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ALLELIC STATE AT THE MICROSATELLITE LOCUS *XGWM261* MARKING THE DWARFING GENE *RHT8* IN EGYPTIAN BREAD WHEAT (*Triticum aestivum* L.) GENOTYPES RELEASED FROM 1947 TO 2004

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Rht8 is widely used in dry environments such as Mediterranean regions where it increases plant adaptability. Variation at the Gatersleben wheat microsatellite *Xgwm261* locus, whose 192-bp allele closely linked to the dwarfing gene *Rht8*, on chromosome 2D within 0.6 cM, was used to screen thirty Egyptian bread wheat genotypes released from (1947-2004) to assess the variation at this locus. There were three microsatellite allelic variants based on size. Screening of this wheat collection showed that the three alleles $Xgwm261_{-165}$, $Xgwm261_{-174}$ and $Xgwm261_{-192}$ bp were the most frequent. The highest allele frequency was observed for a $Xgwm261_{-165}$ bp fragment (65.52%) followed by a $Xgwm261_{-174}$ bp fragment (24.14%). However, the allele frequency of a $Xgwm261_{-192}$ bp fragment among these wheat genotypes was 10.34%. The percentage distribution of dwarfing alleles for the microsatellite locus *Xgwm261* in the Egyptian wheat breeding programs was 30, 20, 20 and 30% for the wheat breeding program Giza, Sakha, Gemmiza and Sids, respectively. PIC for *Xgwm261* was 0.527. Genetic heritage of Egyptian genotypes at the microsatellite locus *Xgwm261* is consequence of new parental components usage, carriers short plant and early maturity attributes and consequent selection progeny with these traits in breeding programs. The present study will be helpful in characterization Egyptian wheat genotypes, as well as in accurate selection of parents for wheat breeding program in Egypt.

Key words: Bread wheat (*Triticum aestivum* L.), *Rht8*, dwarfing gene, microsatellite marker

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INTRODUCTION

Wheat breeding has the opportunity of understanding and improving a crop that has profound strategic importance across countries. It is estimated that over the next decade, grain yield must increase by 15% to meet the global demand and consumption of wheat as a result of a growing human population (EDGERTON, 2009). One strategy to meet this challenge is to increase wheat productivity by optimizing plant architecture such as tillering and ear morphology. A decisive component of plant architecture is stature, mainly determined by stem elongation. Bread wheat is an annual crop with round, hollow and jointed stems. There are usually five elongated internodes in fully grown culms, with each internode progressively longer towards the ear. The last internode, the peduncle, is the longest. Reduced height (*Rht8*) semi-dwarfing gene is one of the few and most widely used in wheat breeding programs together with the Green Revolution genes, to shorten wheat culms and improve lodging resistance without penalizing grain yield (WORLAND and LAW, 1986). One of the most important agronomic characteristics of modern high-yielding bread wheat cultivars is the utilization of reduced height genes (*Rht*), which reduces plant height and simultaneously increases adaptability and grain yield potential (WORLAND *et al.,* 2001; REYNOLDS and BORLAUG 2006; ALGHABARI *et al*., 2014). Short wheat genotypes are less susceptible to lodging and partition more assimilates to developing grain yield (WADDINGTON *et al*., 1986). In wheat, the large increases in yield achieved during the green revolution were associated with the introduction of the reduced height (*Rht*) genes into Mexican wheats by Norman Borlaug. Originally from the Japanese wheat genotype Norin 10, these genes became prevalent in CIMMYT wheats and are now found in the majority of modern wheat genotypes. Using a chromosome substitution line between Cappelle Desprez and the Strampelli wheat cultivar Mara, KORZUN *et al*. (1998) reported a linkage between the dwarfing gene *Rht8* and a *Xgwm261*$_{-192}$ bp allele at the microsatellite locus *Xgwm261* on chromosome 2D within 0.6 cM. Varieties carrying the *Xgwm261*$_{-192}$ bp allele showed a height reduction of 7-8 cm without pleiotropic effects on other agronomic characters except for a slight increase in spikelet fertility (WORLAND *et al*., 1998). The use of dwarfing genes to reduce plant height and improve yield potential has been one of the major strategies in breeding program. Number of studies have surveyed wheat cultivars for the presence of *Rht8* using the Gatersleben wheat microsatellite *Xgwm261* locus as a diagnostic markers for *Xgwm261*$_{-192}$ bp allele, either to determine its prevalence in worldwide wheat cultivars (CHEBOTAR *et al.* 2001; WORLAND *et al.* 2001; AHMAD and SORRELLS 2002; LIU *et al*. 2005; GANEVA *et al*. 2005; ZHELEVA *et al*., 2006, FAYT *et al.,* 2007, SIP *et al.,* 2010, DVOJKOVIĆ *et al.,* 2010, WEIGT *et al.*, 2013) or to ascertain the effect of *Rht8* on other agronomic traits (REBETZKE and RICHARDS 2000; BAI *et al*. 2004). The objective of the present study were to i) analysis the presence of allelic variation in *Xgwm261* microsatellite locus and ii) detect the *Rht8* gene in Egyptian bread wheat genotypes released from (1947-2004).

MATERIALS AND METHODS

Plant material

A total of thirty Egyptian bread wheat genotypes (*Triticum aestivum* L.), released in production during the period from 1947 to 2004, were used for microsatellite screening. A complete list of Egyptian wheat used in this study are presented in Table 1. The seed stocks were obtained from Agriculture Research Center (ARC), Giza, Egypt; USDA Genebank, USA and Genbank Department, IPK, Gatersleben, Germany.

Table 1. Thirty Egyptian bread wheat genotypes used for genotyping with microsatellite marker, year of released and their pedigree.

Genotype	Year	Pedigree
1. Giza 139	1947	Hindi 90/ Kenya B256
2. Giza 144	1958	Rgent/2* Giza 139
3. Giza 157	1977	Giza 155//Pit 62 /LR 64/3/Tzpp/Knott
4. Sakha 8	1977	Indus/Norteno "s"
5. Sakha 61	1980	Inia/RL 4220//7C/Yr "s"
6. Sakha 69	1980	Inia/RL 4220//7C/Yr "s"
7. Giza 160	1982	Chenab70/Giza 155
8. Sakha 92	1987	Napo 63/Inia 66//Wern "s"
9. Giza 162	1987	Vcm//Cno67/7C/3/Kal/BbCM8399-D-4M-3Y-1M-1Y-1M-0Y
10. Giza 163	1987	*T.aestivum*/Bon//Cno/7C CM33009-F-15M-4Y-2M-1M-1M-1Y-0M
11. Giza 164	1987	Kvz/Buha "s"//Kal/Bb CM33027-F-15M-500y-0M
12. Gemmieza 1	1991	Maya 74/On//1160.147/3/Bb/Gall/4/Chat"s" CM58924-1GM-OGM
13. Giza 167	1995	Au/Up301//Gll/Sx/Pew"s"/4/Mai"s"/May"s"//Pew"s"CM67245-C-1M-2Y-1M-7Y-1M-0M
14. Sids 1	1996	HD 2172/Pavon"s"//1158.57/Maya 74 "s" SD46-4SD46-4Sd-2SD-1SD-0SD
15. Sids 2	1996	HD 2206/Hork"s"/3/Napo63/Inia66//Wern "s" SD635-4SD-1SD-1SD-0SD
16. Sids 3	1996	Sakha 69/Giza155 SD723-7SD-1SD-0SD
17. Sids 4	1994	Maya "s"/Mon "S"/CM H74.A592/3/Giza 157*2
18. Sids 5	1994	Maya "s"/Mon "S"/CM H74.A592/3/Giza 157*2 SD10001-7sd-4SD-2SD-0SD
19. Sids 6	1994	Maya "s"/Mon "S"/CM H74.A592/3/Sakha 8*2 SD10002-4SD-3SD-1SD-0SD
20. Sids 7	1994	Maya "s"/Mon "S"/CM H74.A592/3/Sakha 8*2 SD10002-8SD-1SD-1SD-0SD
21. Sids 8	1994	Maya "s"/Mon "S"/CM H74.A592/3/Sakha 8*2 SD10002-14SD-3SD-1SD-0SD
22. Sids 9	1994	Maya "s"/Mon "S"/4//CM H72.428/MRC//jip/3/CMH74A582/5/Giza157*2SD10003
23. Gemmieza 3	1997	Bb/7C*2//Y50/Kal*3//Sakha8/4/Prv/WW/5/3/Bg"s"//OnCGM.4024-1GM13 GM2GM-0GM
24. Gemmieza 5	1998	Vee"s"/SWM 6525 CGM.4017-1GM-6 GM-3 GM-0GM
25. Giza 168	1999	Mil/Buc//Seri
26. Sakha 93	1999	Sakha 92/TR 810328
27. Gemmiza 7	2000	CMH74 A. 630/5x//Seri 82/3/Agent CGM.4611-2GM-3GM-1GM-0GM
28. Gemmiza 9	2000	Ald"s"/Huac"/s"//CMH74A.630/5x CGM.4583-5GM-1GM-0GM
29. Sakha 94	2004	Opata/Rayon//Kauz
30. Gemmieza 10	2004	Maya 74 "s"/On//1160-147/3/Bb/4/Chat"s"/5/Ctow

DNA extraction

Ten seeds of each genotype were germinated and leaf tissue was harvested from 15 days old seedlings. Wheat genomic DNA was extracted from these genotypes according to PLASCHKE *et al.* (1995).

Polymerase Chain Reaction (PCR)

Polymerase chain reactions (PCR) were performed in a volume of 25 µl described by RÖDER *et al*. (1998). The reaction mixture contained the following (1) amplification component, (2) *Xgwm261* primers pair and (3) genomic DNA (Table 2). Amplification for *Xgwm261* locus was

carried out according to the following program conditions, after initial denaturing for 3 min at 94 °C, 45 Cycles were performed at 94°C for 1 minute, 55°C for 1 minute and 72 °C for 2 minutes and a final extension step of 10 minutes at 72 °C.

Table 2. Concentration and volume of polymerase chain reaction (PCR) mix components

	Reaction mix	Stock	Working	Volume per amplification (μl)
1	PCR buffer	10 X	1 X	2.5
	dNTPs	10 mM	0.2 mM	2.0
	Taq polymerase	1 U	0.1 µl	0.1 µl
	Demineraliz H_2O	-	14.1 µl	14.1 µl
2	Forward primer	250 nM	0.65 µl	0.65 µl
	Reverse primer	250 nM	0.65 µl	0.65 µl
3	Genomic DNA	> 50 ng µl	10 ng µl	5.00 µl
				Σ=25.00 µl

Microsatellite marker analysis

The Gatersleben wheat microsatellite marker *Xgwm261* locus on chromosome 2DS as a diagnostic marker for *Rht8* was used for genotyping the Egyptian wheat genotypes according to RÖDER *et al*. (1998). The characteristics of microsatellite *Xgwm261* primers pair shown in Table 3. Wheat microsatellite amplification was carried out as reported by RÖDER *et al*. (1998).

Table 3. Characteristics of microsatellite marker Xgwm261 primer pair

Marker	Chromosome location	Primer sequence	Motif	Ta (°C)
Xgwm261	2DS	*Xgwm261*-F 5'-CTCCCTGTACGCCTAAGGC-3' *Xgwm261*-R 5'-CTCGCGCTACTAGCCATTG-3'	(CT)21	55

Ta (°C); primer annealing temperature

Statistical analysis

To measure the informativeness of the *Xgwm261* locus, the polymorphism information content (PIC) was calculated according to the formula of Nei (1973) using the equation: $\mathrm{PIC} = 1 - \sum_{i=1}^{k} P_i^2$, where k is the total number of alleles detected for a locus of a marker and *Pi* the frequency of the *i*th allele in the set of thirty genotypes investigated.

Polymerase chain reaction and fragment analysis were performed according to RÖDER *et al*. (1998). Denaturing gels with 6% polyacrylamide were prepared. The gels were run in 1X TBE buffer. Photographed gels were analyzed to calculate the allele size. Fragment detection for SSR marker was carried out as given in RÖDER *et al*. (1998), respectively.

RESULTS

Allelic identification and absolute fragment size determination

Wheat microsatellite locus *Xgwm261* was highly polymorphic among the thirty Egyptian bread wheat genotypes examined in the present study. The microsatellite primers amplified three

SSR fragments that varied in size from *Xgwm261*$_{-165}$ bp to *Xgwm261*$_{-192}$ bp (Table 4). All genotypes amplified a single fragment.

Table 4. Classification of Egyptian bread wheat genotypes for allelic variation at the Gatersleben wheat microsatellite locus Xgwm261

Genotype	Year	Fragment size bp for *Xgwm261*		
1. Giza 139	1947	------	*Xgwm261*$_{-174}$	------
2. Giza 144	1958	------	*Xgwm261*$_{-174}$	------
3. Giza 157	1977	*Xgwm261*$_{-165}$	------	------
4. Sakha 8	1977	------	------	*Xgwm261*$_{-192}$
5. Sakha 61	1980	*Xgwm261*$_{-165}$	------	------
6. Sakha 69	1980	*Xgwm261*$_{-165}$	------	------
7. Giza 160	1982	*Xgwm261*$_{-165}$	------	------
8. Sakha 92	1987	*Xgwm261*$_{-165}$	------	------
9. Giza 162	1987	*Xgwm261*$_{-165}$	------	------
10. Giza 163	1987	*Xgwm261*$_{-165}$	------	------
11. Giza 164	1987	*Xgwm261*$_{-165}$	------	------
12. Gemmieza 1	1991	------	*Xgwm261*$_{-174}$	------
13. Giza 167	1995	*Xgwm261*$_{-165}$	------	------
14. Sids 1	1996	------	------	*Xgwm261*$_{-192}$
15. Sids 2	1996	*Xgwm261*$_{-165}$	------	------
16. Sids 3	1996	------	*Xgwm261*$_{-174}$	------
17. Sids 4	1994	*Xgwm261*$_{-165}$	------	------
18. Sids 5	1994	------	*Xgwm261*$_{-174}$	------
19. Sids 6	1994	*Xgwm261*$_{-165}$	------	------
20. Sids 7	1994	*Xgwm261*$_{-165}$	------	------
21. Sids 8	1994	*Xgwm261*$_{-165}$	------	------
22. Sids 9	1994	*Xgwm261*$_{-165}$	------	------
23. Gemmieza 3	1997	*Xgwm261*$_{-165}$	------	------
24. Gemmieza 5	1998	------	*Xgwm261*$_{-174}$	------
25. Giza 168	1999	*Xgwm261*$_{-165}$	------	------
26. Sakha 93	1999	------	------	*Xgwm261*$_{-192}$
27. Gemmiza 7	2000	*Xgwm261*$_{-165}$	------	------
28. Gemmiza 9	2000	------	*Xgwm261*$_{-174}$	------
29. Sakha 94	2004	*Xgwm261*$_{-165}$	------	------
30. Gemmieza 10	2004	------	------	*Xgwm261*$_{-192}$

As the first step for allelic identification, the amplificons of *Xgwm261* of each genotype were compared and the result revealed they can be divided into three groups with different allele size *Xgwm261*$_{-165}$, *Xgwm261*$_{-174}$ and *Xgwm261*$_{-192}$ bp, respectively (Table 4). There was clearly demonstrating three alleles from the longest to the shortest fragment. The 'stuttered' banding pattern, mainly due to the slippage of amplification, was the characteristic of SSR fragment after being separated by standard polyacrylamide gels and visualized by the automated laser fluorescence (ALF) DNA sequencer. In the process of size determination, the most intense upper

band was recorded as the SSR allele size (DECROOCQ ***et al.,*** 2003) and the same criteria were applied in both allele identification and absolute fragment size determination.

The distribution of Xgwm261 allelic variants in Egyptian genotypes

The screening results of the amplified microsatellite marker *Xgwm261* in thirty Egyptian bread wheat genotypes which released from 1947 to 2004 indicated that these genotypes had three different allelic variants at the *Xgwm261* locus (Table 4). Among these microsatellite alleles, the *Xgwm261-165* bp fragment occurred with greatest frequency 65.52% (19 genotypes), followed by *Xgwm261-174* bp 24.14% (7 genotypes) and *Xgwm261-192* bp fragments 10.34% (4 genotypes) (Figure 1), clearly demonstrated the distribution of the allelic variants.

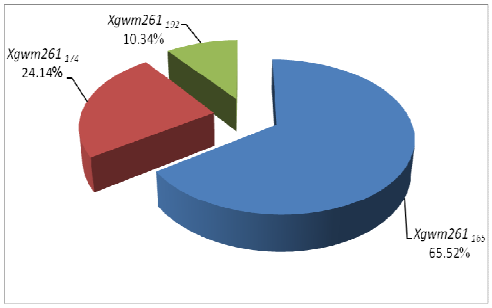

Figure (1): Percentage distribution of three alleles for the microsatellite locus *Xgwm261* in the Egyptian wheat genotypes.

The distribution of Xgwm261 allelic variants in Egyptian breeding program

A collection of thirty Egyptian bread wheat genotypes which released from 1947 to 2004 and representing four Egyptian wheat breeding programs performed at Sakha, Gemmiza, Giza and Sids was analyzed using wheat microsatellite locus *Xgwm261* (Table 5). The number of wheat genotypes have *Xgwm261-165* bp was 7, 4, 2 and 6 for Giza, Sakha, Gemmiza and Sids, respectively. The number of wheat genotypes have *Xgwm261-174* bp was 2, 0, 3 and 2 for Giza, Sakha, Gemmiza and Sids, respectively. The number of wheat genotypes have *Xgwm261-192* bp was 0, 2, 1 and 1 for Giza, Sakha, Gemmiza and Sids, respectively.

The percentage distribution of dwarfing alleles for the microsatellite locus *Xgwm261* in the Egyptian wheat breeding programs was 30, 20, 20 and 30% for the wheat breeding program Giza, Sakha, Gemmiza and Sids, respectively (Figure 2).

Diversity index of Xgwm261

The wheat microsatellite marker *Xgwm261* showed an average PIC value of 0.527, which confirms that this wheat microsatellite marker is highly informative.

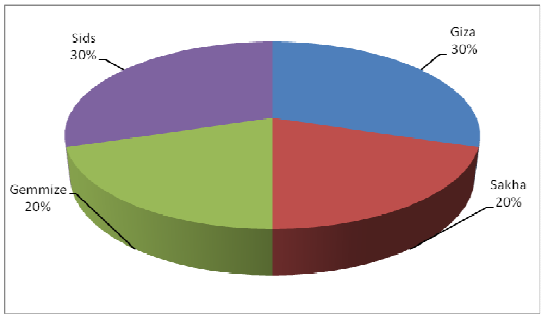

Figure (2): Percentage distribution of dwarfing alleles for the microsatellite locus *Xgwm261* in the Egyptian wheat breeding programs.

Table .5. Alleles distribution of Egyptian wheat genotypes in the wheat breeding programs

			Allele (bp)			
No	Breeding Program		*Xgwm261*$_{-165}$	*Xgwm261*$_{-174}$	*Xgwm261*$_{-192}$	Total
1	Giza	No	7	2	----	9
		%	77.78	22.22	0	
2	Sakha	No	4	----	2	6
		%	66.67	0	33.33	
3	Gemmize	No	2	3	1	6
		%	33.33	50	16.67	
4	Sids	No	6	2	1	9
		%	66.67	22.22	11.11	

DISCUSSION

The genetic diversity at the microsatellite locus *Xgwm261* has been an important diagnostic tool for genotyping the *Rht8* gene (Table 1). Previous studies have shown three different alleles, *Xgwm261*$_{-165}$ bp, *Xgwm261*$_{-174}$ bp and *Xgwm261*$_{-192}$ bp, to be internationally widespread. The majority of the Egyptian genotypes in the present study had either of the first two of these alleles. Some of our PCR products yielded fragments that were sized a few base pairs larger than *Xgwm261*$_{-165}$ bp or *Xgwm261*$_{-174}$ bp, but in accordance with SCHMIDT *et al.* (2004), we did not consider them as distinct alleles, but a result of slippage or "stutter". The *Xgwm261*$_{-165}$ bp or *Xgwm261*$_{-174}$ bp alleles were the most common ones, 65.52 and 24.14% of the homozygotes, respectively. Our genotypes did not include any Japanese or Chinese accessions in crosses. It is therefore not surprising that we detect only four genotypes carry the *Xgwm261*$_{-192}$ bp allele. It has

been suggested that the *Xgwm261*$_{-174}$ bp allele is linked to the *Ppd-D1b* allele. In our genotype, we found both the *Xgwm261*$_{-174}$ bp and the *Xgwm261*$_{-165}$ bp alleles in Egyptian wheats. Although all the genotypes from the same breeding program in a few cases shared the same allele we could not distinguish any clear breeding program pattern in the distribution of the *Xgwm261*$_{-174}$ bp and the *Xgwm261*$_{-165}$ bp alleles. The limited number of genotypes restricts the possibility to recognize breeding program patterns, but the breeding program segregation of allele types (WORLAND**,** *et al.,* 1998, 2001) might actually have arisen later during modern plant improvement, often based on a few key cultivars. In the cultivation data for the Egyptian wheats flowering time (data not shown) was slightly earlier for genotypes with the *Xgwm261*$_{-174}$ bp than those with the *Xgwm261*$_{-165}$ bp allele but not significantly and did thus not show any clear support for linkage to *Ppd-D1b*. Molecular identification of genes involved in domestication and plant improvement has recently accelerated (DOEBLEY *et al.,* 2006 and BURGER *et al.,* 2008). By screening plant genetic diversity present and testing for selection the important alleles can be explored. In the case of dwarfing gene *Rht8* its role in 20th century wheat improvement is well known from extensive screens and documented crossings and pedigrees.

Geographical distribution of the microsatellite locus *Xgwm261* alleles, their linkage relationship to a photoperiod response gene and the respective plant height of the cultivars were discussed by WORLAND *et al.* (1998). Their results indicated that the *Xgwm261-*$_{165}$ and the *Xgwm261-*$_{174}$ bp alleles are associated with a 8-10 cm height increase respectively, as compared to the *Xgwm261-*$_{192}$ bp allele diagnostic for *Rht8*. The *Xgwm261-*$_{192}$ bp allele was observed mostly in Italian, Russian and Yugoslavian wheat genotypes (WORLAND *et al.,* 1998). In the present study, the *Xgwm261*$_{-165}$*, Xgwm261*$_{-174}$ and *Xgwm261*$_{-192}$ bp alleles were the same as those reported by WORLAND *et al*. (2001), BAI *et al*. (2004)**,** GANEVA *et al*. (2005) and ZHELEVA *et al*. (2006). The predominance of the *Xgwm261*$_{-165}$ bp allele in the Egyptian bread wheat genotypes suggests that there may be selection for that allele in Egyptian wheat breeding program. These agree with Worland's results (WORLAND *et al*. 2001) for European wheat genotypes (UK, France and Germany) and South America (Argentina). Preference for taller plants may be caused by drier growing conditions, a shorter growing season or other environmental factors. Biotic factors, such as rain-splashed fungal spores, may reduce lower leaf area and contribute to an advantage for taller plants. The *Xgwm261*$_{-174}$ bp allele that is associated more with shorter plant height than the *Xgwm261*$_{-165}$ bp allele may be favored in the south part of delta in Egypt where there is often more soil moisture available and lodging is an important problem. All *Xgwm261* alleles reported here were observed by WORLAND *et al.* (1998), but they also observed higher frequencies of the *Xgwm261*$_{-165}$ bp and the *Xgwm261*$_{-174}$ bp alleles in their studies. Among the thirty Egyptian wheat genotypes, the diagnostic marker allele for *Rht8* (*Xgwm261*$_{-192}$ bp) was found in only four genotypes (Sakha 8, Sids 1, Sakha 93 and Gemmiza 10). WORLAND *et al.* (1998) stated that CIMMYT wheat cultivars carry the *Xgwm261*$_{-165}$ bp allele, while the *Xgwm261*$_{-174}$ bp allele appears to be present in most of the Great Britain, French and German wheat genotypes. The presence of the higher frequency *Xgwm261*$_{-174}$ bp allele in the Egyptian wheat genotypes suggests it's introduction from CIMMYT wheat germplasm. Interestingly, the presence of the higher frequency *Xgwm261*$_{-165}$ bp allele in Egyptian wheat cultivars suggests that because of wheat breeders subsequently used CIMMYT wheat germplasm in their breeding programs.

The Gatersleben wheat microsatellite *Xgwm261* locus showed a PIC value of 0.527, which confirms that this wheat microsatellite marker is highly informative. BOTSTEIN *et al*. (1980) reported that PIC value > 0.5 is considered as being highly informative marker. PIC obtained in

the present investigation was comparable with previous results on PIC of the *Xgwm261* locus analysis.

Although *Rht8* only reduces plant height by around 8 cm, this new additional information will be practically useful to wheat breeders selecting plant height trait. The present study will be helpful in characterization Egyptian wheat genotypes, as well as in accurate selection of parents for wheat breeding program in Egypt.

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ALELNI STATUS MIKROSATELITSKOG MARKERA *Xgwm261* GENA *Rht8* KOD GENOTIPOVA EGIPATSKE HLEBNE PŠENICE (*Triticum aestivum* L.) PRIZNATIH UPERIODU 1947 - 2014

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Izvod

Rht8 se koristi u klimatskim uslovima Mediterana u kom povećava adaptibilnost biljaka. Microsatelit, *Xgwm261* locus kod pšenice, čiji je alel veličine 192-bp allele blisko ukopčan sa genom Rht8, na hromozomu 2D unutar 0,6cM i kontroliše smanjenje visine biljke, je upotrebljen za skrining 30 genotipova egipatske hlebe pšenice. Clj je bio procena variranja tog lokusa. Utvrđeno je da u kolekciji pšenice postoje tri najfrekventnija alela: $Xgwm261_{-165}$ (65.52%) $Xgwm261_{-174}$ (24,14%) i $Xgwm261_{-192}$ (10,34%). Genetičko nasleđivanje egipatskih genotipova u lokusu mikrosatelita *Xgwm261* je posledica nove roditeljske komponente koja nosi osobinu niske biljke i ranostasnost i daje potomstvo sa ovim osobinama, korisnim za programe oplemenjivanja.

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