+	+
1322	+	+	+	+	+
892	+	-	+	+	+
782	+	+	+	+	+
443	-	+	+	+	-
372	-	+	+	+	-
326	-	-	-	+	-

+ : present band.
- : absent band.

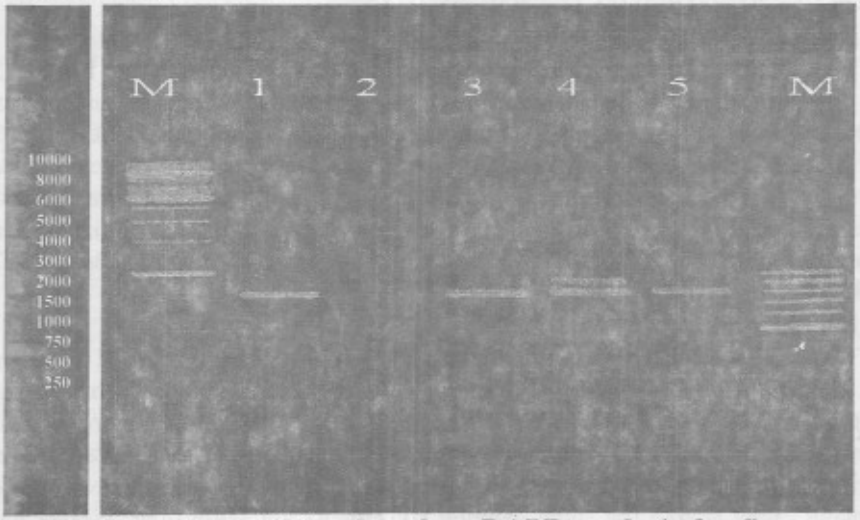

Fig. 5: DNA polymorphism based on RAPD analysis for five genotypes against primer A05

M : Marker
1 : Giza 80
2 : [{G. 83 x (G.75 x 5844)} x G.80]
3 : [{G.83 x (G.75 x 5844)} x {G.83 x (G.72 x Den.)}]
4 : [G. 91 x G. 90]
5 : Giza 90

Table 8. Molecular weights (MW) in base pairs (bp) of amplified DNA fragments that were produced by A08 primer with five different cotton genotypes.

MW Approx band size in bp	Giza 80	[{G. 83 x (G.75 x 5844)} x G.80]	[{G.83 x (G.75 x 5844)} x {G.83 x (G.72 x Den.)}]	[G. 91 x G. 90]	Giza 90
2140	+	-	+	-	-
1719	+	-	+	-	-
1443	+	-	+	+	+
1266	-	-	-	+	+
932	+	+	+	+	+
817	+	+	+	+	+
657	+	+	+	+	+
576	+	+	+	+	+
505	+	+	+	+	+
406	+	-	+	+	+
286	-	-	-	+	+

+ : present band.
- : absent band.

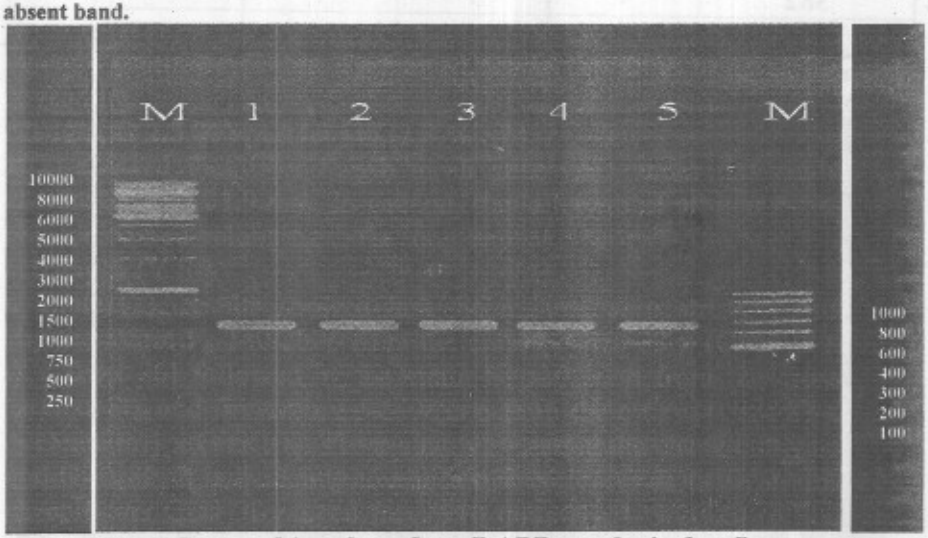

Fig. 6: DNA polymorphism based on RAPD analysis for five genotypes against primer A08

M : Marker
1 : Giza 80
2 : [{G. 83 x (G.75 x 5844)} x G.80]
3 : [{G.83 x (G.75 x 5844)} x {G.83 x (G.72 x Den.)}]
4 : [G. 91 x G. 90]
5 : Giza 90

Table 9. Molecular weights (MW) in base pairs (bp) of amplified DNA fragments that were produced by A09 primer with five different cotton genotypes.

MW Approx band size in bp	Giza 80	[{G. 83 x (G.75 x 5844)} x G.80]	[{G.83 x (G.75 x 5844)} x {G.83 x (G.72 x Den.)}]	[G. 91 x G. 90]	Giza 90
1851	-	-	+	+	+
1604	-	-	+	+	-
1457	-	-	+	-	-
1147	-	-	+	-	+
994	-	+	+	-	+
903	-	+	+	-	+
782	+	+	+	-	+
646	-	+	+	+	+
560	+	+	+	+	+
462	+	+	+	+	+
382	+	+	+	+	+
315	-	+	+	+	+

+ : present band.
- : absent band.

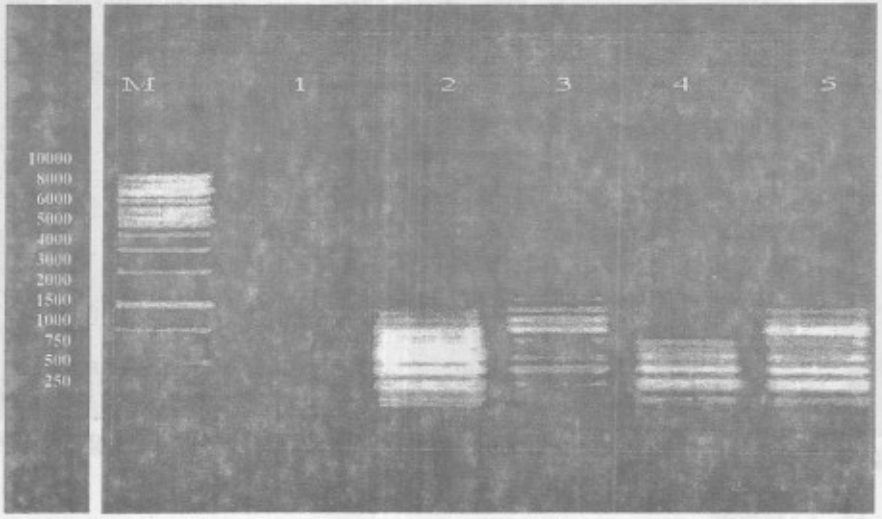

Fig. 7: DNA polymorphism based on RAPD analysis for five genotypes against primer A09

M : Marker
1 : Giza 80
2 : [{G. 83 x (G.75 x 5844)} x G.80]
3 : [{G.83 x (G.75 x 5844)} x {G.83 x (G.72 x Den.)}]
4 : [G. 91 x G. 90]
5 : Giza 90

Primer A11

The products of primer A11 and analysis of these products were illustrated in Table (10) and Figure (8). The results indicated that there were three common bands in all genotypes with MW of 782, 903and 1093 bp. Some genotypes had some specific bands and could be used to distinguish them. For instance [{Giza 83 x (Giza 75 x 5844)} x Giza 80] has one unique band at MW of 508 bp. Meanwhile, Giza 80 variety could be distinguished from the other genotypes by the existence of two unique negative bands at MW 1682 and 2137 bp.

Primer A12

The obtained results of primer A12 are illustrated in Table (11) and Figure (9). This primer produced a range of 1- 6 bands among the studied genotypes with MW ranging from 196 to 746 bp. Bands were polymorphic as they were present in some genotypes and absent in the others. Some genotypes had some specific bands and could be used to distinguish them. For instance [Giza 91 x Giza 90] has two unique bands at MW of 196 and 746 bp. Also, Giza 90 variety exhibited two unique bands at MW of 300 and 462 bp. Three unique positive bands were found in the cross [{Giza 83 x (Giza 75 x 5844)} x {Giza 83 x (Giza 72 x Dendera)}] with MW of 331, 485 and 580 bp. Meanwhile, [{Giza 83 x (Giza 75 x 5844)} x Giza 80] could be distinguished from the other genotypes by the existence of three unique bands, Two of them were considered as positive markers at MW of 236 and 420 bp and the other was a negative one with MW of 382 bp.

Primer A14

The results of RAPD produced using this primer A14 ranged from 4 to 9 bands with MW ranging from 163 to 1600 bp (Table, 12 and Figure, 10]. There were two common bands in all genotypes at MW of 584 and 790 bp. Some genotypes had some specific bands that could be used to distinguish among such genotypes. For instance Giza 90 and [{Giza 83 x (Giza 75 x 5844)} x Giza 80] shared one positive unique band at MW of 966 and 1600 bp, respectively. The same genotypes shared one negative unique band at MW of 1222 and 163 bp, respectively.

Table 10. Molecular weights (MW) in base pairs (bp) of amplified DNA fragments that were produced by A11 primer with five different cotton genotypes.

MW Approx band size in bp	Giza 80	[{G. 83 x (G.75 x 5844)} x G.80]	[{G.83 x (G.75 x 5844)} x {G.83 x (G.72 x Den.)}]	[G. 91 x G. 90]	Giza 90
2137	-	+	+	+	+
1682	-	+	+	+	+
1093	+	+	+	+	+
903	+	+	+	+	+
782	+	+	+	+	+
711	-	+	-	-	+
646	-	-	+	+	-
508	-	+	-	-	-
462	+	-	-	+	+
382	-	-	+	+	+
315	-	-	+	+	+
225	-	-	+	+	-

+ : present band.
- : absent band.

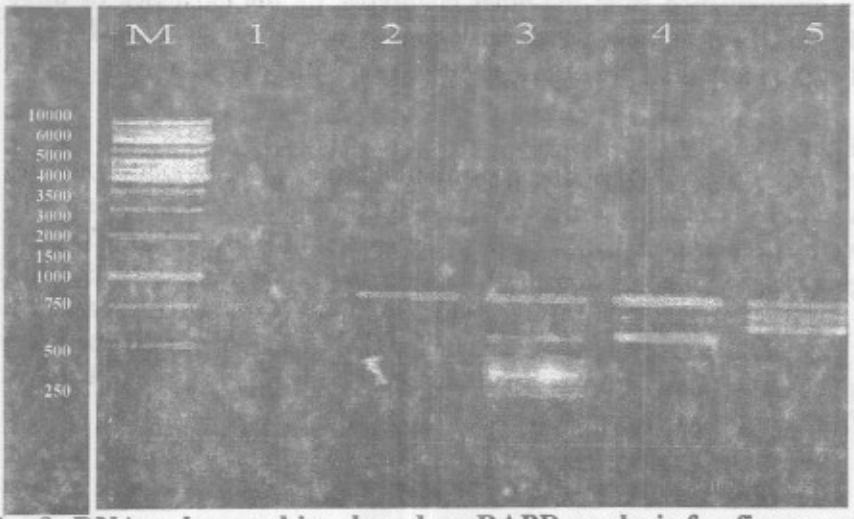

Fig. 8: DNA polymorphism based on RAPD analysis for five genotypes against primer A11

M : Marker
1 : Giza 80
2 : [{G. 83 x (G.75 x 5844)} x G.80]
3 : [{G.83 x (G.75 x 5844)} x {G.83 x (G.72 x Den.)}]
4 : [G. 91 x G. 90]
5 : Giza 90

Table 11. Molecular weights (MW) in base pairs (bp) of amplified DNA fragments that were produced by A12 primer with five different cotton genotypes.

MW Approx band size in bp	Giza 80	[{G. 83 x (G.75 x 5844)} x G.80]	[{G.83 x (G.75 x 5844)} x {G.83 x (G.72 x Den.)}]	[G. 91 x G. 90]	Giza 90
746	-	-	-	+	-
616	-	+	+	-	-
560	-	-	+	-	-
485	-	-	+	-	-
462	-	-	-	-	+
420	-	+	-	-	-
382	+	-	+	+	+
331	-	-	+	-	-
300	-	-	-	-	+
273	-	-	+	+	-
236	-	+	-	-	-
196	-	-	-	+	-

+ : present band.
- : absent band.

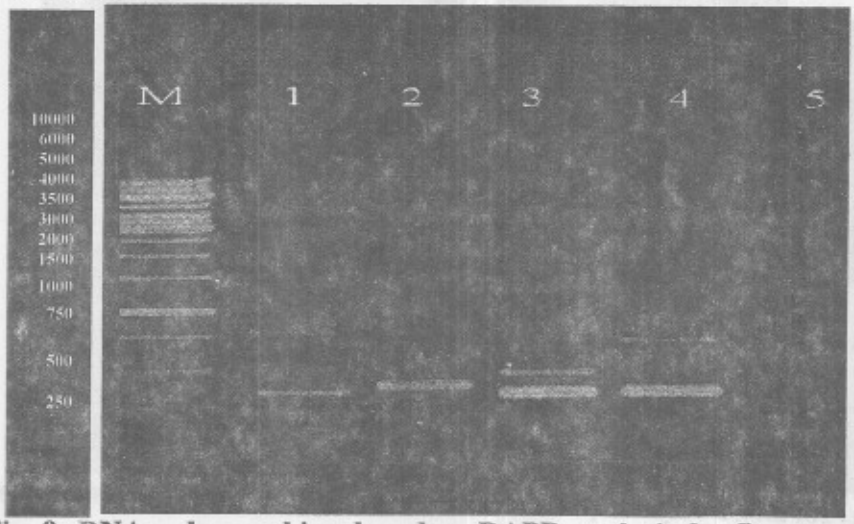

Fig. 9: DNA polymorphism based on RAPD analysis for five genotypes against primer A12

M : Marker
1 : Giza 80
2 : [{G. 83 x (G.75 x 5844)} x G.80]
3 : [{G.83 x (G.75 x 5844)} x {G.83 x (G.72 x Den.)}]
4 : [G. 91 x G. 90]
5 : Giza 90

Table 12. Molecular weights (MW) in base pairs (bp) of amplified DNA fragments that were produced by A14 primer with five different cotton genotypes.

MW Approx band size in bp	Giza 80	[{G. 83 x (G.75 x 5844)} x G.80]	[{G.83 x (G.75 x 5844)} x {G.83 x (G.72 x Den.)}]	[G. 91 x G. 90]	Giza 90
1600	-	+	-	-	-
1398	-	-	-	+	+
1222	+	+	+	+	-
966	-	-	-	-	+
790	+	+	+	+	+
668	-	-	-	+	+
584	+	+	+	+	+
510	-	+	-	+	-
319	-	+	-	+	+
228	-	+	-	+	-
163	+	-	+	+	+

+ : present band.
- : absent band.

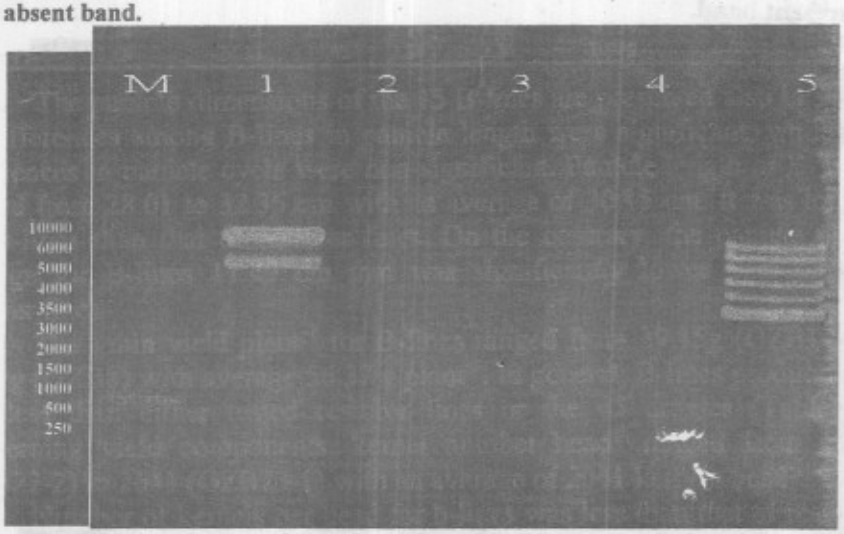

Fig. 10: DNA polymorphism based on RAPD analysis for five genotypes against primer A14

M : Marker
1 : Giza 80
2 : [{G. 83 x (G.75 x 5844)} x G.80]
3 : [{G.83 x (G.75 x 5844)} x {G.83 x (G.72 x Den.)}]
4 : [G. 91 x G. 90]
5 : Giza 90

Unique markers for cotton genotypes by RAPD – PCR analysis

Considering all the data gained in the present study from the RAPD – PCR analysis, it can be concluded that the studied genotypes might be identified through the studied criteria. Some molecular marker was detected for all of the studied genotypes. When the data of the studied 10 primers were combined, complete identification was obtained for the studied genotypes. Some of these primers were more successful in genotype identification such as A01, A03, A04, A09, A12 and A14, where they generated a higher number of RAPD markers than other primers (Table, 13).

From the observed results, it could be concluded that group A of all primers (B, C, D and Z) was more successful than other group for matching with the studied cotton genotypes. Moreover, primer A12 was found to be the most efficient primer since it could distinguish four genotypes 3 of these belonging to the crosses [{Giza 83 x (Giza 75 x 5844)} x Giza 80], [{Giza 83 x (Giza 75 x 5844)} x {Giza 83 x (Giza 72 x Dendera)}], [Giza 91 x Giza 90] and Giza 90 by the existing of unique markers.

As seen from Table (13), there were 41 specific markers for cotton genotypes scored and illustrated. These results indicated that the RAPD - PCR exhibited different unique molecular markers, as previously mentioned. For instance, primer A01 can distinguish three genotypes by distinct bands at MW of about 617 bp for Giza 90, 316 bp and 1019 bp for genotypes from [{Giza 83 x (Giza 75 x 5844)} x {Giza 83 x (Giza 72 x Dendera)}], also at MW 246 and 700 bp for genotypes from [{Giza 83 x (Giza 75 x 5844)} x Giza 80].

Genetic similarity and phylogenetic tree using RAPD – PCR analysis

The genetic similarity and phylogenetic tree have categorized the five studied cotton genotypes into two major groups (Table, 14 and Figure 11). The first group contained the two genotypes Giza 80 and that resulted from the cross [{Giza 83 x (Giza 75 x 5844)} x {Giza 83 x (Giza 72 x Dendera)}] which were in the same cluster with a genetic similarity of 73 %.

The second group was divided into two subgroups. One of these subgroups contains two genotypes [Giza 91 x Giza 90] and Giza 90 with a genetic similarity of 80 %; this close similarity between these two different genotypes should be a matter of future research to explain the close relationship between these genotypes which, fall in different Egyptian cotton categories. As shown in Table (14) the genetic similarity ranged from 65.7 % (between Giza 80 and Giza 90) to 80 % (between [Giza 91 x Giza 90] and Giza 90).

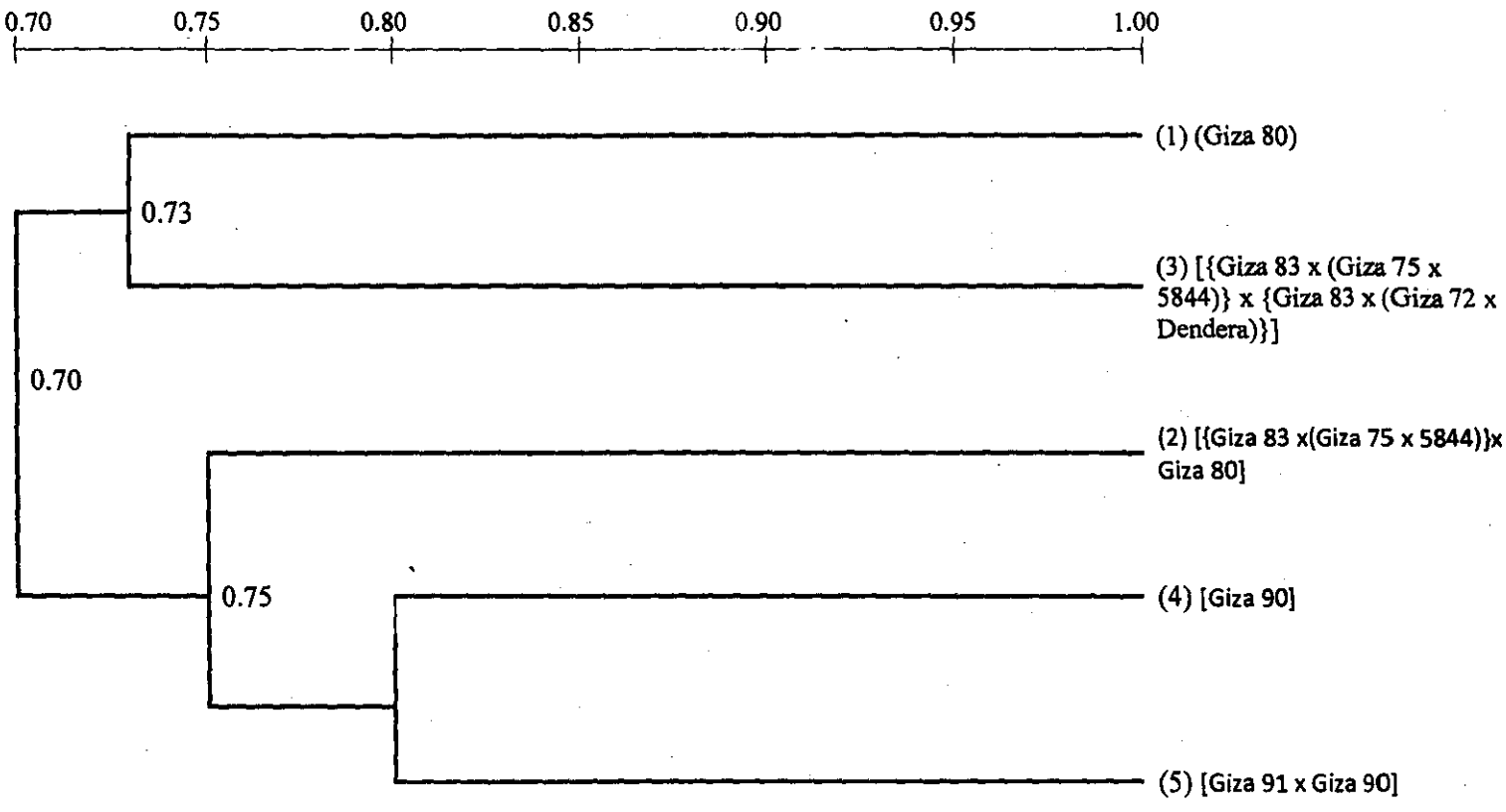

Figure 11. Dendrogram demonstrating the relationships among five cotton genotypes using RAPD – data.

Table 13. Specific molecular markers and their MW for cotton genotypes produced by different primers of RAPD – PCR analysis.

Primers	Giza 80	[{G. 83 x (G.75 x 5844)} x G.80]	[{G.83 x (G.75 x 5844)} x {G.83 x (G.72 x Den.)}]	[G. 91 x G. 90]	Giza 90
A01	-	246 (+) 700 (+)	316 (-) 1019 (-)	-	617 (+)
A02	793 (-)	-	-	291 (+)	-
A03	501 (+) 761 (-) 1156 (-) 1256 (-)	-	-	-	480 (+)
A04	374 (-)	-	-	406 (+) 793 (-)	256 (+)
A05	-	892 (-)	-	326 (+)	-
A08	-	406 (-) 1443 (-)	-	-	-
A09	315 (-) 646 (-)	-	1457 (+)	782 (-)	-
A11	1682 (-) 2137 (-)	508 (+)	-	-	-
A12	-	236 (+) 382 (-) 420 (+)	331 (+) 485 (+) 560 (+)	196 (+) 746 (+)	300 (+) 462 (+)
A14	-	163 (-) 1600 (+)	-	-	966 (+) 1222 (-)

+ : Positive marker, which is absent in all genotypes and present in one genotype.
- : Negative marker, which is present in all genotypes and absent in one genotype.

Table 14. Matrix of the genetic similarity (%) estimated among the studied five cotton genotypes based on RAPD – PCR analysis.

MW Approx band size in bp	Giza 80	[{G. 83 x (G.75 x 5844)} x G.80]	[{G.83 x (G.75 x 5844)} x {G.83 x (G.72 x Den.)}]	[G. 91 x G. 90]	Giza 90
Giza 80	---				
[{G. 83 x (G.75 x 5844)} x G.80]	67.7				
[{G.83 x (G.75 x 5844)} x {G.83 x (G.72 x Den.)}]	73.0	70.3			
[G. 91 x G. 90]	67.6	75.8	73.9		
Giza 90	65.7	74.4	73.7	80.0	---

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تقييم بعض التراكيب الوراثية من القطن المصرى تحت بيئات مختلفة والتعرف الوراثى الجزيئ لسلالات الهجن المبشرة .

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يهدف هذا البحث إلى تقييم بعض سلالات هجن القطن المصرى طويلة التيلة المستنبطة حديثا بالمقارنة بالصنفين المنزرعين (جيزة ٩٠ ، جيزة ٨٠) ، وذلك من خلال أختبار النسل فى تجربة المحصول الأولية (أ) بمحطة البحوث الزراعية بسدس ، وأيضاً فى تجارب المحصول المتقدمة (ب) فى خمس مناطق بالوجه القبلى وهى سدس ، الفيوم ، المنيا ، أسيوط ، وسوهاج فى موسم ٢٠٠٨. كما تم توصيف والتعرف الوراثى الجزيئى لثلاثة من السلالات المبشرة ناتجة من الهجن [(جـ٨٣ × (جـ٧٥ × ٥٨٤٤)} × جـ٨٠] ، [(جـ٨٣ × (جـ٧٥ × ٥٨٤٤)} × {جـ٨٣ × (جـ٧٢ × دندرة)] ، [جـ٩١ × جـ٩٠] مقارنة بالأصناف التجارية جـ٩٠ ، جـ ٨٠.

أوضحت النتائج المتحصل عليها من نتائج تجربة (أ) تفوق هجينين مبشرين من حيث المحصول والصفات التكنولوجية وهذه الهجن هى [جـ٩٠ × بيما س٧٠ (٢٤٢٤)] ، [(جـ٨٣ × (جـ٧٥ × ٥٨٤٤)} × جـ٨٥] . كما أظهرت نتائج تجارب (ب) تفوق ثلاثة هجن مبشرة هى [(جـ٨٣ × (جـ٧٥ × ٥٨٤٤)} × جـ٨٠] ، [جـ٩١ × جـ٩٠] ، [(جـ٨٣ × (جـ٧٥ × ٥٨٤٤)} × {جـ٨٣ × (جـ٧٢ × دندرة)] وأوضحت النتائج بأن الإستمرار فى تربية وتقييم هذه السلالات المبشرة يبشر بأمكانية الحصول على بعض الهجن التى تتفوق فى محصولها وصفات تيلتها عن الأصناف التجارية المنزرعة حالياً.

كذلك أوضحت نتائج هذه الدراسة أن قيم كفاءة التوريث بمعناها الواسع كانت عالية لمعظم الصفات المحصولية فى تجربة (أ) ماعدا صفة محصول القطن الزهر ، ومحصول الشعر. وتشير نتائج التحليل التجميعى لتجارب (ب) عبر المواقع الى وجود تفاعل معنوى بين السلالات والمناطق للصفات المحصولية المدروسة. كما أعطت كفاءة التوريث قيماً عالية لجميع الصفات المحصولية ماعدا صفة متوسط وزن اللوزة حيث أظهرت درجة توريث منخفضة.

ومن نتائج تجارب (أ) ، (ب) يتضح أن هناك عدد من الهجن المبشرة من حيث المحصول والصفات التكنولوجية وهى [(جـ٨٣ × (جـ٧٥ × ٥٨٤٤)} × جـ٨٠] ، [جـ٩١ × جـ٩٠] و [(جـ٨٣ × (جـ٧٥ × ٥٨٤٤)} × {جـ٨٣ × (جـ٧٢ × دندرة)].

وقد تم توصيف لهذه الهجن المبشره مقارنة بصنفى المقارنه جـ٩٠ ، جـ٨٠ على المستوى الجزيئ. وقد أعطت طريقة RAPD – PCR أختلافات بين التراكيب الوراثية الخمسة المدروسة. فقد أختلف عدد الحزم الناتجة عن كل بادئ إستخدم فى هذه الدراسة حيث تراوحت بين ١ إلى ١٤ حزمة. كما أختلفت الأوزان الجزيئية لها ، فقد تراوحت بين ١٦٣ إلى ٢١٤٠ زوج من القواعد. وقد تمكنت هذه البادئات من إظهار حزم مميزة لبعض التراكيب ، فعلى سبيل المثال : أعطى البادئ A01 حزم مميزة للهجين [(جـ٨٣ × (جـ٧٥ × ٥٨٤٤)} × جـ٨٠] عند

الحزم ٢٤٦ ، ٧٠٠ زوج قواعد ، والهجين [(جـ٨٣ × (جـ٧٥ × ٥٨٤٤)) × (جـ٨٣ × (جـ٧٢ × ندرة)] عند الحزم ٣١٦ ، ١٠١٩ زوج قواعد وكذلك للصنف جـ٩٠ عند الحزمه ٦١٧ زوج قواعد.

وكذلك تمكن البادئ A02 من تمييز بعض التراكيب حيث ميز التركيب الوراثى للصنف جـ٨٠ والهجين [جـ٩١ × جـ٩٠] عند الحزم ذات الأوزان الجزيئية ٧٩٣ ، ٢٩١ زوج قواعد على التوالى. أما بالنسبة للبادئ A03 فقد ميز التركيب الوراثى للصنف جـ٩٠ عند الحزمة ٤٨٠ زوج قواعد. وقد ميز الصنف جـ٨٠ عن باقى التراكيب عند الحزم الأربعة ٧٥١ ، ٧٦١ ، ١١٥٦ ، ١٢٥٦ زوج قواعد. بينما أظهر البادئ A04 تميزاً لكل من الصنف جـ٨٠ والهجين [جـ٩١ × جـ٩٠] عند الحزم ٣٧٤ ، ٧٩٣ زوج قواعد على التوالى. وكذلك ميز الصنف جـ٩٠ والهجين [جـ٩١ × جـ٩٠] عند ٢٥٦ ، ٤٠٦ زوج قواعد على التوالى. كما أظهر البادئ A08 تميزاً للهجين [(جـ٨٣ × (جـ٧٥ × ٥٨٤٤)) × جـ٨٠] عن باقى التراكيب عن طريق حزمتين مميزة له عند ٤٠٦ ، ١٤٤٣ زوج قواعد. أما البادئ A11 فقد ميز نفس الهجين السابق عن طريق إنتاج الحزمة المميزة له عند ٥٠٨ زوج قواعد. وكذلك ميز الصنف جـ٨٠ عن باقى التراكيب عند الحزمتين ١٦٨٢ ، ٢١٣٧ زوج قواعد . وقد وجد أن البادئ A12 من أكثر البادئات فاعلية فى إظهار الأختلافات الوراثية محل الدراسة بين الثلاثة هجن المبشرة بالإضافة للصنف التجارى جـ٩٠ ، فقد ميز الهجين [(جـ٨٣ × (جـ٧٥ × ٥٨٤٤)) × جـ٨٠] عند ثلاثة حزم مميزة له عند ٢٣٦ ، ٣٨٢ ، ٤٢٠ زوج قواعد ، والهجين [(جـ٨٣ × (جـ٧٥ × ٥٨٤٤)) × (جـ٨٣ × (جـ٧٢ × ندرة)] بإنتاج حزم مميزة له عند ٣٣١ ، ٤٨٥ ، ٥٦٠ زوج قواعد ، والهجين [جـ٩١ × جـ٩٠] عن طريق تمييز حزمتين عند ١٩٦ ، ٧٤٦ زوج قواعد ، بينما ميز الصنف التجارى جـ٩٠ عند الحزمتين ٣٠٠ ، ٤٦٢ زوج قواعد.

وباستخدام النتائج المتحصل عليها من تحليل RAPD – PCR أمكن دراسة القرابات الوراثية بين التراكيب الوراثية محل الدراسة وبعضها. فقد وجد أن الهجين [جـ٩١ × جـ٩٠] والصنف جـ٩٠ أقرب تركيبين وراثيين إلى بعضهما حيث كانت نسبة التشابه بينهما ٨٠ % ، وعلى الجانب الأخر وجد أن أبعد تركيبين وراثيين عن بعضهما هما جـ٩٠ و جـ٨٠ بنسبة تشابه ٦٥.٧ %.