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دراسة تحمل الإجهاد الحراري في بعض أصناف القمح بإستخدام دلائل الSRAP وال TRAP

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الملخص العربي

تم إستخدام أربعة أصناف من القمح السداسي لتوصيف وتحليل التنوع الوراثي لتحمل الحرارة بإستخدام كل من دلائل ال SRAP وال TRAP وكان اثنان من أصناف القمح مصريه (جيزة ١٦٨ وجميزة ٧) وصنف مكسيكي متحمل للحرارة (SERI 82) بالإضافة إلي صنف صيني حساس للحرارة هو (Chinese Spring). واستخدمت خمسة وعشرين تركيبة من البوادئ لل SRAP و ١٢ لل TRAP لهذا الغرض. تم الحصول على نسبة ٥٩٪ إختلافات وراثية من دلائل ال SRAP في حين أن دلائل ال TRAP انتجت إختلافات وراثية بنسبة ٨١.٨٪. وكان محتوى المعلومات متعددة الأشكال (PIC) من دلائل الTRAP أعلى من دلائل ال SRAP. وقد تم تحديد مجموعة من دلائل ال SRAP و / أو ال TRAP في التراكيب الوراثية المستخدمة و كانت مرتبطة مع صفة تحمل الحرارة. تم تحديد العديد من الدلائل للصنف الصيني الربيعي (Chinese Spring)؛ ويقترح أنها تكون مرتبطة مع الحساسية للحرارة في القمح. وتشير نتائج التحليل العنقودي لكل من نوعي الدلائل الجزيئية إلي أن الأصناف الأربعة من القمح إنفصلت إلي مجموعتين واضحتين إحتوت المجموعة الأولي علي الأصناف (جيزة ١٦٨ وجميزة ٧ والصنف المكسيكي SERI 82) بينما إحتوت المجموعة الثانية علي الصنف Chinese Spring . يمكن القول أنه يمكن استخدام دلائل ال SRAPو / أو دلائل ال TRAP بكفاءة في دراسات توصيف والتفريق بين التراكيب الوراثية المختلفة في درجات تحملها للحرارة في القمح وكذلك في دراسة التنوع الوراثي في القمح.

STUDY OF HEAT STRESS TOLERANCE IN SOME WHEAT (*TRITICUM AESTIVUM* L.) VARIETIES USING SRAP AND TRAP MARKERS

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ABSTRACT: *Four hexaploid wheat varieties; two of them were Egyptians ('Giza 168' and 'Gemmeiza 7'); one Mexican heat tolerant variety ('SERI 82') and one heat susceptible Chinese variety ('Chinese Spring'); were used to study heat tolerance in wheat by using SRAP and TRAP markers. Twenty five SRAP primers combinations and 12 TRAP primer combinations were used for this purpose. A percentage of 59% polymorphism was obtained from the SRAP markers while the TRAP markers generated 81.8% polymorphism. The polymorphic information content (PIC) of the TRAP markers was higher than the SRAP markers. Different SRAP and/or TRAP markers have been assigned to the genotypes and were correlated with heat response. Many markers were assigned to 'Chinese Spring' genotype and proposed to be correlated with the heat susceptibility in wheat. The results of both SRAP and TRAP dendrograms showed same results. The dendrograms separated the four wheat genotypes into two distinct clusters, the first cluster contained the genotypes 'Giza 168', 'Gemmeiza 7' and 'SERI 82' while the 'Chinese Spring' genotype was separated alone in the other cluster. It can be said that SRAP and/or TRAP markers can be used efficiently in differentiating heat tolerant wheat genotypes.*

Key words: *Wheat; SRAP; TRAP; Heat tolerance; Genetic diversity.*

INTRODUCTION

Wheat is a major and temperate crop in the world grows optimally at 18-23ºC (the thermal kinetic window) (Porter and Gawith, 1999). High temperature stress in wheat is a major cause of yield reduction as much as 15% in some regions in Egypt as well as in many wheat-growing regions of the world (Saadalla, 1993; Maestri *et al*.,2002; and Balla *et al.,* 2009). Some attempts to develop heat-tolerant genotypes via conventional plant breeding protocols have been successful and via molecular breeding which provided additional tools to develop crops with improved heat tolerance.

Molecular markers became in the last decades important tools in decision making and revealing genetic relationships among germplasm. PCR-based molecular markers are preferred over other types because of their ease of use. Sequence-related amplified polymorphism (SRAP) is designed to amplify open reading frames (ORFs) (Li and Quiros, 2001) based on two special primer pairs. The forward primers preferentially amplify exonic regions and the reverse primers preferentially amplify intronic regions and regions with promoters. Compared with other molecular markers, SRAP markers are more reproducible, stable, not complicated, and can be used in different materials according to its unique primer design. As a result, SRAPs have been adapted for a variety of research purposes, including germplasm identification, linkage map construction, gene tagging and mapping, gene expression study, map-based cloning, and evolutionary study (Gui *et al.,* 2009; Zhao *et al.,*2010). About the genetic diversity, SRAPs have been demonstrated to be very powerful in many plant species, such as, cotton (Yu *et*

al., 2007), Rice (Zhao *et al.,*2010; Dai *et al.,* 2011) and wheat (Dong *et al*., 2010; Al-Doss *et al.,* 2010).

The target region amplification polymorphism (TRAP) technique (Hu and Vick 2003) is a rapid and efficient PCR-based technique, developed based on SRAP, which utilizes bioinformatics tools

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and expressed sequence tag (EST) database information to generate polymorphic markers, around targeted candidate gene sequences. The technique uses two primers (18 nucleotides in length) to generate markers. One of the primers, the fixed primer, is designed from the targeted EST sequence in the database; the second primer is an arbitrary primer with either an AT- or GC-rich core to anneal with an intron or exon.

As the TRAP technique can be used to generate markers for specific gene sequences, it is useful for genotyping germplasm and generating markers associated with desirable agronomic traits in crop plants for marker-assisted breeding (Hu and Vick, 2003). TRAPs are effectively used in mapping QTL in wheat *(Triticum aestivum L.)* intervarietal recombinant inbred population (Liu *et. al.,* 2005), and in constructing wheat genetic maps (Liu *et al.,* 2007, Chu *et al.,* 2008). SRAP and TRAP marker approaches are multi-loci and multi-allelic features which make them potentially more efficient for genetic diversity analysis. In this study, we used SRAP and TRAP markers to characterize and analyze the genetic differentiation of heat tolerant/susceptible of some wheat genotypes and to determine markers associated with heat tolerance and susceptibility.

MATERIAL AND METHODS:

Plant material

Four different hexaploid wheat varieties were used in this study; two of them were Egyptians ('Giza 168' and 'Gemmeiza 7') and were kindly provided by Agricultural Research Center (ARC), Giza, Egypt; one Mexican variety ('SERI 82') as heat tolerant variety (Ibrahim and Quick 2001) and one Chinese ('Chinese Spring') as heat susceptible variety (Qin *et al.,* 2008). The last two varieties were kindly obtained from CIMMYT. The varieties, their pedigrees and origins are presented in Table (1).

DNA extraction

Surface-sterilized grains from each variety were germinated in sterilized Petri-dishes, containing sterilized filter papers moistened with tap water. Leaves of 10-days seedlings were harvested and crushed into powder with the aid of liquid nitrogen, and the genomic DNA was extracted by modified CTAB method Dellaporta *et al.,* (1983). Working stock solutions were made by diluting the DNA samples to 25ng/µl and stored at -20 °C until using for PCR analysis.

SRAP and TRAP primer designation:

Twenty five SRAP primers combinations and 12 TRAP primer combinations were used to generate and characterize the heat tolerance response of the four wheat genotypes. The different SRAP primers sequences were selected according to literature (Li *et al*., 2009, Dong *et al*., 2010, Al-Doss *et al.,* 2010). The TRAP markers involved using two fixed primers in combinations with six random primers in order to obtain a final 12 primers combinations (Table 2). The TRAP primers were selected such as four of them (W10, W19, W22, and W33) were used by Li *et al.,* (2006) and two primers (T03 and T13) were described by Xu *et al.,* (2003). One of the fixed TRAP primers (RGA2) was described by Zhang *et al.,* (2010) and the other primer (HSP70) was designed from wheat EST sequences (CV066816) in the NCBI database at the website: http://www.ncbi.nlm.nih.gov/nucest/51529993?report=genbank. The EST sequence (CV066816) is similar to the heat shock protein member (HSP70) gene family sequence (AF005993). The primer was

designed using the web-based program PRIMER3 in the NCBI database (http://www.ncbi.nlm.nih.gov/tools/primer-blast) Rosen and Skaletsky (2000). SRAP and TRAP primers were synthesized by Metabion **(**Metabion international AG. Martinsried, Germany, Table 2).

PCR analysis:

PCR analysis was conducted using 25 µl reaction volume containing 5 µl of 5x PCR buffer, 1.5 mM of $MgCl_2$, 0.4 mM of dNTPs, 0.35 µl primers (100 µM) , 25 ng genomic DNA and 1U of GoTaq® DNA Polymerase (Promega, Madison ,USA).

Table (1): Wheat varieties, their pedigrees, origins and year of release.

No	Varieties	Pedigree	Origin	Year of release
1	Giza 168	MRL/BUC//SER CM93046-8M-0Y-0M-2Y-0B	Egypt	--
2	Gemmeiza 7	7CMH74A630/SX//SERI82/AGENT	Egypt	--
3	SERI 82	KVZ/BUHO//KAL/BB	Mexico	1982
4	Chinese Spring	Chinese landrace	China	1932

Table (2): The primers types and sequences of SRAP and TRAP markers.

Primer name	Primer type	Sequence (5′–3′)
	SRAP primers	
F10	Forward	TGAGTCCAAACCGGTGC
Me1	Forward	TGAGTCCAAACCGGATA
Me2	Forward	TGAGTCCAAACCGGAGC
Me3	Forward	TGAGTCCAAACCGGACC
Me4	Forward	TGAGTCCAAACCGGTAG
Em1	Reverse	GACTGCGTACGAATTTGC
Em2	Reverse	GACTGCGTACGAATTGCA
Em3	Reverse	GACTGCGTACGAATTAGC
Em4	Reverse	GACTGCGTACGAATTTAG
Em7	Reverse	GACTGCGTACGAATTCAA
	TRAP primers	
W10	Arbitrary primers	CGTTCCTCAAGTGGTACA
W19	Arbitrary primers	TCATGCCCAGTGATACCT
W22	Arbitrary primers	GCTGACCTTCCATTGAGT
W33	Arbitrary primers	ACTGCTCTAACGGGAAAC
T03	Arbitrary primers	CGTAGCGCGTCAATTATG
T13	Arbitrary primers	GCGCGATGATAAATTATC
Hsp70	Fixed primer	GCGCTGGCCCCAAGATCGAG
RGA2	Fixed primer	CTATGGTGACTATTGCAAGGGGAA

The PCR program for SRAP analysis was carried out using Touchdown PCR program. The main program was performed for 6 cycles at 94oC for 1 min, 51oC for 1 min, decreasing 1oC in every cycle, and 72oC for 1 min; followed by 29 cycles at 94oC for 1 min, 46oC for 1 min and 72oC for 1 min. The previous programs were preceded by a denaturation step at 94oC for 5 min and followed by an extension step at 72oC for 7 min. PCR products were separated on 1.5 % agarose gel

electrophoresis, stained using ethidium bromide and photographed with digital camera. The PCR program for TRAP analysis was performed using Touchdown PCR program. The main program was performed for 8 cycles at 94°C for 1 min, 60°C for 1 min, decreasing 1°C in every cycle, and 72°C for 1 min; followed by 26 cycles at 94°C for 1 min, 52°C for 1 min and 72°C for 1 min. The previous programs were preceded by a denaturation step at 94oC for 5 min and followed by an extension step at 72oC for 7 min. PCR products were separated on 1.5 % agarose gel electrophoresis, stained using ethidium bromide and photographed with digital camera.

Statistical analysis:

All gels of both SRAP and TRAP markers were scored as 0/1 for absence/presence of the bands, respectively. The total number of band and the number of polymorphic bands were calculated as well as the polymorphic information content (PIC) which was calculated according to Anderson *et al.* (1993) using the following simplified formula: $PIC_i = 1- \Sigma p^2_{ij}$

Where pij is the frequency of the jth allele for marker, ith summed across all alleles for the locus. Similarity coefficient matrices were calculated for both SRAP and TRAP markers using simple matching similarity algorithm (Sokal and Sneath, 1963). Phylogenetic dendrograms were constructed using the UPGMA method (Unweighted Pair-Group Method with arithmetical algorithms Averages; Sneath and Sokal, 1973). Goodness of fit and correlations among all obtained similarity matrices (SRAP and TRAP markers) were performed using the Mantel's test (Mantel, 1967). All the above mentioned analyses were performed using the NTSYS PC2.1 software (Rohlf, 1998).

RESULTS AND DISCUSSION:

SRAP and TRAP patterns and polymorphism:

Detection and analysis of genetic variation can help us to understand the molecular basis of various biological phenomena in plants. Using 25 SRAP primers combinations and 12 TRAP primers combinations, four hexaploid wheat varieties having different origins (e.g. Egypt, Mexico and China) and different levels of heat tolerance were screened. The wheat varieties were selected on the base of heat tolerance according to their background on heat stress response. Two Egyptian hexaploid wheat varieties ('Giza 168' as heat tolerant variety and Gemmeiza 7 as heat susceptible variety) were selected according to their heat tolerance (Eldemery 2008). Another two hexaploid wheat varieties were kindly obtained from CIMMYT with information about their backgrounds for the heat tolerance ('SERI 82' as heat tolerant variety and 'Chinese Spring' variety as heat susceptible variety).

The results of SRAP markers revealed that 241 bands were generated from all the 25 primers combinations, 142 out of them were polymorphic (with 59% polymorphism, Table 3). The total number of bands generated from each primer combination varied and ranged from four bands for the combinations (Me1+Em7 and Me2+Em7) to 15 bands for the combination (Me2+Em7). The number of polymorphic bands for the SRAP primers combinations varied also and ranged from only one band for the combination (Me2+Em1) to 13 bands for the primer combination (Me4+Em1, Table 3). The percentage of polymorphism of the SRAP primers combinations was around the 50% for the most of the combinations, but in general it was ranging from 16.7% for the primers combinations (Me2 + Em1) to 100% for the primers combinations (Me1 + Em4 and Me4 + Em1). The polymorphic information content of the SRAP primers combinations was in general intermediate and ranged from 0.28 for the primers combinations (Me2 + Em1) to 0.89 for the primers combinations Me4 + Em2, (Table 3).

The results of TRAP markers showed that 183 bands were generated from all the TRAP primer combinations, 149 out of them were polymorphic (with 81.8% polymorphism, Table 3). The total number of bands generated from each TRAP primer

combination varied and ranged from ten bands for the primers combinations (RGA+W19 and RGA+W33) to 27 bands for the primers combination RGA+W22, (Table 3). The number of polymorphic bands generated from each TRAP primers combinations ranged from three bands for the primers combination (HSP70+W19) to 23 bands for the primers combination (RGA+W22). The percentage of polymorphisms of the TRAP primers combinations ranged from 27.7% for the primers combination (HSP70+W19) to 90% for the primers combinations RGA+W19 and RGA+T03, (Table 3). The polymorphic information content (PIC) of TRAP markers was higher than SRAP markers, Table (3). The PIC ranged from 0.45 for the primers combination (RGA+W19) to 0.86 for the primers combinations (HSP70+W10). These data indicate that the total number and the number of polymorphic bands generated from TRAP markers were in general higher than the bands number generated from the SRAP markers. In the contrary, Al-Doss *et al.,* (2010) reported that SRAP analysis produced 45 polymorphic bands out of 128 bands (35.16%) while in TRAP analysis, 22 out of 55 bands (40.0%) were polymorphic.

Different SRAP and /or TRAP markers have been assigned to the genotypes and correlated with the heat tolerance or susceptibility. For SRAP markers, a marker at molecular weight of about 1100 bp has been assigned to the heat tolerant wheat genotypes (e.g. 'Giza 168' and 'SERI 82') using the primers combinations F10+Em1, (Figure 1). Many other SRAP markers have been assigned to these genotypes separately which characterize them. Molecular weight of 950 bp in length is one of these markers characterizing the heat tolerant genotype 'Giza 168' using the primers combination Me1+Em4, (Figure 1). Similarly, a band with molecular weight of 600 bp was assigned to the heat tolerant wheat genotype 'SERI 82' using the primers combination (F10+Em1) and using the primers combination (F10+Em3) at molecular weigh about 1100 bp in length, (Figure 1). Many SRAP markers have been assigned for the heat tolerant wheat genotypes ('Giza 168' and 'SERI 82') along with the heat susceptible wheat genotype 'Gemmeiza 7'. As an example for these markers a band at molecular weight of 470 using the primers combination (Me2+Em4) and a band of molecular weight of about 130 bp in length using the primers combination Me2+Em7, (Figure 1). The SRAP primers combination (Me3+Em1) is another good example for these types of markers.

The pattern of the genotype 'Chinese Spring' seems to be very different from the other genotypes; hence, many markers were assigned to this genotype and proposed to be correlated with the heat susceptibility in wheat. These markers such as band at molecular weight of 900 bp using the primers combination (F10+Em2), using the primers combination (F10+Em3) at molecular weight of 1200 bp, using the primers combination (Me2+Em4) at molecular weight of both 1200 and 1500 bp, using the primers combination (Me3+Em2) at molecular weight of 1000, 1200 and 1500bp, Figure (1). The same results have been obtained using the TRAP primers combinations (HSP70+W22), (HSP70+W33), (HSP70+T03), (HSP70+T13), (RGA+W33) and (RGA+T03), Figure (2). Thus, it seems that the TRAP fixed primer (HSP70) was very effective in differentiating of heat tolerant and susceptible wheat genotypes. These results suggest that both SRAP and TRAP molecular markers can be used to characterize and analyze the genetic differentiation of heat tolerant wheat genotypes. Castonguay *et al.,* (2010) obtained similar results using SRAP markers in the identification of genetic polymorphisms associated with quantitative traits in alfalfa species and stated that SRAP markers are useful tools for indirect selection of freezing tolerance in alfalfa. Also Chen *et al.,* (2011) recently reported that three TRAP markers were found to be polymorphic between the stripe rust wheat resistant and susceptible DNA bulks as well as their parents.

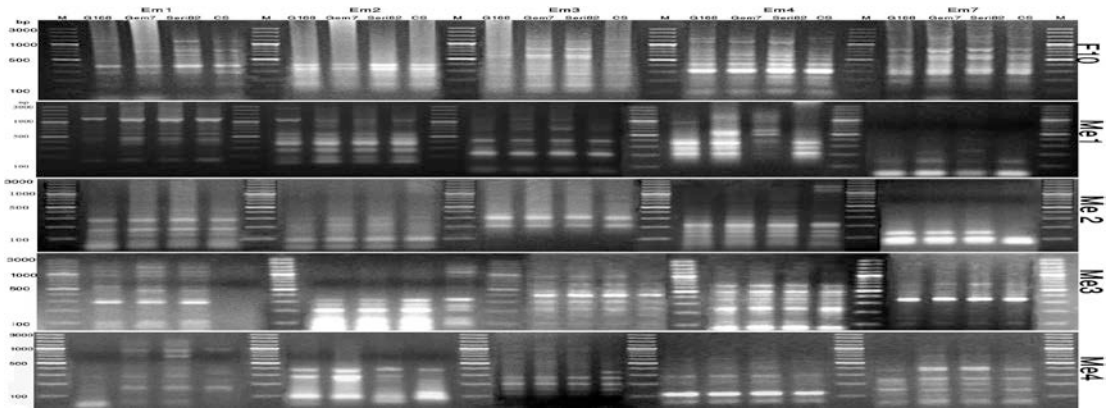

Figure (1): PCR products patterns of 25 SRAP primers combinations on four wheat genotypes differed in heat tolerance response.

Table (3): Number of generated bands and the polymorphism of the different SRAP and TRAP marker combinations.

Primers Combination	Total Bands	Polymorphic. Bands	% Polymorphism	PIC
SRAP Markers	241	142	59	
F10 + Em1	8	4	50	0.69
F10 + Em2	7	4	57	0.69
F10 + Em3	14	11	78.6	0.76
F10 + Em4	12	6	50	0.66
F10 + Em7	10	5	50	0.68
Me1 + Em1	14	9	64.3	0.76
Me1 + Em2	12	5	41.7	0.61
Me1 + Em3	11	5	45.5	0.64
Me1 + Em4	12	12	100	0.78
Me1 + Em7	4	3	75	0.75
Me2 + Em1	6	1	16.7	0.28
Me2 + Em2	5	2	40	0.48
Me2 + Em3	5	2	40	0.60
Me2+ Em4	13	7	53.8	0.67
Me2+ Em7	4	2	50	0.50
Me3 + Em1	9	4	44.4	0.62
Me3 + Em2	13	9	69	0.66
Me3 + Em3	9	3	33.3	0.52
Me3 + Em4	9	3	33.3	0.52
Me3 + Em7	9	6	66.7	0.79
Me4 + Em1	13	13	100	0.82
Me4 + Em2	13	11	84.6	0.89
Me4 + Em3	7	3	42.9	0.61
Me4 + Em4	7	3	42.9	0.61
Me4 + Em7	15	9	60	0.76
TRAP Markers	183	149	81	
RGA + W10	22	18	81.8	0.68
RGA + W19	10	9	90	0.45
RGA + W22	27	23	85	0.67
RGA + W33	10	8	80	0.64
RGA + T03	20	18	90	0.55
RGA + T13	19	17	89	0.74
HSP70 + W10	12	8	66.7	0.86
HSP70 + W19	11	3	27.7	0.82
HSP70 + W22	13	12	92	0.67
HSP70 + W33	11	8	72.7	0.85
HSP70 + T03	17	16	94	0.74
HSP70 + T13	11	9	81.8	0.81

Clear results for this point can be noted from the TRAP primers combinations (RGA+W10) and RGA+W22, (Figure 2) in which many markers appeared to be common for these three genotypes. These results can be expected and explained from the pedigree of the genotypes. The Mexican genotype 'SERI 82' is an ancestor of the Egyptian genotype 'Gemmeiza 7' and thus it may carry some of its genetic background. Using the TRAP primers combination (RGA+W22) explain clearly this relationship between the two genotypes, (Figure 2). Therefore, SRAP and TRAP markers could be used to confirm the genotypes pedigrees. These results are in agreement with the research reported earlier in sugarcane by Alwala *et al.,* (2006). They stated that molecular markers, such as TRAP and AFLP, could be used to confirm the pedigrees. Moreover, molecular markers provide a more direct and precise estimate of allele frequency differences among the parents.

Molecular Cluster analysis:

Both SRAP and TRAP collected data were used to calculate the similarity matrices among the wheat genotypes using the simple matching coefficient algorithm. The similarity matrices were used to construct the separated dendrograms. The similarity matrices and the two dendrograms were compared between the two tested markers.

The results of SRAP dendrogram showed that the four wheat genotypes were distributed into two distinct clusters. The first cluster contained the genotypes 'Giza 168', 'Gemmeiza 7' and 'SERI 82' while the 'Chinese Spring' genotype was separated alone in the other cluster, (Figure 3). The most two related genotypes were 'Gemmeiza 7' and 'SERI 82' varieties (r = 0.83, Table 4). In this study, SRAP marker system was useful in identification and clears the genetic diversity of bread wheat. This findings agreed with the studies reported previously in hard red winter wheat (Fufa *et al.,* 2005), in buckwheat (Li *et al.,* 2009), and recently in wild emmer wheat (Dong *et al.,* 2010). They reported that detected genetic diversity and population structure of 15 wild emmer wheat (*Triticum dicoccoides*) populations from Israel was achieved by using 30 SRAP primer pairs (primers combinations). They stated that the SRAP marker is an effective technique for the diversity evaluation of the *T. dicoccoides* due to its capacity to reveal relatively more informative bands leading to desirable discrimination ability.

The results of TRAP dendrogram showed almost the same results which were obtained from the SRAP dendrogram (Figure 4). The four wheat genotypes were divided also into two distinct clusters; the first cluster contained the genotypes 'Giza 168', 'Gemmeiza 7' and 'SERI 82' while the other cluster contained the variety 'Chinese Spring', Figure (4). The most two related genotypes were 'Gemmeiza 7' and 'SERI 82' varieties (r = 0.91, Table 4). Previously, Xu *et al.,* (2003) successfully used TRAP markers to estimate the genetic diversity in stock of tetraploid wheat (*T. turgidum* L., 2n =4x =28, AABB genomes). Liu *et al.*, (2005) and (2007) also reported that TRAP markers, which allowed linkage groups to be joined and many gaps to be filled. Moreover, they were very efficient for rapidly generating a large number of markers scattered across the genome and constructing intervarietal genetic linkage map in hard red spring wheat.

It seems that the results of both SRAP and TRAP dendrograms are similar. This fact can be inferred from the very high correlation between their matrices according to Mantel's test (r = 0.82). These results are in disagreement with those obtained by Al-Doss *et al.,* (2010). They reported that the dendrogram based on SRAP markers differed from that based on TRAP markers, when they used SRAP (19 primers) and TRAP (9 primers) markers to determine the genetic diversity of 6 durum wheat genotypes. It can be said that both SRAP and TRAP markers were able to differentiate between heat tolerant and susceptible wheat genotypes. Furthermore, different molecular markers have been assigned to the tolerant and susceptible wheat genotypes.

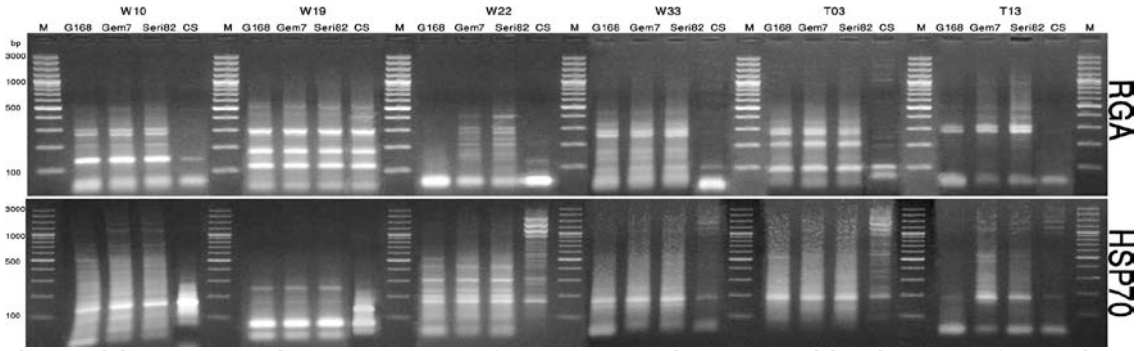

Figure (2): PCR products patterns of 12 TRAP primers combinations on four wheat genotypes differed in heat tolerance response.

Table (4): Similarity correlation coefficients of wheat genotypes using SRAP (lower part) and TRAP (upper part) markers.

Correlation	Giza168	Gemmeiza7	SERI83	Chinese Spring
Giza168		0.77	0.75	0.40
Gemmeiza7	0.72		0.91	0.30
SERI83	0.67	0.83		0.27
Chinese Spring	0.60	0.66	0.62	

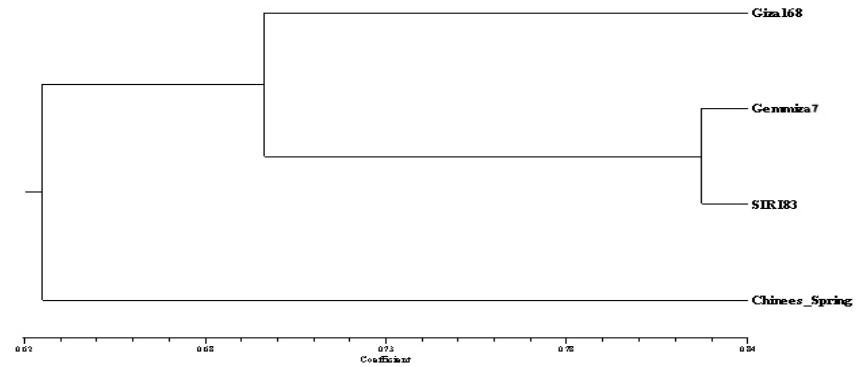

Figure (3): SRAP cluster analysis of four wheat genotypes depending upon simple matching coefficient and using the UPGMA clustering method.

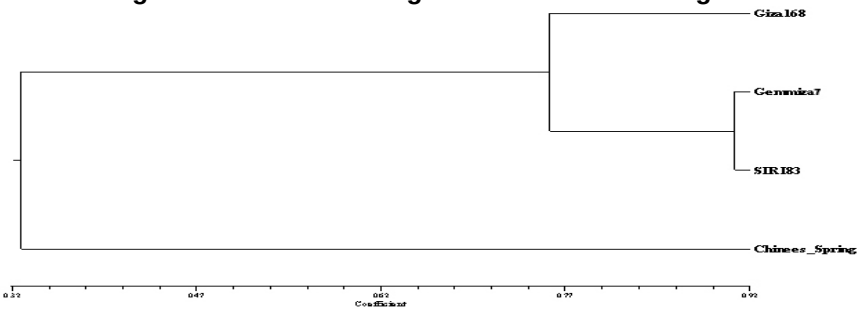

Figure (4): SRAP cluster analysis of four wheat genotypes depending upon simple matching coefficient and using the UPGMA clustering method.

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دراسة تحمل الإجهاد الحراري في بعض أصناف القمح بإستخدام دلائل الSRAP وال TRAP

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الملخص العربي

تم إستخدام أربعة أصناف من القمح السداسي لتوصيف وتحليل التنوع الوراثي لتحمل الحرارة بإستخدام كل من دلائل ال SRAP وال TRAP وكان اثنان من أصناف القمح مصريه (جيزة ١٦٨ وجميزة ٧) وصنف مكسيكي متحمل للحرارة (SERI 82) بالإضافة إلي صنف صيني حساس للحرارة هو (Chinese Spring). واستخدمت خمسة وعشرين تركيبة من البوادئ لل SRAP و ١٢ لل TRAP لهذا الغرض. تم الحصول على نسبة ٥٩٪ إختلافات وراثية من دلائل ال SRAP في حين أن دلائل ال TRAP انتجت إختلافات وراثية بنسبة ٨١.٨٪. وكان محتوى المعلومات متعددة الأشكال (PIC) من دلائل الTRAP أعلى من دلائل ال SRAP. وقد تم تحديد مجموعة من دلائل ال SRAP و / أو ال TRAP في التراكيب الوراثية المستخدمة و كانت مرتبطة مع صفة تحمل الحرارة. تم تحديد العديد من الدلائل للصنف الصيني الربيعي (Chinese Spring)؛ ويقترح أنها تكون مرتبطة مع الحساسية للحرارة في القمح. وتشير نتائج التحليل العنقودي لكل من نوعي الدلائل الجزيئية إلي أن الأصناف الأربعة من القمح إنفصلت إلي مجموعتين واضحتين إحتوت المجموعة الأولي علي الأصناف (جيزة ١٦٨ وجميزة ٧ والصنف المكسيكي SERI 82) بينما إحتوت المجموعة الثانية علي الصنف Chinese Spring . يمكن القول أنه يمكن استخدام دلائل ال SRAPو / أو دلائل ال TRAP بكفاءة في دراسات توصيف والتفريق بين التراكيب الوراثية المختلفة في درجات تحملها للحرارة في القمح وكذلك في دراسة التنوع الوراثي في القمح.