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Effect of the glutenin genes on quality parameters in common wheat

M. Erkan BAYRAM[1] (✉), Kayıhan Z. KORKUT[2]

[1] Maize Research Institute, 54580 Sakarya, Turkey

[2] Field Crops, Faculty of Agriculture, Namık Kemal University, 59030 Tekirdağ, Turkey

✉ Corresponding author: mebayram11@gmail.com

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ABSTRACT

Association of glutenin alleles with bread quality has long been known and identification of glutenin alleles may be very informative for the quality of the breeder's material. In this study, 64 wheat genotypes were evaluated for high and low molecular weight glutenin alleles (Glu-1 and Glu-3) and some quality parameters. Of the identified glutenin alleles, eleven were at the *Glu-1* loci and 15 were at the *Glu-3* loci. Highly significant (P<0.001) differences were found among the genotypes for all quality parameters. Associations of glutenin alleles with the quality parameters were also found significant. The positive effective glutenin alleles of Glu loci on quality traits were *1* at *Glu-A1*, *13+16*, *17+18* and *7+8* at *Glu-B1* and *5+10* at *Glu-D1*, and *A3d*, *A3e*, *A3f* and *A3b* at *GluA3*, *B3a*, *B3b* and *B3g* at *Glu-B3* and *D3a* at *Glu-D3*. The negative effective glutenin alleles of *Glu* loci on quality traits were *null* allele at *Glu-A1*, *7*, *7+9* and *14+15* at *Glu-B1*, *2+12* at *Glu-D1* loci, and *A3a*, *A3c* at *Glu-A3*, *B3f*, *B3c* at *Glu-B3* and *D3c* at *Glu-D3*.

Keywords: bread wheat, glutenin alleles, marker-assisted selection, plant breeding

INTRODUCTION

Large differences are present among wheat cultivars considering grain composition (Pena, 2002). Therefore one cultivar may be suitable for producing one food type rather than several food types. As a result of the need of high quality wheat crop, the breeders in wheat breeding programs started to investigate the quality content of their breeding material in detail, to target quality based crosses and to seek ways to eliminate poor quality genotypes and to select higher quality material during selection.

Classical wheat flour quality tests such as alveograph or baking tests require more wheat grains, time and effort. Applications of these tests are usually difficult in the early generations of breeding programs due to the need of higher seed material. High molecular weight (HMW) and low molecular weight (LMW) glutenin subunits (GSs) include more information about quality values of wheat genotypes and *Glu-1* and *Glu-3* genes referring HMW and LMW glutenin subunits may easily be identified by SDS-PAGE electrophoresis requiring quite less seed. Payne et al. (1981) reported that some certain allelic subunits installed different effects on gluten quality. Branland and Dardevet (1985) also reported associations of alveograph values with HMW-GSs. Many studies have reported the associations of LMW-GSs allelic variation with the significant changes in bread making quality of wheat flour (Payne, 1987; Gupta et al., 1989, 1994; Cornish, 1995; Cornish et al., 1999).

Protein is one of the most important quality factors in determining bread quality. Protein quantity analysis is a significant quality control parameter for wheat and flour, since there is a close relationship between the amount of protein and physicochemical properties of flour (Park et al., 2006). Flour and bread making qualities of wheat flour with the same protein amount can be different.

Both quantity and quality of protein are quite important for bread-making and they may significantly influence the dough strength properties of wheat flours (Pena, 2002).

Among various quality tests, Zeleny sedimentation is one of the quickest and easiest methods to determine the bread making quality of flour obtained from wheat (Zeleny, 1947; Zeleny et al., 1960, AACC, 2000). Sedimentation value indicates gluten quantity and quality. Zeleny sedimentation test values and slower sedimentation refers to higher gluten content and better gluten quality (Huruskova and Famera, 2003). Therefore, it is a very useful method to evaluate wheat with different gluten quality or to determine protein quantities of wheats with the same gluten quality (Yıldız, 2011). The result obtained from this test may provide important information about the quality and structure of the bread to be made from the wheat flour.

The alveograph is accepted as one of the important tests in the assessment of the quality characteristics of wheat flour and it has previously been used in various countries (Khattak et al., 1974; Bettge et al., 1989; Indrani et al., 2007; Boros et al., 2009; Codina et al., 2011; Mironeasa and Codina, 2013). It was also suggested for breeding studies in Turkey (Kaya and Şahin, 2015). Among the all alveograph parameters W (energy) value has been considered for assessing the quality in most of the bread-making quality studies (Bloksma, 1957; Faridi and Rasper, 1987). Chen and D'Appolonia (1985) stated that the alveograph W value measures bread-making potential accurately and is an acceptable predictor of the end-use bread-baking quality of the flour. The quality of the dough obtained from wheat flour is very important in the production of baked goods. Alveograph W value which is an important indicator of flour strength shows the energy required for dough swelling and measures the strength of dough extensibility. The value obtained is expressed in joules ($x10^{-4}$) and is an indication of the gluten quality required for bread-making in the desired quality.

The gluten index value was developed as a rapid method to measure gluten quality in wheat (Perten, 1990). The gluten index, a measure of the strength of wheat flour, has been widely used in the determination of gluten protein quality (Özer and Ünal, 1998). It has been explained that optimum cooking quality is obtained for flours with gluten index value between 60-90% (Elgün et al., 2001). On the other hand, according to Perten (1990) if the index value is more than 95%, wheat flour is too strong for optimum bread-making and weak for below 40%.

Wet gluten gives information on the quantity and estimates the quality of gluten in wheat (WMC, 2004). Wet gluten is a structure unique to wheat and is an important quality measure in the production of leavened bread. It indicates appropriateness of the dough for bread-making. Wet gluten composed of glutenin protein which is elastic and gliadin protein which is viscous in nature (Day, 2011). Glutenin has been reported to form a network-like structure when the dough is kneaded, allowing CO^2 to be retained by the yeast during fermentation, making bread more voluminous (Tayyar, 2008). It has been stated that high gluten content indicates good bread quality (Bulut, 2012).

In this study, 64 four genotypes from a breeding program were investigated for bread quality. Using sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) method HMW and LMW glutenin alleles of 64 genotypes were identified to reveal higher quality genotypes for breeding programs as gene resources. Also, some quality parameters of these genotypes were determined including kernel protein content (%), Zeleny sedimentation volume (mL), alveograph energy (J), gluten index (%), wet gluten content (%). Finally, the associations of glutenin alleles with the quality parameters were identified.

MATERIAL AND METHODS

Sixty four genotypes having different quality traits were used (Table 1). Of the 64 genotypes 21 were advanced lines and 13 were lines and cultivars from the MRI (Maize Agricultural Research Institute) wheat breeding program. Thirty of the genotypes were cultivars from other research institutions or countries.

Table 1. The names and features of the genotypes used in the study

No.	Genotype**	Feature	No.	Genotype	Feature
1	Pamukova-97/Sönmez	Adv.Line	33	Ocoroni 86	Cultivar
2	Tnmu/3/HD2206/Hork// Buc/Bul	Adv.Line	34	Pastor	Cultivar
3	Ocoroni 86/ Pewit3	Adv.Line	35	Pewit3	Cultivar
4	Tahirova2000/Zornitcha	Adv.Line	36	Pamukova-97	MRI-Cultivar
5	Tahirova2000/Zornitcha	Adv.Line	37	Prostor	Cultivar
6	Ağrı/Bjy"S"//Vee"S"/Mmtc /4/LL/3/ Orso/Akv/Ska	Adv.Line	38	Sibia/Milan	MRI-Line
7	Pamukova-97/Arostor	Adv.Line	39	Sönmez	Cultivar
8	Pamukova-97/Arostor	Adv.Line	40	Stozher	Cultivar
9	Momtc/4/LL/3/Orso//Akv/ Ska/Prostor	Adv.Line	41	Sultan-95	Cultivar
10	Stozher/3/Kal/Mus//Har	Adv.Line	42	Sunco	Cultivar
11	Sunvale/Sultan95	Adv.Line	43	Sunvale	Cultivar
12	Stozher//Sibia/Milan	Adv.Line	44	Tahirova-2000	MRI-Cultivar
13	Stozher//Sibia/Milan	Adv.Line	45	Tinamou	Cultivar
14	Sunco/Pastor	Adv.Line	46	Yakar-99	Cultivar
15	Doğu-88/Ziyabey98	Adv.Line	47	Ziyabey-98	Cultivar
16	Adana-99/Sultan95	Adv.Line	48	Zornitcha	Cultivar
17	Adana-99/Sultan95	Adv.Line	49	Basribey-95	Cultivar
18	Aköz/Galil	Adv.Line	50	Osmaniyem	Cultivar
19	Aköz/Dariel	Adv.Line	51	Gönen-98	Cultivar
20	Bau/Kauz// Tahirova2000	Adv.Line	52	Pehlivan	Cultivar
21	Tahirova-2000/Yakar	Adv.Line	53	Aldane	Cultivar
22	Adana-99	Cultivar	54	Flamura 85	Cultivar
23	Ağrı/BJy"S"//Vee"S"	MRI-Line	55	Tosunbey	Cultivar
24	Aköz	Cultivar	56	Konya-2002	Cultivar
25	Arostor	Cultivar	57	Harmankaya-99	Cultivar
26	Bau/Kauz	MRI-Line	58	Çetinel-2000	Cultivar
27	Dariel	Cultivar	59	Yıldız 98	Cultivar
28	Lancer	Cultivar	60	Bezostaya-1	MRI-Cultivar
29	Galil	Cultivar	61	Momtchil	MRI-Cultivar
30	HD2206/Hork//Buc/Bul	MRI-Line	62	Bandırma-97	MRI-Cultivar
31	Kal/Mus//Har	MRI-Line	63	Beşköprü	MRI-Cultivar
32	Momtc/4/LL/3/Orso/Akv/Ska	MRI-Line	64	Hanlı	MRI-Cultivar

**The genotypes 4-5, 7-8, 12-13, 16-17 are sisters

This research was carried out in the fields of MRI, Sakarya and in the biotechnology laboratory of Transitional Zone Agricultural Research Institute (TZARI), Eskişehir and in the quality laboratory of Field Crops Central Research Institute (FCCRI), Ankara, under Republic of Turkey Ministry of Food, Agriculture and Livestock.

The materials were planted as 1 m long 30 ear rows in Sakarya field of MRI in November 2011. To maintain seed purity, 25 ears from each genotype were isolated with paper bags in order to prevent fertilization of the foreign pollens. Non-homogeneous or mixed rows were discarded. All of the 25 ears of each genotype, grown isolated, were harvested and threshed separately in July 2012. Ten healthy ears having homogeneous seeds from 25 ears were selected for SDS-PAGE electrophoresis of HMW and LMW glutenin subunits. Remained rows were harvested and threshed in July 2012. Using the cleaned seeds of each genotype the trial was planted in Pamukova field of MRI in November 2012 in an 8x8 partially balanced lattice design with three replicates (Cochran and Cox 1957). The plot size of the trial was 12.5 m^2 (1mx12.5m) in planting and it was reduced to 10 m^2 in harvest for exclusion of border effect. The trial planting area with an altitude of 73 m in Pamukova has clay loam soil having medium organic matter with pH 7.64 and with a mean season rainfall of 486 mm. During the growing season monthly the minimum and maximum temperatures were 5.5 and 22.4 °C, respectively. The rows were fertilized with 80 kg N ha^{-1} and 80 kg P_2O_5 ha^{-1} at the planting and 70 kg N ha^{-1} in spring at tillering. The trial was harvested in July 2013. Since the trial environment quite favorable for wheat production, by using one environment year and location effect on quality parameters were kept limited.

Gluten electrophoresis method and sample preparation

For the glutenin extraction and SDS-PAGE electrophoresis, we used a standard method described by UPOV (UPOV, 1994) with some modifications. Studies of Glutenin SDS-PAGE electrophoresis were completed in October 2013. Nine varieties, Chinese Spring, Gabo, Courtot, Norman, Opata, Buck Pingo, Halberd, Ruso, Neepawa, which were kindly requested from CIMMYT (International Maize and Wheat Improvement Center-Mexico) were used as standards in the glutenin analyses. These cultivars were suggested as standards for determination of HMW-GS and LMW-GS alleles (Liu et al., 2009, 2010). Identification of banding patterns of HMW-GS and LMW-GS of studied genotypes were conducted according to the standard cultivars.

Quality Analyses

Protein amount analyses (AACC, 2000) were performed according to AACC Method 46-30 (Crude Protein / Combustion Method) on a Velp Scientifica model NDA-701 Dumas Nitrogen Analyzer protein determination device. Zeleny sedimentation test applications were made according to AACC Method 56-60, 56-61A (AACC, 2000). Alveograph energy analyses were made according to ICC Standard No: 121 (ICC, 2008) using a Chopin Alveograph NG (France) instrument. Flour grinding was carried out according to AACC Method No: 26-21 and 26-31 (AACC, 2000). Gluten index analyzes were performed using AACC Method 38-12A (AACC, 2000). Wet gluten analyses were performed using AACC Method 38-12A (AACC, 2000). The gluten index value (%) obtained at the end of the analyzes was calculated by the following formula.

Ig (Gluten Index) % = [Stiff wet gluten remaining on the sieve (g) / total wet gluten (g)] x100

Variance analyzes of the obtained quality values were made according to the MSTAT-C version 3.00 / EM packet statistical program (MSTAT, 1982). Associations between HMW-GSs and LMW-GSs and quality parameters were determined by applying 'Pearson Correlation'.

RESULTS AND DISCUSSION

Glutenin alleles

Twenty six of glutenin alleles were identified in total. Eleven of the identified glutenin alleles were at the *Glu-1* loci and 15 were at the *Glu-3* loci. Three alleles were identified at the locus *Glu-A1*, among which the subunit *2** was the most frequent with the frequency of 68.8%.

Six alleles were identified at the locus *Glu-B1* and subunits *7+9*, *17+18* and *7+8* had high frequencies of 42.1%, 23.4% and 18.8%, respectively. Two alleles were identified at the locus *Glu-D1* and subunit *5+10* had higher frequency than *2+12*, 68.8% and 31.2%, respectively. Six alleles were identified at the locus *Glu-A3*, among these six alleles the subunit *c* was the most frequent with the frequency of 28.1%. Seven alleles were identified at the locus *Glu-B3*, and subunit *b* had the highest frequency of 35.9%. Two alleles were identified at the locus *Glu-D3* and subunit *c* had higher frequency than subunit *a*, (92.2% and 7.8%, respectively). In total, 52 different *Glu* loci combinations were determined. Within the 52 combination, the number of combinations repeated twice was 6, and the number of combinations repeated three times was 3 including 3 pairs of the sister genotypes.

Identified HMW and LMW allele composition of 64 genotypes were previously documented by Bayram (2016). Therefore, only the correlations of these alleles were given in this manuscript.

Quality parameters

The differences among the genotypes were found to be highly significant at the 0.1% level in terms of all quality parameters. The mean quality values of the genotypes and significance groups were identified (Table 2).

Protein content

The genotype means for kernel protein content (KPC) ranged from 10.6% to 14.3% (Table 2). The trial mean of KPC was 11.8%. Thirty genotypes have KPC above the mean. While the genotype Ocoroni-86/Pewit-3 reached the highest KPC with 14.3%, Aldane (13.8%) and Pewit-3 (13.3%), also reached the highest KPC by sharing the same statistical group (a). Konya-2002 cultivar was the genotype with the lowest KPC at 10.6%.

Köksel et al. (2000) classified wheat flours according to amount of protein as bulgur (>13%), bread (10-13%) and biscuits and crackers (<10%). Similarly, Pena (2002) classified breads according to protein quantity as leavened (>13%), flat and steamed (10-13%) and cookies, cakes, pastries (<10%). All genotypes in this study yielded KPC above 10% indicating good bread making quality. Genotypes with 13% or more KPC in this study were Tinamou/3/Hd2206/Hork//Buc/Bul, Pamukova-97/Arostor, Pewit-3, Aldane and Ocoroni-86/Pewit-3. In the study conducted by Kaya and Akcura (2014) in Central Anatolia, the KPC of the genotypes varied between 10.1% and 13.2% and the mean KPC of all genotypes was 11.6%. Aktaş and Baloch (2017) reported the mean KPC range of their genotypes from 11.7% to 14.8% in the three location of Southeastern Region of Turkey.

Zeleny sedimentation volume

The genotype means of ZSV values ranged from 26.9 mL to 63.1 mL and the trial mean was 43.8 mL (Table 2). Thirty-four genotypes gave ZSV values above the mean. While Aköz/Dariel genotype reached the highest sedimentation value with 63.1 mL, the other high ZSV genotypes were Aköz/Galil (60.2 mL), Ocoroni-86 (59.0 mL) and Pamukova-97 (58.5 mL). The genotype Çetinel-2000 gave the lowest sedimentation value with 26.90 mL. In a study conducted by Kahrıman (2007), high ZSV value (62.7 mL) of Pamukova-97 was also reported.

The sedimentation value of flours has been set in four classes (Elgün et al., 1998; Köksel et al., 2000); weakest (less than 15 mL), weak (between 15-16 mL and 24 mL), good (between 25 mL and 36 mL) and very good (more than 36 mL). In this study, 48 genotypes (75.0%) were over 36 mL. Therefore they were accepted as very good-sedimentation genotypes. Since 16 (25%) genotypes were found under the ZSV value of 36 mL. by entering into the good ZSV class of Elgün et al. (1998) and Köksel et al. (2000), they were accepted as genotypes with good-quality sedimentation. Although all genotypes in the study were in the class of good and very good ZSV, 3 genotypes were the genotypes had lowest ZSV values remaining below 30 mL ZSV value. These were Çetinel-2000, Zornitcha and Tahirova 2000/Zornitcha (no.5).

Table 2. The mean quality values of the genotypes and significance groups

No.	PC		No.	ZSV		No.	AE		No.	GIN		No.	WGC	
3	14.23	a	19	63.19	a	3	444.70	a	31	100.00	a	3	36.59	a
53	13.78	a	18	60.32	ab	36	426.45	a	19	99.92	ab	35	35.46	ab
35	13.32	b	33	59.45	b	35	357.52	b	18	99.84	ab	2	34.45	bc
7	13.28	b	36	58.73	b	19	350.21	b	29	99.78	ab	13	33.69	cd
2	12.92	bc	35	55.24	c	31	343.64	bc	27	99.72	ab	21	33.57	cde
36	12.89	bcd	53	55.10	c	53	343.51	bcd	59	99.54	abc	4	33.51	cde
13	12.77	cde	54	54.83	cd	16	329.60	cde	16	99.50	abc	50	33.43	cde
50	12.71	cde	63	54.51	cd	51	328.50	c-f	46	99.43	abc	60	32.55	def
21	12.64	c-f	64	54.02	cde	43	327.32	c-f	23	99.38	abc	14	32.46	def
19	12.59	c-g	60	53.65	c-f	22	326.57	c-f	55	99.36	abc	24	32.32	efg
45	12.58	c-h	43	52.32	c-g	54	323.87	c-g	15	99.03	a-d	5	32.00	fgh
4	12.45	d-i	31	52.29	c-g	29	322.72	d-h	36	98.81	a-e	12	31.76	f-i
44	12.42	e-i	40	51.89	d-h	42	321.66	e-i	64	98.70	a-f	48	31.70	f-i
8	12.36	e-J	3	51.33	e-i	27	312.54	e-J	17	98.67	a-f	7	31.68	f-i
14	12.35	e-J	8	51.23	e-i	18	309.31	e-k	33	98.43	a-f	32	31.42	f-J
60	12.33	e-J	7	51.06	e-i	61	308.42	f-l	63	98.18	a-f	53	31.41	f-J
54	12.23	f-k	22	50.65	f-i	17	305.95	g-l	22	97.78	a-f	44	31.13	g-k
12	12.23	f-l	14	49.88	g-J	10	305.16	g-l	42	97.25	a-g	1	30.92	h-l
38	12.21	f-m	46	49.87	g-J	40	302.30	h-l	43	97.23	a-g	20	30.72	h-m
48	12.17	g-n	13	49.44	g-J	60	300.93	ı-m	41	97.22	a-g	38	30.53	i-n
61	12.16	g-n	42	49.31	g-J	55	300.88	J-m	56	96.74	a-g	36	30.51	i-n
5	12.12	h-o	55	49.12	hiJ	8	298.20	J-n	8	96.10	a-h	61	30.38	J-o
18	12.10	i-o	15	48.84	iJ	33	293.66	J-o	51	96.08	a-h	25	30.00	k-p
10	12.05	i-p	61	48.38	iJk	11	293.22	J-o	40	95.84	a-i	62	29.92	k-r
32	12.03	i-p	16	47.46	Jkl	34	292.91	J-o	37	95.02	a-i	45	29.81	l-s
24	11.94	J-r	12	47.36	Jkl	38	292.58	J-o	57	94.44	b-J	58	29.80	l-s
9	11.92	J-s	17	45.48	klm	57	291.22	k-p	7	94.15	b-k	30	29.77	l-s
20	11.85	k-s	11	45.19	lm	56	291.02	k-p	30	92.91	c-l	6	29.74	l-s
33	11.83	k-t	32	45.03	lm	15	287.94	l-p	54	92.60	d-l	47	29.73	l-s
16	11.78	l-u	41	44.99	lm	6	282.03	m-r	10	92.16	e-m	8	29.68	l-s
43	11.75	m-u	37	44.92	lm	23	280.87	m-r	53	92.13	f-n	22	29.62	m-t

Table 2. Continued

No.	PC		No.	ZSV		No.	AE		No.	GIN		No.	WGC	
42	11.71	o-v	23	44.58	lm	12	279.00	n-s	11	90.86	g-o	54	29.59	m-u
17	11.71	o-v	51	43.79	mn	45	278.96	n-s	34	90.82	g-o	9	29.42	n-u
49	11.70	n-v	27	43.74	mn	2	274.71	o-t	61	89.60	h-p	26	29.30	n-u
40	11.68	o-y	10	43.74	mn	30	274.28	o-t	3	89.43	i-p	19	29.28	n-u
22	11.61	p-y	56	43.32	mn	7	273.74	o-t	45	88.34	J-r	43	29.27	n-u
26	11.58	p-z	29	41.42	no	14	273.38	o-t	9	87.53	k-s	49	29.10	o-v
6	11.55	r-A	30	40.99	nop	32	271.99	p-u	25	86.77	l-t	28	29.01	p-v
34	11.51	r-B	47	40.17	opr	62	263.30	r-v	49	86.24	m-t	39	28.94	p-y
31	11.47	s-C	57	39.40	opr	64	261.84	r-y	14	85.67	n-t	42	28.84	p-y
28	11.46	s-D	45	39.13	opr	13	260.26	s-y	35	85.38	o-u	40	28.70	r-Z
30	11.38	t-E	25	39.10	opr	63	258.40	s-y	12	83.26	p-v	41	28.62	s-A
1	11.38	t-E	38	38.32	o-s	50	257.41	t-y	60	82.30	r-v	52	28.42	t-B
11	11.35	u-F	62	38.05	p-t	37	254.21	t-z	52	81.76	s-v	34	28.34	u-B
57	11.35	u-F	39	37.94	p-t	20	251.78	u-A	39	80.79	tuv	57	27.91	v-C
25	11.32	u-G	34	37.84	r-u	41	247.82	v-B	26	79.16	uvy	37	27.88	v-D
46	11.30	v-G	50	37.83	r-v	26	244.52	v-B	6	78.25	vyz	10	27.68	y-E
55	11.23	y-H	59	35.75	s-v	49	244.43	v-B	62	76.80	v-A	18	27.53	z-F
29	11.23	y-H	6	35.32	t-y	44	241.94	y-C	47	73.90	y-B	11	27.49	z-F
47	11.15	z-İ	9	35.10	t-y	52	237.00	z-C	20	73.25	y-C	33	27.38	A-G
59	11.12	z-İ	2	34.82	u-z	4	232.49	A-C	38	72.22	z-C	29	27.20	B-G
41	11.10	B-İ	21	34.69	v-A	25	228.77	B-D	32	72.02	z-C	17	27.14	B-G
64	11.09	B-İ	52	34.59	v-z	39	221.17	C-E	13	71.24	ABC	51	26.89	C-G
15	11.04	C-J	44	34.54	v-A	24	210.35	D-F	24	70.05	BCD	56	26.83	C-G
27	11.01	D-K	49	34.43	v-A	21	209.45	D-G	44	68.13	B-E	23	26.66	D-G
37	10.97	E-K	20	34.18	v-A	46	203.26	E-H	28	68.12	B-E	63	26.65	D-G
23	10.97	E-K	24	32.48	y-B	48	198.45	F-H	50	66.83	CDE	31	26.55	EFG
52	10.91	F-K	28	32.48	y-B	1	195.16	F-H	5	63.72	DEF	16	26.42	FG
58	10.88	G-K	1	32.01	z-B	5	194.74	F-H	2	63.19	DEF	46	26.36	FG
62	10.84	H-K	26	31.91	z-B	59	188.79	G-H	4	61.56	EFG	15	26.21	G
63	10.82	H-K	4	31.58	AB	9	186.00	H	48	59.16	FG	55	26.19	G
51	10.69	İJK	5	30.15	BC	47	185.63	H	21	59.10	FG	64	26.14	G
56	10.61	JK	48	28.32	CD	58	158.94	I	1	56.60	GH	27	26.13	G

Table 2. Continued

No.	PC		No.	ZSV		No.	AE		No.	GIN		No.	WGC	
39	10.56	K	58	26.72	D	28	155.36	I	58	51.37	H	59	23.52	H
CV(%)	2.21			4.0			4.24			4.4			2.5	
LSD(0.05)	0.47			3.06			20.82			6.38			1.28	
Mean	11.82			43.81			275.20			86.11			29.56	

Means sharing same letter differ non-significantly (P>0.05)
PC: Protein content, ZSV: Zeleny sedimentasyon volume, AE: Alveograph energy value
GIN: Gluten index value, WGC: Wet gluten content

The ZSV values in this study are in line with previous work findings. Kahrıman (2007) reported ZSV values as 28.1-62.7 mL range and 40.3 mL trial mean for 20 cultivars in Southern Marmara Region. In Central Anatolia condition, Aydoğan et al. (2013) also found similar results for ZSV values (19.5-62.5 mL range and 45.9 mL mean) for 21 cultivars.

Alveograph energy

Mean alveograph energy values (AEV) of the genotypes varied from 155.4 J to 442.7 J and the trial mean was 275.20 J (Table 2). Thirty-four genotypes gave AEV above the mean. The genotypes Ocoroni86/Pewit3 and Pamukova-97 reached the highest AEV with 442.7 J and 426.5 J, respectively. Pewit-3 (357.0 J) and Akova/Dariel (351.2 J) genotypes were the other high AEV given genotypes. However, the genotypes Lancer and Çetinel-2000 had the lowest AEV with 155.4 J and 159.4 J, respectively.

According to Williams et al. (1988), the AEVs in the range of 300-400 J express strong dough, the AEVs in the range of 200-300 J express moderate strength dough and the AEVs in the range of 100-200 J express medium dough. In this study, since 21 genotypes (32.8%) were ranked between 300.9 J and 442.7 J, they were described as genotypes in the class with strong doughs. On the other hand, 35 genotypes (54.7%) remained in the range of 200-300 J indicating moderate strength dough. The eight genotypes (12.5%) were between 100-200 J and accepted as medium class dough.

In a winter wheat quality study, AEVs of 59 genotypes ranged from 48 J to 380 J and the mean of the all genotypes was 153 J in Central Anatolia condition (Yıldız, 2011). In another study in Central Anatolia, the average of AEVs of 13 genotypes ranged from 139 J to 257.5 J and the mean of the trial was 193 J (Aydoğan et al. 2006). On the other hand, Kaplan Evlice (2016) reported AEV as high as 412 J in 98 cultivars and 406 J in 101 lines, and the mean AEVs for all those genotypes 192 J and 200J, respectively. The higher mean AEVs in this study come from incorporating better genotypes into the study probably. Quite high AEVs were reported for 100 hard red winter wheat samples (the range 208-573J, the mean 350J) and 100 hard red spring wheat samples (the range 109-793 J, the mean 500 J) from the USA (Maghirang et al., 2006). The genotypes having higher AEVs in this study such as Bezostaya-1, Tosunbey, Konya-2002 also had similar high AEVs in the studies of Aydoğan et al. (2006) and Yıldız (2011).

Gluten index

Gluten index (GIN) value of the genotypes ranged from 52.41% to 100.0% and the trial mean was 86.11% (Table 2). Thirty-eight genotypes gave GIN values above the mean. The Kal/Mus//Har genotype reached the highest GIN value with 100% and Tosunbey and Doğu-88/Ziyabey were the other genotypes had the highest GIN values (99.90% and 99.88%, respectively). However, Çetinel-2000 was the genotype with the lowest GIN value (52.4%).

Elgün et al., (2001) put wheat flour doughs into 3 group according to gluten index values), strong doughs (>80% index values), moderate doughs (50-80% index values) and weak and sticky doughs (<50% index values). Of the genotypes in this study, 44 (68.75%) gave a GIN value of over 80%, referring to strong doughs and 20 (31.25%) gave a GIN value between 50-80% referring to moderate doughs. There was no any genotype below 50% GIN value, indicating that all the genotypes included in the study are good quality genotypes considering their doughs.

Similar GIN ranges were reported by various researchers; Kahrıman (2007), Yıldız (2011) and Kaplan Evlice et al. (2016) (43.7-94.3%, 37.8-99.7% and 45.9-100.0%, respectively).

Wet gluten Content

Wet gluten Content (WGC) value of the genotypes ranged from 23.6% to 36.6% and the trial mean was 29.6% (Table 2). Thirty-one genotypes (48.4%) gave WGC values above the mean. The Ocoroni-86 / Pewit-3 genotype reached the highest WGC value with 36.6%, Pewit-3 and Tnmu/3/HD2206/Hork//Buc/Bul were the other genotypes had the highest WGC values (35.2% and 34.6%, respectively). However, Yıldız-98 had the lowest WGC value (23.6%).

According to Elgün et al. (2001), wet gluten values higher than 27% indicate high bread quality, wet gluten values between 20% and 27% indicate medium bread quality and lower than 20% of wet gluten values indicate low bread quality. Fifty-two genotypes (81.25%) in this study were above the WGC ratio of 27%. These genotypes have high bread quality according to the WGC values. However, 20 genotypes (18.75%) in this study have moderate quality since they were in the range of WGC values between 20-27%.

Kaya and Akcura (2014) reported the range of WGC as 28-37% and the trial WGC mean as 32% for 20 wheat genotypes. Kahrıman (2007) found the range of WGC for 20 wheat genotypes as 25.3-43.6% and the trial WGC mean as 34.2%. Aktaş and Baloch (2017) reported the mean WGC range of the three locations as 25.9-31.4%. However, Yıldız (2011) found the range of WGC for 59 wheat genotypes as 16.5-43.8% and the trial WGC mean as 28.3%, and

Kaplan Evlice et al. (2016) reported the WGC range as 16.1-44.6% and the WGC mean as 30.7% for 101 wheat lines, and the range of WGC as 14.8-47.5% and the mean of WGC as 33.5% for 98 wheat cultivars. An increase in the number of genotypes may promote variation in WGC values. Our findings showed similarity to previous reports of WGC values in wheat.

Relationships between glutenin alleles and the quality parameters

The mean quality values of the glutenin alleles belong to the HMW-GSs and the LMW-GSs and the significant correlation coefficients of the quality parameters and glutenin alleles were presented (Table 3).

In this study, the highest PC value obtained from the allele *A1-1* (11.98%) at the *Glu-A1* locus and the relationship between PC and the allele *A1-1* was found significantly positive (r = 0.16, P<0.05). There was no significant relationship between PC and the other two alleles at the *Glu-A1* locus. The highest PC value at the *Glu-B1* locus obtained from *B1-7+9* allele (12.09%) and the relationship between PC and the allele *B1-7+9* was found significantly positive (r= 0.28, P<0.001). Contrarily, the association of PC with the allele *B1-7* was significantly negative (r = - 0.29, P<0.001). The PC values of the alleles *D1-2+12* and *D1-5+10* at the *Glu-D1* locus were close to each other (11.63%, 11.90 respectively), and the allele *D1-5+10* was significantly positively and the allele *D1-2+12* was significantly negatively correlated with PC (r = 0.15, P<0.05; r = - 0.15, P<0.05, respectively).

At the *Glu-A3* locus, the highest PC values were found at the *A3d* allele (12.5%) and *A3a* allele (12.2%), and the relationship between PC and the alleles *A3d* and *A3a* were found significantly positive (r = 0.31, P<0.001; r = 0.15, P<0.05). At the *Glu-B3* locus, the highest PC value (12.1%) was obtained from the *B3f* allele, and PC associated significantly positively with only the *B3f* allele (r = 0.14, P <0.05).

Table 3. The mean quality values of the glutenin alleles belong to the HMW-GSs and the LMW-GSs and the significant correlation coefficients (r) between the quality parameters and glutenin alleles

L	Allele	DAN	KPC		ZSV		AEV		GIN		WGC	
			%	r	mL	r	J	r	%	r	%	r
	N	2	11.48	-	36.25	-0.15*	223.30	-0.16*	81.65	-	28.37	-
Glu-A1	1	18	11.98	0.16*	46.10	-	299.90	0.27***	90.30	-	29.39	-
	2*	44	11.70	-	43.21	-	267.40	-0.20**	84.50	-	29.68	-
	7	8	11.22	-0.29***	40.73	-	242.50	-0.22**	86.32	-	27.72	-0.27***
	7+8	12	11.71	-	46.97	0.17*	292.70	0.15*	91.02	0.17*	29.40	-
	7+9	27	12.09	0.28***	40.74	-0.30***	263.90	-0.17*	78.55	-0.47***	30.91	0.44***
Glu-B1	13+16[x]	1	11.31	-	50.00	-	204.30	-0.16*	98.73	-	26.73	-
	14+15[x]	1	11.62	-	32.50	-0.16*	155.50	-0.27***	69.37	-0.15*	28.73	-
	17+18	15	11.80	-	48.77	0.31***	311.60	0.35***	95.94	0.40***	28.49	-0.23**
	2+12	20	11.63	-0.15*	41.56	-0.17*	271.69	-	82.92	-0.16*	30.02	-
Glu-D1	5+10	44	11.90	0.15*	44.82	0.17*	276.79	-	87.53	0.16*	29.35	-
	a	5	12.23	0.15*	32.80	-0.36***	224.50	-0.26***	65.10	-0.44***	32.17	0.29***
	b	14	11.81	-	45.54	-	296.80	0.20**	89.71	-	29.29	-
	c	18	11.65	-	40.89	-0.21**	268.00	-	85.74	-	29.03	-
Glu-A3	d	9	12.46	0.31***	47.06	0.15*	291.70	-	83.41	-	31.76	0.34***
	e	15	11.63	-	47.47	0.23**	264.90	-	90.88	0.19**	28.36	-0.26***
	f	3	11.29	-	43.50		304.10	-	90.77	-	29.11	-
	a	3	11.98	-	52.67	0.22**	331.50	0.22*	96.95	0.18*	29.11	-
	b	23	11.69	-	45.75	0.16*	287.70	0.17*	91.19	0.28***	28.64	-0.27***
	c[x]	1	11.62	-	32.50	-0.16*	155.50	-0.27***	69.37	-0.15*	28.73	-
Glu-B3	f	12	12.06	0.14*	33.99	-0.53***	242.80	-0.27***	71.71	-0.50***	31.11	0.29***
	g	13	11.91	-	45.50	-	296.00	0.18*	87.46	-	30.61	0.20**
	h	5	11.55	-	47.83	-	258.20	-	85.32	-	28.70	-
	i	7	11.83	-	46.05	-	256.30	-	89.89	-	28.91	-
	a	5	11.84	-	48.60	0.16*	300.85	-	89.89	-	28.94	-
Glu-D3	c	59	11.82	-	43.40	-0.16*	273.02	-	85.77	-	29.61	-

*P<0.05, **P<0.01, ***P<0.001.

L: Locus, DAN: Determined allele numbers in 64 genotypes, KPC: Kernel protein content (%),

ZSV: Zeleny sedimentation value (mL), AEV: Alveograph energy value (J), GIN: Gluten index value (%), WGC: Wet gluten content (%)

[x] determined in one genotype

The PC values of the alleles *D3a* and *D3c* at the *Glu-D3* locus showed similarity (11.84%, 11.82%), and PC association with the alleles at the *Glu-D3* locus were not significant.

The alleles having high PC in this study were also reported by Kaya and Akcura (2014) as high PC exhibiting alleles. According to Kaya and Akcura (2014), alleles with high PC values, were the alleles *A1-1* (12%) at the *Glu-A1*, *B1-7+8* (12%), *B1-7+9* (11%), *B1-17+18* (12%) at the *Glu-B1*, *D1-5+10* (11.9%) at the *Glu-D1*, *A3b* (13%), *A3d* (12%), *A3e* (12%) at the *Glu-A3*, *B3b* (12%), *B3f* (13%) and *B3g* (13%) at the *Glu-B3*. The allele *A1-1* was also reported by Liatukas et al. (2008) as the allele having higher PC (10.10%) comparing to the *null* allele at the *Glu-A1* locus. Similarly, Aktaş and Baloch (2017) reported that alleles with high PC values were the alleles *A1-1* (12.1%) at the *Glu-A1* locus, *B1-7+8* (15.4%) and *B1-13+19* (15.4%) at the *Glu-B1*, *D1-5+10* (12.4%) and *D1-2+12* (12.3%) at the *Glu-D1*, *A3b* (13.8%), and *A3e* (13.5%) at the *Glu-A3*, *B3b* (13.3%), *B3c* (14%) and *B3h* (13.3%) at the *Glu-B3*.

The allele *A1-1* gave the highest ZSV (46.1 mL) at the *Glu-A1* locus, and the association between ZSV and *A1-1* allele was not significant. Although, a significant association was found only between the *null* allele and ZSV at the *Glu-A1* locus, this association was negative (r = - 0.15, P<0.05). The highest ZSV value at the *Glu-B1* locus was obtained from *B1-13+16* allele (50.0 mL). The *B1-17+18* allele at the *Glu-B1* also reached to high ZSV value (48.8 mL). Significantly positively correlated *Glu-B1* alleles with ZSV were *B1-7+8* (r = 0.17, P<0.05) and B1-17+18 (r = 0.31, P<0.001). At the *Glu-D1* locus the *D1-5+10* allele gave higher ZSV than the *D1-2+12* allele (44.8 mL, 41.6 mL, respectively). Associations of these two alleles with ZSV were significant. However, only the *D1-5+10* allele correlated with ZSV positively (r = 0.17, P<0.05).

At the *Glu-A3* locus *A3e* and *A3d* alleles gave the highest ZSV values (47.5 mL, 47.1 mL, respectively), and their correlation with ZSV were significantly positive (r = 0.23, P<0.01; r = 0.15, P<0.05, respectively). Contrastingly, at the *Glu-A3* locus *A3a* and *A3c* alleles were significantly negatively correlated with ZSV (r = - 0.36, P<0.001; r = - 0.21, P<0.01, respectively). At the *Glu-B3* locus the allele *B3a* gave the highest ZSV (52.7 mL), and its correlation with ZSV were significantly positive (r = 0.22, P<0.01). The *b* allele at the *Glu-B3* locus was the other significantly positively correlated (r = 0.16, P<0.05) allele with ZSV value (45.75 mL). The correlations between ZSV and the alleles *B3f* and *B3c* at the *Glu-B3* locus were found significantly negative (r = - 0.53, P<0.001; r = - 0.16, P<0.05, respectively). The *D3a* allele at the *Glu-D3* locus had higher ZSV (48.6 ml), and the correlation of this allele with ZSV was found to be significantly positive (r = 0.16, P <0.05). In contrast, the *D3c* allele at the *Glu-D3* locus was significantly negatively correlated with ZSV value (r = - 0.16, P<0.05).

The high ZSV giving alleles of this study, *A1-1* at the *Glu-A1*, *B1-7+8* at the *Glu-B1*, *D1-5+10* at the *Glu-D1*, *A3b* and *A3d* at the *Glu-A3*, *B3b* at the *Glu-B3* and *D3a Glu-D3* have been described as the alleles giving high ZSV value by Kaya and Akcura (2014). The high ZSV giving alleles, *A3d* allele at the *Glu-A3* locus, *B3b*, *B3g* and *B3i* alleles at *Glu-B3* were also found as high ZSV having alleles by Zhang et al. (2012). Of this study, high ZSV related alleles, *A1-1* at the *Glu-A1*, *B1-13+16*, *B1-17+18* at the *Glu-B1*, *D1-5+10* at the *Glu-D1*, *A3d* at the *Glu-A3*, *B3b* and *B3i* at the *Glu-B3* were similarly reported as high ZSV giving alleles by Branlard et al. (2001). Recently, high ZSV giving alleles of this study, *Glu-A1-1* and *Glu-A1-2**, *Glu-B1-7+8*, *Glu-B1-17+18*, *Glu-D1-5+10*, *Glu-A3d* and *Glu-A3e*, *Glu-B3b*, *Glu-B3g*, *Glu-B3i*, and *Glu-D3a* were also reported as high ZSV having alleles by Aktaş and Baloch (2017).

Glu-A1-1 allele had the highest AE value (299.9 J). The association of this allele with AE value was significant and positive (r = 0.27, P <0.001). The association of other alleles with AE value at *Glu-A1* were also significant but negative (Table 3). *Glu-B1-17+18* allele had the highest AE value (311.6 J). The correlation of this allele with AE value was positive and significant (r = 0.35, P<0.001). The other allele, having significant and positive correlation with AE at the *Glu-B1* locus was *B1-7+8* allele (r = 0.15, P<0.05) with 292.7 J AE value. On the contrary, the alleles B1-7, *B1-7+9*, *B1-13+16* and *B1-14+15* at the

Glu-B1 locus correlated significantly but negatively with AE (Table 3). At the *Glu-D1* locus, *D1-5+10* allele had a higher AE value than *D1-2+12* allele had (276.8 J and 271.7 J, respectively) and their correlations with AE were not significant.

The *A3f* allele at the *Glu-A3* locus gave the highest AE (304.1 J). However, the correlation of *A3f* allele with AE was not significant. The *A3b* allele at the *Glu-A3* locus had a significant positive correlation with AE (r = 0.20, P<0.01), but, the *A3a* allele at the *Glu-A3* locus had a negative significant correlation with AE (r = - 0.26, P<0.001). *Glu-B3*a allele had the highest AE value (331.5 J), and the correlation of this allele with AE value was significantly positive (r = 0.22, P<0.05). The other alleles, having significant and positive correlations with AE at the *Glu-B3* locus were *B3b* and *B3g*, (r = 0.17, P<0.05; r = 0.18, P<0.05) with 287.7 J and 296.0 AE values, respectively. Adversely, the correlation of the alleles *B3c* and *B3f* at the *Glu-B3* locus with AE were significantly negative (r = - 0.27, P<0.001; r = - 0.27, P<0.001). Although *Glu-D3a* allele had a higher AE value (300.9 J) than *Glu-D3c* allele had, the correlations of the alleles at this locus with AE values were not significant.

The high AE value giving alleles in this study, *A1-1* allele at the *Glu-A1*, *B1-17+18* allele at the *Glu-B1*, *D1-5+10* allele at the *Glu-D1*, *A3d* and *A3f* alleles at the *Glu-A3* and *B3b* and *B3g* alleles at the *Glu-B3* and *D3a* allele at the *Glu-D3* were also reported by Branlard et al. (2001) as the alleles that having high AE values. Similar to the present study, Sharma et al. (2012) stated in conclusion that *B1-17+18* allele at the *Glu-B1*, *D1-5+10* alleles at the *Glu-D1*, *A3d* allele at the *Glu-A3* and *B3g* allele at the *Glu-B3* positively affect gluten strength.

Glu-A1-1 allele had the highest GIN (90.3%). The relationships between GIN and the three alleles at this locus were not significant. At the *Glu-B1* locus *B1-13+16* allele gave the highest GIN value (98.7%). However, the GIN relationship with the *B1-13+16* allele was not significant. At the *Glu-B1* locus *B1-17+18* allele also gave a high GIN value (95.9%), and the association of *B1-17+18* allele with GIN was found to be highly significant (r = 0.40, P <0.001). Having 91.0% GIN value, at the *Glu-B1* locus *B1-7+8* allele was also found significantly positively correlated with GIN (r = 0.17, P<0.05). However, the correlation of the *B1-7+9* and *B1-14+15* alleles at the *Glu-B1* locus with GIN were significantly negative (r = - 0.47, P<0.001; r = - 0.15, P<0.05, respectively). At the *Glu-D1* locus the allele *D1-2+12* significantly negatively and the allele *D1-5+10* significantly positively correlated with GIN values (r = - 0.16, P<0.05; r = 0.16, P<0.05). GIN value of the allele *D1-5+10* was higher than that of the allele *D1-2+12* (Table 3).

Glu-A3e and *Glu-A3f* alleles have the highest GIN values (90.9% and 90.8%, respectively) and the relationship between *Glu-A3e* allele and GIN was significantly positive (r = 0.19, P<0.01). Whereas, at the same locus the correlation of *Glu-A3a* allele with GIN was significantly negative (r = - 0.44, P<0.001). At the *Glu-B3* locus, *Glu-B3a* and *Glu-B3b* alleles have the highest GIN values (97.0%, 91.2%, respectively) with significant positive correlations (r = 0.18, P<0.05; r = 0.28, P<0.001, respectively).

Tabiki et al. (2006) similarly reported that the *D1-5+10* allele at the *Glu-D1* and the *B3b* allele at *GluB3* increased GIN values significantly. Sharma et al. (2012) listed *A1-1* allele at the *Glu-A1*, *B1-17+18* alleles at the *Glu-B1*, *D1-5+10* alleles at the *Glu-D1*, *A3d* allele at the *Glu-A3* and *B3g* allele at the *Glu-B3*, *D3a* allele at the *Glu-D3* as the alleles having higher GIN values than other alleles. Likewise, the alleles conferring high GIN values stated by Sharma et al. (2012) also showed high GIN values in the present study.

*Glu-A1-2**allele had the highest WGC (29.7%). At the same locus, the allele *A1-1* had similar WGC (29.4%). All alleles at this locus were not associated with WGC. At the *Glu-B1* locus *B1-7+9* allele gave the highest WGC (30.9%). The relationship of WGC and *B1-7+9* allele was determined as highly significant and positive (r = 0.44, P <0.001). The WGC values of *D1-2+12* and *D1-5+10* alleles at the *Glu-D1* locus were close to each other (30.02%, 29.35%, respectively). However, the associations of these two alleles with the WGC were not significant.

At *Glu-A3*, the *A3a* allele had the highest WGC (32.2%). The association of the WGC with *A3a* allele was found highly significant (r = 0.29, P <0.001). At *Glu-A3*, the *A3d* and *A3a* alleles also gave highly significant correlations with WGC (r = 0.34, P <0.001; r = 0.29, P<0.001, respectively). In contrast, the *A3e* allele gave a significant negative correlation with WGC (r = - 0.26, P <0.001) at the *Glu-A3*. At *Glu-B3*, the *B3f* and *B3g* alleles had the highest WGC values and their association with WGC were significant (31.1%, r = 0.29, P<0.001; 30.6%, r = 0.20, P<0.01, respectively). At *Glu-B3*, only the *B3b* allele gave a significant negative correlation with WGC (r = - 0.27, P <0.001). The associations of WGC with the alleles at the *Glu-D3* locus were negligible and *D3c* allele gave a little higher WGC than the *D3a* allele gave (29.6% and 28.94%, respectively).

The high WGC giving alleles in this study, *A1-2** allele at the *Glu-A1*, *B1-7+9* allele at the *Glu-B1* and *D1-2+12* allele at the *Glu-D1* were also found by Tabiki et al. (2006) as the alleles with high WGC. Also, the high WGC giving alleles in this study, *A3a* and *A3d* alleles at the *Glu-A3*, *B3f* allele at the *Glu-B3* were also reported by Kaya and Akcura (2014) as the alleles having high WGC.

Consequently, considering the quality parameters, the glutenin alleles may be graded as, PC increasing HMW-GS alleles *A1-1*, *B1-7+9*, *D1-5+10* and LMW-GS alleles *A3d*, *B3f*, *D3a*; ZSV increasing HMW-GS alleles *A1-1*, *B1-13+16 / B1-17+18*, *D1-5+10* and LMW-GS alleles *A3e*, *B3a*, *D3a*; AE increasing HMW-GS alleles *A1-1*, *B1-17+18*, *D1-5+10* and LMW-GS alleles *A3f/b*, *B3a/g*, *D3a*; GIN increasing HMW-GS alleles *A1-1*, *B1-13+16 / B1-17+18*, *D1-5+10* and LMW-GS alleles *A3e/f*, *B3a/b*, *D3a*; WGC increasing HMW-GS alleles *A1-2**, *B1-7+9*, *D1-2+12* and LMW-GS alleles *A3a/d*, *B3f/g*, *D3c*.

On the other hand, the negative effective alleles may be expressed as; PC reducing HMW-GS alleles *A1-null*, *B1-7*, *D1-2+12* and LMW-GS alleles *A3f*, *B3h*, *D3c*; ZSV reducing HMW-GS alleles *A1-null*, *B1-7+9/B1-14+15*, *D1-2+12* and LMW-GS alleles *A3a/c*, *B3f/c*, *D3c*; AE reducing HMW-GS alleles *A1-null*, *B1-14+15/B1-7/B1-7+9*, *D1-2+12* and LMW-GS alleles *A3a*, *B3c/f*, *D3c*; GIN reducing HMW-GS alleles *A1-null*, *B1-7+9/B1-14+15*, *B1-2+12* and LMW-GS alleles *A3a*, *B3f/c*, *D3c*; WGC reducing HMW-GS alleles *A1-null*, *B1-7/B1-13+16/B1-17+18*, *D1-5+10* and LMW-GS alleles *A3e*, *B3b/h*, *D3a*.

CONCLUSIONS

Breeding high-quality wheat cultivars has been one of the basic aims of the wheat breeding programs beside grain yield since the demand of high quality flour has risen. To meet the need of wheat cultivars having high quality, breeding programs started to use intense quality tests as early as possible during breeding steps. Revealed information might be helpful for the bread wheat breeders for selection of high quality genotypes carrying quality promoting glutenin alleles, and for discarding low quality genotypes carrying quality reducing glutenin alleles during their breeding applications. Also, high quality genotypes identified in this study can be used in wheat crossing programs as gene resources.

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