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Screening Bread Wheat Genotypes for High Molecular Weight Glutenin Subunits and Some Quality Parameters

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ABSTRACT

High Molecular Weight Glutenin Subunits (HMW-GS) compositions of 122 genotypes from bread wheat crossing block were investigated in terms of some quality traits such as grain Protein Content (PC), Sodium Dodecyl Sulphate (SDS), the Particle Size Index (PSI), and Thousand Kernel Weight (TKW), by using SDS-PAGE. In total, 12 different HMW-GS combinations were determined. Considerable diversity in terms of three *Glu-A1*, *Glu-B1* and *Glu-D1* loci were identified. In *Glu-A1* locus, 1/2*, 1 and 2* alleles were found with the frequency of 2.5, 12.3 and 85.5%, respectively. Whereas, in *Glu-B1*, out of 7 reported alleles, 7+8 (20.5%) and 17+18 (17.2%) were detected. Existence of 2 alleles at the locus *Glu-D1* was revealed; in fact, 54.1% of them demonstrated the subunits 5+10 correlated with good bread making properties. The *Glu-1* score of genotypes ranged from 6 to 10. Among the genotypes, only 23 (18.9%) had 10 *Glu-1* quality score value. In the evaluation using the Genotype-Traits (GT) Biplot graph, PC and PSI were involved in section I while SDS sedimentation value and *Glu-1* score were involved in section II. On the other hand, section III included the only TKW which was negatively associated with other traits. The desired genotypes can be used for the crossing programs to improve technological quality of bread wheat.

Keywords: Biplot, HMW-GS, Landraces, Quality.

INTRODUCTION

Wheat is one of the most important products in the world with the due to its ability to adapt to environmental conditions and its use for a wide diversity of food products (Shewry and Tatham, 1997). Also, wheat is among the leading cereals in Turkey (TUİK, 2014). Wild emmer wheat (*Triticum dicoccoides* Körn ex Asch. and Graebn.) Thell. is the wild progenitor of domesticated wheat. Natural populations of the species are confined to the Fertile Crescent (Zohary and Hopf, 1993; Jaradat, 2011). Nowadays, *Aegilpos speltoides*, *Triticum monococcum* and *Triticum dicoccoides* grow spontaneously on the basaltic rocky slopes of the Karacadag Mountains in southeastern Anatolia. Bread wheat improvement of south-eastern Anatolia is mainly targeted to develop high yielding, widely adapted and disease resistant varieties; with inadequate emphasis on grain quality. Different genotypes are necessary in favourable environments and breeder may contribute to the improvement of yield and baking quality (Tarakanovas and Ruzgas, 2007). In breeding programs, the main objective is to improve the quality of the germplasm bank in order to make it possible to develop wheat with adequate gluten strength and extensibility for bread-making (Costa *et al*., 2013). Bordes *et al*. (2008) have reported that wheat produced in

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different parts of the world differ greatly in their actual protein qualities and quantities, the quantity is affected mainly by environmental factors, but the protein quality is primarily a heritable characteristic. Improvement of wheat genotypes with good bread making quality is a most important goal for many wheat breeders. Gluten, which is a sub unit of protein, is responsible for bread making quality (Branlard and Dardevet, 1985). Gluten is a storage protein found in the endosperm of the grain and composed of two prolamine groups, gliadins, and glutenin. Gluten is composed of glutenins, which consist of Low- and High-Molecular-Weight (LMW and HMW) complex subunits and constitute about 30-40% of flour protein (Kaya and Akçura, 2014). The quality of wheat flour for bread making depends on the viscoelastic properties of the dough, which are influenced by the quantity and quality of the gluten-forming storage proteins of the endosperm. These proteins consist of two classes, i.e. monomeric gliadins and polymeric glutenins (Weegels *et al*, 1996; Pfluger, 2007). Glutenin subunits can be divided in two main groups: HMW-GS and LMW-GS, based on the relatives mobilities in SDS-polyacrylamide gel electrophoresis (SDS-PAGE). Three different loci, located on the long arms of group 1 chromosomes, code for the HMW-GS *Glu-A1*, *Glu-B1* and *Glu-D1*. (Payne, 1987). The SDS-PAGE electrophoresis test is a conventional method utilized for separating protein components. It allows the division of the subunits from gluten proteins by detecting the glutenin subunits of HMW-GS (Keser and Pena, 2004; Liang *et al*., 2010; Zheng *et al*., 2011). Molecular studies have shown that the HMW-GS have the highest effect on the rheological properties of dough and bread-making quality (Zheng *et al*., 2011; Hernandez *et al*., 2012). He *et al*. (2005) reported that the alleles 1 and 2* of *Glu-A1* have been discovered to have a better effect on bread-making quality when compared to a null allele. The 5+10 alleles of the *Glu-D1* have been correlated with higher dough strength, while the 2+12 alleles have been correlated with low bread-making quality (Gianibelli *et al*., 2001). Payne *et al*. (1987) have identified a score of each HMW-GS which allowed a statistical evaluation of the amount of variation in bread-making quality attributable to the HMW-GS. For British- and Spanish-grown wheat cultivars, 47 and 68%, respectively, of the variation in quality is directly related to *Glu-1* score (Payne *et al*., 1987; Payne, 1988). For Canadian-grown wheat, 59-69% of the variation in bread-making quality is directly related to this score (Lukow *et al*., 1989). The objectives of this research were to: (i) Determine the interrelationship among wheat traits using GT biplot procedure, and (ii) Provide information on HMW-GS variation of wheat (*Triticum aestivum* L.) breeding lines and cultivars. This will benefit the improvement of wheat quality in breeding programs.

MATERIALS AND METHODS

In this study, 122 wheat (*Triticum aestivum* L.) genotypes (14 of which were registered as cultivars of Turkey, 15 of which were local and 93 were from foreign lines) from the crossing blocks of the bread wheat breeding program were used. The genotypes are listed in Table 3. The experiment was located at Diyarbakır, Turkey, with an altitude of 602 m; clay loam soil and with a mean annual rainfall of 501 mm. The seeds were sown in experimental field of GAP-IARTC in the city of Diyarbakır, Turkey in 2001-2002 growing season. The plots were fertilized with 60 kg N ha^{-1} and 60 kg P_2O_5 ha^{-1} at the planting and 60 kg N ha^{-1} in spring at stem elongation for drought conditions. Grain Colour (GC), Thousand Kernel Weight (TKW), grain Protein Content (PC), and Particle Size Index (PSI) for each wheat genotype were determined by the method of Williams *et al*. (1988). SDS-sedimentation volume was determined according to the method described by Pena *et al*. (1990).

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SDS-PAGE Electrophoresis

Seeds crushed into a fine powder were used to extract the endosperm storage proteins. Electrophoresis of glutenins was performed on vertical gel according to the SDS-PAGE protocol described by Singh *et al*. (1991) and fractionated in vertical SDS-PAGE slabs at a polyacrylamide concentrations of 8 and 10% (w/v, C: 1.28%) with and without 4 M urea according to Lafiandra *et al*. (1993). Electrophoresis was applied at a constant current of 30 mA gel^{-1} at 18ºC. After 18 hours, the gels were stained in 12.5% (w/v) trichloroacetic acid, 0.01% (w/v) Coomassie Brilliant Blue R250 and distained with distilled water (Akhtar *et al*., 1994). The HMW -GS were identified using the numbering system of Payne and Lawrence (1983). Quality and HMW-GS analysis were made by Field Crops Central Research Institute laboratory. The *Glu-1* score was calculated according to the catalogue of alleles for HMW-GS (Payne *et al*., 1987) (Table 1).

Statistical Analysis

The Genotype Trait (GT) biplot method, as described by Yan and Rajcan (2002), was established by plotting the First Principal Component (PC1) scores of the genotypes and the traits against their respective scores for the Second Principal Component (PC2). The correlation coefficient between any two traits was approached by the cosine of the angle between their vectors. Acute angles indicated positive correlations, wide angles negative correlations, and right angles no correlation. A short vector may suggest that the trait is not related to other traits (Mohammadi and Amri, 2011). The biplot method presented in this study was generated using Gen Stat 12th statistical software (Payne *et al*., 2009).

RESULTS AND DISCUSSION

Physicochemical Characterization of the Wheat Grains

The results obtained by evaluation of grain quality are summarized in Tables 1 and 3. Williams *et al*. (1988) reported that bread wheat quality may be classified by its PC as very low (< 9.0%), low (9.1-11.5%), medium (11.6-13.5%), high (13.6-15.5%), very high (15.6-17.5%), and extra high (> 17.6%). In this study, the genotypes mean values of PC ranged from 9.3-16.1%, PSI from 33.9 to 80.5%, SDS sedimentation values from 13.0 to 34.0 mL, TKW from 25.1 to 42.2 g. The HMW-GS play the major role in determining the functional properties of flour and dough (Shewry and Jones, 2012). The SDS-sedimentation volume

Table 1. HMW-GS compositions, PSI, TKW, PC, GC and SDS-sedimentation volume of 122 wheat genotypes at the three loci.

	Subunits	*PSI*%	TKW g^{-1}	PC%	SDS ml^{-1}	Red grain%	White grain%
Glu-A1	1	59.2	31.3	13.2	27.3	37.5	62.5
	2*	56.7	32.2	13.0	24.5	49.5	50.5
	1/2*	59.7	29.4	13.2	23.0	33.3	66.7
Glu-B1	13+16	55.4	31.9	12.9	24.0	33	67
	17+18	55.8	31.0	12.6	27.0	19	81
	6+8	68.9	33.2	12.2	23.4	40	60
	7+8	60.6	31.3	13.4	24.5	44	56
	7+9	54.8	32.4	13.1	24.7	52.8	47.2
	7	59.7	32.7	13.0	23.3	77	33
	7+8/7+9	54.2	32.5	12.8	24.0	100	0
Glu-D1	5+10	55.8	31.8	12.8	25.3	51	49
	2+12	58.7	32.1	13.2	24.3	41	59

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correlated with the amount of total HMWG subunits and individual HMWG subunits (Kanenori *et al*., 2003). Also, Tahir (2009) reported that the SDS sedimentation volume correlated with the amount of total HMW-GSs and individual HMWG subunits. Some subunits were positively correlated, and the others were negatively correlated with sedimentation volume (Seilmeier *et al*., 1991). The HMW subunits play the major role in determining the functional properties of flour and dough.

Composition of HMW-GS

Allelic variations at *Glu-1* loci in wheat samples separated by SDS-PAGE are represented in Tables 1, 2, and 3. From all genotypes, 12 different subunits of HMW-GS were observed. While the most frequent patterns were 2*, 7+8, 7+9, 5+10 and 2+12, other subunits were found less frequent. The HMW-GS of all of the genotypes (Table 2) were found to have three allelic variations in *Glu-A1* [subunits 2* (85.5%), 1 (12.3%), and 1/2* (2.5%)], seven in *Glu-B1* [subunits 7+9 (45.1%), 7+8 (20.5%), 17+18 (17.2%), 7 (9%), 13+16 (6%) and 6+8(4.1%)], and two in Glu-D1 [subunits 5+10 (54.1%), 2+12 (45.9%)]. The two major alleles at the *Glu-D1* locus, 5+10 and 2+12, have repeatedly shown a contrasting effect on quality traits (Gupta *et al*., 1994; He *et al*., 2005; Guzmán *et al*., 2016). Whereas, correlations and genetic studies of HMW-GS (Pogna *et al*., 1986; Payne *et al*., 1987) established subunits with both positive (5+10) and negative (2+12) effects on bread making quality.

The *Glu-1* quality score of the genotypes varied from 6 to 10 (Table 2). The scores 9 and 10 were the most frequent due to the higher frequency of 2* allele in Glu-A1, 7 + 9 alleles in *Glu-B1*, and 5+10 alleles in *Glu-D1*. Thus, Costa *et al*. (2013) reported that there was a positive correlation between the *Glu-1* quality score and the volume of sedimentation (r= 0.521) and the TKW (r= 0.510).

The mean values of quality parameters of the genotypes grouped by individual glutenin subunits are demonstrated in Table 3. At locus *Glu-A1*, the genotypic groups possessing subunits 1 and 2*; at locus *Glu-B1*, subunits 17+18 showed higher values of wheat on SDS sedimentation value than the other group of subunits. Also, subunits 1 and 2*, therefore, have positive effects on the dough strength parameters (Liang *et al*., 2010). These results agree with those of Lukow *et al*., 1989; Keser and Pena, 2004, and Yıldız, 2011. Within the Turkish commercial varieties, "Bezostaya, Gerek-79, Pehlivan, Dağdaş-94 and Gün-91" are mostly grown in winter zone of Turkey and these varieties have 2*, 7+9, 5+10; 2*, 7+8, 2+12; 2*, 7+9, 2+12; 2*, 7+8, 5+10; 2*,

Table 2. *Glu-1* quality score and allele frequencies of HMW-GS studied by SDS-PAGE in bread wheat genotypes.

Locus	HMW-GS	Frequency	%	*Glu-1* score
Glu-A1	1	15	12.3	3
	2*	104	85.5	3
	1/2*	3	2.5	3
Glu-B1	17+18	21	17.2	3
	7+8	25	20.5	3
	13+16	6	4.9	3
	7+9	55	45.1	2
	7	9	7.4	1
	6+8	5	4.1	1 (Poor)
	7+8/7+9	1	0.82	-
Glu-D1	5+10	66	54.1	4 (Good)
	2+12	56	45.9	2

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Table 3. Pedigree, quality traits, HMW-GS and *Glu-1* score of the 122 bread wheat genotypes evaluated.

No	Name	Orig	GC	*PSI*	TKW	PC	SDS	HMW-GS			*Glu-1*
				%	g^{-1}	%	ml^{-1}	*Glu-A1*	*Glu-B1*	*Glu-D1*	score*
G1	Kırkpınar-79	C	W	50.7	29.9	10.8	25	2*	13+16	5+10	10
G2	Cumhuriyet-50-1	BL	W	56.5	39.1	10.3	25	2*	17+18	5+10	10
G3	Gerek 79	C	W	76.6	30.0	13.1	27	2*	7+8	2+12	6
G4	Dağdaş-94	C	W	58.1	31.8	13.7	23	2*	7+8	5+10	10
G5	Gün-91	C	R	62.7	28.9	13.7	34	2*	17+18	5+10	10
G6	Kınacı-97	C	R	71.4	27.2	13.5	26	1	7+8	5+10	10
G7	Pehlivan	C	R	58.5	42.2	13	30	2*	7+9	2+12	7
G8	Bezostaja-1	C	R	34.4	35.7	12.1	26	2*	7+9	5+10	9
G9	Katae A-1	C	R	52.0	31.4	12.3	28	1	7+8	2+12	8
G10	Malabadi	C	W	50.7	28.0	12.2	29	2*	17+18	2+12	8
G11	Gemini	C	R	55.5	28.2	12.9	21	2*	7	2+12	6
G12	Flamura-85	C	R	65.5	35.2	14	28	2*	7+8	5+10	10
G13	Yüreğir-89	C	W	54.2	34.0	12.5	30	2*	17+18	2+12	8
G14	Nurkent	C	W	59.0	30.2	12.5	22	1/2*	17+18	2+12	8
G15	Seyhan-95	C	W	57.2	29.6	12.9	24	2*	7+9	5+10	9
G16	Kırmızı Buğday	L	R	54.2	32.5	12.8	24	2*	7+8/7+9	5+10	7
G17	Ağdenli	L	W	42.7	29.6	11.1	25	2*	17+18	2+12	8
G18	Dışbudak	L	R	62.3	37.8	14.2	26	2*	7	2+12	6
G19	Cumakalesi	L	W	49.0	28.4	12.3	27	2*	17+18	5+10	10
G20	İsimsiz	L	W	60.2	29.9	14.9	25	2*	17+18	2+12	8
G21	İsimsiz	L	W	64.1	38.2	13.2	18	2*	7+8	2+12	8
G22	Beytülşebap-Beyaz	L	W	70.2	28.3	13.9	15	2*	7+8	2+12	8
G23	Buhare-Beytülşebap	L	K	63.9	26.3	16.5	26	2*	7+8	2+12	8
G24	Şırnak	L	R	71.8	34.0	14.1	20	2*	7+8	2+12	8
G25	Beytülşebap- Kırmızı	L	R	70.2	31.8	14.4	25	2*	7	2+12	6
G26	Lanchester-Kızıltepe	L	W	61.3	33.7	13.5	28	2*	13+16	5+10	10
G27	Akbaşak-Malatya	L	W	69.6	38.1	14.3	22	2*	7+8	2+12	8
G28	Zerun-Malatya	L	W	69.6	32.0	14.6	30	2*	7+8	2+12	8
G29	Aşure	L	W	70.8	32.8	14.4	26	2*	7+8	2+12	8
G30	Serdari	L	W	73.0	40.8	12.2	20	2*	6+8	2+12	6
G31	Sevinç-Azeri	L	R	61.1	32.9	14.5	18	2*	7+8	2+12	8
G32	Cham 6 (S/F)	F	W	62.5	29.6	10.8	27	2*	6+8	2+12	6
G33	Ykt-406	F	R	39.1	32.5	12	24	2*	7+8	2+12	8
G34	Partizanka	F	R	51.6	34.9	11.6	27	2*	7+9	5+10	9
G35	Zg.1004-82	F	R	57.5	37.0	13.1	18	2*	7+9	5+10	9
G36	Sremica	F	R	56.4	30.7	14.4	30	2*	7+9	5+10	9
G37	Mv-4	F	R	43.0	35.1	12.7	30	1	7	2+12	6
G38	Emu/Rmn	F	W	52.2	32.8	12.8	25	2*	7+9	5+10	9
G39	Kanred/Funo	F	R	52.3	34.8	11.9	23	2*	7+9	5+10	9
G40	Tamw-105	F	R	46.4	25.5	13.1	21	2*	7+8	5+10	9
G41	Cleo-74	F	W	58.9	31.7	11.9	26	2*	7+8	5+10	10
G42	Anza	F	W	47.1	28.6	12.2	24	2*	7+8	2+12	10
G43	Festa	F	R	61.3	33.0	14	32	2*	7+9	5+10	9
G44	Vilmorin 23 (W)	F	W	73.8	27.9	14.6	25	2*	7+8	2+12	8
G45	Emu"s"	F	R	52.3	34.6	12	24	2*	7+8	2+12	8
G46	Nacozari-76	F	R	39.2	29.7	12.1	24	2*	17+18	2+12	8
G47	Fengang-15	F	R	42.8	30.0	11.8	30	2*	7+8	2+12	8
G48	Ildıko/F.29-76	F	R	68.8	34.1	12.5	18	2*	7	5+10	8
G49	Mini Mano	F	R	60.9	34.7	14.5	13	2*	7+9	2+12	7
G50	Falcon	F	R	69.0	35.0	12.1	23	2	17+18	2+12	6
G51	Mol	F	W	56.9	25.7	13.5	29	1	17+18	2+12	8
G52	Pvn 1R (1B)	F	W	61.3	25.3	13.8	27	1/2*	7+9	5+10	9
G53	Heines Kolben (S)	F	R	74.3	29.2	15.2	27	1	7+9	5+10	9
G54	Clement (W)	F	R	76.4	29.1	13.3	18	2*	6+8	2+12	6
G55	Au	F	R	50.1	34.5	13.8	20	2*	7+9	2+12	7
G56	Pj-62/Abn-43	F	R	45.0	30.6	12.4	24	2*	7+9	5+10	9
G57	Nai-60/Hn-7//Buc	F	W	48.8	34.8	12.4	24	2*	7+9	5+10	9

Table 3 continued…

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Continued of Table 3.

No	Name	Orig	GC	*PSI*	TKW	PC	SDS	HMW-GS			*Glu-1*
				%	g^{-1}	%	ml^{-1}	*Glu-A1*	*Glu-B1*	*Glu-D1*	score*
G58	Mit	F	R	46.0	25.2	12.5	22	2*	7+8	5+10	10
G59	138.1.2/Nad//Bez/3/Coc	F	R	56.1	36.7	11.7	25	2*	6+8	5+10	8
G60	Lee/Kkz/3/Cc//Ron/Cho	F	W	52.8	28.5	11.8	24	2*	7+8	5+10	10
G61	Buc"s"/Pvn"s"	F	W	48.0	33.9	11.2	25	2*	7+9	2+12	7
G63	Line.1280-170/Nar-79	F	W	45.9	33.8	12.3	34	2*	7+8	2+12	8
G64	Gvz/Gv	F	W	47.3	32.6	12.1	32	1	17+18	5+10	10
G65	S.Sfm//Soty/Jn(3)	F	R	44.7	32.2	11.8	30	2*	7+9	5+10	9
G66	Carpentero/Carp	F	R	33.9	32.4	11.8	26	2*	7+9	5+10	9
G67	Prl"s"	F	W	43.0	33.3	10.7	29	2*	7+9	2+12	7
G68	C.183-24.C.168/3/Cno/7C*2//Cc/Tob	F	W	35.2	36.1	10.6	22	2*	7+9	5+10	9
G69	C.182-24.C.168/3/Cno/7C*2//Cc/Tob	F	W	39.4	32.3	10.9	24	2*	7+9	5+10	9
G70	Gen/Pew"s"	F	K	40.5	31.7	11.7	24	2*	7+9	5+10	9
G71	Nac/Trm	F	W	37.7	29.5	11.5	25	2*	17+18	2+12	8
G72	Jup/Bjy"s"//Ures=Kauz"s"	F	W	57.9	28.0	12.6	20	2*	7	5+10	9
G73	Mn-72131/Mor"s"	F	W	62.7	32.7	13.1	26	2*	7	5+10	9
G74	Chr/4/Inia"s"/7C//Cno"s"/Gll/3/Pci"s"//Bb	F	W	47.6	31.7	12.6	21	2*	7	2+12	6
G75	85-7	F	W	73.5	32.4	14.7	28	2*	7+8	2+12	8
G76	85-19	F	W	70.4	27.0	12.4	24	2*	17+18	2+12	8
G77	(N-10/B-1)	F	R	62.0	33.8	14	22	2*	7+9	2+12	7
G78	Brg/Kkz	F	R	58.1	33.6	14.5	15	2*	7+9	2+12	7
G79	Edch/Cfn"s"//Au/Era	F	W	59.2	30.7	13.6	18	2*	7+9	2+12	7
G80	Asp"s"//Hys/Peep"s"	F	R	69.7	33.0	13.1	33	2*	7+9	2+12	7
G81	Prl"s"	F	W	56.0	31.9	13	25	2*	7+9	5+10	9
G82	Prl"s"//Car-422/Ana	F	W	62.8	32.1	13.7	26	2*	7+9	5+10	9
G83	Bow""s"	F	W	68.5	30.4	9.3	24	2*	7+9	5+10	9
G84	Dove"s"/Bow"s"	F	W	50.9	31.6	12.9	24	2*	17+18	5+10	10
G85	Rbs/Anza/3/Kvz/Hys//Ymh/Tob/4/Bow"s"	F	W	53.4	30.2	13.3	25	2*	7+9	2+12	7
G86	Rbs/Anza/3/Kvz/Hys//Ymh/Tob/4/Bow"s"	F	W	50.0	28.1	13.9	24	2*	7+9	2+12	7
G87	Rbs/Anza/3/Kvz/Hys//Ymh/Tob/4/Bow"s"	F	W	58.4	26.7	13.7	26	1	7+9	2+12	7
G88	Bow"s"/Vee"s"	F	W	58.1	34.0	13.5	26	2*	7+9	2+12	7
G89	Tr.380-16-3A614/Chat"s"	F	W	55.4	35.1	13	25	2*	7+9	2+12	7
G90	Nac F.76/Ald"s"	F	W	53.5	31.3	13.4	28	2*	17+18	5+10	10
G91	Gh"s"/Anza	F	W	64.9	35.9	13.6	23	2*	17+18	5+10	10
G92	Br-6427	F	R	58.7	34.9	13.3	30	2*	17+18	5+10	10
G93	Anza/3/Pı/Nar//Hys/4/Vee"s"	F	R	55.2	27.5	13.1	25	1	7+9	2+12	7
G94	Buc"s"//7c/Ald"s"	F	W	60.2	35.9	12.4	30	1	7+9	5+10	9
G95	Bow"s"/Vee"s"//71 St 2959/Crow"s"	F	R	58.6	25.1	14.3	25	2*	7+9	5+10	9
G96	Ns.732/Her	F	W	60.2	33.9	12.6	20	2*	17+18	2+12	8
G97	Ures/Bow"s"	F	W	57.4	37.0	12.7	27	1	7+9	5+10	9
G98	Buc"s"/Dga//Hpo"s"	F	R	65.6	31.1	13.2	26	2*	7+9	5+10	9
G99	Hahn"s"/Mji//Lira"s"	F	W	59.6	32.2	15.1	27	1	7+9	5+10	9
G100	Kauz"s"	F	W	59.2	34.4	15.1	22	2*	7+9	2+12	7
G101	Myna"s"/3/F 35.70/Mo//Nac	F	R	59.2	29.9	13.1	22	2*	7+9	5+10	9
G102	Ns.732/Her	F	R	59.2	30.1	12.2	22	2*	7+9	5+10	9
G103	Chen/Aegilops squarrosa (Taus)//Bcn	F	W	58.8	32.6	13.3	20	1/2*	7+9	5+10	9
G104	Chen/Aegilops squarrosa(Taus)//Bcn	F	W	67.1	33.3	13.5	28	2*	7+8	5+10	10
G105	Era/Chm//Sal.75/3/Cndr"s"/Ana//Cndr"s"	F	R	50.9	31.0	12.9	22	2*	13+16	5+10	10
G106	Au//Kal/Bb/3/Bon/4/Bow"s"	F	R	55.9	30.7	14	28	2*	7+9	5+10	9
G107	Dowe"s"/Tsi/5/Gu/4/D.6301/Nai//Wrm	F	R	52.5	34.5	12.6	22	1	13+16	2+12	8
G108	Flk"s"//Hork/6/Wa.4767/391//56D.8114.53	F	W	70.8	30.9	11.7	30	1	17+18	5+10	10
G109	Kvz//Cno/Pj.62/5/Tuc"s"/4/Tob/Cc//Pato/	F	R	61.4		13.6	32	2*	7+9	5+10	9
G110	Kvz/Pak.20/5/Maya-74"s"/On//II 60-	F	W	54.8	34.1	14.6	28	1	7+9	5+10	9
G111	Au//Kal/Bb/3/Bon/4/Kvz//Cno/Fj-62	F	W	80.5	30.4	13.5	22	2*	7+8	2+12	7
G112	Kvz/Pak.20/5/Maya-74"s"/On//II 60-147/	F	R	57.5	35.4	13.8	19	2*	7+9	5+10	9
G113	Sn.64/Hn.4//Rex/3/Edch/Mex/4/Sls"s"/	F	W	56.6	35.6	12.9	21	2*	7+9	5+10	9
G114	Ures.81//Hd.2206/Hork"s"	F	W	45.9	33.6	14.2	23	2*	7+9	2+12	7
G115	Cno//Lr/Son.64/3/Rbs 47.51/4/7	F	R	64.7	31.9	13.4	30	2*	17+18	2+12	8

Table 3 continued…

[DOR: 20.1001.1.16807073.2017.19.6.11.6]

Continued of Table 3.

No	Name	Orig	GC	*PSI*	TKW	PC	SDS	HMW-GS			*Glu-1*
				%	g^{-1}	%	ml^{-1}	*Glu-A1*	*Glu-B1*	*Glu-D1*	score*
G115	Cno//Lr/Son.64/3/Rbs 47.51/4/7	F	R	64.7	31.9	13.4	30	2*	17+18	2+12	8
G116	Kasyon/Glennson.81	F	R	57.2	34.5	13.4	26	2*	7+9	5+10	9
G117	Sn.64/Hn.4//Rex/3/Edch/Mex/4/Sls"s"/5/	F	W	62.8	33.2	14.2	24	2*	13+16	5+10	10
G118	Au//Kal/Bb/3/Bon/4/Bow"s"	F	R	60.0	28.5	14	23	2*	7+9	5+10	9
G119	Seri-82/5/Ald"s"/4/Bb/Gll//Cno.67/7c//Kvz	F	W	57.5	29.5	12.9	20	2*	7+9	5+10	9
G120	Sn.64/Hn.4//Rex/3/Edch/Mex/4/Sls"s"/5/Bo	F	W	54.4	29.1	13.3	23	1	13+16	5+10	10
G121	Vee"s"//Sannine/Ald"s"	F	W	62.3	27.9	13.3	32	1	17+18	5+10	10
G122	Vee"s"/5/Skh.8/4/Rrv/Ww.15/3/Bj"s"//On*	F	R	52.8	28.0	14.2	23	2*	7+9	5+10	9
Means				57.1	32.0	13.0	24.9				
Sd				9.71	3.31	1.59	3.99				

*According to the Payne and Lawrence nomenclature (1983), BL: Breeding Line; C: Commercial; F: Foreign; GC: Grain Color; W: White; R: Red; *PSI*: Part Size Index; TKW: Thousand Kernel Wight, SDS: Sedimentation volume.

17+18, 5+10, respectively. Bezostaya is accepted as high quality variety, while Gerek-79 is accepted as medium quality by milling and baking industry (Demir *et al*., 2015). In Turkish commercial winter varieties, subunit 5+10, associated with good bread-making quality, appeared to have higher frequencies than in Turkish spring varieties.

Additionally, quality scores were assigned to each subunit band produced by alleles at the *Glu1* loci of chromosomes A, B, and D as defined by Payne *et al*. (1987). Quality scores demonstrated high significant correlation with dough strength, thus, providing a useful method for selecting HMW glutenin compositions with good quality (Belderol *et al*., 2000). In order to predict the bread-making quality of wheat genotypes, *Glu-1* score was calculated for the wheat genotypes on the basis of HMW glutenin subunits detected. Our data demonstrated that the *Glu-1* score in Turkish commercial wheat varieties varied within an interval from 6 to 10. The lowest *Glu-1* score was recorded in cultivars Gemini, Pehlivan and Gerek-79. However, the cultivars Dağdaş-94, Gün-91, Kınacı-97 and Flamura-85 accounted for the highest *Glu-1* score, reflecting high baking quality (Table 3). These results are in accordance with those reported by Keser and Pena (2004); Demir *et al*. (2015), and Yıldız (2011). Within local genotypes, the highest value of *Glu-1* score was achieved by Cumakalesi, while Dışbudak showed the lowest score value (Table 3).

Principal Component Analysis

The Genotype-by-Trait (GT) biplot is a statistical tool for evaluating cultivars based on multiple traits and for identifying lines that are superior (Mıshra *et al*., 2015). The GT biplot explains superior genotypes with favourable traits effect which would be useful for the breeding of new genotypes for each target entry, thus, it will help breeders explore the interactions among entries and subsets of tester (Dehghani *et al*., 2008). Also, GT biplot was built to identify the genetic variability and the relationships among wheat genotypes.

Figure 1 represents polygon view of a GT biplot generated from 4 quality traits and *Glu-1* score of 122 genotypes data. Biplot analysis was used to examine the relationships between the genotypes and quality traits studied together with Glu-1 score (Figure 1). The first two PCAs (Principal Components 1 and 2) accounted for 56.17% (PC1= 31.98% and PC2= 24.19%) of the relationships between the genotypes and quality traits. The PC, *PSI* and *Glu-1* score had long vectors, suggesting that there was a relatively large variation among genotypes. In contrast, TKW and

[DOR: 20.1001.1.16807073.2017.19.6.11.6]

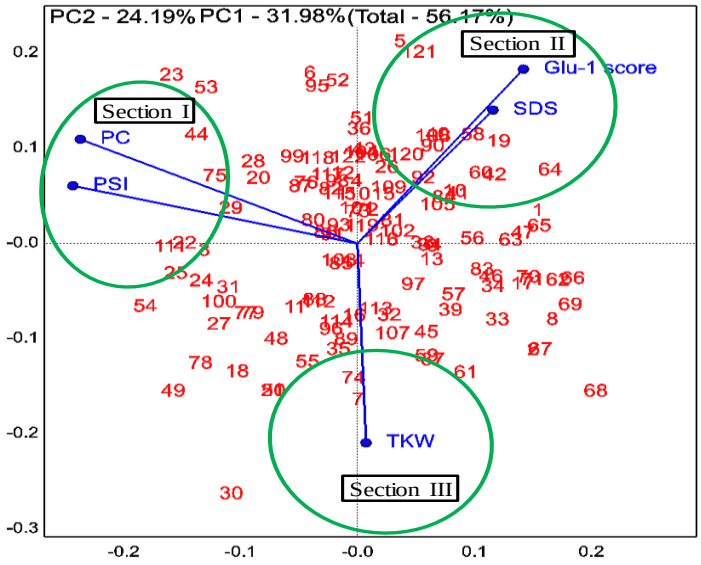

Figure 1. The biplot showing the relation among genotypes and quality traits.

SDS had shorter vectors, suggesting that there were relatively little variation among genotypes. The cosine of the angle between the vectors of two traits measures the correlation between them relative to their variation among genotypes. Two traits are positively correlated if the angle between their vectors is < 90°, negatively correlated if the angle is > 90°, and independent if the angle is 90° (Dehghani *et al*., 2012). Therefore, *Glu-1* score and SDS had acute (< 90°) angles between them, demonstrating that their variations were similar. On the contrary, TKW had obtuse (> 90°) angles with *Glu-1* score, SDS, PC and *PSI*, indicating negatively correlated variation. Traits were grouped into three sections and are presented in Figure 1. Protein Content (PC) was positively correlated with *PSI* at section I. Salmanowicz *et al*. (2012) reported that the relationship between grain hardness and PC was uncertain. Section II included *Glu-1* score which was strongly correlated with SDS sedimentation. These were in agreement with results of Schuster *et al*. (1997) that reported positive and significant relationship between *Glu-1* score and SDS sedimentation test and baking strength ("W"). Therefore, *Glu-1* score can be used as a helpful guide in selection for bread-making quality in the first generation of the breeding programs, when quantities of seeds necessary for the conventional test are not available (Schuster *et al*., 1997). Section III included the only TKW which was negatively associated with other traits. Our findings were in agreement with results of Şahin *et al*. (2001) and Akçura (2011). In a previous study, O'Brien and Ronalds (1984) reported negative relationship between TKW and Zeleny SDS sedimentation test and PC. The Genotype by Trait (GT) biplot can be used to compare cultivars on the basis of multiple traits and to identify cultivars that are particularly good in certain traits and, therefore, can be candidates for parents in plant breeding program (Dolatabad *et al*., 2010). Figure 1 is a GT biplot with a polygon view that presents the data of 122 wheat genotypes. It seems that G121, G58, Cumakalesi, and G64 had the highest values of *Glu-1* score and SDS; G44, G75, G22 and G114 had the highest values of PC and *PSI*. Also, Figure 1 indicates that Pehlivan and G74 were highest in TKW.

CONCLUSIONS

This study concerning HMW-GS and some quality traits evaluation of local, old, and new genotypes and breeding lines

[DOR: 20.1001.1.16807073.2017.19.6.11.6]

revealed that bread wheat (*Triticum aestivum* L) crossing blocks have potential value in wheat breeding programs. Twenty three of the studied genotypes with the highest ranking in HMW *Glu-1* score (Glu-1 score> 10) have the potential for breeding wheat varieties with higher protein quality. The *Glu-1* quality score can be used as a parameter for selecting lines in terms of the baking quality of bread in Turkish wheat breeding programs.

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غربالگری ژنوتیپ های گندم نان برای زیرواحدهای گلوتنین با وزن مولکولی بالا و برخی صفات کیفیتی

ه. کیلیک، ت. سانال، ی. اردمسی، و ک. کاراکا

چکیده

در این پژوهش، در ۱۲۲ ژنوتیپ گندم نان محلی برگرفته از بلوک های دو رگ گیری، ترکیب زیرواحدهای گلوتنین با وزن مولکولی بالا (HMW-GS)برحسب چند صفت کیفیتی مانند محتوای پروتئین(PC) ، سولفات دودسیل سدیم (SDS) ، نمایه اندازه ذرات (particle size index)، و وزن هزار دانه (TKW) با روشSDS-PAGE بررسی شد. درکل، ۱۲ ترکیب متفاوت HMW-

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GSتعیین شد. همچنین، بر حسب جایگاه (loci) آلل های *Glu-A1*،*Glu-B1*، و *Glu-D1* گوناگونی وتنوع زیادی شناسایی شد. در جایگاه *Glu-A1*، بسآمد آلل های *1/2*، ۱ و *2 به ترتیب ۲/۵٪، ۱۲/۳٪، و ۸۵/۵٪ شناسایی شد ، در حالیکه در*Glu-B1*، از ۷ آلل گزارش شده، آلل ۸+۷ (۲۰/۵٪) و ۱۸+۱۷ (۱۷/۲٪) شناسایی شد. وجود دو آلل در جایگاه *Glu-D1*نیز آشکار شد. در واقع، ۵۴/۱٪ آنها نشان دادند که زیر واحد های ۱۰+۵ با خواص نانوایی خوب همبستگی داشتند. امتیازجایگاه *Glu-1*ژنوتیپ ها در محدوده ۶ تا ۱۰ بود. در میان این ژنوتیپ ها، فقط ۲۳ تا (۱۸/۹٪) دارای امتیاز ۱۰ *Glu-1*بودند. در ارزیابی ژنوتیپ- صفت (GT) با استفاده از نمودار بای پلات، صفات PCو PSI در بخش I نقش داشتند در حالیکه معیار ته نشینی SDSو امتیاز *Glu-1*در بخش IIنقش داشتند. از سوی دیگر، بخش III تنها TKW را شامل بود که با صفات دیگر همراهی منفی داشت. بنا بر این، ژنوتیپ های مطلوب را می توان برای برنامه های دو رگ گیری به منظور بهبود کیفیت تکنولوژیکی گندم های نان استفاده کرد.

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