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Effects of genotype and environment on grain yield and quality traits in bread wheat (*T. aestivum* L.)

Yuksel KAYA[1,2]*, Mevlut AKCURA[3]

Abstract

Genotype (G), environment (E) and their interaction (GEI) play an important role in the final expression of grain yield and quality attributes. A multi-environment trial in wheat was conducted to evaluate the magnitude of G, E and GEI effects on grain yield and quality of wheat genotypes under the three rainfed locations (hereafter environment) of Central Anatolian Plateau of Turkey, during the 2012-2013 cropping season. Grain yield (GY) and analyses of test weight (TW), protein content (PC), wet gluten content (WGC), grain hardness (GH), thousand kernel weight (TKW) and Zeleny sedimentation volume (ZSV) were determined. Allelic variations of high and low molecular weight glutenin subunits (HMW-GS and LMW-GS) and 1B/1R translocation were determined in all genotypes evaluated. Both HMW-Glu-1, 17+18, 5+10 and LMW-Glu-3 b, b, b corresponded to genotypes possessing medium to good quality attributes. Large variability was found among most of the quality attributes evaluated; wider ranges of quality traits were observed in the environments than among the genotypes. The importance of the growing environment effects on grain quality was proved, suggesting that breeders' quality objectives should be adapted to the targeted environments.

Keywords: bread wheat; quality; genotype; environment; HMW-GS; LMW-GS.

1 Introduction

Development of wheat cultivars with good bread making quality is a challenging objective for many wheat breeding programs. The major wheat endosperm protein, the gluten, is responsible for bread making quality (Branlard & Dardevet, 1985). Gluten is composed of two prolamine groups, gliadins, and glutenin. Glutenins consist of low- and high-molecular-weight (LMW and HMW) complex subunits and constitute about 30-40% of flour protein. It has been reported that HMW glutenin subunits have the largest effect on bread making quality even though they constitute only 10% of the total storage proteins as compared to LMW, which contributes with 40%. The HMW-GSs described as Glu-A1, Glu-B1, and Glu-D1 are encoded by multi-allelic genes located on the long arms of chromosomes 1A, 1B and 1D respectively (Payne et al., 1984). It has been reported that HMW-GSs are encoded by three loci, Glu-A1, Glu-B1, and Glu-D1 (Payne & Lawrence, 1983). LMW-GSs are encoded by three loci, Glu-A3, Glu-B3, and Glu-D3 (Gupta & Shepherd, 1990).

Worldwide, the wheat-rye 1B/lR chromosome translocation is used because of the presence of genes for resistance to diseases. Unfortunately, wheat cultivars with 1B/lR translocation display poor bread making quality as a result of dough stickiness and poor mixing tolerance (Pena et al., 1990).

It is important to determine and quantify the extent to which factors like the environment (E) and genotype x environment interaction (GEI) contribute to variations in each wheat quality parameter. The influence of E on certain quality parameters vary, but it is generally stronger on PC and protein related parameters (Fowler & De La Roche, 1975). In order to minimize the masking effect of GEI, breeders should determine a quality parameter or parameters that perform consistently in the Es (Lin & Binns, 1994).

Plant breeders use heritability estimates to determine the influences of the environmental and genetic factors on the trait of interest and choose the selection procedure that should be implemented to make improvements. Heritability can be defined as the proportion of the observed variation in a progeny that is inherited (Poehlman & Sleper, 2006). The extent to which replicated testing is required for selection will depend on the heritability estimate (Nyquist, 1991). This estimate gives plant breeders an understanding to what extent a trait is influenced by the G as opposed to E.

Correlations, although reliable only for the range of material tested, may point to relationships that can be utilised in making a selection programme more effective (Baker et al., 1971). A correlation coefficient between two quality attributes that is unusually high suggests a strong heritable association and possibly a narrow gene base (Gaines, 1991).

The objectives of this research were i) to determine the relative contributions of G, E, and GEI to the variation in GY and quality traits of 20 wheat genotypes tested across three locations, ii) to analyze the relationships between GY and quality traits, iii) to identify high and low molecular weight glutenin subunits

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[1] *Graduate School of Natural Sciences, Onsekiz Mart University, Canakkale, Turkey, e-mail: yuksel_k@yahoo.com*
[2] *Bahri Dagdas International Agricultural Research Institute, Konya, Turkey*
[3] *Field Crops Department, Agricultural Faculty, Onsekiz Mart University, Canakkale, Turkey*
**Corresponding author*

(HMW-GS and LMW-GS) associated with quality traits, and iv) to find the best wheat genotypes based on GY and quality traits.

2 Material and method

2.1 Genotype characteristics

Among the 20 genotypes tested across three environments, G1 (Gerek-79), G2 (Karahan-99), G3 (Sonmez-01), G4 (Mufitbey), and G5 (Bayraktar) were the most widely grown cultivars under the rain-fed conditions of the Central Anatolian Plateau (CAP), covering about 40 % of total wheat cultivated land of Turkey (Table 1).

Among the genotypes G6-G20, the advanced inbred lines identified were those from the IWWIP (International Winter Wheat Improvement Program-http://www.iwwip.org), a joint program between Turkey, CIMMYT and ICARDA (Table 1).

2.2 Climate and soil characteristics

Soil conditions for conducting the field trials were suitable. During the crop cycle, temperature pattern was similar to that of the long term average. As for the precipitation pattern, it was totally different from that of the long term average; considering the total amount of precipitation during the whole crop cycle, it was lower than that of the long term average. As a consequence, the water deficit, difference between the cropping season and long term average of precipitation, caused a remarkable reduction in grain yield and quality traits (data not shown).

2.3 Quality analysis

Flour milling

The wheat grains were stored for 48 h at 14% moisture and milled using a Quadrumat Senior mill (Brabender, Germany). Flours of approximately 65 % extraction were used for further quality analyses (American Association of Cereal Chemists International, 2000).

Wet gluten content (%)

Wet gluten content (WGC) was analyzed using a Glutomatic 2200 (Perten Instruments) according to American Association of Cereal Chemists International, (2000).

Protein content (%)

Flour samples were evaluated for protein content (PC) using (American Association of Cereal Chemists International, 2000)

Zeleny sedimentation volume (mL)

Zeleny sedimentation volume (ZSV) was determined using (American Association of Cereal Chemists International, 2000)

Grain hardness (PSI)

(12)'s Near-Infrared Reflectance Method was used for grain hardness (GH).

Test weight (kg/hL)

Test weight (TW) was recorded as kilograms/hectoliter (kg/hL) based on (American Association of Cereal Chemists International, 2000).

Thousand kernel weight (g)

Thousand kernel weight (TKW) was recorded as grams/1000 kernels of cleaned wheat.

2.4 SDS-PAGE analysis

HMW-GS and LMW-GS were separated by sodium dodecyl-sulfate polyacrylamide gel electrophoresis (SDS-PAGE) based on the extraction method described by (Sıngh et al., 1991), with modifications reported by (Liu et al., 2005; 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.

2.5 Statistical analysis

Variance (ANOVA) and Pearson's correlation analyses were performed using (SAS Instıtute Inc., 2004), and a comparison of the means was performed using the LSD test ($p<0.01$) and the same software. Principal component and Biplot analyses were performed using Biplot and Singular Value Decomposition Macros for Excel© (Lipkovich & Smith, 2002).

Broad sense heritability (H) estimates were calculated according to (Singh & Ceccarelli, 1996).

Table 1. Genotypes.

Code	Pedigree
G1	GEREK-79
G2	KARAHAN-99
G3	SONMEZ-01
G4	MUFITBEY
G5	BAYRAKTAR
G6	VEE/TSI//GEREK/3/NS55.03/5/C126.15/COFN//6/TAM200/KAUZ
G7	BOEMA/ALTAY//ALTAY 2000
G8	AUS GS50AT34/SUNCO//CUNNINGHAM
G9	SUNCO/2*PASTOR
G10	BILINMEYEN96.7
G11	BURBOT-6
G12	VRATZA/3/ORF1.148/TDL//BLO/4/PONY/OPATA
G13	TAM200/KAUZ/3/SPN/NAC//ATTILA/4/F885K1.1/SXL
G14	ZCL/3/PGFN//CNO67/SON64(ES86-8)/4/KA../4/BEZOSTAYA-1/NAD//KZM (ES85.24)/3/F900K
G15	SHARK-1/3/INDIANDWARF/KORB DOLI//DUKATI
G16	CHIRYA.3/GK OTHALON
G17	VORONA/PARUS//HATUSHA/3/LUT112/4/PEHL//RPB8-68//CHRC
G18	ALAMOOT/CATBIRD
G19	OVERLEY*3/AMADINA
G20	VEE#8//JUP/BJY/3/F3.71/TRM/4/BCN/5/KAUZ/6/163

3 Results

3.1 Genotype (G) means and ranges over the environments studied (E)

G means and ranges were calculated for GY and quality characteristics (Table 2). In general, Gs had relatively low GY (range 2.26-3.05 t/ha, mean = 2.71 t/ha), and PC (range 10.1-13.2 %, mean = 11.6 %). WGC and ZSV were moderate (range 28-37 %, mean = 32 %) (range 24-33 mL, mean = 29 mL, respectively). GH had medium soft hardness, ranging from 48 to 60 PSI with mean = 55 PSI. TKW ranged from 28 g to 33 g (mean = 30 g) and TW varied from 76 to 82 kg/hL (mean = 79 kg/hL).

Generally speaking, genotypes with higher GY, TKW, and TW had inferior quality values (e.g. G1, G3, G19 and G20) or vice versa. Comparing the means of quality traits of the genotypes tested, it can be said that G4, G5, G7, G8, G9, G12, G13, and G14 had better quality values than those of the other genotypes (Table 2).

3.2 Genotype x Environment Interaction (GEI)

The influence of G, E, and GEI on GY and 6 quality traits was determined. Table 3 shows that G, E, and GEI had significant effects on all the traits analyzed. The E was the main factor controlling GY, TKW, and TW, accounting for 70.2 %, 78.5 % and 63 % of the total variance, respectively. In addition, most of the total variance in the remaining quality traits was determined partially by the E, along with G, and GEI also showed influence in defining PC, WGC, ZSV and GH. Therefore, the effects of E and the GEI cannot be ignored when breeding wheat for end-use quality.

3.3 Broad Sense Heritability (H)

H values estimated for traits of interest are given in Table 3. H ranged from 0.32, for TKW, to 0.52, for ZSV. The H values ranged from low to moderate values for all of the characteristics studied due to larger E variance (with GEI), indicating the E effect. H values for PC, WGC, ZSV, and TW were relatively larger than those of GY, GH, and TKW. The H values for the GY were 0.45, 0.41, 0.52, and 0.42, whereas for the TWK they were 0.33, 0.34, and 0.32, respectively.

3.4 High Molecular Weight Glutenin Subunites (HMW-GS)

The loci and allele's numbers and frequencies of HMW-GS observed in the 20 genotypes are shown in Table 4. A total of 8 alleles at the Glu-1 loci were detected among the genotypes examined. Two alleles were observed at the locus Glu-A1, among which the subunit 2* (allele b) was most frequent with the frequency of 65 %. The frequency of subunit 1 (allele a) was 35 %. Four alleles were present at the locus Glu-B1. Subunit combinations 7+9 (allele c) and 7 + 8 (allele b) had high frequencies of 35 and 50 %, respectively, followed by subunit 7 (allele a) (10 %) and 17+18 (allele i) (5 %). SDS-PAGE differentiated 2 alleles at the locus Glu-D1. Subunit combinations 2 + 12 (allele a) and 5+10 (allele d) were almost equally dominant with the frequencies of 55 and 45 %, respectively (Table 4).

Table 2. Means of grain yield and quality traits of genotypes in the environments studied.

Genotype	GY†	PC	WGC	ZSV	GH	TKW	TW
G1‡	2.96	10.1	28	27	56	32	81
G2	2.50	12.0	30	26	55	29	80
G3	2.95	10.2	29	27	50	30	82
G4	2.82	13.2	33	28	48	32	79
G5	2.90	11.2	31	29	52	32	79
G6	2.55	10.9	30	32	60	28	77
G7	2.70	12.0	33	28	54	30	78
G8	2.50	13.0	32	33	50	30	79
G9	2.68	13.0	33	32	55	30	79
G10	2.75	11.2	31	29	52	32	78
G11	2.83	11.0	35	28	60	32	77
G12	2.63	12.0	33	30	56	29	79
G13	2.52	12.0	36	33	55	30	80
G14	2.51	13.0	35	32	58	32	76
G15	2.68	12.0	37	29	56	28	80
G16	2.62	10.2	31	30	60	29	79
G17	2.95	10.1	29	26	50	30	77
G18	2.26	10.7	28	26	56	29	75
G19	2.82	13.0	29	26	58	33	78
G20	3.05	11.6	30	24	60	29	81
Mean	2.71	11.6	32	29	55	30	79
$LSD_{(0.01)}$	0.46	0.55	1.42	1.89	2.56	1.21	2.45

†GY, Grain yield (t/ha); PC, Protein content (%); WGC, Wet gluten content (%) ZSV, Zeleny sedimentation volume (mL); GH, Grain hardness (PSI); TKW, Thousand kernel weight (g) TW; Test weight (kg/hL); ‡G, Genotype.

Table 3. ANOVA and G, E, and GEI variances for grain yield and quality traits across environments.

	Mean Square			Variance (%)[¥]					
	G[‡]	E	GEI	G	E	GEI	$CV_{(\%)}$	R^2	H
GY[†]	16.83**	660.31**	6.35**	17.0	70.2	12.8	15.68	0.81	0.33
PC	6.84**	80.12**	1.84**	36.1	44.4	19.4	6.55	0.87	0.45
WGC	363.44**	4994.21**	121.01**	32.2	46.6	21.3	6.21	0.83	0.41
ZSV	422.33**	5061.25**	85.61**	37.5	47.3	15.2	7.54	0.89	0.52
GH	802.43**	10177.31**	316.71**	32.0	42.7	25.2	12.30	0.81	0.34
TKW	82.32**	5128.21**	32.53**	12.0	78.5	9.5	15.12	0.79	0.32
TW	697.73**	16078.25**	148.63**	26.0	63.0	11.1	11.93	0.80	0.42

**P<0.01; [†]GY, Grain yield (t/ha); PC, Protein content (%); WGC, Wet gluten content (%); ZSV, Zeleny sedimentation volume (mL); GH, Grain hardness (PSI); TKW, Thousand kernel weight (g); TW, Test weight (kg/hL); [‡]G, Genotype; E, Environment; GEI, Genotype x environment interaction; $CV_{(\%)}$, Coefficient of variation; R^2, Coefficient of determination; H, Broad sense heritability; [¥] Variance (%), ration of G, E, GEI SS to sum of G, E, GEI SS

Table 4. Allele numbers (#) and frequencies (F) and statistical analysis of the effects of HMW-GS and LMW-GS on grain yield and quality traits.

Locus	Subunit	#	F (%)	GY[†]	PC	WGC	ZSV	GH	TKW	TW
Glu-A1	1	7	35	2.73	12	32	29	54	30	79
	2*	13	65	2.70	11	31	28	56	30	79
Glu-B1	7	2	10	2.74	11	33	30	53	30	81
	7+8	10	50	2.69	12	32	29	55	30	79
	7+9	7	35	2.72	11	31	28	56	30	78
	17+18	1	5	2.70	12	33	28	54	30	78
Glu-D1	5+10	9	45	2.63	12	33	30	55	30	79
	2+12	11	55	2.80	11	30	28	55	30	78
Glu-A3	a	3	15	2.74	11	32	28	56	31	79
	b	4	20	2.59	13	34	32	55	30	79
	c	7	35	2.78	11	31	28	54	31	79
	d	3	15	2.71	12	32	30	58	29	79
	e	2	10	2.54	12	29	26	57	31	76
	f	1	5	2.95	10	29	26	50	30	77
Glu-B3	b	5	25	2.60	12	35	29	56	29	79
	e	7	35	2.90	11	33	28	56	30	79
	f	1	5	2.82	13	33	28	48	32	79
	g	3	15	2.56	13	33	32	54	31	78
	h	1	5	2.75	11	31	29	52	32	78
	j	3	15	2.68	11	29	26	55	31	77
Glu-D3	a	5	25	2.73	12	32	29	52	31	79
	b	7	35	2.72	12	31	29	57	31	79
	c	7	35	2.74	11	32	28	55	30	79
	d	1	5	2.26	11	28	26	56	29	75
1B/1R	-	17	85	2.71	12	32	29	55	30	79
	+	3	15	2.68	11	29	26	55	31	77
LSD (0.05)				0.41	0.85	1.58	1.91	2.45	1.35	2.54

[†]GY, Grain yield (t/ha); PC, Protein content (%); WGC, Wet gluten content (%); ZSV, Zeleny sedimentation volume (mL); GH, Grain hardness (PSI); TKW, Thousand kernel weight (g); TW, Test weight (kg/hL).

3.5 Low Molecular Weight Glutenin Subunites (LMW-GS)

The loci and allele's numbers and frequencies of LMW-GS observed in the 20 genotypes are shown in Table 4. A total of 16 alleles at the Glu-3 loci were detected among the genotypes examined. Six alleles were observed at the locus Glu-A3, among which the subunit Glu-A3's two alleles (b and c) were most frequent with the frequencies of 20 and 35 %, respectively. Six alleles were present at the locus Glu-B3. Among them, alleles b and e located on Glu-B3 locus had high frequencies of 25 and 35 %, respectively, followed by allele g (15 %) and allele j (15 %). Alleles f and h had low frequencies of 5 %. Four alleles were detected on the locus Glu-D3. Alleles b and c were equally dominant with the frequencies of 35 %. Allele a had also relatively high frequency of 25 %.

3.6 1B/1R translocations

Among all genotypes, merely G17, G18 and G19 (15 %) contained 1B/lR translocation. Comparing the means of the quality traits of the 1B/1R translocated genotypes with those of the non 1B/1R translocated genotypes; the means of the

quality traits of the 1B/1R translocated genotypes were low, indicating that 1B/1R translocations affected the quality traits adversely (Table 4).

3.7 Relationships between grain yield (GY) and quality traits

GY was significantly positively correlated (r = 0.511, p<0.05) with TW, but negatively correlated with ZSV (r = -0.485, p<0.05). It was also negatively correlated with PC, WGC, and GH, but positively correlated with TKW. However, they were not statistically significant.

PC showed a significant positive correlation with WGC (r = 0.498, p<0.05), whereas it was positively correlated with ZSV although the relationship was statistically non-significant.

WGC did not show any significant relationship with GH, TKW, and TW; however, it was positively correlated with ZSV (r = 0.565, p< 0.01).

3.8 Biplot analysis

Biplot analysis was used to examine the relationships between the genotypes and GY together with quality traits (Figure 1). The first two PCs (principal components 1 and 2) accounted for 55 % (PC1 = 33 % and PC2 = 22 %) of the relationships between the genotypes and all of the traits. PC, WGC, and ZSV were grouped on the positive PC1 axis of the biplot, suggesting strong relationships among them. Therefore, they were called protein related traits.

Like PC, WGC, and ZSV, the genotypes G7, G8, G9, G12, G13, G14, and G15 were also grouped on the positive PC1 axis. Therefore, it was suggested that these genotypes showed similar responses for PC, WGC, and ZSV in the environments.

Unlike the protein related traits, GY, TKW, and TW were grouped on the negative PC1 axis of the biplot, suggesting strong relationships among them. Thus, they were called yield related traits.

Like GY, TW and TKW, the genotypes G3, G4, G5, G10, and G19 were also grouped on the negative PC1 axis. Therefore, it was suggested that those showed similar responses for GY, TW, and TKW across environments.

4 Discussion

4.1 Genotype x environment interaction (GEI) and Broad sense heritability (H)

GY and quality traits were affected more intensely by the E than by the G, and GY, GH, and TKW reacting more expressively to the changes in E than to changes in PC, WGC, ZSV, and TW. PC was one of the most responsive traits since it was predominantly affected by E and GEI (Wıllıams et al., 2008). It appears that GEI effects, although significant, were lower than the effects of G and E, for all of the traits (Mladenov et al., 2001).

H of a trait is important since it determines the response to selection (Sharma & Smith, 1986). The magnitude of H was affected by the type of genetic material and yield level of the environment due to the fact that the studied characters are created by the effects of genes and growing seasons. In the present study, Hs for GY was examined, and the quality traits varied from low to moderate (Baker et al., 1971).

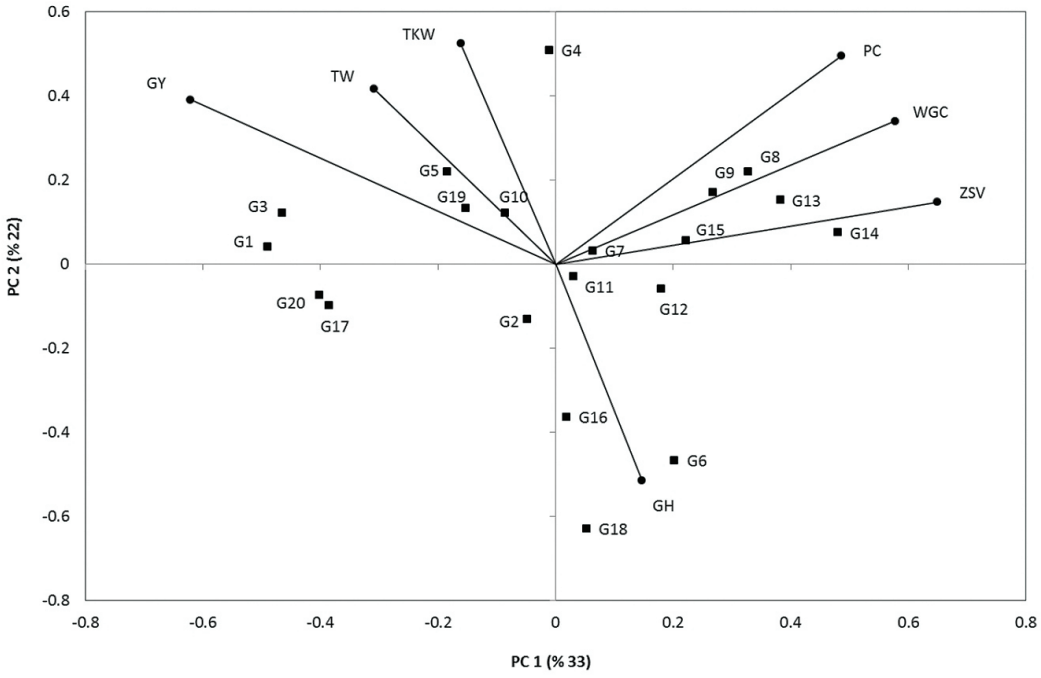

Figure 1. Biplot analysis for grain yield and quality traits. GY, Grain yield (t/ha); PC, Protein content (%); WGC, Wet gluten content (%); ZSV, Zeleny sedimentation volume (mL); GH, Grain hardness (PSI); TKW, Thousand kernel weight (g); TW, Test weight (kg/hL); G, Code for genotypes.

Selection for PC in wheat is affected by the negative relationship with GY. Our results were in agreement with those reported by (Clarke et al., 2000). In addition, Klatsikes & Lee (1971) found low H for TKW. Although ZSV was widely used in early generation selection parameters for bread wheat, H for ZSV is low in this study. Like our results, H for ZSV varies from intermediate to high values in wheat (Clarke et al., 2000; Akcura, 2009). Barnard et al. (2002) determined medium-high H for PC, ZSV, TW and TKW and reported that a successful and rapid selection with respect to quality criteria may be in question only for the characters with high heritability. Zanetti et al. (2001) determined high H for PC and TKW. The same researchers suggested that the GY and PC seem to be controlled by genotypes more than by the environment in comparison with test weight. The heritability estimated in our study was much lower than that estimated in the study conducted by (Zanetti et al., 2001).

In the present study, H for GY was low. Sharma & Smith (1986) reported that GY was highly influenced by the E and is known to have low H. The most common justification for conducting selection in optimum environments, regardless of the nature of the target environment, was the lower H found by (Ceccarelli, 1994) in low yielding Es. Furthermore, Ceccarelli (1996) reported that a lower H value was expected in low input conditions. In the present study, low estimates of heritability were observed for grain yield and quality traits. Akcura (2009) also reported moderate to low values of H for GY in wheat.

4.2 High and low molecular weight glutenin subunits (HMW-GS and LMW-GS) and 1B/1R translocation

In this study, the effect of subunit 1, being significantly higher than 2* in the genotypes, at Glu-A1 on quality was better, in agreement with results of other studies (Payne et al., 1984; Liu et al., 2005). Subunit 1 expressed higher values for PC, WGC, and ZSV than those of 2*. However, the effect of subunit 2* on quality was divergent.

Glu-B1 locus subunits 17+18 and 7+ 8 had positive effects on PC, WGC, and ZSV determined in the present study. Payne et al. (1987) ranked Glu-B1 subunits in descending order of baking quality as 17+18, 7+ 8, 7 + 9, 6 + 8, and 7.

Glu-D1d (5+10) is a HMW-GS allele conferring better quality (Guo et al., 2010). Positive effect of Glu-D1d was present on the genotypes used in this study. Sultana et al. (2007) screened some Pakistani wheat varieties for HMW-GS allele and Glu-D1d (5+10) using SDS-PAGE and found similar results to those of the present study.

Payne et al. (1987) found that, in general, genotypes containing HMW-GSs 5+10 have higher quality compared with that of genotypes containing 2+12. In this study, such conclusion could be drawn for the examined genotypes and the analyzed traits. Taking Glu-D1 locus subunits into consideration, 5+10 showed the best average mean for PC, WGC, ZSV, and TW, but lower values for 2+12, which is in agreement with the results of the authors mentioned above. It has been proved that the subunits designated as: Glu A1-1, Glu A1 (2*), Glu B1 (7 + 9), Glu B1 (17 + 18), or Glu D1 (5 + 10) are related to high technological quality, whereas their allelic variants such as Glu A1 (null), Glu B1 (6 + 8), or Glu D1 (2 + 12) are related to lower quality (Gıanıbellı et al., 2001). Judging by the HMW-GS composition, only one genotype (G7) is expected to have good quality, due to the presence of subunits 2*, 5+10, and 17+18 (Payne et al., 1987).

In our study, there was no significant increase in GY, comparing non 1B/1R translocated genotypes with the translocated ones. The translocation was associated with lower PC, WGC, ZSV, and higher TW. Therefore, it negatively affected most of the quality traits. Several reports, however, have reported that some genotypes with translocation might have good dough quality (Bullrich et al., 1998).

LMW-GS encoded by Glu-B3 allele plays a key role in gluten strength (Flaete & Uhlen, 2003). Zhang et al. (2008) reported that genotypes with positive allele of 1B/1R are negative for Glu-B3 allele. In our study, the positive allele of Glu-B3 was present in 85% wheat genotypes, whereas 15% of the genotypes did not have this allele. Our results also revealed a positive association between Glu-B3 and PC, WGC, and ZSV. This indicates that the marker assisted selection for Glu-B3 can be useful to select genotypes with desirable PC, WGC, and ZSV.

In our study, Glu-A3b, Glu-B3b, and Glu-D3b were LMW-GS alleles, which exert a positive effect on PC, WGC, and ZSV. Cornısh et al. (1993) found that the Glu-3 composition b, b, b (at loci Glu-A3, Glu-B3 and Glu-D3, respectively) gave the best extensibility. They also reported that Glu-A3e, Glu-B3c, d, and g alleles were associated with medium to weak dough properties. However, the contribution of alleles encoding LMW-GSs to quality also varies (Eagles et al., 2006).

4.3 Biplot and correlation analyses

The biplot analysis indicated that the traits studied were clustered into two groups. Like the traits, the genotypes studied were also seperated into the two groups. These results are in agreement with those of (Saınt Pıerre et al., 2008), which indicated that the grouping of genotypes in the biplot showed that the genotypes within the quality groups reacted similarly to the combinations of the quality traits.

In general, the genotypes containing HMW-GSs 2*, 7+9, 2+12 were positioned exclusively on the negative side of the PC1 axis, while the genotypes containing 1, 7+8, 5+10 were located on the positive side. Our findings were in agreement with the results of (Panozzo & Eagles, 2000). Meanwhile, relatively higher yielding genotypes, with the subunits 2*, 7+9, and 2+12 were located on the negative PC1 axis, while relatively lower yielding genotypes, with the subunits 1, 7+8, and 5+10 were positioned on the positive PC1 axis. It may be concluded that genes confering GY could be negatively associated with genes determining protein quantity and quality for genotypes used in this study.

Traits of wheat may be correlated to each other in a positive or a negative manner. The direction of the correlation is independent of the breeding objectives and may change from one production environment to another. GY and PC

are negatively correlated with each other (O'Brien & Ronalds, 1987). This negative relationship between GY and PC is highly undesirable for the development of cultivars eligible for grades of the market class (Depauw et al., 2007).

The association between ZSV and PC was highly significant, which was expected since the influence of PC on the ZSV is well known. ZSV is significantly influenced by PC, and the magnitude of the effect varies according to the genotype (Cubadda et al., 2007).

The negative correlation between ZSV and GY was highly significant. This is in accordance with other reports (Cubadda et al., 2007). This is probably also linked to the highly significant correlation of ZSV with PC, in which high PC is known to be negatively associated with GY.

5 Conclusion

The present study showed that GY and quality traits were determined mainly by E, whereas the influence of G is of less importance. GEI was of smaller size compared to G and E in terms of all the studied quality parameters. The majority of advanced breeding lines had low quality values for all environments. Negative association between high yield and good quality should be an important target for the next breeding efforts.

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