PERFORMANCE AND GENETIC RELATIONSHIPS AMONG TEN EGYPTIAN WHEAT CULTIVARS AS REVEALED BY RAPD-PCR ANALYSIS

Clara R. Azzam[1] and M. A. Mahrous[2]

[1]Cell Res. Dept., Field Crops Res. Inst., Agricultural Res. Center., Giza, Egypt
[2]Wheat Res. Dept., Field Crops Res. Inst., Agricultural Res. Center., Giza, Egypt

ABSTRACT

This study was conducted to develop molecular fingerprints of ten bread wheat cultivars by RAPD technique and to estimate the genetic distances and the relationships among these cultivars. Mean performance of the measured yield-related traits indicated that significant differences among studied cultivars were found across the two seasons for all studied traits. A wide range of genomic diversity was observed among all studied genotypes, qualifying them to be prime candidates as parents of wheat breeding program for improving specific traits and broadening the genetic base. Random amplified polymorphic DNA (RAPD) analysis was used to fingerprint these ten wheat cultivars. Ten random primers were used to differentiate among wheat cultivars. The genetic similarity matrix based on all possible pairs of cultivars ranged from 49.4% to 82.7%. The lowest genetic similarity value was between Gemmeiza 7 and Gemmeiza 11. The highest genetic similarity was noted between Sids 12 and Sids 13. The dendrogram based on genetic similarities divided the ten cultivars into two main clusters, cultivar Gemmeiza 11 was separated alone in the first cluster, while all the other cultivars were grouped in the second one. Some unique cultivar specific bands were detected, which may be associated with some important economic traits such as grain yield and earliness, which could be useful for wheat breeding program.

Key words: *Triticum aestivum, Mean Performance, Molecular Markers, RAPD, Genetic similarity and Dendrogram.*

INTRODUCTION

In Egypt, bread wheat (*Triticum aestivum* L.) is considered one of the most important crops to the human diet. DNA marker systems are useful tools for assessing genetic diversity levels among germplasm (Lee 1995 and Karp *et al* 1996). As compared with pedigree information, DNA marker-based diversity estimates better reflect actual DNA differences among lines. Molecular markers are applied in breeding programs, where they have proved to be powerful tools in the assessment of genetic variation both within and between plant populations by analyzing large numbers of loci distributed throughout the genome (Powell *et al* 1995). Many molecular marker techniques are available today. PCR-based approaches are in

demand because of their simplicity and requirement for only small quantities of DNA sample. Fingerprinting and genetic relationships using molecular markers are important steps required for gene conservation and breeding programs. Vierling and Nguyen (1992) used RAPD markers to determine the genetic diversity of two diploid wheat species, *Triticum monoccocum* and *T urartu*. They reported that the RAPD technique would make an excellent tool for monitoring and determining the genetic diversity in all germplasm collections and in determining the genetic relationships among genotypes. These RAPD markers are useful in studies of genome evolution, analysis of genome composition, and genome identification. Cao *et al* (1999) estimated genetic diversity within and between spelta and macha wheats. The classification of spelta and macha accessions, based on RAPD markers, was consistent with their geographical origin. The results indicated that the germplasm of macha wheat was more diverse than that of spelta wheat. Thus, it was suggested that RAPD analysis could be used to estimate genetic diversity and identify duplicate accessions in wheat germplasm collections. Garg *et al* (2001) reported that the highest number of polymorphic bands per assay unit was observed for AFLPs (39.7), followed by RAPDs (12.7) and SSRs (4.0). Based on estimation of genetic similarities, more realistic dendrogram was obtained from SSR compared to that obtained from AFLP or RAPD data. Most of the cultivars could be uniquely identified with SSR and RAPD markers but not with AFLPs. Ichii *et al* (2003) emphasized the usefulness of RAPD markers in the identification and selection of the desired genotype in segregating populations during breeding programmes. Abdel-Tawab *et al* (2008) emphasized the usefulness of RAPD markers in the identification and selection of the desired genotype for a variety of traits of economic importance in segregating populations during breeding programmes. The objectives of this study were to develop molecular fingerprints of ten bread wheat cultivars by RAPD technique and to estimate the genetic distances and the relationships among these cultivars.

MATERIALS AND METHODS
Materials

This study was carried out in the Laboratory of the Department of Cell Res., Field Crops Res. Institute and the field experiments were carried out at the experimental farm of wheat Res. Dept., Field Crops Res. Institute of the ARC, Gemmeiza Station, Gharbyia Governorate. Ten Egyptian hexaploid bread wheat cultivars (*Triticum aestivum* L.) were used as shown in Table (1).

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Table 1. The code, name and pedigree of the ten wheat cultivars.

Code	Cultivar	Pedigree
1	Gemmeiza 7	CMH74A.630/SX//Seri82/3/Agent
2	Gemmeiza 9	AId "S"/Huac "S" //CMH74A.630/SX
3	Gemmeiza 10	MAYA74"S"/ON//1160-47/3/BB/GLL/4/CHAT"S"/5/CROW "S"
4	Gemmeiza 11	BOW"S"/KVZ"S"//7C/SERI82/3/Giza168/SAKTN61.
5	Sakha 93	Sakha92/TR810328
6	Sakha 94	Sakha 94 = OPATA/RAYON//KAUZ
7	Giza 168	MRL/BUC//SERI
8	Sids 12	BUC//7C/ALD/5/MAYA74/ON//1160.147/3/BB/GLL/4/CHAT"S"/6/MAYA/VUL//CMH74A.630/4*SX
9	Sids 13	ALMAZ-19=KAUZ"S"//TSI/SNB"S".
10	Shandaweel 1	SITE/MO/4/NAC/ON///1160.147/3/TH.AC//3*PVN/3/MIRLO/BUC

Field experiments

The ten wheat cultivars (Table 1) seeds were sown on the third week of November in both winter seasons of 2008-2009 and 2009-2010. The experiments were laid out in randomized complete block design having four replications, using a constant seeding rate (80 kg/fed). Plot area was 12 m². The normal cultural practices for growing wheat were applied as recommended. The recorded data were; plant height (cm) (, days to flower, days to maturity, seed index, number of spikes/m², number of grains/spike and grain yield (ard/fed). The data of the two seasons were statistically analyzed by Cosat computer statistical analysis program as combined analysis and the differences among means were compared using Duncan's new multiple range test (Duncan 1955).

RAPD-PCR analysis

Genomic DNA extraction

Young and fresh leaf samples were collected separately from 10 plants for each cultivar, all the selected leaves were normal and free from any pathogenic symptoms and all leaf samples were saved in ice box and quickly transported to laboratory. Plant tissues were ground under liquid nitrogen to a fine powder, then bulked DNA extraction was performed using DNeasy plant Mini Kit (QIAGEN).

Polymerase chain reaction (PCR).

PCR amplification was performed using ten random 10-mer arbitrary primers synthesized by Operon Biotechnologies, Inc. Germany, with the sequences represented in Table (2).

Table 2. Random primer names and their nucleotide sequences for RAPD-analysis.

No	Name	Sequence	No	Name	Sequence
1	OP-AQ15	5` TGC GAT GCG G 3`	6	OP-D15	5` CAT CCG TGC T 3`
2	OP-AX06	5` AGG CAT CGT T 3`	7	OP-E06	5` AAG ACC CCT C 3`
3	OP-C03	5` GGG GGT CTT T 3`	8	OP-E19	5` ACG GCG TAT G 3`
4	OP-C10	5` TGT CTG GGT G 3`	9	OP-G05	5` CTG AGA CGG A 3`
5	OP-D01	5` ACC GCG AAG G 3`	10	OP-F04	5` GGT GAT CAG G 3`

Amplification was conducted in 25 µl reaction volume containing the following reagents: 2.5 µl of dNTPs (2.5 mM), 2.5 µl MgCl$_2$ (2.5 mM), and 2.5 µl of 10 x buffer, 3.0 µl of primer (10 pmol), 3.0 µl of template DNA (25 ng / µl), 1 µl of *Taq* polymerase (1U/ µl) and 10.5 µl of sterile dd H$_2$O. The DNA amplifications were performed in an automated thermal cycle (model Techno 512) programmed for one cycle at 94° C for 4 min followed by 45 cycles of 1 min at 94° C, 1 min at 36° C, and 2 min at 72° C. The reaction was finally stored at 72° C for 10 min. Amplified products were size-fractioned using ladder marker (100 bp) Fermentas CO, by electrophoresis in 1.5 % agarose gels in TBE buffer at 120 V for 1 h. The bands were visualized by ethidium bromide under UV florescence and photographed.

Genetic relationships

Similarity indices were calculated and the consensus tree was developed based on the banding patterns of the ten bread wheat cultivars in RAPD analysis using SPSS statistical analysis program to study the genetic relationships among them on the molecular level. Unweighted pair group method using Arithmetic averages (UPGMA) according to Sneath and Sokal (1973) was followed.

RESULTS AND DISCUSSION

Mean performance

Mean values of the measured yield-related traits indicated that significant differences among studied cultivars were found across the two seasons for all studied traits, the differences between theses cultivars are labeled with different letters (Duncan's Multiple Range Test) as shown in (Table 3). A wide range of genomic diversity was observed among all the genotypes, proving them to be prime candidates as parents of breeding programs for improving specific traits and broadening the genetic base. Across studied seasons, cultivar Gemmeiza 7 was the highest in plant height with an average of 120 cm, while cultivar Sids 13 was the shortest one with an average of 83 cm. Regarding days to flower, Sids 12 was the earliest cultivar (81 days to flower), while Gemmeiza 10 was the latest cultivar that need about 106 days to flower. Sids 12 also was the earliest cultivar regarding maturity beside Gemmeiza 11 (134 and 135 days, respectively). Earliness is an important trait in wheat breeding. Earlier wheat is strongly desired by farmers for enhancing land utilization and the possibility of selecting early breeding materials could be examined with one or more molecular methods. Wheat breeding for earliness is important to obtain new varieties which can tolerate adverse environmental conditions such as diseases and abiotic stresses. Conventional breeding programs to choose the earlier wheat cultivars need long time, effort and costs. However, molecular markers are good techniques to predict for suitable genotypes in a much shorter time.

Gemmeiza 11 and Gemmeiza 7 revealed the highest seed index (56 and 55 g, respectively), while Sakha 93 recorded the lowest seed index (39 g), as shown in Table (3). Regarding number of spikes/m^2, Gemmeiza 10 surpassed all other studied cultivars and revealed 439 spikes/m^2, while Sakha 93 gave the lowest number of spikes/m^2 (310). Sids 12 and Shandaweel 1 showed the lowest number of grains per spike (60), while Gemmeiza 7 gave the highest one (86 grains/spike). Regarding the grain yield (ard/fed), both Giza 168 and Gemmeiza 10 gave the highest grain yield; they gave 28 and 27 ard/fed, whereas Gemmeiza 7 gave 20 ard/fed. Grain yield of cereals is a particularly complex trait, reflecting the culmination of all the processes of vegetative and reproductive growth and development, and their interactions with the edaphic and aerial environments; yet yield is usually the trait of most importance to plant breeders. Stably expressed genes leading to higher grain yield are important targets of wheat breeding. Grain yield and associated agronomic traits are important factors in bread wheat improvement. Knowledge regarding the number, genomic location, and effect of quantitative trait loci (QTL) would facilitate marker-assisted selection and the development of cultivars with desirable characteristics (Marza *et al* 2006). Ma *et al* (2007) reported that

Table 3. Mean values of some yield-related traits combined across the two seasons (2008-2009 and 2009-2010) for the ten bread wheat cultivars grown at Gemmeiza Station.

Genotype	Plant height (cm)	Days to flower	Days to maturity	Seed index (g)	No of spikes/ m^2	No. of grains/ spike	Grain yield (ard/fed)
Gemmeiza 7	120 [a]	95 [d]	150 [c]	55 [a]	320 [i]	86 [a]	20 [c]
Gemmeiza 9	110 [b]	100 [b]	160 [a]	50 [b]	388 [c]	71 [b]	21 [cd]
Gemmeiza 10	102 [d]	106 [a]	154 [b]	45 [d]	439 [a]	68 [cd]	27 [a]
Gemmeiza 11	103 [cd]	83 [f]	135 [g]	56 [a]	352 [f]	69 [bc]	22 [bcd]
Sakha 93	95 [f]	84 [f]	145 [de]	39 [f]	310 [j]	63 [e]	22 [bcd]
Sakha 94	104 [c]	98 [c]	150 [c]	50 [b]	410 [b]	66 [d]	23 [bc]
Giza 168	103 [cd]	83 [f]	144 [e]	42 [e]	340 [g]	67 [cd]	28 [a]
Sids 12	89 [g]	81 [g]	134 [g]	42 [e]	335 [h]	60 [f]	21 [cd]
Sids 13	83 [h]	88 [e]	138 [f]	47 [c]	354 [e]	66 [d]	22 [bcd]
Shandaweel 1	99 [e]	87 [e]	146 [d]	45 [d]	381 [d]	60 [f]	24 [b]

Means not sharing a common letter in a column differ significantly at 0.05% level of probability.

grain number per spike is one of the most important yield components of wheat.

RAPD fingerprints

In this study, ten random primers were used to differentiate between ten wheat cultivars by RAPD analysis. The primers produced multiple bands with a number of amplified DNA fragments ranging from 8 (primer G05) to 25 (primer AX06), as shown in Table (4). The total number of reproducible fragments amplified by the ten primers reached 174 bands, from which 132 were polymorphic, which indicated high level of polymorphism (83%). These results agreed with those of Cao et al (1999) and Freitas et al (2000) who reported that RAPD analysis could be used in many different applications involving variety identification and phylogenetic studies in wheat. Also, Maric et al (2004) showed that RAPD markers gave high level of polymorphism among the studied wheat cultivars.

RAPDs can produce a large set of markers, which can be used for the evaluation of genetic variations between and within species, more rapidly and easily than isoenzymes and microsatellites (Guadognuolo et al 2001). The ten cultivars can be uniquely identified (fingerprinted) with cultivar-specific RAPD markers as shown in Figures (1 through 4). The highest number of unique markers was observed in cultivar Gemmeiza 9 (Table 4) which scored seven unique markers at molecular size (MS) of 197.18 bp, 956.31 bp and 150.15 bp of primers: AQ15, AX06 and D15,

Table 4. Levels of polymorphism and unique cultivar-specific bands based on RAPD analysis.

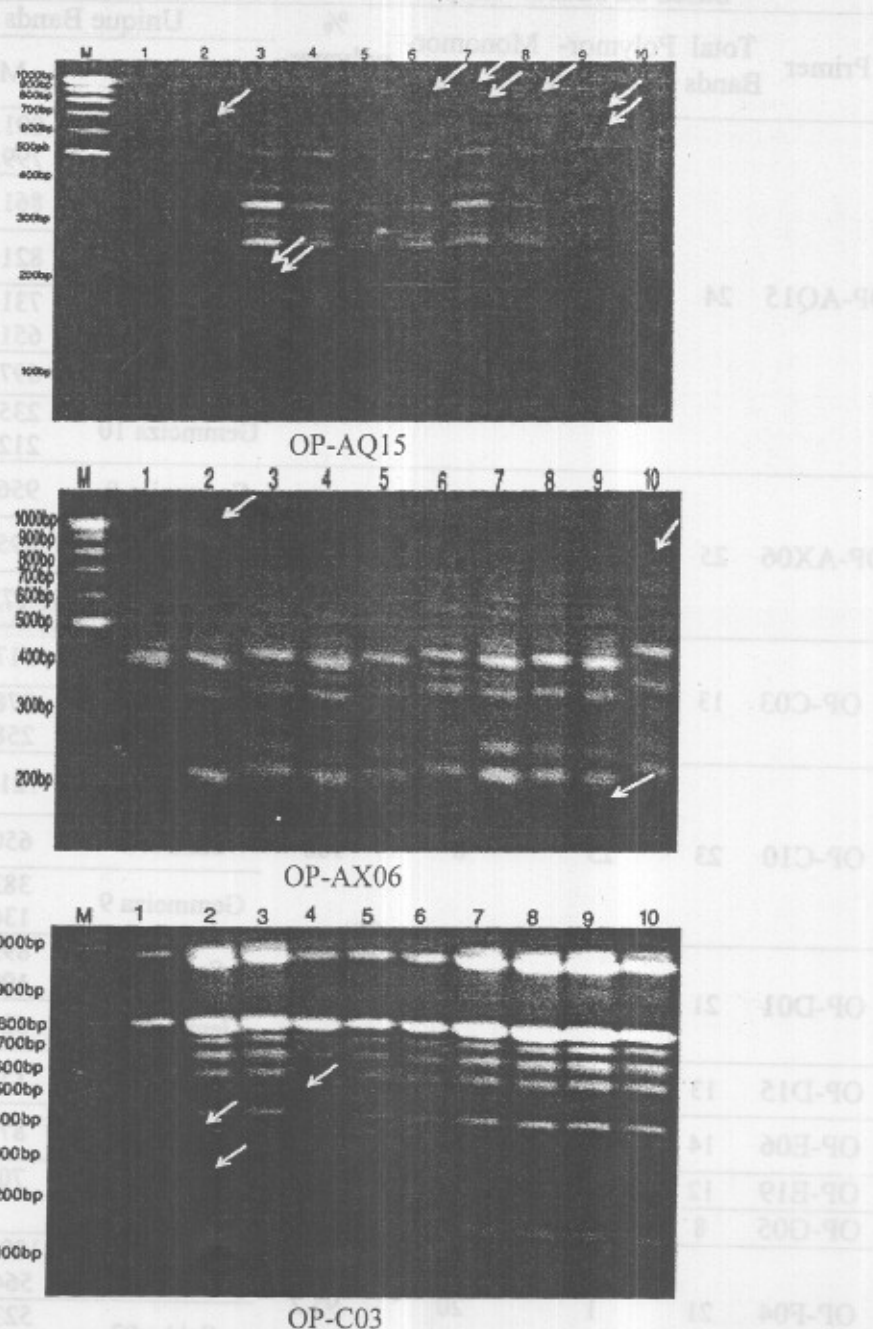| Primer	Total Bands	Polymorphic bands	Monomorphic bands	% polymerrphism	Unique Bands Cultivar	MS
OP-AQ15	24	23	1	96	Giza 168	891.74 799.34
					Sids 12	861.77
					Sakha 94	821.50
					Sids 13	731.35 651.10
					Gemmeiza 9	697.18
					Gemmeiza 10	235.08 212.17
OP-AX06	25	23	2	92	Gemmeiza 9	956.31
					Shandaweel 1	895.94
					Sids 13	173.6
OP-C03	13	6	7	46.2	Gemmeiza 11	517.97
					Gemmeiza 9	378.37 258.52
OP-C10	23	23	0	100	Gemmeiza 10	1214.73
					Sakha 93	650.00
					Gemmeiza 9	383.32 136.66
OP-D01	21	21	0	100	Sakha 93	899.59 199.81
					Gemmeiza 7	526.40
OP-D15	13	11	2	84.6	Gemmeiza 9	150.15
OP-E06	14	13	1	92.86	Shandaweel 1	873.86
OP-E19	12	4	8	33.3	Gemmeiza 11	702.71
OP-G05	8	7	1	87.5	-	-
OP-F04	21	1	20	95.2	Gemmeiza 7	1004.82 564.96
					Sakha 93	523.21 171.87
Total	174	132	42	83		

Fig. 1. DNA polymorphism of the ten wheat cultivars using randomly amplified polymorphic DNA with primer OP-AQ15, OP-AX06 and OP-C03, where M= Molecular Marker, 1= Gemmeiza 7, 2= Gemmeiza 9, 3= Gemmeiza 10, 4= Gemmeiza 11, 5= Sakha 93, 6= Sakha 94, 7= Giza 168, 8= Sids 12 , 9= Sids 13 and 10= Shandaweel 1
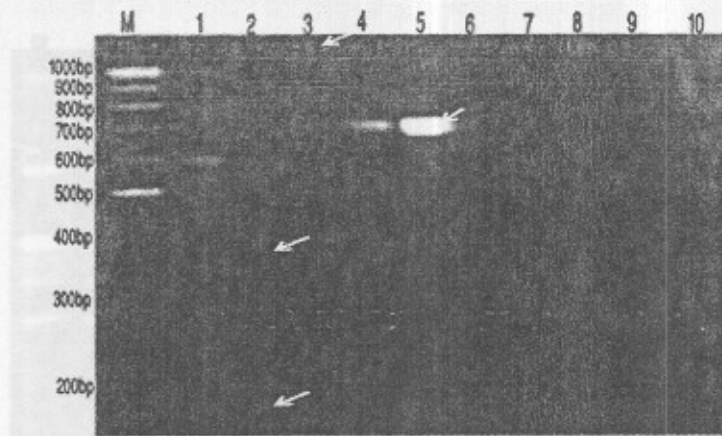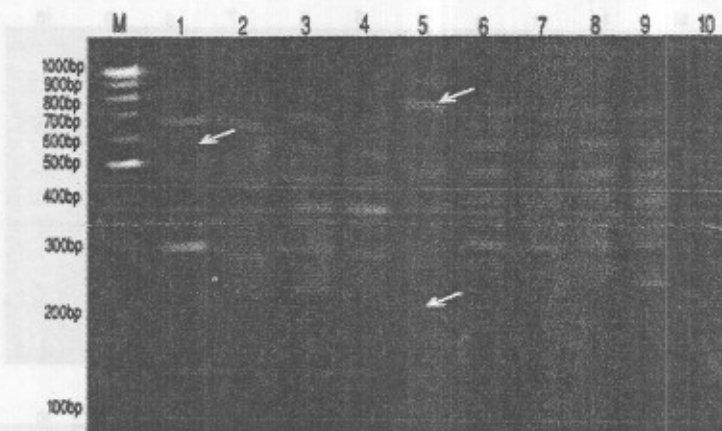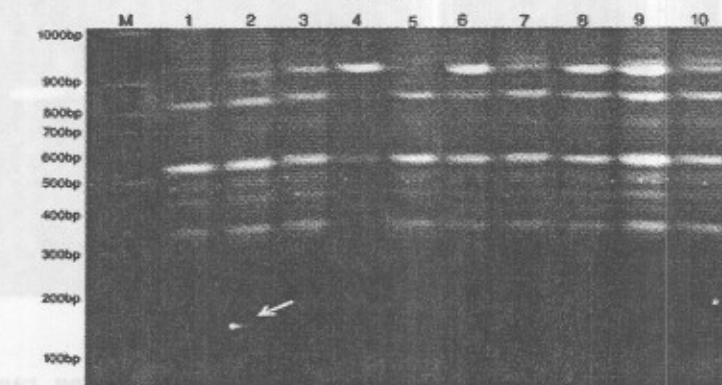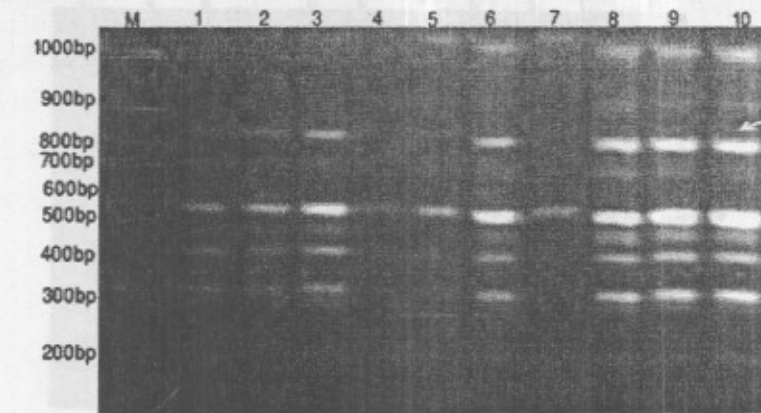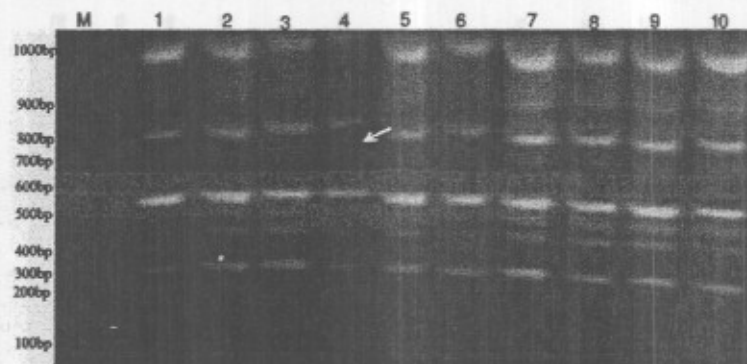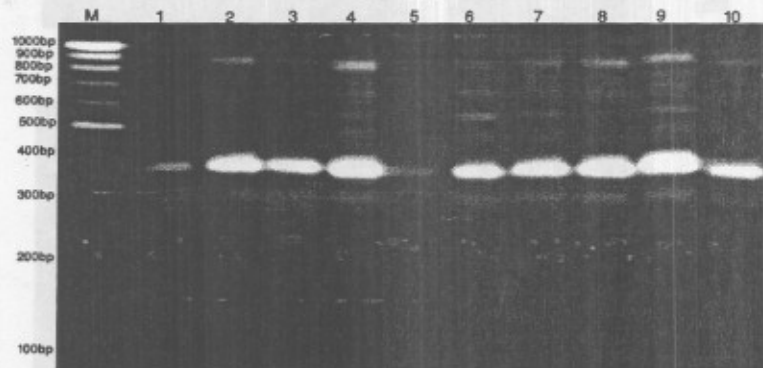
Fig. 2. DNA polymorphism of the ten wheat cultivars using randomly
amplified polymorphic DNA with primer OP-C10, OP-D01 and OP-
D15, where M= Molecular Marker, 1= Gemmeiza 7, 2= Gemmeiza 9,
3= Gemmeiza 10, 4= Gemmeiza 11, 5= Sakha 93, 6= Sakha 94,
7= Giza 168, 8= Sids 12 , 9= Sids 13 and 10= Shandaweel 1

OP-E06

OP-E19

OP-G05

Fig. 3. DNA polymorphism of the ten wheat cultivars using randomly
amplified polymorphic DNA with primer OP-E06, OP-E19 and OP-
G05, where
M= Molecular Marker, 1= Gemmeiza 7, 2= Gemmeiza 9,
3= Gemmeiza 10, 4= Gemmeiza 11, 5= Sakha 93, 6= Sakha 94,
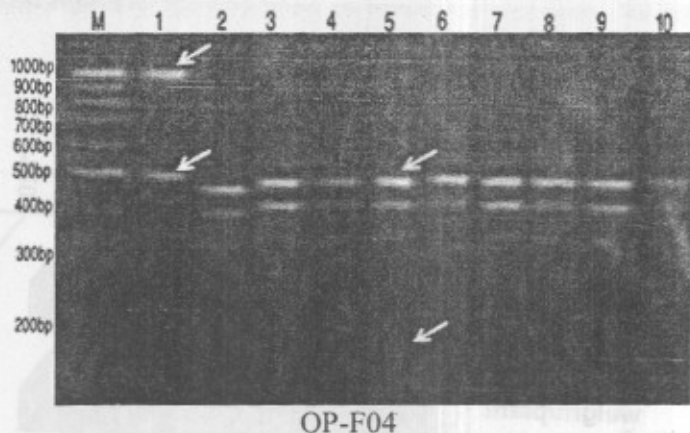7= Giza 168, 8= Sids 12 , 9= Sids 13 and 10= Shandaweel 1

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Fig. 4. DNA polymorphism of the ten wheat cultivars using randomly
amplified polymorphic DNA with primer OP-F04, where
M= Molecular Marker, 1= Gemmeiza 7, 2= Gemmeiza 9,
3= Gemmeiza 10, 4= Gemmeiza 11, 5= Sakha 93, 6= Sakha 94,
7= Giza 168, 8= Sids 12 , 9= Sids 13 and 10= Shandaweel 1

respectively beside two unique markers at MS of 378.37 bp and 258.52 bp
of primer C03 and also two unique markers at MS of 383.32 bp and 136.66
bp of primer C10. Sakha 93 scored four unique markers; band number 9 of
primer C10 at MS of 650 bp, bands number 2 and 20 of primer D01 at MS
of 899.59 bp and 199.81 bp, and band number 12 of primer F04 at MS of
523.21 bp. Cultivars Gemmeiza 7, Gemmeiza 10 and Sids 13 showed three
unique markers at band no.3 and 11 of primer F04 at MS of 1004.82 bp and
564.96 bp and also at band number 10 of primer D01 at MS of 526.4 bp for
Gemmeiza 7 cultivar, while for Gemmeiza 10, band no.22 and 23 of primer
AQ15 at MS of 235.08 bp and 212.17 bp and also at band number 1 of
primer C10 at MS of 1214.73 bp, where band no. 5 and 7 of primer AQ15 at
MS of 731.35bp and 651.10 bp, respectively, and band no.25 of primer
AX06 at MS of 173.6 bp.

On the other hand, cultivar Gemmeiza 11, Giza 168 and Shandaweel
1 gave two unique markers both at band no.8 of primer C03 at MS of 517.97
bp, band no. 5 of primer E19 at MS of 702.71 bp for Gemmeiza 11 cultivar,
while at band no.1 and 4 of primer AQ15 at MS of 891.74bp and 799.34 bp
for Giza 168 wheat cultivar, while for Shandaweel 1 cultivar at band no.2 of
primer AXQ06 at MS of 894.94 bp, band no.5 of primer E06 at MS of
873.86 bp. Each of cultivar Sids 12, Sakha 94 and Gemmeiza 9 exhibited
only one unique band at band no.2, 3 and 6 of primer AQ15 at MS of
861.77, 821.50 bp and 697.18 bp, respectively.

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These results indicated that RAPD-PCR markers gave adequate distinctions among all the ten tested cultivars. These unique cultivar specific bands may be associated with some important economic traits such as grain yield and earliness, which could be useful for wheat breeding program.

Also, Abdel-Tawab et al (1998) identified nine sugarcane cultivars using SDS-protein, isozymes and RAPD-PCR markers and found that RAPD-PCR gave more reliable markers. After that Abdel-Tawab et al (2001) found some unique bands, which could be used as DNA markers for cultivar identification in sweet sorghum.

Genetic similarity and cluster analysis

The RAPD data developed by all primers of this study were used to estimate the genetic similarities among the ten cultivars. The genetic similarity matrix based on all possible pairs of cultivars ranged from 49.4% to 83% (Table 5). The lowest genetic similarity value was between cultivar Gemmeiza 7 and Gemmeiza 11 (49.4%). While, the highest genetic similarity was noted between cultivar Sids 12 and Sids 13 (82.7%) followed by Sids 12 and both Gemmeiza 10 and Giza 168 (78%).

Table 5. Similarity matrix among the ten wheat cultivars based on RAPD analysis.

Cultivar	1	2	3	4	5	6	7	8	9
2	0.693								
3	0.652	0.720							
4	0.494	0.610	0.648						
5	0.601	0.659	0.718	0.609					
6	0.540	0.632	0.729	0.605	0.621				
7	0.599	0.704	0.738	0.686	0.700	0.670			
8	0.621	0.673	0.779	0.629	0.667	0.764	0.784		
9	0.603	0.677	0.731	0.633	0.670	0.736	0.735	0.827	
10	0.620	0.705	0.730	0.592	0.552	0.735	0.681	0.755	0.726

1= Gemmeiza 7, 2= Gemmeiza 9, 3= Gemmeiza 10, 4= Gemmeiza 11, 5= Sakha 93, 6= Sakha 94, 7= Giza 168, 8= Sids 12, 9= Sids 13 and 10= Shandaweel 1

The dendrogram developed from RAPD data using unweighted pair group method of arithmetic means (Fig. 5) divided the ten cultivars into two main clusters. Cultivar Gemmeiza 11 was separated alone in the first cluster, while all other cultivars were grouped in the second cluster, which was separated into two sub-clusters where cultivars Gemmeiza 7 and Gemmeiza 9 were grouped together in the same sub-cluster and the other sub-cluster comprised the remaining cultivars.
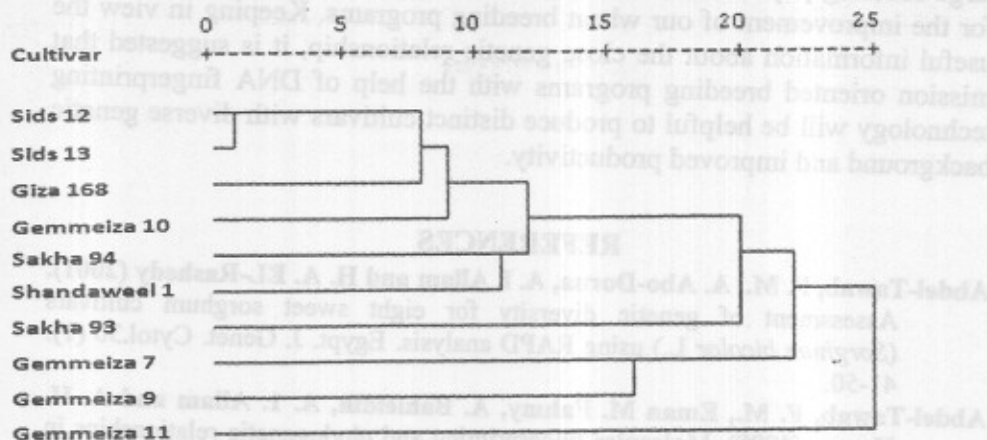
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                    0         5        10        15        20        25
      Cultivar      +--------+---------+---------+---------+--------+
      Sids 12       ┐
      Sids 13       ┤
      Giza 168      ┤
      Gemmeiza 10   ┤
      Sakha 94      ┤
      Shandaweel 1  ┤
      Sakha 93      ┤
      Gemmeiza 7    ┤
      Gemmeiza 9    ┤
      Gemmeiza 11   ┘
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Fig. 5. Dendrogram of ten wheat genotypes developed from RAPD data using unweighted pair group method of arithmetic means (UPGMA).

RAPD analysis seemed to be one of the effective tools for detecting polymorphism and could discriminate between all the ten cultivars. These results agreed with Vierling and Nguyen (1992) who reported that the RAPD technique was an excellent tool for monitoring and determining the genetic diversity present in all germplasm and in determining the genetic relationships among wheat genotypes.

Barakat *et al* (2000) used RAPD analysis to construct a similarity matrix and found that the genetic similarity among all the wheat cultivars ranged from 41% to 84%. This indicated that RAPD analysis might help in studying genetic relationships between different wheat cultivars. Guadognuolo *et al* (2001) reported that the best-resolved dendrogram was obtained using RAPD data and it could detect the highest levels of genetic diversity in wheat. Also, Bered *et al* (2002) found that, based on the use of RADP markers, the average genetic similarity value among all genotype pairs was 0.88, showing high genetic relationships in the wheat germplasm.

The data obtained in this experiment confirmed the efficiency of the RAPD technique for determination and estimation of genetic distances and relatedness among different plant genotypes. The RAPD analysis has been found to a valuable DNA marker system to evaluate genetic diversity. The information about genetic similarity will be helpful to avoid any chance of elite germplasm becoming genetically uniform. Because of the simple experimental procedures, the requirement of minimal amount of plant tissue and the possibility of automation, RAPD analysis should be very useful in breeding for rapid and early identification of most diverse individuals in

large seedling populations, allowing the detection of true to type genotypes for the improvement of our wheat breeding programs. Keeping in view the useful information about the close genetic relationship, it is suggested that mission oriented breeding programs with the help of DNA fingerprinting technology will be helpful to produce distinct cultivars with diverse genetic background and improved productivity.

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الأداء والعلاقات الوراثية بين عشرة اصناف قمح مصرية باستخدام تحليل الكشافات الوراثية الجزيئية RAPD-PCR

كلارا رضا عزام [1] و محروس عبد الغنى محروس [2]

[1] قسم بحوث الخلية- معهد بحوث المحاصيل الحقلية- مركز البحوث الزراعية- الجيزة- مصر
[2] قسم بحوث القمح- معهد بحوث المحاصيل الحقلية- مركز البحوث الزراعية- الجيزة- مصر

تمت هذه الدراسة بغرض تحديد بعض الكشافات الجزيئية المميزة لبعض الأصناف تحت الدراسة. تمت زراعة عشر أصناف من القمح لمدة موسمين متتاليين و تم أخذ بعض القياسات لبعض الصفات المرتبطة بالمحصول و النمو فى القمح وحساب اداء الأصناف فى هذه الصفات. واشار مؤشر اداء الصفات المرتبطة بالمحصول لوجود اختلافات معنوية بين جميع الصفات المدروسة خلال الموسمين لجميع الصفات المدروسة. ولوحظ وجود مدى واسع من التنوع الجينى بين جميع التراكيب الوراثية التى تمت دراستها، والتى تؤهلهم ليكونوا مرشحين لاستخدامهم كآباء فى برنامج تربية القمح لتحسين صفات محددة وتوسيع القاعدة الوراثية. تم اجراء تحليل الـ RAPD بإستخدام العديد من بادئات تفاعل بلمرة الـ DNA للوقوف على السلوك الجزمى لهذه الأصناف. و كذلك لمعرفة الحزم الناتجة و المرتبطة ببعض الصفات الإنتاجية و الحزم المميزة

للأصناف تحت الدراسة كما تم عمل شجرة القرابة و العلاقات التطورية على اساس السلوك الحزمى للأصناف باستخدام تقنية RAPD. من خلال القياسات التى أجريت على الصفات المرتبطة بالإنتاجية فى القمح لموسمين متتاليين تم تحديد بعض الكشافات الجزيئية المرتبطة ببعض هذه الصفات باستخدام تقنيات الــ RAPD كـذلك تم تحديد بعض الكشافات الجزيئية المميزة لبعض الأصناف تحت الدراسة. كما دلت نتائج نسبة التشابه عـلـى ان أكثر الأصناف تشابها هما سدس ١٢ و سدس ١٣ و بنسبة تشابه (٨٢,٧%) و ان أكثر الأصناف إختلافـا هما الاصناف جميزة ٧ وجميزة ١١ ونسبة تشابه (٤٩,٤%). كما دلت نتائج رسم شجرة القرابة و العلاقات التطورية على أساس السلوك الحزمى للأصناف باستخدام تقنية الــ RAPD على إنقسام الأصناف لمجموعتين رئيسيتين و تشمل المجموعة الأولى الصنف جميزة ١١ كما تضم المجموعة الثانية باقى الاصناف تحت الدراسـة. تـم الكشف عن بعض الحزم الوراثية المعلمة للصنف والتى يمكن ان تكون مرتبطة ببعض الصفات الاقتصادية الهامـة مثل محصول الحبوب و التبكير والتى يمكن الاستفادة منها فى برامج تربية القمح .

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