Genetic diversity for high- and low-molecular weight glutenin subunits in local and commercial bread wheat cultivars released since 1951 in Iran: I- Irrigated

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Received: February 2017
Accepted: August 2017

ABSTRACT

Esmaeilzadeh Moghaddam, M., Jalal Kamali, M. R., Pena, R. J. and Najafian, G. 2017. Genetic diversity for high- and low-molecular weight glutenin subunits in local and commercial bread wheat cultivars released since 1951 in Iran: I- Irrigated. **Crop Breeding Journal 7 (1 & 2): 1-7.**

Allelic variations at the *Glu-1* and *Glu-3* loci play an important role in determining dough visco-elastic properties and bread making quality. Fifty-nine bread wheat cultivars released in Iran since 1951 from four different agro-climate zones, were examined for their high (HMW-GS) and low-molecular-weight glutenin subunit (LMW-GS) composition, controlled at the *Glu-1* and *Glu-3* loci, respectively. In addition, the presence of the 1B.1R translocation was investigated. Three, eight, and four allelic variations were present at *Glu-A1*, *Glu-B1*, and *Glu-D1* loci, respectively. Subunits 2*, 7+8, 7+9, and 2+12 are the dominant HMW-GS, at *Glu-A1*, *Glu-B1*, and *Glu-D1*, with frequencies of 45.8, 39, 25.4, and 59.3%, respectively. Five, eight and four allelic variations were present at the *Glu-A3, Glu-B3* and *Glu-D3* loci, with *Glu-A3c*, *Glu-B3b and Glu-D3b* LMW-GS dominating, with frequencies of 52.5, 39 and 59.3%, respectively. The frequencies of allelic variation at *Glu-1* and *Glu-3* differ greatly in different regions. Among the 59 cultivars/varieties examined in this study, four genotypes were local varieties (6.8%), 27 (45.8%) bred in the national breeding program and 28 (47.4%) originated from international nurseries. The average quality scores based on HMW-GS for local varieties, genotypes from the national breeding program and international nurseries were 5.5, 7.6 and 7.7 respectively. It was concluded that integration of desirable subunits at *Glu-1* such as 1, 7+8, 5+10, must be used as the core focus of the breeding program, which could lead to the improvement of gluten quality in Iranian bread wheat cultivars.

Key words: Glutenin, allelic variation, SDS-PAGE, *Triticum aestivum*

INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is the most widely grown field crop in the world. Currently the area grown to wheat is estimated at about 220 million hectares with a total annual production of about 750 million tons (FAOSTAT). Wheat is the major crop in 43 countries and supplies food for at least 35% of the world population (Trethowan and Pfeiffer, 1999).

World population has reached 7.6 billion people and is projected to increase to around 9.0 billion by 2050 (UNFPA, 2017). Wheat seed storage proteins represent an important source of food and energy. Additionally, they are involved in the determination of baking quality. The protein content in the wheat grain is highly dependent on genotype but it is also strongly influenced by environmental conditions such as nitrogen availability, water access and temperature during growth, especially through the grain filling period (Dupont and Altenbach, 2003; Johansson *et al.,* 2004; Torbica *et al.,* 2007). Wheat protein (8 to 20% of the grain) mainly contains albumins, globulins, gliadins and glutenins. Glutenin protein is a polymer of a long chain of polypeptide subunits linked by inter polypeptide disulfide bonds. The reduction of these inter-chain bonds allows the separation of the subunits into high molecular weight (HMW) (80-130 kDa) and low molecular weight (LMW) (10-70 kDa) glutenin subunits (Bietz and Wall, 1972). Glutenins are divided into high molecular weight glutenin subunits (HMW-GS) and low molecular weight glutenin subunits (LMW-GS), accounting for 12% and 33% of the endosperm proteins, respectively; these are known to be the responsible for the viscoelasticity of gluten and bread making quality. The HMW glutenin subunits are encoded by two types of genes (x:y) that are located at *Glu-Al,Glu-Bl* and *Glu-Dl* loci close to the

`chromosomes lA, 1B and lD, respective1y (Payne *et al.,* 1982). The x-gene encodes for high molecular weight x-type subunit, whereas the y-gene encodes for LMW y-type subunit (Shewry *et al.,* 1992; Gu *et al.,* 2006). Gliadins are classified into α, β, γ, and ω types, based on their mobility in A-PAGE, and are mainly related to dough extensibility and ductility (Metakovsky *et al.,* 1984; Payne, 1987).

Bread wheat is expected to contain six different HMW glutenin subunits, but due to the silencing of some genes (x,y), most bread wheat cultivars possess three to five subunits. Thus, *Glu-A1* locus encodes for none or one active subunit (y-type of this locus is not expressed) and loci *Glu-B1* and *Glu-D1* encode for one or two x-type subunits each (Payne and Lawrence, 1983). On the other hand, genes encoding for LMW glutenin subunits are located on the short arms of homologous group 1 chromosomes at *Glu-A3*, *Glu-B3* and *Glu-D3* loci, and are tightly linked to *Glu-1* loci (Liu *et al.,* 2010). The *Glu* loci make different contributions to dough strength. Gupta, *et al.* (1994) reported that the contributions by loci could be ranked as *Glu-D1 >Glu-B1 >Glu-B3 >Glu-A3>Glu-D3 =Glu-A1*, with respect to maximum dough resistance. Zhang, *et al.* (2009) reported that *Glu-D1*and *Glu-B3* play the most important roles in determining dough properties. Moreover, the presence or absence of specific HMW glutenin subunits largely determines bread making quality of wheat. It is well known that the HMW-GS pair 5+10 encoded by *Glu-D1d* contributes to strong dough and good bread-making quality (Campbell *et al.,* 1987; Lagudah *et al.,* 1987). HMW-GS 1 and 2* encoded by *Glu-A1a* and *Glu-A1b*, respectively, and 7+8, 7+9, and 17+18 encoded by *Glu-B1b*, *Glu-B1c*, and *Glu-B1i*, respectively, also contribute to strong dough and good bread making quality (Eagles *et al.,* 2002; He *et al.,* 2005). In general, subunits null, 6+8, and 2+12 at *Glu-A1*, *Glu-B1* and *Glu-D1*, respectively, are negatively related to break making quality (Payne *et al.*, 1987; Weegels *et al.*, 1996). The present study was conducted to determine high molecular weight glutenin subunits of Iranian commercial bread wheat varieties released over the past 60 years.

MATERIALS AND METHODS

Plant material

Fifty-nine irrigated bread wheat cultivars released since 1951 in Iran were evaluated for high and low molecular weight (HMW & LMW) glutenins subunit composition. Seeds from single heads were collected from demonstration plots at the Cereal Research Department of Seed and Plant Improvement Institute (SPII) in the 2012-13 cropping seasons, and the samples were sent to the International Maize and Wheat Improvement Center (CIMMYT) quality laboratory for SDS-PAGE electrophoresis analysis. They scored high and low molecular weight glutenin subunits.

SDS-PAGE analysis

HMW-Glutenins and LMW-Glutenins were separated by sodium-dodecyl-sulfate polyacrylamide gel electrophoresis (SDS-PAGE) based on the extraction method described by Singh, *et al.* (1991), with modifications reported by Liu, *et al.* (2005) and He, *et al.* (2005). The presence of the 1B.1R translocation was determined by SDS-PAGE of alcohol-soluble and alcohol-insoluble protein extracts, detecting the presence of *Sec-1* secalins in the first test and the presence of the *Glu-B3j* allele in the second test.

RESULTS AND DISCUSSION

Allelic variation at *Glu-1*

The identification of the HMW-GS composition of the varieties included in the historical series revealed differences between breeding periods (Table 1). Three allelic variations were observed at *Glu-A1*, subunit 2* and the null allele predominated, with frequencies of 45.8 and 30.5%, respectively, whereas subunit 1 was the least frequent (23.7%). The null allele predominated in local varieties and modern varieties, but subunit 2* was seen mostly in the varieties that were released between 1995 and 2007. The highest frequency of these two subunits (2* and null) was seen in varieties that adapted and released for temperate zone (Tables 1 & 2). Seven *Glu-B1*alleles were present, subunits 7+8 and 7+9 were found in high proportions (39 and 25.4%, respectively), followed by subunit 17+18 (15.2%). Subunits 21+19, 13+16, 7 and 20, were found in three, two, five and one genotypes, respectively. Uncommon subunit(s) 21+19 were present in the cultivars Pishgam, Mihan and Uroum, three Iranian cultivars adapted for cold areas and originating from the national breeding program. The other low-frequency subunit, 13+16, was seen in Parsi and Tajan cultivars. Parsi is adapted to the temperate zone and originated from the national breeding program, whereas Tajan, an advanced CIMMYT line, was released for the northern warm and humid zone in Iran, and it is no longer planted for commercial use (Tables 1 & 2).

Four allelic variations were observed at the *Glu-D1* locus. The frequencies of 2+12 and 5+10 were 59.3 and 37.3%, respectively. Subunit 2.1+ 11 and 3+12 were present in one genotype respectively. The

Table 1. Description of irrigated bread wheat varieties used in the study and their allelic composition at the high molecular weight glutenin subunits (HMW-GS) loci.

Variety	Pedigree	Year of Release	High Molecular Weight Glutenin Subunits		
			Glu-*A1*	Glu-*B1*	Glu-*D1*
Tabasi	Local Variety	1951	Null	7+8	2+12
Omid	Local Variety	1956	Null	7+8	2+12
Sholeh	Local Variety	1957	Null	7	2+12
Roshan	Local Variety	1958	Null	7+8	2+12
Navid	(Kirkpinar 79)63-112/66-2*7C	1968	2*	7	5+10
Bezostaya		1969	2*	7+9	2+12
Karaj 1	(200H*Vfn)Rsh	1973	Null	7+8	2+12
Karaj 2	(Fa*Th-Mt)Omid	1973	2*	7+8	2+12
Arvand	Rsh(Mt-Ky*My48)	1973	Null	7+8	2+12
Karaj 3	Drc/Mxp//Son64/Tzpp-Y54/3/Nai60	1976	2*	20	2+12
Bayat	C271/Wte-Son64//CIR	1976	Null	7+8	2+12
Golestan	Alondra"s"	1986	2*	17+18	2+12
Azadi	(4820*1-32-15409)* Mexp	1989	2*	7+8	2+12
Ghods	Rsh/5/Wt/4/Nor10/K54*^{2}//Fn/3/Ptr/6/Omid//Kal/Bb	1989	2*	7+8	5+10
Falat	Seri82	1990	1	7+9	2+12
Hirmand	Byt/4/Jar//Cfn/Sr70/3/jup''s''	1991	2*	17+18	2+12
Maroon	Avd*Pchu((28mt54A*N10-Brv21-1c/Kt5B)Nar59,1039))7c	1991	1	7+8	2+12
Rasoul	Veery"s	1992	1	7+9	2+12
Mahdavi	Ti/Pch/5/Mt48/3/Wt*//Nar59/Tota63/4/Mus	1995	1	7+8	5+10
Nikenejad	F13471/Crow"s"	1995	2*	7+9	5+10
Alamoot	KVZ/Ti71/3Maya"s"//Bb/Inia/4/Kj2/5/Inza/3/Pi/Ndr//Hys	1995	Null	7+9	5+10
Alvand	1-27-6275/CF1770	1995	1	7+8	2+12
Zarin	PK15841	1995	1	17+18	2+12
Tajan	Bow"s"/Nkt"s"	1995	2*	13+16	2+12
Darab 2	Maya"s"/Nac	1995	2*	17+18	5+10
Atrak	Kauz"s"	1995	2*	7+9	5+10
Shiroodi	Attila, (CM85836-4Y-OM-OY-8M-OY-OPZ)	1997	1	7	2+12
Chamran	Attila, (CM85836-50Y-OM-OY-3M-OY)	1997	2*	7	5+10
Kavir	Stm/3/Kal//V534/Jit716	1997	2*	17+18	5+10
Marvdasht	HD2172/Bloudan//Azadi	1999	2*	7+8	2+12
Pishtaz	Alvand//Aldan/Ias58.	2001	2*	7+8	5+10
Shiraz	Gv/D630//Ald"s"/3/Azd	2001	2*	7+8	5+10
Shariyar	Kvz/Ti71/3/Maya "s"//Bb/Inia/4/Karaj2/5/Anza/3/Pi/Nar//Hys	2001	2*	7+8	5+10
Tous	"Spn/Mcd//Cama/3/Nzr"	2001	2*	7	5+10
Dez	Kauz*2/Opata//Kauz	2001	2*	7+9	5+10
Hamoon	Falat/Roshan	2001	Null	7+9	2+12
Sepahan	Azd/5/L2453/1347/4/Kal//Bb/Kal/3/Au//Y50E/Kal *3	2007	2*	17+18	5+10
Bahar	Bloyka	2007	2*	7+8	2+12
Moghan 3	Luan/3/V763.23/V879.c8//Pvn/4/Picus/5 /opata	2007	2*	7+9	2+12

rare subunit, 2.1+11 was present in Sivand cultivar. This genotype was released in 2009 for the temperate zone, deriving from crosses between CIMMYT line (Kauz"s'') and Iranian variety, Azadi. The second rare allele, 3+12, was seen only in Mihan. This cultivar was released 2010 for the cold area and originated from national breeding program and crossed between one Iranian lines, Barakat, and Chinese variety (90-Zhong 87), (Table 1 &2).

Quality Scores Based on HMW-GS composition

HMW-GS quality score of all the genotypes ranged from four -10 with an average of 7.5, shown in Table 3. The quality scores for cultivars/varieties that were released for northern warm and humid zones ranged from five-eight with high frequency

Continued Table 1.

Variety	Pedigree	Year of Release	High Molecular Weight Glutenin Subunits		
			Glu-*A1*	Glu-*B1*	Glu-*D1*
Darya	SHA4/CHIL	2007	2*	7+9	2+12
Bam	Vee "s"/Nac //1-66-22	2007	Null	7+8	5+10
Neishabour	1-63-31/3/12300/Tob//Cno/Sx	2007	Null	7+8	5+10
Sistan	Bank"s"/Vee"s"	2007	Null	7+8	2+12
Pishgham	Bkt/90-Zhong 87	2008	1	21+19	5+10
Parsi	Dove"s"/Buc"s"/2*Darab	2009	Null	13+16	5+10
Sivand	kauz"s"/Azd	2009	2*	7+8	2.1+11
Morvarid	Milan/Sha7	2009	Null	7+9	2+12
Arg	1-66-22/Inia	2009	Null	7+8	2+12
Uroum	Alvand//NS732/Her	2010	1	21+19	2+12
Zare	130L1.11//F35.70/Mo73/4/Ymh/Tob//Mcd/3/Lira	2010	2*	7+9	2+12
Mihan	Bkt/90-Zhong 87	2010	1	21+19	3+12
Aflak	HD160/5/Tob/ Cno / 23854 /3/ Nai60//Tit/ Son64 /4/LR/ Son64	2010	Null	17+18	5+10
Sirvan	PRL/2*PASTOR	2011	1	7+9	2+12
Gonbad	ATRAK/WANG - SHUI-BAI	2011	1	7+9	2+12
Ofogh	GF-gy54/Attila	2012	2*	7+8	5+10
Chamran 2	Attila 50y//Attila/Bacanora	2013	1	7+9	2+12
Shoush	◦ CBRD-3/STORK X DICOCCOIDES	2014	Null	17+18	2+12
Mehregan	OASIS/SKAUZ//4*BCN/3/2*PASTOR	2014	1	17+18	5+10
Heidari	Ghk"s"/Bow"s"//90Zhong87/3/Shiroodi	2015	Null	7+8	2+12

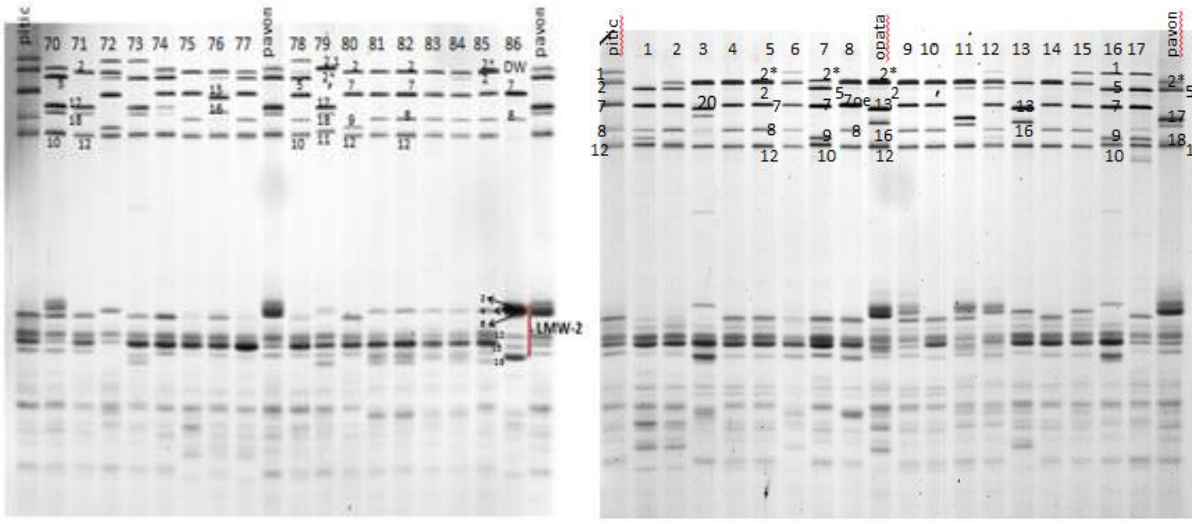

Fig. 1. SDS-PAGE profile of high molecular weight (HMW) glutenin alleles in a set of studied wheat/varieties cultivars. Since the same gel was used for both HMW and low molecular weight (LMW) glutenins, the LMW profile is also shown in the figure. Pitic, Opata, and Pavon were used as standard varieties.

Table 2. Frequencies (%) of high molecular weight glutenin subunits in 59 irrigated wheat genotypes from four agro-ecological zones in Iran.

Locus	Allele/Subunit	Number	Mean frequency	Zone I	Zone II	Zone III	Zone IV
Glu-*A1*	2*	27	45.8	14.8	18.5	40.7	25.9
	1	14	23.7	21.4	28.6	14.3	35.7
	N	18	30.5	11.0	33.4	27.8	27.8
Glu-*B1*	7+8	23	39	0	13.0	65.2	21.7
	7+9	15	25.4	33.3	33.3	13.4	20.0
	17+18	9	15.2	11.1	55.6	22.2	11.1
	others	12	20.4	16.7	16.7	16.6	50.0
Glu-*D1*	5+10	22	37.3	0	27.3	50.0	22.7
	2+12	35	59.3	22.9	25.7	25.7	25.7
	others	2	3.4	0	0	50.0	50.0

Table 3. Frequencies (%) and distribution of scores based on high molecular weight – glutenin subunits in 59 irrigated bread wheat genotypes from four agro-ecological zones in Iran.

Locus	Allele/Subunit	Number	Mean frequency	Zone I	Zone II	Zone III	Zone IV
Glu-*A3*	d	4	6.8	0	25	50	25
	c	31	52.5	6.5	32.3	38.7	22.5
	e	11	18.5	18.2	18.2	27.3	36.3
	b	13	22.2	30.7	15.3	30.7	23.3
Glu-*B3*	b	23	39.0	17.4	26.1	30.4	26.1
	c	5	8.4	0	40.0	20.0	40.0
	j	9	15.3	0	22	56	22
	g	9	15.3	11.2	22.2	44.4	22.2
	other	13	22.0	23.0	23.0	31.0	23.0
Glu-*D3*	a	9	15.3	0	22.2	55.6	22.2
	b	35	59.3	14.3	28.6	31.4	25.7
	c	12	20.3	16.7	25.0	41.6	16.7
	d	3	5.1	33.3	0	0	66.7

for a score (50%) of seven. In the second zone, southern warm and dry zone, the range for quality scores was between four -10, with high frequency for a score of eight (27%). Darab 2 and Mehregan, two CIMMYT lines, scored 10 for this zone. The second cultivar is planted in the southern part of Iran with high adaptability (Table 3).

In the temperate zone, the range of quality scores was between six-10 with an average of eight. Thirty three percent of studied cultivars related to this zone had a score of 10. Among cultivars/varieties related to cold zone, the range was between 5-10 with high frequency of eight score (33%) (Table 3).

Among 59 cultivars/varieties that used in this study, four genotypes were local varieties (6.8%), 27 (45.8%) came from the national breeding program and 28 (47.4%) originated from international nurseries. The average of quality scores based on HMW-GS for local varieties, genotypes from national breeding program and international nurseries was 5.5, 7.6 and 7.7, respectively (Table 4).

Table 4. Mean frequency of score based on high molecular weight – glutenin subunits composition and origin of studied genotypes

Origin	No.	Mean frequency	Quality scores Based on Glu-1
Local varieties	4	6.8	5.5
National breeding program	27	45.8	7.6
International nurseries	28	47.4	7.7

Allelic variation at *Glu-3*

The frequencies of LMW glutenin subunits observed in 59 genotypes are presented in Table 5. Four allelic variations were observed at the *Glu-A3* locus, predominating allele *Glu-A3c* (52.5%), followed by *Glu-A3b*, *Glu-A3e*, and *Glu-A3d*, respectively. *Glu-A3d* was present only in four genotypes from northern warm and humid and temperate zones of Iran. Three of these genotypes were CIMMYT lines, and two of them Morvarid and Sirvan, are still grown in farmers' fields. Eight allelic variations were present at the *Glu-B3* locus, with *Glu-B3b* representing almost 23% of the tested germplasm. *Glu-B3c*, *Glu-B3j*, and *Glu-B3g* represented 5, 9, and 9% of the population, respectively. Allele *Glu-B3*b', which (migrates in SDS-PAGE slightly faster than *Glu-B3b*), was present in six genotypes from temperate and cold zones. For *Glu-D3,* four allelic variants were observed in the 59 studied genotypes, with *Glu-D3b* representing 59%, and *Glu-D3a*, *Glu-D3c* and *Glu-D3d* represented 15%, 20% and 5% respectively. The diversity in *Glu-3* alleles at the three loci (at least four alleles at each loci) and the low frequency of the Glu-B3j allele in most of the zones (except zone III) is very encouraging regarding the further improvement of the quality of Iranian wheat for diverse food uses. The high frequency of *Glu-B3*j in zone III warrants further efforts to decrease the presence of the 1B. IR translocation in lines for this zone.

Table 5. Frequencies (%) of low molecular weight - glutenin subunits) in 59 wheat genotypes from four agro-ecological zones in Iran

Quality scores Based on Glu-1	Number	Mean frequency	Zone I	Zone II	Zone III	Zone IV
10	10	16.9	0	20.0	70.0	10.0
9	3	5.1	0	67.0	33.0	0
8	17	28.8	11.8	23.5	35.3	29.4
7	11	18.6	36.4	18.2	9.0	36.4
6	13	22	7.7	23.1	46.1	23.1
5	4	6.8	25.0	25.0	0	50.0
4	1	1.7	0	100	0	0

Table 6. Allelic composition at the Low molecular weight glutenin subunits (LMW-GS) loci and 1B/1R translocation status in studied genotypes.

	Low Molecular Weight Glutenin Subunits			Status of 1B/1R		Low Molecular Weight Glutenin Subunits			Status of 1B/1R
Variety	Glu-*A3*	Glu-*B3*	Glu-*D3*	Translocation	Variety	Glu-*A3*	Glu-*B3*	Glu-*D3*	Translocation
Tabasi	e	b	a	1B/1B	Pishtaz	c	b	c	1B/1B
Omid	c	b	a	1B/1B	Shiraz	c	h	b	1B/1B
Sholeh	c	b	a	1B/1B	Shariyar	c	b	b	1B/1B
Roshan	e	b'	a	1B/1B	Tous	b	g	b	1B/1B
Navid	e	g	b	1B/1B	Dez	c	j	b	1B/1R
Bezostaya	c	b	b	1B/1B	Hamoon	c	b	b	1B/1B
Karaj 1	e	b	a	1B/1B	Sepahan	c	i	b	1B/1B
Karaj 2	e	b	a	1B/1B	Bahar	b	i/e	b	1B/1B
Arvand	c	b	b	1B/1B	Moghan 3	e	j	b	1B/1R
Karaj 3	d	g	c	1B/1B	Darya	c	g/j	b	1B/1B-1B/1R
Bayat	c	g	c	1B/1B	Bam	b	c	c	1B/1B
Golestan	b/c	b/j	a	1B/1B-1B/1R	Neishabour	b	c	c	1B/1B
Azadi	c	b	b	1B/1B	Sistan	b	b	c	1B/1B
Ghods	c	b	b	1B/1B	Pishgham	c	d	b	1B/1B
Falat	c	j	b	1B/1R	Parsi	b	b	a	1B/1B
Hirmand	e	g	b	1B/1B	Sivand	c	b	b	1B/1B
Maroon	c	b	b	1B/1B	Morvarid	d	g	c	1B/1B
Rasoul	d	j	c	1B/1R	Arg	b	c/b	c	1B/1B
Mahdavi	c	b	d	1B/1B	Uroom	e	b'	c	1B/1B
Nikenejad	c	b	b	1B/1B	Zare	e	b'	b	1B/1B
Alamoot	e	b'	d/a	1B/1B	Mihan	c	d	b	1B/1B
Alvand	e	b'	b	1B/1B	Aflak	c	b	b	1B/1B
Zarin	b	b'	d	1B/1B	Sirvan	d	g	b	1B/1B
Tajan	c	d	a	1B/1B	Gonbad	c	j	b	1B/1R
Darab 2	b	i	b	1B/1B	Ofough	b	c	b	1B/1B
Atrak	c	j	b	1B/1R	Chamran 2	c	j	c	1B/1R
Shiroodi	c	j	b	1B/1R	Shoush	c	b	b	1B/1B
Chamran	c	j	c	1B/1R	Mehregan	c	g	b	1B/1B
Kavir	b	c	b	1B/1B	Heidari	b	b	b	1B/1B
Marvdasht	c	b	b	1B/1B					

The frequency (15%) of the 1B.1R translocation in the studied genotype was relatively low. Most of the commercial varieties evaluated in this study did not have this translocation. However, Falat, Rasoul, Atrak, Chamran, Dez, Moghan3, Shiroodi cultivars from CIMMYT nurseries, and two commercial varieties Chamran 2 and Gonbad from the national breeding program, all showed the 1B/1R translocation (Table 6).

The frequencies of the 1B.1R translocation in agro-ecological zones I, II, III, and IV were 44.4, 44.4, 11.2, and 0%, respectively. This was not unexpected since CIMMYT lines carrying the 1B.1R translocation such as Kauz, Attila, were widely and successfully used in breeding programs in zones I and II, and III.

CONCLUSIONS

This study confirmed there is wide genetic variability for both in HMW-GS and LMW-GS in different kinds of cultivated bread wheat released since 1951. At locus *Glu-1A*, the 2* subunit was found in large frequency. Subunits 7+8 at locus *Glu-1B*, was very frequent in the studied germplasm. Surprisingly, *Glu-1D*, subunit 2+12 was found in high frequency among the 59 studied varieties/cultivars. The quality scoring system for HMW-GS was developed by Payne, *et al*. (1987), in which individual subunits are graded with numbers based on dough visco-elastic parameters. A given cultivar can be assigned a HMW-GS quality score, which is the sum of contributions of each of the three *Glu-1* loci. The HMW-GS quality score has more influence in some sets of wheat than in others (MacRitchie and Wrigley, 1990). Ten cultivars (Ghods, Kavir, Pishtaz, Shiraz, Shariyar, Sepahan, ofough, Mahdavi, Darab 2 & Mehregan) showed the maximum HMW-GS quality score of 10, which would be best suited for bread making. Normally the lines with 5+10 subunits are supposed to have strong gluten and thus their HMW-GS quality score is at the higher side (Payne *et al.*, 1987; MacRitchie and Wrigley, 1990).

Among 59 studied cultivars, some genotypes possessed low HMW-GS quality scores six, five and four. The lowest quality score of four was found in sholeh, one local varieties released 1957 that was adapted for the southern warm and dry zone. A HMW-GS score of five was found in four cultivars including Hamoon, Morvarid, Uroom and Mihan. These lines with low HMW-GS score, consisted of 2+12 and 3+12 subunits. These subunits are supposed to have weak gluten and thus, their quality score should have been on the lower side. The study also revealed that a few cultivars of the last two decades have low HMW-GS quality scores, as well as the presence of the undesirable 1B.IR translocation. This warrants putting more emphasis

on improving the glutenin composition (*Glu-1* and *Glu-3*) through breeding and more strict quality testing. The electrophoretic analysis of glutenin subunit composition was very useful in cultivar and end use quality product identification.

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