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BIOCHEMICAL AND MOLECULAR MARKERS ASSOCIATED WITH EARLINESS TRAIT IN BREAD WHEAT

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ABSTRACT: This study was aimed to find out some biochemical and molecular genetic markers associated with earliness trait in bread wheat *(Triticum aestivum L.)*. Six parental genotypes of wheat were used that represent a wide range of variability for earliness trait namely; Sids- 4 and Sakha- line (early), Sakha-93and Gemmeiza-7 (medium), Gemmeiza-9 and Milan(late). F_1 seeds were obtained for five crosses were chosen to make biochemical analysis using SDS – PAGE Banding Pattern. These crosses were (Sids-4 × Sakha-line), (Sakha-93 × Gemmeiza-7), (Gemmeiza-9 × Milan), (Sids-4×Milan) and (Sids-4 ×Gemmeiza-7). The obtained results showed that, there are a biochemical and molecular markers associate with earliness trait in wheat. Two bands with molecular weight ranged from (90.276 to 77.181 KD) in the cross (Sids-4 × Milan), that appeared only in F_1. So, these bands could be used as a selective biochemical marker for earliness trait in wheat.

Regarding to the molecular analysis, only one cross (Sid-4 × Milan), was chosen for the wide variation between its parents. RAPD–PCR analysis was carried out using F_2 bulked segregant analysis technique. The obtained results showed that, the primer (OPB–10) exhibited only one negative marker with 637bp that appeared in late parent and late bulked F_2. In addition, in primer (OPD–05) one positive marker with 1463bp that appeared in early parent and early bulked F_2. These two bands could be used as marker for earliness in wheat breeding programs.

Key words: Wheat, earliness, molecular markers, RAPD, SDS- PAGE.

INTRODUCTION

Wheat *(Triticum aestivum L.)* is one of the major staple foods all over the world. In Egypt, wheat is the main cereal crop. Breeding for high yielding cultivars is an ongoing process for increasing the wheat production. However, we are needed for early cultivars with high yielding. Characterization of the new genotypes should include their performance, DNA and/or protein patterns. Molecular markers are the best tools for determining genetic relations of domestic cultivars in a short period of time. In wheat, RAPD technique is mainly used to mark and locate target genes; identify and mark fragments of (alien) chromosomes; determine the genetic relationships between *Triticum sp.* and related species; and analyze the genetic diversity of wheat varieties (Yu *et al.*, 2004) Several studies have been carried out to determine genetic variability and/or similarity using RAPD molecular markers (Suvarna, 2001). And (Svetlana *et al.*, 2007) determined the levels of genetic polymorphism in the collection of spring common wheat genotypes based on RAPD -PCR analysis. In addition, proteins are usually considered as the direct product of genes and the environment does not influence their expression. Among the biochemical techniques, SDS-PAGE is widely used due to its simplicity and effectiveness for describing the genetic structure of crop germplasm. The analysis of storage protein variation in wheat has proved to be useful tool not only for diversity studies but also to optimize variation in germplasm collections. SDS- PAGE can be used as a promising tool for distinguishing cultivars of particular crop species (kaleem *et al.*, 2008).

The objective of this investigation was to develop some molecular and biochemical markers, using SDS-PAGE protein banding pattern and RAPD markers, associated with earliness trait in wheat genotypes employing bulked segregant analysis technique.

In addition, the relationship between some wheat genotypes was also studied.

MATERIALS AND METHODS

This study was carried out at Experimental Farm of Gemmeiza, Agricultural Research Station, Egypt through three successive seasons of 2004/2005, 2005/2006 and 2006/2007.Chemical analysis were carried out at the Molecular Genetic Lab. Genetics Dept., Fac. of Agriculture, Zagazig University and Agriculture Genetic

Engineering Research Institute (AGERI) Giza, Egypt. Six parental genotypes of spring wheat *(Triticum aestivum L.)* were used in this study namely; Sids-4, Sakha- line, Gemmeiza-7, Gemmeiza-9, Sakha-93 and Milan were chosen which represent a wide range of earliness variability. The name, origin and pedigree of these cultivars are presented in Table 1. In the first season, the parental genotypes were planted in three different sowing dates. Simultaneously, pair crosses (half diallel), were performed to obtain the F_1 seeds. In the second season, the hybrid seeds were sown. Meanwhile, F_1 plants were self–pollinated to produce F_2 seeds. In third season, the obtained seeds of these populations i.e., P_1, P_2, F_1 and F_2 for the cross (Sids-4 × Milan) is evaluated using a randomized complete block design. Each plot consists of 30 individual guarded plants for P_1, P_2 and F_1, and 300 plants for the F_2 and the following analysis were done:

SDS – PAGE Analysis

Protein analysis was performed using sodium dodecyl sulphate polyacrlamide gel electrophoresis (SDS–PAGE) according to Laemmli (1970) for five crosses (Sids 4× Sakha line), (Sakha 93 × Gemmeiza 7), (Gemmeiza 9 × Milan), (Sids 4 × Milan) and (Sids-4 × Gemmeiza-7).

RAPD DNA Analysis

DNA analysis was performed using RAPD technique. Six random primers used against the template DNA presented in Table 2. Fresh leaves were collected from parents, F_1, bulked from early F_2 plants and bulked late F_2 plants at heading stage. DNA was extracted according to (Dellaporta *et al.,* 1983).

Statistical Analyses

The data was computed using (numerical taxonomy and multivariate analysis system according to (Rohlf exeter software, 2000).

RESULTS AND DISCUSSION

Protein Analysis

Data in Fig. 1 and Table 3 illustrate SDS–PAGE protein profiles of the studied wheat genotypes. The electrophoretic profiles of the studied genotypes revealed that, the total number of protein banding patterns was thirty one, distributed widely among wheat entries, and having a range of molecular weights of 34.237 to 133.994 KD. Twenty eight bands (90.323%) out of the thirty one

Table 1. The name, origin and pedigree of wheat genotypes used in this study

	Name	Origin	Pedigree	Character
1	**Sids 4**	**Egypt**	Maya"s"/ Mons"s"// CMH74A.592/3/ Sakha 8*2 SD/000/-2SD-2SD-0SD	**Early**
2	**Sakha Line**	**Egypt**	Sakha12/5/Kvz//CNO67/Pj62/3/YD"s"Bios"s"/4/K13 4(60)VEE S14665-4S-1S-0SY-0S	**Early**
3	**Sakha 93**	**Egypt**	Sakha92/ TR81032 S8871-1S-2S-1S-0S	**Medium**
4	**Gemmeiza 7**	**Egypt**	CMH74 A.630/Sx//Seri82/3/Agent CGM4611-2GM-3GM-1GM-0GM	**Medium**
5	**Gemmeiza 9**	**Egypt**	Ald"s"/Huac"s"//CMH74 A.630/Sx CGM583-5GM-1GM-0GM	**Late**
6	**Milan**	**Mexico**	VS73.600/MRL/3/BOW//YR/TRF CM75113.B-5M-2Y-3B-0Y-0CF-0M-0CHL-0AP	**Late**

Table 2. Sequence and operon codes of the random primers used to detection of variation in wheat

Primer codes	Sequence (5˙ to 3˙)
OPB-10	CTG CTG GGA C
OPD-05	TGA GCG GAC A
OPC-20	ACT TCG CCA C
OPA-11	CAA TCG CCG T
OPB-18	CCA CAG CAG T
OPB-05	TGC GCC CTT C

bands were polymorphic Table 4. Otherwise, the three monomorphic bands were no. 1, 30 and 31 exerted in molecular weight 133.994, 41.149 and 34.237 KD. Some unique amplified bands characterize these genotypes such band no. 5 (Mw= 121.969), no. 6 (Mw = 120.701), no. 8 (Mw = 114.318), no. 9 (Mw = 112.658), no. 13 (Mw = 100.848), no. 15 (Mw = 96.72), no. 16 (Mw = 96.317), no. 17 (Mw = 95.316), no. 20(Mw = 93.15), no. 21 (Mw = 90.276) , no. 22 (Mw = 89.337), no. 23 (Mw = 84.79), no. 24 (Mw = 81.32), no. 25 (Mw =80.475), no. 26 (Mw = 77.991) and no. 27 (Mw = 77.181) Table 5. Regarding the number of observed bands among the genotypes while Table 3 showed that the presence of light variation between the six parents (8 and 9 bands). Meanwhile the number of bands observed belong different crosses showed a wide variation. The highest number of bands was 9 bands for (Sids-4 × Gemmeiza-7) and the lowest number of bands was 6 bands observed in (Sids-4 × Sakha line). The obtained results for crosses could be attributed to the interactions between the parents as well as the crosses. Also, Table 3. showed that some specific bands restricted in early parent (Sids-4, no. 4) as well as (band no. 29 for Sakha line) these specific bands restricted only in parents but not appeared in F_1, this results can be attributed to recessive or masking behavior for this region. Moreover this table no. 3 showed an interesting

Table 3. SDS-PAGE protein bands of wheat genotypes as appeared in Fig. 1

Band no.	1	2	3	4	5	6	7	8	9	10	11
1	+	+	+	+	+	+	+	+	+	+	+
2	-	-	-	-	-	+	+	+	-	-	-
3	-	-	+	+	-	-	-	-	-	-	-
4	+	+	-	-	-	-	-	-	-	-	-
5	-	-	-	-	+	-	-	-	-	-	-
6	-	-	-	-	-	-	-	-	+	-	-
7	-	-	-	-	-	-	-	-	-	+	+
8	-	-	-	-	-	-	+	-	-	-	-
9	-	-	-	-	-	+	-	-	-	-	-
10	+	+	+	+	+	-	-	-	-	-	-
11	-	-	-	-	-	-	-	+	+	-	-
12	-	-	-	-	-	-	-	-	-	+	+
13	-	-	-	-	-	-	-	+	-	-	-
14	+	+	+	+	+	+	-	-	-	-	-
15	-	-	-	-	-	-	-	+	-	-	-
16	-	-	-	-	-	-	-	-	+	-	-
17	-	-	-	-	-	-	-	-	-	-	+
18	-	-	-	-	+	+	-	-	-	-	+
19	-	-	+	+	-	-	-	-	-	-	-
20	+	-	-	-	-	-	-	-	-	-	-
21	-	-	-	-	-	-	-	-	-	+ *	-
22	-	-	-	-	-	-	-	-	-	-	-
23	-	-	-	-	+	-	-	-	-	-	-
24	-	+	-	-	-	-	-	-	-	-	-
25	-	-	+	-	-	-	-	-	-	-	-
26	-	-	-	-	-	-	-	-	-	-	+
27	-	-	-	-	-	-	-	-	-	+ *	-
28	+	-	-	+	+	+	+	+	+	+	+
29	-	+	+	-	-	-	-	-	-	-	-
30	+	+	+	+	+	+	+	+	+	+	+
31	+	+	+	+	+	+	+	+	+	+	+

1- Sids4 2- Sakha line 3 - Sakha93 4- Gemmeiza7 5- Gemmeiza9 6- Milan 7- Sids4 x Sakha line 8- Sakha93 x Gemmeiza7 9- Gemmeiza9 x Milan 10- Sids4 x Milan 11- Sids4 x Gemmeiza7

+ = present, - = absent * = protein marker

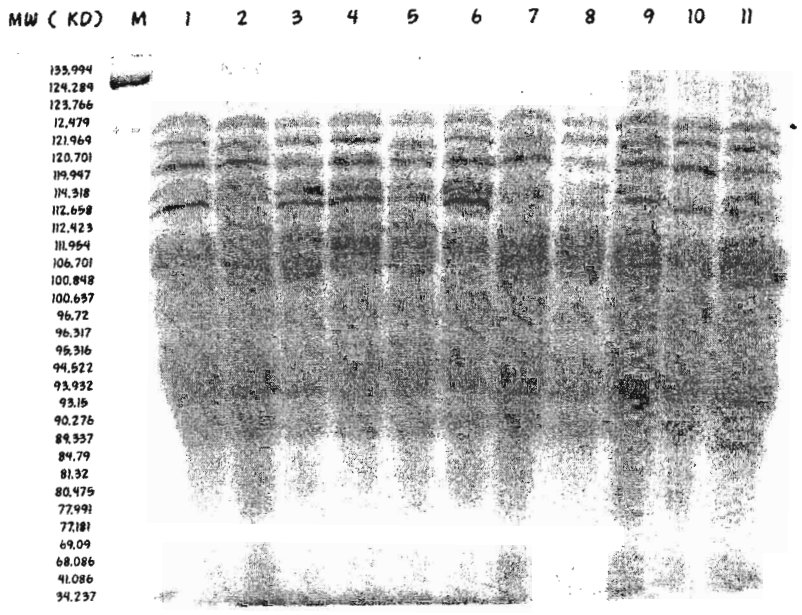

Fig. 1. SDS – PAGE profiles of wheat genotypes associated with earliness trait in wheat

1. Sids-4
2. Sakha-line
3. Sakha-93
4. Gemmeiza-7
5. Gemmeiza-9
6. Milan
7. Sids-4 x Sakha line
8. Sakha-93 x Gemmeiza-7
9. Gemmeiza-9 x Milan
10. Sids-4 x Milan
11. Sids-4 x Gemmeiza-7

Table 4. Protein banding polymorphism for wheat genotypes and their crosses

Monomorphic bands	3
Polymorphic (without unique)	12
unique bands	16
Polymorphic (with unique)	28
Total number of bands	31
Polymorphism (%)	90.323%
Mean of band frequency	0.258

bands observed in F_1 for the cross (Sids-4 × Milan) represent the early parent (Sids -4) and the late parent (Milan) these bands were no. 21 and 27 at the zones of molecular weight varied from (90.276KD to 77.181 KD) that appeared in F_1 and not observed in either these parents, that can be attributed to the interaction between the two different genotype. These results were agreement with those obtained by Altenbac *et al.* (2001), Dovřáček and Čurn (2005) Shauib *et al.* (2007) and Kaleem *et al.* (2008).

Regarding to the dendogram that demonstrates the relationships among the wheat genotypes based on data recorded from polymorphism of protein patterns. Fig. 2 illustrated that, the tested entries of wheat were dividedbasically into two main groups. First group included 5 parents Sids 4, Sakha line, Sakha - 93, Gemmeiza -7 and Gemmeiza - 9, meanwhile, the second group included the 6th parents and all crosses.

The protein banding patterns of wheat resulted from direct genetic control and in general not affected by environmental conditions. In addition, because wheat is essentially a self-pollinated crop, protein composition of the different varieties of wheat remains stable for plant generation (El-Morshidy *et al.*, 2003). Therefore, the protein composition of wheat can be characterized and thus to identify its variety.

Table 5. Relative frequencies and polymorphism distribution for SDS-PAGE bands in different wheat genotypes

Band no.	RF	Mw	Frequency	Polymorphism
1	0.133	133.994	1	*
2	0.169	124.284	0.273	***
3	0.171	123.766	0.182	***
4	0.176	12.479	0.182	***
5	0.178	121.969	0.091	**
6	0.183	120.701	0.091	**
7	0.186	119.947	0.182	***
8	0.209	114.318	0.091	**
9	0.216	112.658	0.091	**
10	0.217	112.423	0.455	***
11	0.219	111.954	0.182	***
12	0.242	106.701	0.182	***
13	0.269	100.848	0.091	**
14	0.270	100.637	0.545	***
15	0.289	96.72	0.091	**
16	0.291	96.317	0.091	**
17	0.296	95.316	0.091	**
18	0.300	94.522	0.182	***
19	0.303	93.932	0.182	***
20	0.307	93.15	0.091	**
21	0.322	90.276	0.091	**
22	0.327	89.337	0.091	**
23	0.352	84.79	0.091	**
24	0.372	81.32	0.091	**
25	0.377	80.475	0.091	**
26	0.392	77.991	0.091	**
27	0.397	77.181	0.091	**
28	0.45	69.09	0.818	***
29	0.457	68.086	0.182	***
30	0.698	41.086	1	**
31	0.786	34.237	1	**

* Monomorphic fragment ** Unique fragment
*** Polymorphic fragment

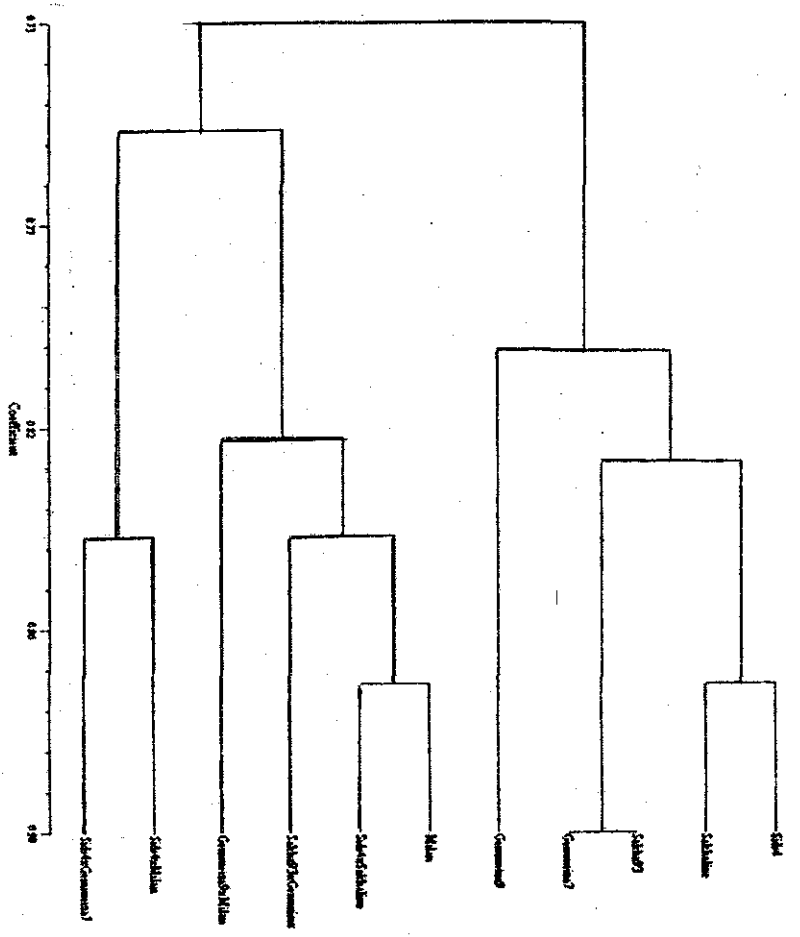

Fig. 2. Dendogram demonstrating the relationships among the wheat genotypes based on data recorded from polymorphism of protein pattern

The previous view of protein patterns in the studied wheat genotypes could be used as a selective marker for desirable trait as suggested by (Lin *et al.*, 1999).

DNA Analysis

RAPD-PCR analysis was used to determine the genetic variation and to obtain molecular markers for wheat genotypes. Depending upon the previous results, which were detected from the field experiments and protein profiles, cross (Sids-4 × Milan) was chosen represent the extremes for earliness trait to continue the molecular analysis. The five genotypes represent by P_1, P_2, and F1, bulk F_2 early and bulk F_2 late were carried out. Six primers (OPB–10, OPD–05, OPC–20, OPA–11, OPB–18 and OPB–05) were used to differentiate between the five genotypes Fig. 3. A total of 46 DNA bands varied from 257 bp (OPA– 11) to 1627 bp (OPB–05) were amplified through the six random primers. Six bands out of the fourty six bands (13.04%) were polymorphic Table 6. The number of RAPD–PCR bands generated by each primer varied from seven bands (OPB–10, OPC– 20 and OPB–18) to nine bands (OPD–05) with an average of 7.66 Table 7.

Also the number of polymorphic bands through each primer ranged from 1 band (OPB–10) to 2 bands (OPB-05) with an average 1 band/primer. The highest number of amplificated and polymorphic bands were generated by (OPD–05) (9, 2) followed by primer (OPB-18) (7, 2), respectively. On the other hand, the lowest primer was (OPB – 10) (7, 1).The polymorphic band no. 1 with size 1463bp showed banding pattern by application of primer (OPD–05) from the early parent (Sids 4) and early bulked F2 but not detected in bulked late F_2. In addition, the primer (OPB–10) exhibited only one negative band no. 6 with size 637bp that appeared in late parent (Milan) and late bulked F_2. These results were agreement with (Joshi and Nquyen, 1993), Lin *et al.* (1999), Gerashchenkov *et al.* (2000), El-Morshidy *et al.* (2003), Mari *et al.* (2004), Bhutta *et al*, (2006), Nalini *et al.* (2006), Halima *et al.* (2007), Hanocq *et al.* (2007) and Kunpu *et al.* (2008).

So, these bands could be used as a selective molecular marker associated with earliness gene (s) for wheat breeding to select the early genotypes.

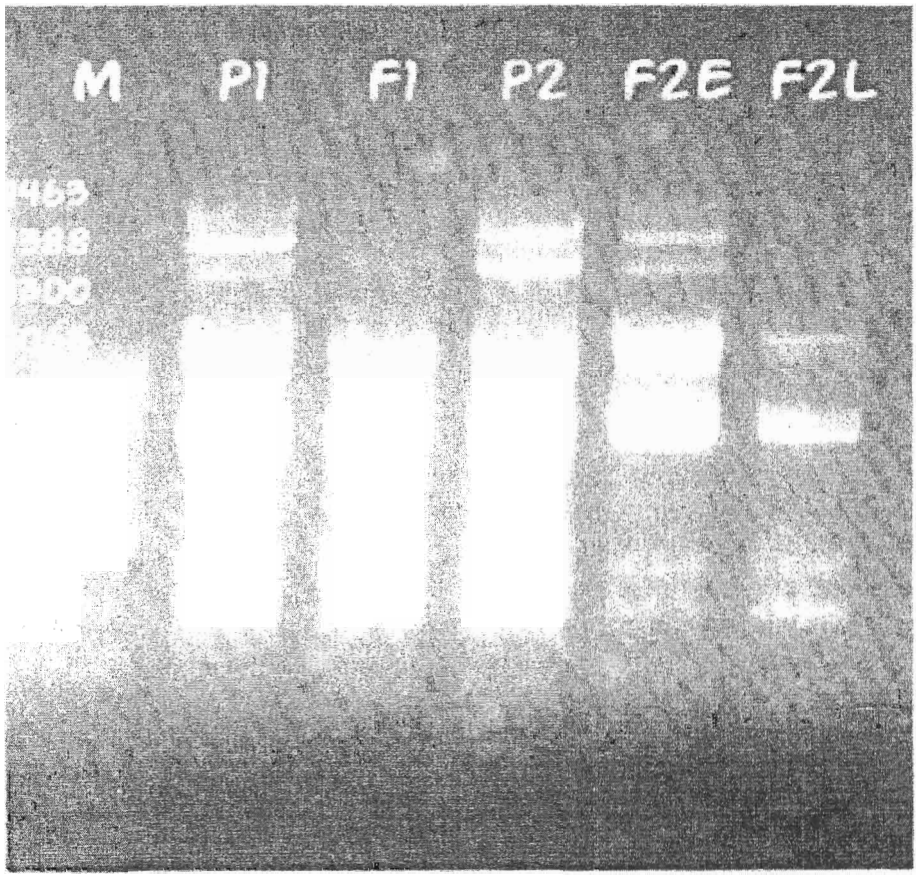

Fig. 3. RAPD-PCR DNA banding patterns of wheat genotypes associated with earliness trait in wheat using primer OPD-05

P_1: Sids-4 P_2: Milan F_1: Sids-4 x Milan

F_2E: Bulk of F2 early F_2L: Bulk of F2 late

Table 6. RAPD-PCR bands of wheat genotypes using primres OPB-10

NO.	bp	P_1E	F_1	P_2L	F_2E	F_2L
1	1583	+	+	+	+	+
2	1442	+	+	+	+	+
3	1333	+	+	+	+	+
4	1192	+	+	+	+	+
5	837	+	+	+	+	+
6	637	-	+	+	-	+
7	317	+	+	+	+	+

Table 6. Cont.
OPD-05

NO.	bp	P_1E	F_1	P_2L	F_2E	F_2L
1	1463	+	-	-	+	-
2	1388	+	+	+	+	-
3	1300	+	+	+	+	+
4	1063	+	+	+	+	+
5	983	+	+	+	+	+
6	815	+	+	+	+	+
7	751	+	+	+	+	+
8	444	+	+	+	+	+
9	350	+	+	+	+	+

Table 6. Cont.
OPC-20

NO.	bp	P_1E	F_1	P_2L	F_2E	F_2L
1	1100	+	+	+	+	+
2	848	+	+	+	+	+
3	706	+	+	+	+	+
4	631	+	+	+	+	+
5	580	+	+	+	+	+
6	357	+	+	+	+	+
7	260	+	+	+	+	+

Table 6. Cont.

OPA-11

NO.	bp	P_1E	F_1	P_2L	F_2E	F_2L
1	1350	+	+	+	+	+
2	1160	+	+	+	+	+
3	909	+	+	+	+	+
4	631	+	+	+	+	+
5	569	+	+	+	+	+
6	496	+	+	+	+	+
7	315	+	+	+	+	+
8	257	+	+	+	+	+

Table 6. Cont.

OPB-18

NO.	bp	P_1E	F_1	P_2L	F_2E	F_2L
1	1482	+	+	+	+	-
2	1273	+	+	-	+	+
3	1191	+	+	+	+	+
4	1036	+	+	+	+	+
5	863	+	+	+	+	+
6	652	+	+	+	+	+
7	589	+	+	+	+	+

Table 6. Cont.

OPB-05

NO.	bp	P_1E	F_1	P_2L	F_2E	F_2L
1	1627	-	+	+	+	+
2	1409	+	+	+	+	+
3	1273	+	+	+	+	+
4	1100	+	+	+	+	+
5	981	+	+	+	+	+
6	793	+	+	+	+	+
7	612	+	+	+	+	+
8	505	+	+	+	+	+

+ = band present, - = band absent.

Table 7. Number of amplified and polymorphic DNA fragments for 5 tested wheat genotypes

Primers	Genotypes					No. of amplified bands	No. of polymorphic bands
	P_1E	F_1	P_2L	F_2E	F_2L		
OPB-10	6	7	7	6	7	7	1
OPD-05	9	8	8	9	8	9	2
OPC-20	7	7	7	7	7	7	0
OPA-11	8	8	8	8	8	8	0
OPB-18	7	7	6	7	6	7	2
OPB-05	7	8	8	8	8	8	1
Total	44	45	44	45	44	46	6
Mean	7.33	7.5	7.33	7.5	7.33	7.66	1

REFERENCES

Altenbac, S.B., W.J. Hurkman, W.H. Vensel, K.M. Cronin, C. Tanaka and D. Ladencia-Chingcuanco. 2001. Molecular characterization of wheat grain development by transcript and protein profiling. Annual Meeting of American Association of Cereal Chemists (AACC), October 14-18, 2001.

Bhutta W.M., J. Akhtar, M. Ibrahim and A. Shahzad. 2006. Genetic variation between Pakistani Wheat *(Triticum aestivum L.)* genotypes as revealed by Random Amplified polymorphic DNA (RAPD) markers. South African Journal of Botany, 72 (2): 280-283.

Dellaporta S.I., Wood and J.B. Hicks. 1983. A plant DNA mini preparation. Ver III plant Mol. Biol. 1: 19 – 21.

Dovřáček V. and V. Čurn. 2005. Evaluations of protein fractions as biochemical markers for identification of spelt wheat cultivars *(Triticum spelta L.)*. Plant Soil Environ., (3): 99 – 105.

El-Morshidy M.A., A. Abo El-wafa and A.Y. Allam. 2003. Assessment of some new wheat lines variability using RAPD and protein patterns. Assiut J. of Agric. Sci. 35 (5): 27 – 52.

Gerashchenkov G.A, V. Garbunova, L. Zarianov, N.A. Rozhnova and V. Bakhitov. 2000. RAPD–PCR analysis of the variability of spring common wheat cultivar genomes and their androclinal double haploid from Genetika 36, 1081 – 1087.

Halima H.H., A.A. Bahy, H.H. Tian, D.N. Qin, X.M. Wang and Q.D. Xie. 2007. Use of Ramdom Amplified polymorphic DNA analysis for economically important food crops. Journal of integrative plant Biology, 49 (12): 1670 – 1680.

Hanocq E., A. Laperche, O. Jaminon, A. Lainè and J. Gouis. 2007. Most significant genome regions involved in the control of earliness trait in bread wheat, as revealed by QTL meta analysis. Theoretical and Applied Genetics, 114 (3) 569 – 584.

Joshi C.P. and H.T. Nquyen. 1993. RAPD (random amplified polymorphic DNA) analysis based intervarietal genetic relationship among hexaploid wheats. Plant Science, 93 (1-2). 95 – 103.

Kaleem A., A. Ahmed, Z. Abbas, M. Gulfraz, M.S. Masood and N.S. Kisana. 2008. Genetic diversity in wheat *(Triticum aestivum L.)* as revealed by SDS–PAGE. International Journal of Applied Agricultural Research, 3 (1): 1– 8.

Kunpu Z., T. Hichum, Z. Laing, L. Bin and F.C. Guang. 2008. Detection of Quantitative trait loci for heading date based on the douple haploid progeny of two elite Chinese wheat cultivars. Genetica Springer Netherlands (on line).

Laemmli U.K. 1970. Cleavage of structural proteins during the assembly of the head of bacteriophage T4. Nature, 227: 680 – 685.

Lin. Z.Q., Y. Pei and Z.J. Pu. 1999. Relationship between hybrid performance and genetic diversity based on RAPD markers in wheat *(Triticum aestivum L.)*. Plant Breeding, 118 (2): 119 – 123.

Mari A.S., S. Bolari, J. Martin, I. Peji and V. kozumplik. 2004. Genetic diversity of hexaploid wheat cultivars estimated by RAPD markers, morphological traits and coefficients of parentage. Plant breeding, 123 (4): 366 – 369.

Nalini E., N. Jawali and S.G. Bhagwat. 2006. Analysis of QTL for Earliness components in bread wheat *(Triticum aestivum L.)*. FOUNER'S DAY, ISSUE no. 285: 183 – 189.

Rohlf F.J. 2000. NTSYS–PC: numerical taxonomy and multivariate analysis system, version 2.1 Exeter Software. New York

Shuaib M., Z. Alam, A. Zahir, A. Waqar, A. Taufiq and K. Ikhtiar. 2007. Characterization of wheat varieties by seed storage protein electrophoresis. African Journal of Biotechnology, 6 (5): 497 – 500.

Suvarna T.T. 2001. Molecular analysis of wheat genome using ISSR and RAPD markers. M. Sc. Thesis, Pune Uni., India.

Svetlana L., V. Korzun and A. Birner. 2007. Molecular markers. Actual and potential contributions to wheat genome characterization and breeding Euphytica, 156 (3): 271–296.

Yu G., M.A. Hong Xiang, X. Zhang, L.J. REN, O.Z. Ma and L. Weizhong. 2004. Cloning a DNA marker associated to wheat scab resistance J. Appl. Genet. 45, 17-25.

الواسمات البيوكيميائية والجزيئية المرتبطة بصفة التبكير فى قمح الخبز

شيماء الدسوقى إبراهيم[1] – عبد الرحمن السيد مندور[1]

أنـــور عبد الخالق عجيـــز[2]– محمـــد يحيـــى هيكـــل[1]

١– قسم الوراثة– كلية الزراعة– جامعة الزقازيق.

٢– قسم بحوث القمح – مركز البحوث الزراعية – الجيزة– محطة بحوث الجميزة.

تهدف هذه الدراسة الى التعرف على بعض الواسمات البيوكيميائية والجزيئية المرتبطة بصفة التبكير فى قمح الخبز. وذلك باستخدام ٦ أباء من القمح والتى بها مدى واسع من الاختلافات بالنسبة لصفة التبكير وهى: سدس ٤، والسلالة سخا (مبكر)، سخا ٩٣، جميزة ٧ (متوسط)، جميزة ٩، ميلان (متأخر). وتم الحصول على حبوب الـــ F_1بالنسبة للخمسة هجن التى تم اختيارها لإجراء التحليل البيوكيميائى باستخدام تحليل الـــ SDS-PAGE. banding patternهذه الهجن كانت (سدس٤×السلالة سخا)، (سخا ٩٣×جميزة ٧)، (جميزة ٩ × ميلان)، (سدس ٤× ميلان)، (سدس٤× جميزة ٧). أظهرت النتائج المتحصل عليها وجود واسمات بيوكيميائية وجزيئية مرتبطة بصفة التبكير فى القمح. وجود حزمتين ذات وزن جزيئى يتراوح بين (٧٧,١٨١ الى٩٠,٢٧٦ كيلو دالتون) فى الهجين (سدس٤ × ميلان) والتى ظهرت فقط فى الجيل الأول لذلك يمكن اعتبار هذه الحزم كواسم بيوكيميائى لصفة التبكير. بالنسبة للتحليل الجزيئى تم اختيار الهجين (سدس ٤ × ميلان) فقط لإجراء التحليل لوجود الاختلافات الكبيرة بين الأبوين. تم أجراء تحليل الـــ RAPD-PCR مستخدما تكنيك Bulk segregant analysis. وأظهرت النتائج المتحصل عليها أن البادئ (OPB-10) اظهر حزمة سالبة ذات حجم ٦٣٧ فى الأب المتأخر ونباتات الـــ F_2 المتأخرة بالإضافة إلى أن البادئ (OPD-05) اظهر حزمة موجبة ذات حجم ١٤٦٣ فى الأب المبكر ونباتات الـــ F_2 المبكرة. وبذلك يمكن اعتبار هاتين الحزمتين كواسمات لصفة التبكير فى برامج تربية القمح.