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GENETIC RELATIONSHIPS OF SOME EGYPTIAN AND YEMENI WHEAT VARIETIES DETECTED BY RAPD AND ISSR MARKERS

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ABSTRACT

Two types of molecular markers, Randomly Amplified Polymorphic DNA (RAPD) and Inter-Simple Sequence Repeats (ISSR), were assayed to determine the genetic diversity of four hexaploid Egyptian wheat varieties [(Giza١٦٤, Giza١٦٨, Sakha٦١ and Sakha٩٢) (Triticum aestivum)], and four tetraploid Yemen's wheat genotypes [Behows١٤, Smara'a, Mysany and Saba'a (Triticum durum)]. In RAPD analysis, six used primers displayed RAPD profiles with polymorphic bands. A total of ٢٤ bands out of ٥٨ bands for the Egyptian and Yemeni varieties were polymorphic (٤١.٣٨% of polymorphism) consist of DNA fragments with molecular weights ranged from ١١٣ to ١١٧٥ base pairs. The Yemeni genotypes were distinguished via OP-A٠٣ and HB-١١ primers that generated two bands at molecular weight of ١٥٣.٢٢ and ٣٧٤.١٦ base pairs, respectively. The Egyptian varieties were distinguished via OP-A١٠ and HB-١٢ primers that generated two bands at molecular weight of ٤٨٣.٩٨ and ٧٠٧.٧٩ base pairs, respectively. In ISSR analysis, six used primers generated variable banding patterns with amplified bands ranged from ٧٤ to ١١١٩ base pairs. Thirty five bands out of ٧١ bands were polymorphic for the Egyptian varieties and Yemeni genotypes with ٤٩.٣% of polymorphism. Primer ٨٩-B gave a specific marker for the Yemeni genotypes with molecular weight of ٢٨٧.٤٠ base pairs. While primer HB-١٠ gave a specific marker for the Egyptian varieties with molecular weights of ٥٠٢.٦٩ and ٥٥٠.٠٥ base pairs. Dendrogram was constructed for the tested cultivars using UPGMA algorithm based on RAPD and ISSR analysis. The dendrogram indicated that the Egyptian varieties were grouped in one cluster and the Yemeni ones were separated in the other cluster. The present study showed that RAPD and ISSR analyses are useful tools for generating candidate specific markers of genetic characterization and distinguishing between the tetraploid and hexaploid wheat genotypes and necessity for protection of Egyptian royalties of the landraces.

Key Words: ***Wheat, Genetic diversity, Molecular markers, RAPD marker, ISSR marker.***

INTRODUCTION

Wheat is considered as the most important gramineae plants. The past limitation associated with pedigree data and morphological, physiological and cytological markers for assessing genetic diversity in cultivated and wild plant species have largely been circumvented by the development of DNA markers such as Random Amplified Polymorphic DNAs (RAPD) (Williams *et al* ١٩٩٠). This method has proven to be useful for germplasm

identification and elucidation of genetic relationships of numerous plant cultivars and species (Williams *et al* ١٩٩٠; Halward *et al* ١٩٩٢ and Levi and Rowland ١٩٩٧).

Molecular markers have proved to be valuable tools in the characterization and evaluation of genetic diversity within and between species and populations; different markers might reveal different classes of variations (Russell *et al* ١٩٩٧). The generated DNA polymorphism reflects both the distance between two annealing sites and the pattern of their distribution throughout the genome of a particular cultivar or species (Williams *et al* ١٩٩٠).

The advent of the Polymerase Chain Reaction (PCR) favored the development of different molecular techniques such as RAPD and Inter-Simple Sequence Repeat polymorphic DNA (ISSR) etc. (Nagaoka and Ogihara ١٩٩٧). RAPDs proved to be useful as genetic markers in the case of self pollinating species with a relatively low level of intra-specific polymorphism, such as tetraploid, hexaploid wheat (Joshi and Nguyen ١٩٩٣ and Ramiz *et al* ٢٠٠٧) and cultivated barley (Tinker *et al* ١٩٩٣). RAPD and ISSR techniques do not require the use of radioactive materials and are simple to use and able to detect a significant degree of polymorphism (Williams *et al* ١٩٩٠). Many authors referred to the validity of RAPD analysis for taxon characterization. In this regard, Gregor *et al* (١٩٩٤) used RAPD analysis to fingerprint some *Prunus domestica.* They stated that comparing DNA from various cultivars of the same species have proved the reliability of this method. Also, Dollo *et al* (١٩٩٥) suggested that RAPD analysis can provide a new alternative for cultivar identification and classification, and can be effectively incorporated into breeding programs. ISSR markers, have become good DNA molecular markers for research on populations of the same species, and could be used to assess genetic diversity (Qian *et al* ٢٠٠١). ISSRs have been used for cultivar identification in maize (Pejic *et al* ١٩٩٨), potatoes (Prevost and Wikinson ١٩٩٩), wheat (Ammiraju *et al* ٢٠٠١), and barley (Tanyolac ٢٠٠٣).

It is clear that numerous species-specific markers are required for documentation of the Egyptian and Yemeni wheat genotypes. This study demonstrated that molecular markers are needed to identify wheat cultivars and differentiate between the Egyptian and Yemeni wheat varieties. DNA molecular markers have received considerable attention in the recent years. ISSR marker has been utilized in gramineae plants to identify markers associated with seed size in wheat (Ammiraju *et al* ٢٠٠١) and fingerprinting in rice (Blair *et al* ١٩٩٩) as well as in other crops, e.g., in fingerprinting cashew (Archak *et al* ٢٠٠٣).

The objective of this study was to detect molecular genetic fingerprints and to determine the genetic relationships for four hexaploid Egyptian and

four tetraploid Yemeni wheat varieties using two types of molecular markers; RAPD and ISSR.

MATERIALS AND METHODS

Plant materials

This study was carried out at the Genetic Department, Faculty of Agriculture, Ain Shams University, during ٢٠٠٨. Four hexaploid Egyptian wheat varieties were kindly provided by Field Crop Research Institute, Agricultural Research Center (ARC). Other four tetraploid Yemeni genotypes were kindly provided by Faculty of Agriculture, Sana'a University. The names and ploidy levels of these genotypes are listed in Table ١.

Table ١. Names and ploidy levels of the hexaploid Egyptian and tetraploid Yemeni wheat genotypes.

No.	Egyptian varieties	Ploidy level	No.	Yemeni genotypes	Ploidy level
١	Giza١٦٤	Hexaploid	٥	Behows١٤	Tetraploid
٢	Giza١٦٨	Hexaploid	٦	Smara'a	Tetraploid
٣	Sakha٩٢	Hexaploid	٧	Mysany	Tetraploid
٤	Sakha٦١	Hexaploid	٨	Saba'a	Tetraploid

Extraction of genomic DNA

The DNA was extracted from grains of the eight Egyptian and Yemeni wheat entries using DNeasy plant Mini Kit (QIAGEN).

RAPD-PCR Analysis

PCR amplification was performed using six random ١٠-mer arbitrary primers synthesized by Operon biotechnologies, Inc. These primers and their nucleotides sequences are listed in Table ٢. Amplification was conducted in ٢٥µl reaction volume containing the following reagents: ٢.٥µl of dNTPs (٢.٥mM), ٢.٥µl of $MgCl_٢$ (٢.٥mM), and ٢.٥µl of ١٠x buffer, ٣.٠µl of primer (١٠pmol), ٣.٠µl of DNA template (٢٥ng/µl), ١µl of *Taq* polymerase (١U/µl) and ١٠.٥µl of sterile dd $H_٢O$. The DNA amplifications were performed in an automated thermal cycle (model Techno ٥١٢) programmed for one cycle at ٩٤ºC for ٤ min followed by ٤٥ cycles of ١ min at ٩٤ºC, ١ min at ٣٦ºC, and ٢ min at ٧٢ºC. The reaction was finally stored at ٧٢ºC for ١٠ min. Amplified products were size-fractioned [using ١٠٠ bp ladder marker (Axygen Biosciences)] by electrophoresis in ١.٥% agarose gels in TBE buffer at ١٢٠ V for ١ h. The bands were visualized by ethidium bromide under UV fluorescence and were photographed.

ISSR-PCR Analysis

Selected primers based on dinucleotide, tetranucleotide or pentanucleotide repeats were used for ISSR analysis. PCR amplification was performed using six ISSR primers that produced clear and reproducible bands. These primers and their nucleotides sequences are listed in Table ٢. Amplification was conducted in ٢٥µl reaction volume containing the following reagents: ٢.٥µl of dNTPs (٢.٥mM), ٢.٥µl of $MgCl_2$ (٢.٥mM), and ٢.٥µl of ١٠x buffer, ٣.٠µl of primer (١٠pmol), ٣.٠µl of template DNA (٢٥ng/µl), ١µl of *Taq* polymerase (١U/µl) and ١٢.٥µl of sterile dd H_2O. The PCRs were programmed for one cycle at ٩٤°C for ٤ min to pre-denature, followed by ٤٥ cycles of ١ min at ٩٤°C, ١ min at ٥٧°C, and ٢ min at ٧٢°C. The reaction was finally extension at ٧٢°C for ٥ min, and eventually stored at ٤°C. Amplified products were electrophoresed in ١% agarose gel with ٠.٥x TBE buffer. After staining the gel with ethidium bromide, band patterns were visualized with an UV transilluminator. Fragments sizes were estimated with the ١٠٠ bp ladder DNA marker.

Table ٢. Primers and their nucleotide sequences used for RAPD and ISSR analyses.

RAPD Primers			ISSR Primers		
No.	**Name**	**Sequence**	**No.**	**Name**	**Sequence**
١	OP-A٠٣	٥´ AGT CAG CCA C ٣`	١	٤٤-A	٥` (GT)٨GG ٣`
٢	OP-A٠٧	GAA ACG GGT G	٢	٨٩-B	(CA)٨GT
٣	OP-A١٠	GTG ATC GCA G	٣	٩٩-B	(CA)٨ GG
٤	OP-B٠٧	GGT GAC GCA G	٤	HB-١٠	(GA)٨ CC
٥	OP-B١١	GTAGACCCGT	٥	HB-١١	(GT)٨ CC
٦	OP-B١٢	CCT TGA CGC A	٦	HB-١٢	(CAC)٣GC

Data analysis for RAPD and ISSR fragments were scored for presence (+) or absence (-) by using the Phoretix ١D image analysis system (Phoretix International, London) to integrate the data. The similarity matrix and the dendrogram among the eight wheat genotypes were determined using Unweighted Pair Groups Method with Arithmetic average (UPGMA) cluster analysis program.

RESULTS AND DISCUSSION

Molecular genetic fingerprints of wheat genotypes

RAPD Analysis

Six random primers (OP-A٠٣, OP-A٠٧, OP-A١٠, OP-B٠٧, OP-B١١ and OP-B١٢) were used in the present study to identify the tested eight wheat genotypes (Fig. ١). Thirty four monomorphic and twenty four polymorphic distinct fragments (٤١.٣% of polymorphism) were detected (Table ٣). The results of RAPD analysis showed that all used primers were polymorphic. OP-A٠٧ primer showed the highest polymorphism level among the tested cultivars (٦٠% of polymorphism), while OP-A٠٣ primer showed the lowest polymorphism level (٣٣.٣٣% of polymorphism) (Fig. ٣). The compiled data for the six used primers recorded ٤١.٣٨% of polymorphism.

Some genotype(s)-specific markers were detected among the eight studied wheat cultivars as shown in Table ٤. OP-A٠٣ primer gave a specific marker for Saba'a Yemeni genotype with molecular weight of ٨٨٠.٠٨ base pairs. Primer OP-A٠٣ and HB-١١ primer gave two specific markers for the tetraploid Yemeni varieties with molecular weights of ١٥٣.٢٢ and ٣٧٤.١٦ base pairs, respectively. OP-A٠٧ and OP-A١٠ primers showed two specific markers for Smara'a genotype with molecular weights of ١١٧٥.١٣ and ١٠٧٢.١٢ base pairs, respectively. Also OP-A١٠ and HB-١٢ primers showed two specific markers for the hexaploid Egyptian varieties with molecular weights of ٤٨٣.٩٨ and ٧٠٧.٧٩ base pairs, respectively. Finally, HB-١٢ primer showed two specific markers for Behows١٤ with molecular weights of ٣٦٢.٢٥ and ٢٢١.٢٣ base pairs. Shehata (٢٠٠٤) studied genotyping variability of some wheat cultivars including Giza١٦٤ and Giza١٦٨ using eight RAPD primers (OP B-٠١,-٠٢, -٠٣, ٠٨ and OP I-٠٣, -٠٩, -١٤ and -١٨). A total of ٦٧ polymorphic bands out of ٨٦ ones were generated by these eight primers. OP I-٠٣ primer generated four unique bands for Giza١٦٤. Abdollahi (٢٠٠٨) used ٢٢ random operon primers of OPA, OPB, OPC and OPD series for exploring the polymorphism among some Indian wheat cultivars. OP A٠٣ primer generated only ٢٦ polymorphic bands. Moreover, OP A٠٧ primer was used with other RAPD primers to generate polymorphic bands and distinguishing between some diploid and tetraploid wheat cultivars (Aliyev *et al* ٢٠٠٧).

ISSR Analysis

Six ISSR primers (٤٤-A, ٨٩-B, ٩٩-B, HB-١٠, HB-١١ and HB-١٢) were used in the present study to identify the eight wheat varieties (Fig. ٢). Thirty six monomorphic and thirty five polymorphic distinct fragments (٤٩.٣٠% of polymorphism) were detected (Table ٣). The results of ISSR

analysis showed that all used primers were polymorphic. HB-١٢ primer showed the highest polymorphism level among the tested varieties (٧٢.٧٣% of polymorphism), while HB-١١ primer showed the lowest polymorphism level (٣٣.٣٣% of polymorphism) (Fig. ٣). The compiled data for the six used primers recorded ٤٩.٣٠% of polymorphism.

Table ٣. Levels of polymorphism detected with each RAPD and ISSR primer tested in the eight studied wheat varieties.

	Primer name	OP-A٠٣	OP-A٠٧	OP-A١٠	OP-B٠٧	OP-B١١	OP-B١٢	Total
RAPD	Monomorphic bands	٦	٤	٧	٥	٥	٧	٣٤
	Polymorphic bands	٣	٦	٤	٤	٣	٤	٢٤
	Total	٩	١٠	١١	٩	٨	١١	٥٨
	Polymorphism %	٣٣.٣٣	٦٠.٠٠	٣٦.٣٦	٤٤.٤٤	٣٧.٥٠	٣٦.٣٦	٤١.٣٨
	Primer name	**٤٤-A**	**٨٩-B**	**٩٩-B**	**HB-١٠**	**HB-١١**	**HB-١٢**	**Total**
ISSR	Monomorphic bands	٥	٧	٧	٨	٦	٣	٣٦
	Polymorphic bands	٥	٤	٨	٧	٣	٨	٣٥
	Total	١٠	١١	١٥	١٥	٩	١١	٧١
	Polymorphism %	٥٠.٠٠	٣٦.٣٦	٥٣.٣٣	٤٦.٦٧	٣٣.٣٣	٧٢.٧٣	٤٩.٣٠

Some genotype(s)-specific markers were detected among the eight studied wheat varieties as shown in Table ٤. The ٨٩-B primer gave a specific marker for the tetraploid Yemeni genotypes with molecular weight of ٢٨٧.٤٠ base pairs and two unique bands for Mysany and Smara'a with molecular weights of ٤٠٨.٩٠ and ٢٠٧.٤٦ base pairs, respectively. The HB-١٠ primer gave also two specific markers for the hexaploid Egyptian cultivars with molecular weights of ٥٥٠.٠٥ and ٥٠٢.٦٩ base pairs as well as Behows١٤ Yemeni variety with molecular weight of ٧٤.٧٤ base pairs. The ٩٩-B primer showed a specific marker for Sakha٦١ Egyptian cultivar with molecular weight of ١١٩.١١ base pairs. HB-١٢ primer showed a specific marker for Sakha٩٢ Egyptian variety with molecular weight of ٤٢٦.٢٠ base pairs and at molecular weight of ١١١٩.٧٠ base pairs for Saba'a Yemeni genotype. Heikal *et al* (٢٠٠٧) used different RAPD and ISSR primers to fingerprint some Egyptian gramineae species. The ISSR primers (HB-١٠, HB-١١ and HB-١٢) scored highly polymorphic bands for the tested species.

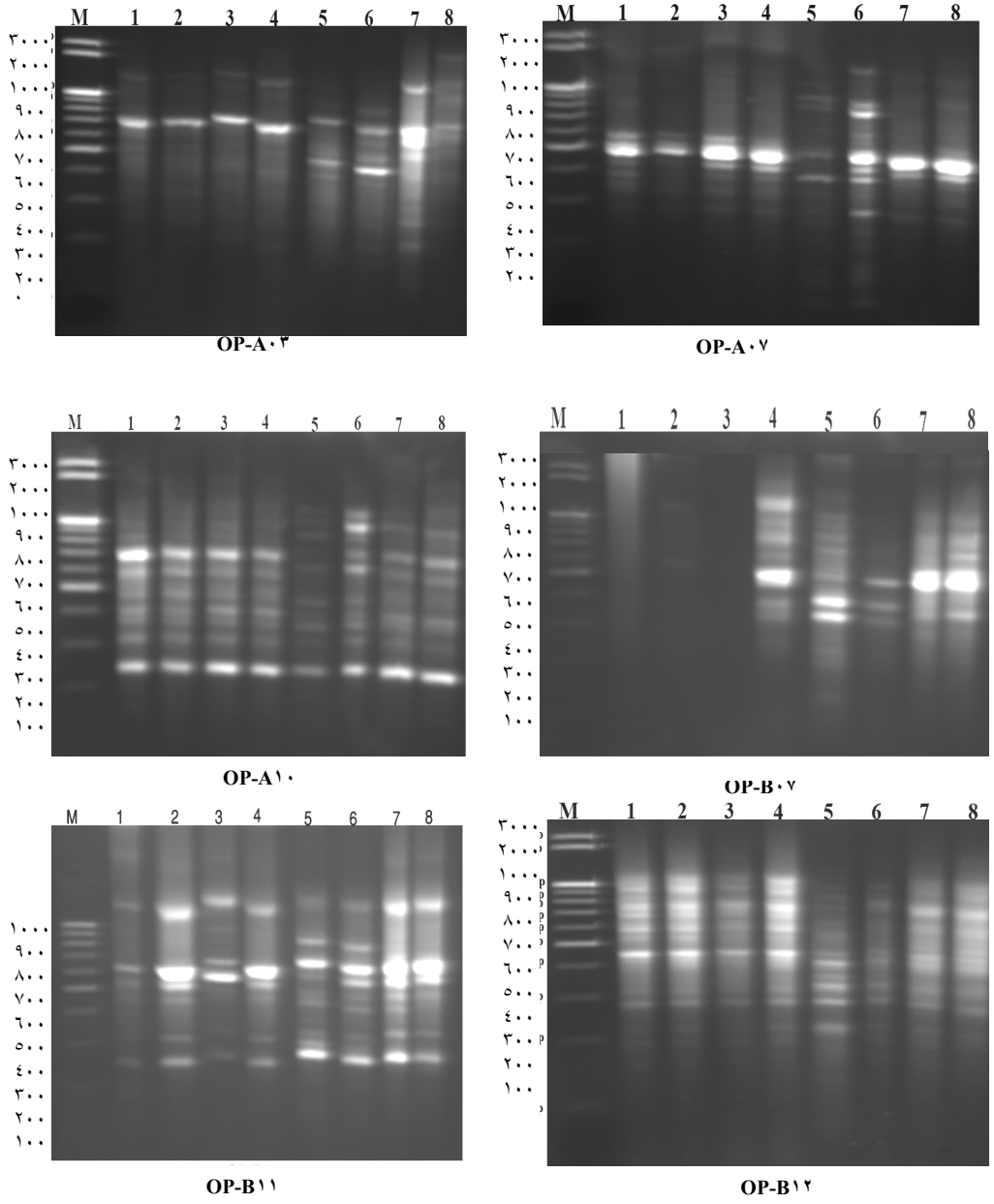

Fig. (١): PCR products by six RAPD primers (OP-A٠٣, OP-A٠٧, OP-A١٠, OP-B٠٧, OP-B١١ and OP-B١٢) for the eight studied wheat genotypes. M DNA marker.

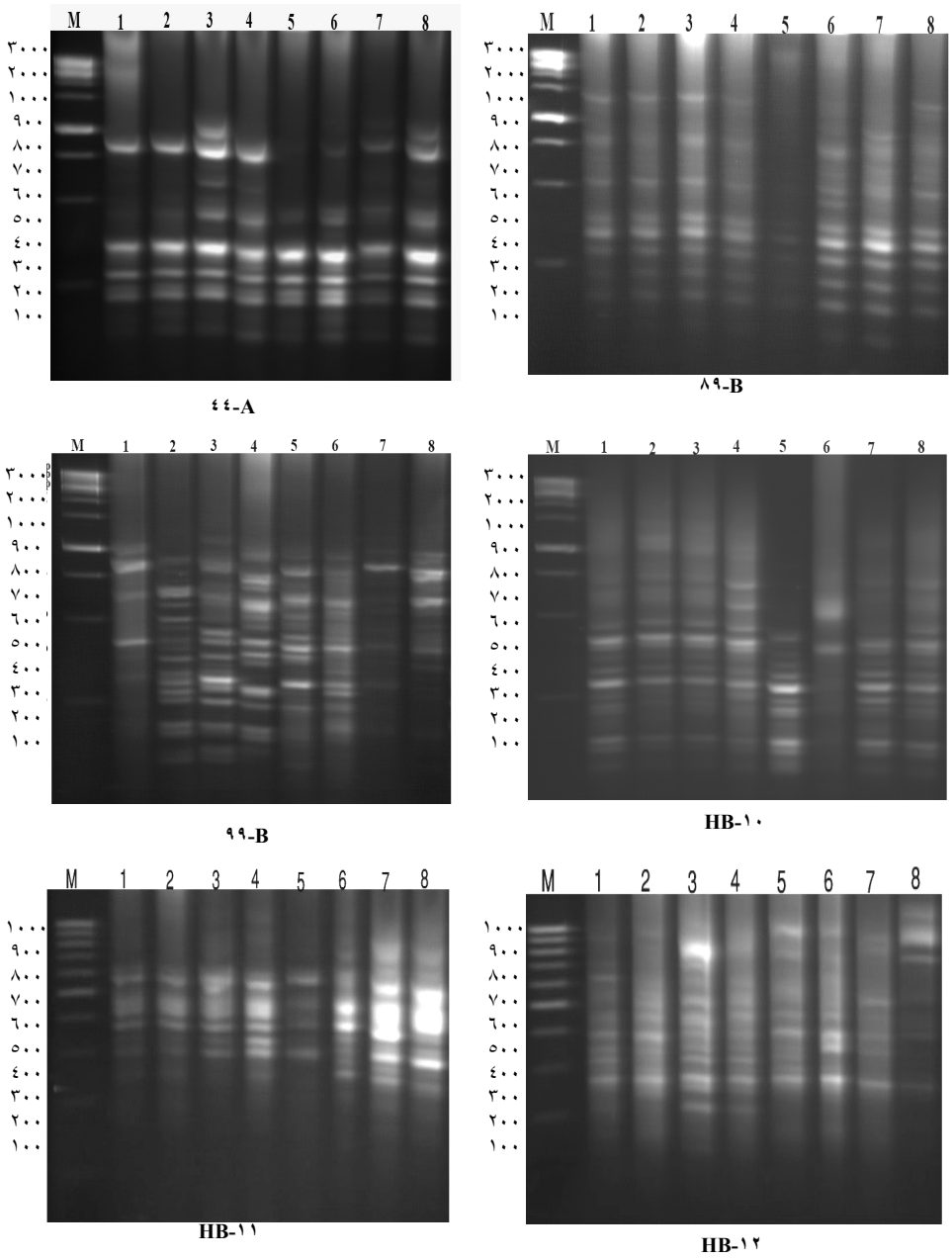

Fig. (٢): PCR products by six ISSR primers (٤٤-A, ٨٩-B, ٩٩-B, HB-١٠, HB-١١and HB-١٢) for the eight studied wheat genotypes. M DNA marker.

Table ٤. Variety(s)-specific markers in the eight studied wheat genotypes based on RAPD and ISSR analyses.

	Primer name	Band No.	MW (bp)	١	٢	٣	٤	٥	٦	٧	٨	Variety(s)-specific marker
RAPD	OP-A٠٣	٢	٨٨٠.٠٨	-	-	-	-	-	-	-	+	Saba'a (٨)
		٩	١٥٣.٢٢	-	-	-	-	+	+	+	+	Yemeni* (٥,٦,٧,٨)
	OP-A٠٧	١	١١٧٥.١٣	-	-	-	-	-	+	-	-	Smara'a (٦)
	OP-A١٠	١	١٠٧٢.١٢	-	-	-	-	-	+	-	-	Smara'a (٦)
		٦	٤٨٣.٩٨	+	+	+	+	-	-	-	-	Egyptian** (١,٢,٣,٤)
	OP-B١١	٦	٣٧٤.١٦	-	-	-	-	+	+	+	+	Yemeni (٥,٦,٧,٨)
	OP-B١٢	٤	٧٠٧.٧٩	+	+	+	+	-	-	-	-	Egyptian (١,٢,٣,٤)
		٨	٣٦٢.٢٥	-	-	-	-	+	-	-	-	Behows١٤ (٥)
		١١	٢٢١.٢٣	-	-	-	-	+	-	-	-	Behows١٤ (٥)
ISSR	٨٩-B	٢	٤٠٨.٩٠	-	-	-	-	-	-	+	-	Mysany (٧)
		٤	٢٨٧.٤٠	-	-	-	-	+	+	+	+	Yemeni (٥,٦,٧,٨)
		٦	٢٠٧.٤٦	-	-	-	-	-	+	-	-	Smara'a (٦)
	٩٩-B	١١	١١٩.١١	-	-	-	+	-	-	-	-	Sakha٦١ (٤)
	HB-١٠	١	٥٥٠.٠٥	+	+	+	+	-	-	-	-	Egyptian (١,٢,٣,٤)
		٢	٥٠٢.٦٩	+	+	+	+	-	-	-	-	Egyptian (١,٢,٣,٤)
		١٥	٧٤.٧٤	-	-	-	-	+	-	-	-	Behows١٤ (٥)
	HB-١٢	١	١١١٩.٧٠	-	-	-	-	-	-	-	+	Saba'a (٨)
		٦	٤٢٦.٢٠	-	-	+	-	-	-	-	-	Sakha٩٢ (٣)

***Yemeni = tetraploid, **Egyptian = hexaploid**

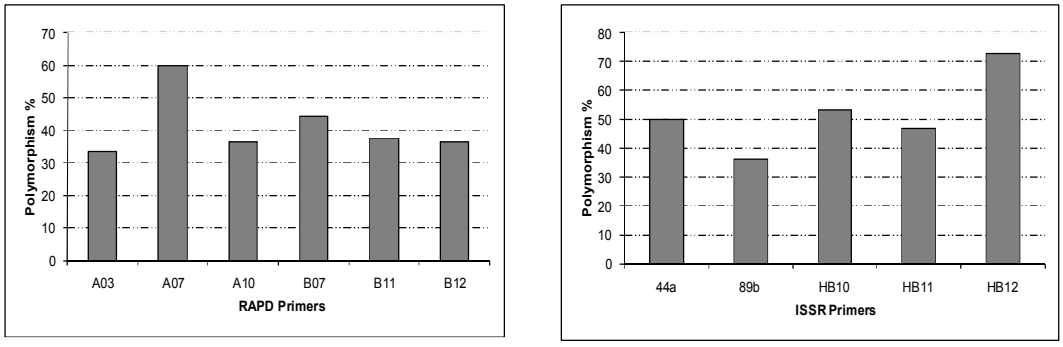

Fig. (٣): Polymorphism percentage for each primer used with the eight studied wheat varieties.

Genetic similarity analysis

The dendrogram tree among the studied wheat varieties based on RAPD, ISSR and overall markers were constructed using UPGMA cluster analysis program depending on the similarity matrix present in Table ٥. The analysis was based on the number of markers that were similar between any given pair of cultivars. The Egyptian hexaploid varieties, Giza١٦٤ and

Table ٥. Similarity matrix based on the overall marker polymorphism for the studied eight wheat varieties.

Variety	Giza١٦٤	Giza١٦٨	Sakha٩٢	Sakha٦١	Behows١٤	Smara'a	Mysany	Saba'a
Giza١٦٤	١							
Giza١٦٨	٠.٩٤٦	١						
Sakha٩٢	٠.٩٣٢	٠.٩٤٢	١					
Sakha٦١	٠.٩٥٣	٠.٩٣٢	٠.٩٤٩	١				
Behows١٤	٠.٨٢٣	٠.٨١٣	٠.٨٢٤	٠.٨٣٤	١			
Smara'a	٠.٨٢٨	٠.٨٣٨	٠.٨٢٩	٠.٨٤٩	٠.٩١٣	١		
Mysany	٠.٨٥٤	٠.٨٦٥	٠.٨٣٣	٠.٨٦٥	٠.٨٦٠	٠.٨٨٤	١	
Saba'a	٠.٨٦٣	٠.٨٥٣	٠.٨٤٣	٠.٨٧٣	٠.٨٥٩	٠.٨٨٢	٠.٩٣٢	١

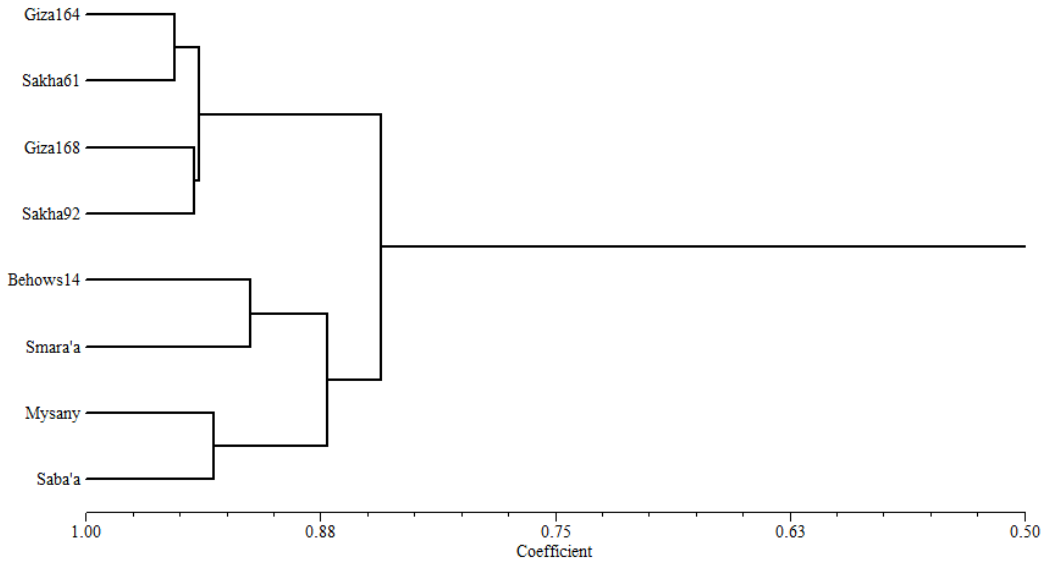

Fig. (٤): Dendrogram tree for the Egyptian and Yemeni wheat varieties based on RAPD and ISSR analyses.

Sakha ٦١ were highly related to each other with similarity value of ٠.٩٥٣, while variety pairs (Giza١٦٤ and Sakha٩٢) and (Giza١٦٨ and Sakha٦١) showed the lowest similarity value of ٠.٩٣٢. Concerning the tetraploid Yemeni genotypes, the highest similarity value (٠.٩٣٢) was observed between Mysany and Saba'a cultivars, while the similarity value between Behow١٤ and Saba'a was the lowest one (٠.٨٥٩). Concerning the Egyptian and Yemeni varieties, the lowest similarity value (٠.٨١٣) was observed between the Egyptian cultivar Giza١٦٨ and the Yemeni

Behows١٤, while the highest similarity value (٠.٨٧٣) was observed between Egyptian variety Sakha٦١ and the Yemeni Saba'a.

Dendrogram tree separated the eight varieties into two major clusters as shown in Fig. ٤. The first cluster was divided into two groups for the Egyptian hexaploid entries which showed variety pairs (Giza١٦٤ and Sakha٦١) and (Giza١٦٨ and Sakha٩٢). They were highly related to each others. The second cluster was divided into two groups for the Yemeni tetraploid genotypes which showed that pairs (Behows١٤ and Smara'a) and (Mysany and Saba'a) were remotely related to each others. However, the relationships among the studied wheat genotypes based on RAPD and ISSR analyses were in agreement with the origin ploidy level of these cultivars.

In conclusion, genetic background of the Egyptian varieties revealed that these studied cultivars were related to each other based on RAPD and ISSR analyses. Besides, the results illustrate that tetraploid cultivars could be distinguished by using molecular markers analyses. Moreover, these molecular markers could distinguish unique bands as specific markers for some Egyptian and Yemeni genotypes.

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تصنيف العلاقات الوراثية لبعض أصناف القمح المصري واليمنى باستخدام نوعين من الكشافات الجزيئية (RAPD & ISSR)

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تم استخدام نوعين من الكشافات الجزيئية (RAPD&ISSR) في هذه الدراسة بهدف تحديد العلاقات الوراثية بين أربعة أصناف من القمح المصري سداسي المجموعة الكروموسومية وهى (جيزة ١٦٤– جيزة ١٦٨ – سخا ٩٢ – سخا ٦١) و كذلك أربعة أصناف من القمح اليمنى وهى (بحوث ١٤ – سمراء – ميسانى – سبا) اقماح رباعية المجموعة الكروموسومية. و بتحليل نتائج الـ RAPD لقطع الـ DNA باستخدام ستة بادئات كان العدد الكلى لقطع الـ DNA الناتجة من الـ PCR هي ٥٨ قطعة. و كان هناك تعدد مظهري مختلف للقطع الناتجة (٢٤ قطعة للأصناف المصرية و اليمنية كانت ذات تعدد مظهري مختلف بنسبة ٤١,٣٨%) يتراوح وزنها الجزيئى من ١١٣ إلى ١١٧٥ قاعدة.

و بتحليل نتائج أل ISSR لقطع أل DNA باستخدام ستة بادئات كان العدد الكلى لقطع الـ DNA الناتجة من أل PCR هي ٧١ قطعة (٣٥ قطعة DNA في الأصناف المصرية و اليمنية ذات تعدد مظهري مختلف ٤٩,٣%). و كان هناك تعدد مظهري مختلف للقطع الناتجة يتراوح وزنها الجزيئى بين ٧٤ إلى ١١١٩ قاعدة.

الارتباط بين نتائج الـ RAPD لأصناف القمح المصرية و اليمنية اظهر تعدد مظهري مختلف بنسبة ٤٦,٤%.

وضحت شجرة علاقة القرابة باستخدام دليل النشابة بين الأصناف أن بعض الأصناف كانت متقاربة و البعض الآخر غير متقارب.

ومن هذه الدراسة اتضح أن الكشافات الجزيئية (RAPD&ISSR) مفيدة ككشافات خاصة و محددة للتوصيف الوراثى الجزيئى و تحديد العلاقات الوراثية بين أصناف القمح المختلفة ويمكن بواسطتها التمييز بين أصناف القمح ذات المجموعات الكروموسومية الرباعية والسداسية والمحافظة عليها.