



Original article

## Genotypes by Environment Interaction of Bread Wheat (*Triticum aestivum* L.) Genotypes on Yield and Quality Parameters under Rainfed Conditions

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### Abstract

The significant genotype (G) by environment (E) interaction and genetic diversity in the breeding programs are an essential issue for the breeder to develop new cultivars. The experiment was conducted in the Trakia region, Turkey at five environments during the 2015-2016 growing cycles. In the study, 25 advanced genotypes were used in randomized complete block design with four replications. Data on grain yield, days to heading, plant height, 1000-kernel weight, test weight, protein ratio, wet gluten content, gluten index, hardness, and sedimentation value were investigated. The results of variance analyses showed that there were significant differences ( $P < 0.01$ ) among genotypes based on all parameters investigated. Genotypes when tested across different environmental conditions often showed significant variation in grain yield. Mean grain yield across five locations ranged from the highest 6673 kg ha<sup>-1</sup> to the smallest 5008 kg ha<sup>-1</sup>. Burgaz location was found near the ideal test environment of the average environment coordination. Therefore, location Burgaz should be regarded as the most suitable to select widely adapted genotypes. With the longest vectors from the origin, environments Edirne1 and Edirne2 were the most discriminating location. Considering simultaneously mean yield and stability, G7 and G12 were the best genotypes. G3 is more ideal genotype because it is located in the ideal center. So these genotypes can be used as for the evaluation of bread wheat genotypes in the region. With the longest vectors from the origin, traits plant height, gluten index and protein ratio was the most discriminating parameters. In the evaluation of genotypes, G2 and Pehlivan are quite stable because they are located close to the center of the horizontal axis. Genotype G3 is very favourable because it is located near the center of the horizontal axis and on all traits. G7, G24 and Aldane are located above the axis vertical genotypes are desirable based on parameters profiles.

**Keywords:** Bread Wheat, Environment, Genotypes, Yield, Agronomic Characters, Biplot.

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## **INTRODUCTION**

Bread wheat is a widely produced crop in the Trakia region of Turkey. Because of the various environmental conditions yield and quality in wheat varies and GGE biplot analysis provides an easy and comprehensive solution to genotype by environment interaction and it not only allows effective evaluation of the genotypes but also allows a comprehensive understanding of the target environment and the test environments. Various environment conditions is mainly abiotic stress factor affect bread wheat yield and quality (Öztürk and Korkut 2018; Öztürk, 2001). Almost all breeding programs in the world aim to improve varieties with stable yields. The yield stability is generally grouped as static or dynamic stability (Pfeiffer and Braun, 1989). Evaluation of genotypes across diverse environments and over several years is needed in order to identify spatially and temporally stable genotypes that could be recommended for release as new cultivars and/or for use in the breeding programs (Sharma et al., 2010). GGE biplot analysis has been widely used to determine performance stability in multilocation trials when identifying superior genotypes (Yan et al., 2007; Sharma et al., 2010). G×E interactions are of major importance, because they provide information about the effect of different environments on cultivar performance and have a key role for assessment of performance stability of the breeding materials (Moldovan et al., 2000). To develop varieties for different environments, very essential for breeders to evaluate their genotypes based on many years and several locations. Environmental variations are important in determining performance of elite materials (Solomon et. al., 2018). Variety trials provide essential information for selecting and recommending crop cultivars. However, variety trial data are rarely utilized to their full capacity. Although data may be collected for many traits, analysis may be limited to a single trait usually yield and information on other traits is often left unexplored (Yan and Tinker, 2006). Environmental factors play a main role in the expression of genotype characteristics (Peterson et al., 1998). In wheat, grain yield and baking quality are dependent on the environment, genetic factors and the interaction between them (Yan and Holland, 2010; Coventry et al., 2011). Genotypes when tested across different environmental conditions often show significant variation in grain yield. This fluctuation is generally known as GE interaction. However, GE interaction is likely to be more severe in stress conditions which complicate the process of selecting high yielding stable genotypes (Cooper and Byth, 1996). Therefore, breeding programs are tended to test extensively newly developed material in diverse environments to increase the chances of success (Alwala et al., 2010). The study was carried out to test developed 25 advanced bread wheat genotypes at five environments under rainfed conditions to identify high yielding stable wheat genotypes and assessment of the genotypes for quality parameters.

## **MATERIALS and METHODS**

The experiments were designed to determine the environment effect for grain yield, quality and agronomic traits in bread wheat. The experiments were conducted at five environments (Edirne1,

Edirne2, Burgaz, Keşan and Tekirdağ) in Trakya region, Turkey, in 2015-2016 cropping seasons. Tekirdağ and Keşan are located in the coastal zone of the region, in the north of Edirne1 and Edirne2, and Burgaz in the middle of the region constitutes different locations in terms of climate and soil characteristics. Each location in each year was considered as single environment. Twenty five winter wheat genotypes, 5 of them was local check (G1: Aldane, G5: Selimiye, G10: Bereket, G15: Pehlivan, G20: Gelibolu) and 20 advanced lines developed from breeding program, were examined. The wheat genotypes were grown in a randomized complete block design with four replications at each cropping seasons. Plot size was 6.0 m<sup>2</sup>, 6 rows with 6 m long, and 17 cm between rows. A seed rate of 500 seeds m<sup>2</sup> was used.

In the research; grain yield, days to heading, plant height, 1000-kernel weights and test weight, (Blakeney et al., 2009), protein ratio, grain hardness, wet gluten content, gluten index, and sedimentation (Perten H. 1990; Anonymous, 1990; Anonymous, 2002) were investigated. The quality analysis of Zeleny sedimentation test and wet gluten content were determined according to ICC standard methods No. 116/1 and 106/2, respectively (Anonymous, 1972; Anonymous, 1984). 1000-kernels were randomly counted from each plot's seed package and weighed to determine TKW. To determine TW, two samples with a grain volume of 500 mL were used. The days to heading was determined from the date of 01 January up to the date when the tips of the spike first emerged from the main shoots on 50% of the plants in a plot. A combined analysis of variance was conducted to test the significance of environment, genotype, and GE interaction. Genotype and genotype x environment (GGE) biplot analyses were used (Yan and Kang, 2002) to determine performance and stability for grain yield, 1000-kernel weight, test weight, protein ratio and wet gluten content. Data were analysed statistically for analysis of variance the method described by Gomez and Gomez (1984). The significance of differences among means was compared by using Least Significant Difference (L.S.D. at a %5) test. In order to visually display relations of observed traits and genotypes multivariate biplot analysis (genotype by trait biplot), described by Yan and Rajcan, (2002), Yan and Tinker (2006) and Yan and Kang (2003) was used.

## **RESULTS and DISCUSSION**

The results of variance analysis of the research are presented in Table 1. The data of 25 bread wheat genotypes in multi-location and year trials were analyzed to determine whether the effect of the genotype and environment was significant; means were separated using the least significant differences (LSD) test with significance set at  $P < 0.01$ . Data were also graphically analyzed by the genotype  $\times$  trait biplot method as recommended by Yan and Thinker (2005). The combined ANOVA revealed significant differences among environments for all parameters ( $P < 0.01$ ) and highly significant differences ( $P < 0.01$ ) were recorded among the genotypes for all parameters investigated.

**Table 1.** Mean square and F ratio for yield, morphological and quality parameters measured in 25 bread wheat genotypes grown across five environments

Parameters	Genotypes (G)		Environment (E)	
	MS	F Ratio	MS	F Ratio
Grain yield (GY)	10728.47	2.32**	160200.37	34,67**
Days of heading (DH)	105.85	29.53**	557.77	155.61**
Plant height (PH)	511.92	28.54**	132.51	7.38**
1000-kernel weight (TKW)	81.44	12.82**	379.40	53.21**
Test weight (TW)	24.01	12.42**	100.80	52.16**
Protein ratio (PRT)	3.33	13.18**	1.48	5.84**
Gluten value (GLT)	53.26	9.47**	35.13	6.25**
Gluten index (IND)	1384.50	19.06**	1078.14	14.84**
Sedimentation (SED)	354.12	31.31**	66.37	5.87**
Hardness (HARD)	34.15	6.89**	98.11	19.79**

\*, \*\* Significant at  $p < 0.05$  and  $p < 0.01$  respectively.

The results of variance analyses showed that there were significant differences ( $P < 0.01$ ) among genotypes. Genotypes when tested across different environmental conditions often show significant variation in grain yield. Mean grain yield across five locations ranged from the highest 6673 kg ha<sup>-1</sup> to the smallest 5008 kg ha<sup>-1</sup>. The mean grain yield was 5770 kg ha<sup>-1</sup>. The highest grain yield was performed by genotypes G7 and followed by G12 (Table 2). Early heading plays an important role in grain filling in the majority of crops including wheat. Late heading provides lesser time for grain filling which ultimately reflects in lower grain weight (Nasarullah et al., 2017). The adaptation strategies of the plants to drought stress include drought escape, drought avoidance and drought tolerance. Among these strategies, escaping drought involves the completion of the life cycle before the onset of the drought period. Therefore, early maturity has been known as a major drought escaping mechanism, particularly in terminal drought stresses (Levitt, 1980; Chaves et al., 2002). Due to the fluctuation of rainfall in the region mid-early genotypes generally are favourable in the wheat breeding program. Mean days to heading of the genotypes indicated that cultivar Aldane was noted with early heading (105.0 days), across environments. Similarly, G7 (105.6 days) and G8 (106.6 days), was also early in heading thus confirmed as early heading line across eight environments (Table 2). Plant height is an important character for bread wheat and its contribution to yield is indirect. The highest plant height causes yield losses, as tall stature plants become more susceptible to lodging problems hence moderate to short plant height is favourable for production. Lodging is also one of the main problems in the Trakya region so plant height is an important trait to evaluating genotypes. There was a significant difference among genotypes for plant height. With regard to genotypic effects, G23 (77.4 cm) and G22 (78.8 cm) exhibited the lowest plant height. On the other hand, genotype G14, which was showed the highest plant height of 114.4 cm, and followed by G3 and G25 (Table 2). Reducing plant height has played an important role in improving crop yields. The success of a breeding program relies on the source of dwarfing genes. For

a dwarfing or semi-dwarfing gene to be successfully used in a breeding program, the gene should have minimal negative effects on yield and perform consistently in different environments (Wang et al. 2014).

High yield performance is attributed to high 1000-grain weight and it is the most important yield component which contributes to plant yield. Losses in grain yield occur due to a decrease in 1000-grain weight (Akram et al., 2004). The number of grains in a spike in wheat has predominant importance for grain yield and kernel weight is known to be a major yield component. There were significant differences among genotypes based on 1000-kernel weight and test weight. 1000-kernel weight ranged from 30.0 g (G4) to 48.1 g (G18) among genotypes and the mean value was 39.7 g across five locations. Genotypes G18 had the highest 1000-kernel weight and followed by G19 (Table 2). Test weight of wheat genotypes indicated that the highest test weight in genotype G7 (85.7 kg), cultivar Pehlivan (84.3 kg) and G3 (84.1 kg), whereas, the lowest test weight was observed in G23 (78.3 kg).

Protein quality and quantity is the most important components of wheat grains governing end-use quality (Pena, 2008). Protein quality and quantity have received more attention than other quality attributes, partly owing to the significant influence imparted by protein on the end-use product quality of both common wheat and durum wheat. Environmental factors, such as nitrogen fertilization, water and temperature, influence protein ratio (Sissons et al., 2005). Table 3 shows that mean and ranges of variation for protein ratio in all genotypes were evaluated across five locations. In this study, protein ratio varied between 10.09% (Bereket) and 12.9% (G8) in the genotypes and mean was 11.1% in genotypes. Wet gluten content ranged from 25.4% (G4) to (G8) among genotypes and mean was 32.2%. The highest wet gluten content was measured in genotypes G8 and followed by G14, G25 and cultivar Aldane. Also, there was significant variation in sedimentation among genotypes and ranged from 27.8 ml to 59.8 ml and cultivar Aldane had the highest sedimentation (59.8 ml) and followed by genotypes G7, G3 and G25. The mean sedimentation was 41.4 ml. There were significant variation among genotypes for gluten index and minimum and maximum were 41.2 (G19)-93.1% (G7), respectively.

**Table 2.** The mean value and standard deviation of the genotypes on yield, morphological and quality characters

No	Genotypes	GY	DH	PH	TKW	TW
1	G1 (Aldane)	5951±1051 <sup>a-e</sup>	105.0±6.3 <sup>h</sup>	99.4 d±5.7 <sup>g</sup>	45.7±4.2 <sup>ab</sup>	83.2±1.7 <sup>b-f</sup>
2	G2	6144±1071 <sup>abc</sup>	111.4±3.4 <sup>de</sup>	109.2±7.7 <sup>abc</sup>	33.1±3.4 <sup>ij</sup>	81.6±1.4 <sup>e-h</sup>
3	G3	5008±747 <sup>f</sup>	117.6±6.8 <sup>ab</sup>	112.8±6.0 <sup>ab</sup>	35.5±2.0 <sup>hi</sup>	84.1±1.8 <sup>abc</sup>
4	G4	5924±1169 <sup>a-e</sup>	109.0±3.4 <sup>f</sup>	88.6±3.8 <sup>j</sup>	30.0±2.9 <sup>j</sup>	81.0±2.0 <sup>gh</sup>
5	G5 (Selimiye)	5284±1147 <sup>def</sup>	109.0±4.9 <sup>f</sup>	97.2±4.9 <sup>e-h</sup>	40.1±3.8 <sup>de</sup>	84.9±1.6 <sup>ab</sup>
6	G6	6362±1227 <sup>ab</sup>	111.6±4.4 <sup>de</sup>	100.4±2.9 <sup>def</sup>	38.8±6.2 <sup>d-h</sup>	79.3±3.1 <sup>jk</sup>
7	G7	6673±556 <sup>a</sup>	105.6±5.3 <sup>h</sup>	98.0±2.9 <sup>e-h</sup>	35.7±3.5 <sup>ghi</sup>	85.7±1.9 <sup>a</sup>
8	G8	6275±1008 <sup>ab</sup>	106.6±8.5 <sup>gh</sup>	95.0±4.3 <sup>ghi</sup>	36.1±4.8 <sup>f-i</sup>	83.2±2.3 <sup>b-f</sup>
9	G9	5149±1168 <sup>ef</sup>	118.8±5.0 <sup>ab</sup>	83.0±6.2 <sup>k</sup>	38.8±6.3 <sup>d-g</sup>	78.3±2.1 <sup>k</sup>
10	G10 (Bereket)	5065±1189 <sup>f</sup>	109.0±2.7 <sup>f</sup>	102.4±6.2 <sup>de</sup>	38.2±3.0 <sup>e-h</sup>	82.0±1.9 <sup>d-g</sup>
11	G11	5842±1252 <sup>a-f</sup>	110.4±3.0 <sup>ef</sup>	94.0 ±3.3 <sup>hi</sup>	38.9±4.5 <sup>d-g</sup>	81.6±3.1 <sup>fgh</sup>
12	G12	6581±1124 <sup>a</sup>	110.6±4.0 <sup>def</sup>	98.8±4.8 <sup>e-h</sup>	41.5±3.7 <sup>cde</sup>	80.2±2.7 <sup>hij</sup>
13	G13	5928±720 <sup>a-e</sup>	111.8±4.1 <sup>de</sup>	98.4±2.1 <sup>e-h</sup>	38.3±3.8 <sup>e-h</sup>	79.1±2.6 <sup>jk</sup>
14	G14	5312±782 <sup>c-f</sup>	118.8±5.3 <sup>ab</sup>	114.4±3.4 <sup>a</sup>	39.0±2.9 <sup>d-g</sup>	81.6±1.3 <sup>fgh</sup>
15	G15 (Pehlivan)	5345±1325 <sup>c-f</sup>	110.2±5.0 <sup>ef</sup>	108.2±4.0 <sup>bc</sup>	44.2±5.4 <sup>bc</sup>	84.3±2.1 <sup>abc</sup>
16	G16	5960±1070 <sup>a-e</sup>	106.4±7.7 <sup>h</sup>	95.4±4.9 <sup>f-i</sup>	36.3±3.6 <sup>f-i</sup>	83.5±2.2 <sup>bcd</sup>
17	G17	6056±965 <sup>a-d</sup>	111.0±3.8 <sup>def</sup>	91.4±6.1 <sup>ij</sup>	40.4±5.3 <sup>de</sup>	83.4±3.1 <sup>b-e</sup>
18	G18	5666±1157 <sup>b-f</sup>	115.2±5.4 <sup>c</sup>	109.6±5.8 <sup>abc</sup>	48.1±3.7 <sup>a</sup>	83.7±1.1 <sup>bcd</sup>
19	G19	5849±556 <sup>a-f</sup>	112.8±5.9 <sup>d</sup>	104.6±3.0 <sup>cd</sup>	47.0±6.9 <sup>ab</sup>	79.7±4.1 <sup>ijk</sup>
20	G20 (Gelibolu)	6102±882 <sup>a-d</sup>	108.8±4.1 <sup>fg</sup>	96.8±2.2 <sup>fgh</sup>	39.0±5.8 <sup>d-g</sup>	83.7±2.3 <sup>bcd</sup>
21	G21	5951±409 <sup>a-e</sup>	112.4±5.1 <sup>de</sup>	100.0±6.4 <sup>d-g</sup>	44.6±6.4 <sup>bc</sup>	79.3±4.9 <sup>ijk</sup>
22	G22	5535±1232 <sup>b-f</sup>	119.2±4.1 <sup>ab</sup>	78.8±2.9 <sup>kl</sup>	39.0±4.5 <sup>def</sup>	78.6±1.9 <sup>jk</sup>
23	G23	5353±1066 <sup>c-f</sup>	119.4±4.1 <sup>a</sup>	77.4±4.0 <sup>l</sup>	39.3±5.2 <sup>def</sup>	78.6±2.1 <sup>jk</sup>
24	G24	5282±1291 <sup>def</sup>	118.8±4.8 <sup>ab</sup>	111.4±4.9 <sup>ab</sup>	44.2±6.2 <sup>bc</sup>	83.0±1.6 <sup>c-f</sup>
25	G25	5663±1140 <sup>b-f</sup>	117.0±2.2 <sup>bc</sup>	112.0±4.6 <sup>ab</sup>	41.9±5.2 <sup>cd</sup>	83.2±1.7 <sup>b-f</sup>
	Mean	5770	112.3	99.1	39.7	81.8
	C.V (%)	11.7	1.7	4.3	6.7	1.7
	L.S.D (0.05)	83.30	2.35	5.28	3.32	1.72

GY: Grain yield (kg ha<sup>-1</sup>), DH: Days of heading, PH: Plant height (cm), TKW: 1000-kernel weight (g), TW: Test weight (kg)

Genotype × trait biplot analysis is highlighted among the multivariate methodologies because it assesses genotypes based on multiple traits and identifies those that are superior to the desired variables; these can be used as parents in breeding programs or even as possible commercial cultivars. A quick and practical visualization of the genetic correlation between traits is also provided by this analysis. Less important (redundant) traits can be detected and identified as the most suitable to indirectly select a favorable trait (Yan and Tinker, 2006). Trait values across five locations of 25 bread wheat genotypes are displayed in Tables 2 and 3. These data were used to create a biplot and the goodness of fit of the biplot is relatively strong because it represents 65.25% of the variation

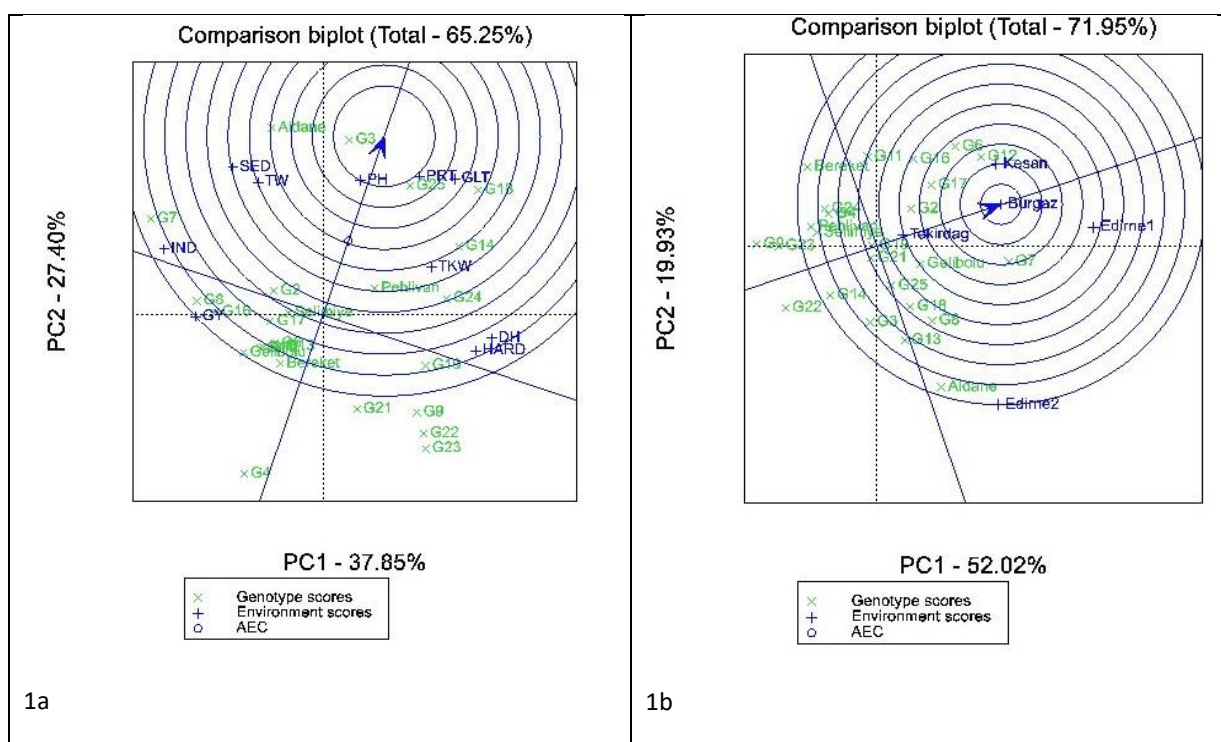
**Table 3.** The mean of the quality parameters and standard deviation of the genotypes

No	Genotypes	PRT	GLT	IND	HARD	SED
1	G1 (Aldane)	12.8±0.6 <sup>a</sup>	36.3±2.4 <sup>ab</sup>	89.7±3.9 <sup>ab</sup>	46.6±4.6 <sup>jk</sup>	59.8±3.9 <sup>a</sup>
2	G2	11.3±0.7 <sup>de</sup>	31.6±3.9 <sup>c-g</sup>	73.4±18.7 <sup>d-g</sup>	48.6±1.1 <sup>f-j</sup>	44.4±5.0 <sup>efg</sup>
3	G3	12.7±0.3 <sup>ab</sup>	36.7±2.4 <sup>ab</sup>	84.4±7.8 <sup>abc</sup>	47.4±2.1 <sup>ijk</sup>	55.4±5.0 <sup>b</sup>
4	G4	10.4±0.6 <sup>ijk</sup>	25.4±2.3 <sup>i</sup>	62.8±17.6 <sup>gh</sup>	49.0±2.0 <sup>f-j</sup>	29.0±0.7 <sup>m</sup>
5	G5 (Selimiye)	10.4±0.7 <sup>h-k</sup>	31.1±2.3 <sup>d-h</sup>	72.5±19.4 <sup>efg</sup>	48.6±1.1 <sup>f-j</sup>	39.6±5.6 <sup>h-k</sup>
6	G6	10.9±0.8 <sup>e-i</sup>	30.3±3.0 <sup>fgh</sup>	80.6±8.3 <sup>b-e</sup>	49.6±1.8 <sup>e-i</sup>	44.6±1.3 <sup>ef</sup>
7	G7	11.3±0.5 <sup>ef</sup>	30.5±2.7 <sup>e-h</sup>	93.1±1.9 <sup>a</sup>	45.6±2.7 <sup>k</sup>	56.2±2.9 <sup>ab</sup>
8	G8	10.5±0.5 <sup>g-k</sup>	30.7±2.3 <sup>e-h</sup>	83.4±9.1 <sup>a-d</sup>	46.8±1.6 <sup>jk</sup>	49.4±3.9 <sup>cd</sup>
9	G9	11.3±0.4 <sup>ef</sup>	33.1±1.9 <sup>c-f</sup>	54.6±10.0 <sup>hi</sup>	51.2±2.3 <sup>c-f</sup>	36.8±4.1 <sup>i-l</sup>
10	G10 (Bereket)	10.0±0.5 <sup>k</sup>	29.5±2.1 <sup>gh</sup>	75.8±14.8 <sup>c-f</sup>	47.4±2.3 <sup>ijk</sup>	36.2±4.2 <sup>kl</sup>
11	G11	10.6±0.2 <sup>g-k</sup>	29.8±1.0 <sup>gh</sup>	78.0±10.5 <sup>c-f</sup>	47.6±1.1 <sup>h-k</sup>	42.8±2.8 <sup>e-h</sup>
12	G12	10.5±0.2 <sup>g-k</sup>	29.8±0.4 <sup>gh</sup>	82.9±5.8 <sup>a-e</sup>	50.2±2.9 <sup>e-h</sup>	43.6±2.6 <sup>e-h</sup>
13	G13	10.8±0.2 <sup>e-i</sup>	30.0±1.3 <sup>gh</sup>	85.0±5.2 <sup>abc</sup>	49.8±2.0 <sup>e-i</sup>	46.8±2.8 <sup>cde</sup>
14	G14	11.9±0.3 <sup>cd</sup>	38.4±2.0 <sup>a</sup>	46.9±6.3 <sup>ijk</sup>	51.8±1.9 <sup>b-e</sup>	40.2±2.3 <sup>g-j</sup>
15	G15 (Pehlivan)	10.8±0.3 <sup>e-i</sup>	34.0±1.8 <sup>bcd</sup>	43.5±5.5 <sup>jk</sup>	49.0±3.2 <sup>f-j</sup>	35.6±2.7 <sup>kl</sup>
16	G16	10.3±0.3 <sup>ijk</sup>	30.6±1.2 <sup>e-h</sup>	83.2±7.9 <sup>a-e</sup>	48.0±1.0 <sup>g-k</sup>	47.0±2.5 <sup>cde</sup>
17	G17	10.6±0.3 <sup>f-j</sup>	30.7±1.4 <sup>e-h</sup>	82.1±8.5 <sup>b-e</sup>	50.4±1.1 <sup>d-g</sup>	45.2±3.3 <sup>de</sup>
18	G18	12.9±0.6 <sup>a</sup>	38.6±4.8 <sup>a</sup>	53.2±15.5 <sup>hij</sup>	54.6±1.5 <sup>a</sup>	39.6±2.4 <sup>h-k</sup>
19	G19	11.0±0.4 <sup>e-h</sup>	34.2±1.8 <sup>bc</sup>	41.2±7.4 <sup>k</sup>	51.0±2.6 <sup>c-f</sup>	27.0±4.2 <sup>m</sup>
20	G20 (Gelibolu)	10.1±0.6 <sup>jk</sup>	28.4±2.2 <sup>hi</sup>	84.6±6.3 <sup>abc</sup>	51.0±1.2 <sup>c-f</sup>	40.6±3.1 <sup>f-i</sup>
21	G21	10.6±0.5 <sup>f-j</sup>	30.1±5.3 <sup>gh</sup>	41.5±8.4 <sup>k</sup>	47.4±3.9 <sup>ijk</sup>	29.2±1.9 <sup>m</sup>
22	G22	11.4±0.6 <sup>de</sup>	32.5±1.9 <sup>c-g</sup>	53.4±10.3 <sup>hij</sup>	53.6±4.3 <sup>abc</sup>	34.6±2.9 <sup>l</sup>
23	G23	11.1±0.5 <sup>efg</sup>	31.6±1.1 <sup>c-g</sup>	54.4±8.6 <sup>hi</sup>	54.2±5.2 <sup>ab</sup>	35.0±3.5 <sup>l</sup>
24	G24	11.1±0.9 <sup>efg</sup>	33.3±3.4 <sup>cde</sup>	54.7±12.3 <sup>hi</sup>	54.4±4.8 <sup>ab</sup>	37.2±4.8 <sup>l-l</sup>
25	G25	12.2±1.1 <sup>bc</sup>	37.4±3.6 <sup>a</sup>	68.4±11.8 <sup>fg</sup>	53.0±6.0 <sup>a-d</sup>	50.4±6.9 <sup>c</sup>
	Mean	11.1	32.2	68.9	49.8	41.4
	C.V (%)	4.5	7.4	12.4	4.5	8.0
	L.S.D (0.05)	0.61	2.95	10.67	2.77	4.19

PRT: Protein ratio (%), GLT: Gluten (%), IND: Gluten index (%), HARD: Hardness, SED: Sedimentation (ml)

The discrimination and representativeness of genotypes based on traits are displayed in Figure 1a. This figure shows that a representative “ideal center” over the property mean values and allows evaluating genotypes according to their nearness or distance to this center (Yan et al., 2000; Yan and Tinker, 2005). The most ideal genotypes are located in the center, whereas genotypes located on the mean vertical axis, but far from the center, are ideal; genotypes located below the vertical axis are undesirable. According to Figure 1a, G3 is more ideal genotype because it is located in the ideal center, followed by G25 because it is the nearest genotypes to the ideal center, while G4 and G9, G21, G22, G23, and G24 are located under the vertical axis and far from the ideal center so these are undesirable varieties. Also, the discrimination and representativeness of the environment based on traits are

displayed in Figure 1b. According to Figure 1b, Burgaz is a more ideal environment because it is located in an ideal center, followed by Keşan because of the nearest genotypes to the ideal center.



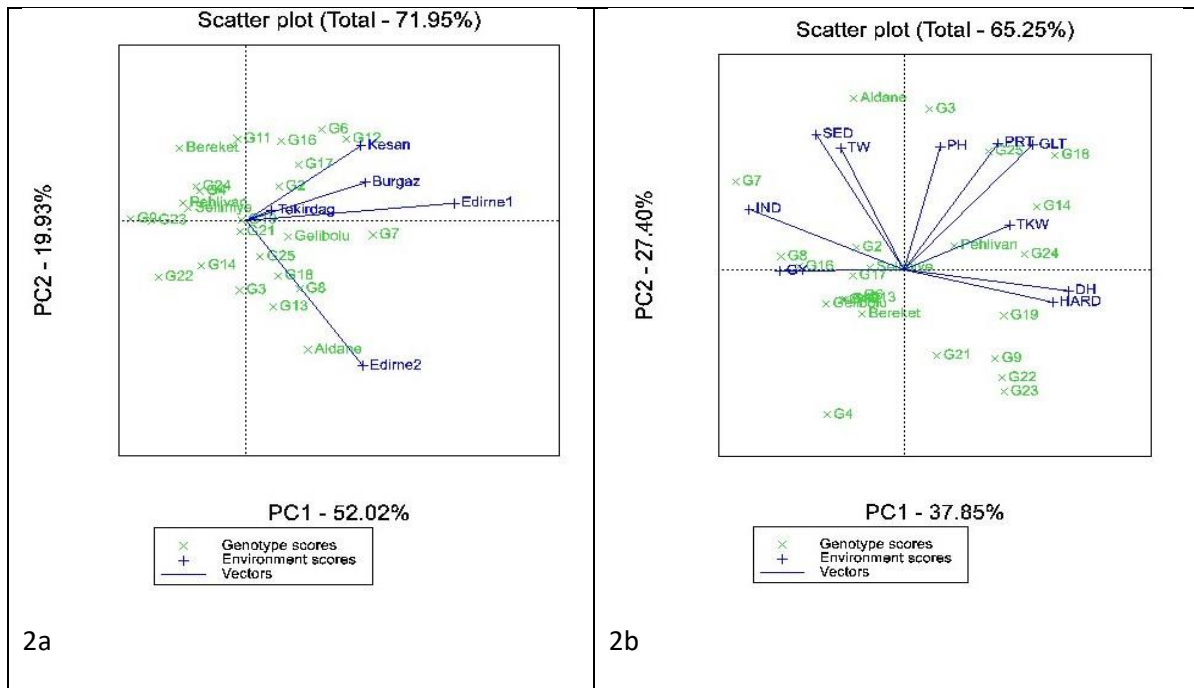
**Figure 1.** GGE biplot graph based on genotype-focused scaling for comparison of parameters with ideal genotype (1a), and GGE-biplot based on genotype-focused scaling for comparison of the genotypes with the ideal environment (1b).

Further information about the discriminating power of environments, together with a representation of their mutual relationships, can be obtained by the environment-vector view of the GGE-biplot. In this case, a long environmental vector reflects a high capacity to discriminate the genotypes. Furthermore, the cosine of an angle between vectors of two environments approximates the correlation between them: a wide obtuse angle indicates a strong negative correlation, an acute angle indicates a positive correlation while a close to 90° angle indicates lack of correlation (Yan and Tinker 2006). With the longest vectors from the origin, environments Edirne1 and Edirne2 were the most discriminating. Locations Keşan and Burgaz were moderately discriminating, while Tekirdağ was least discriminating. Considering the angles between environmental vectors, yield results in Keşan and Burgaz were strongly correlated, similarly to those obtained in Burgaz and Edirne1 (Figure 2a).

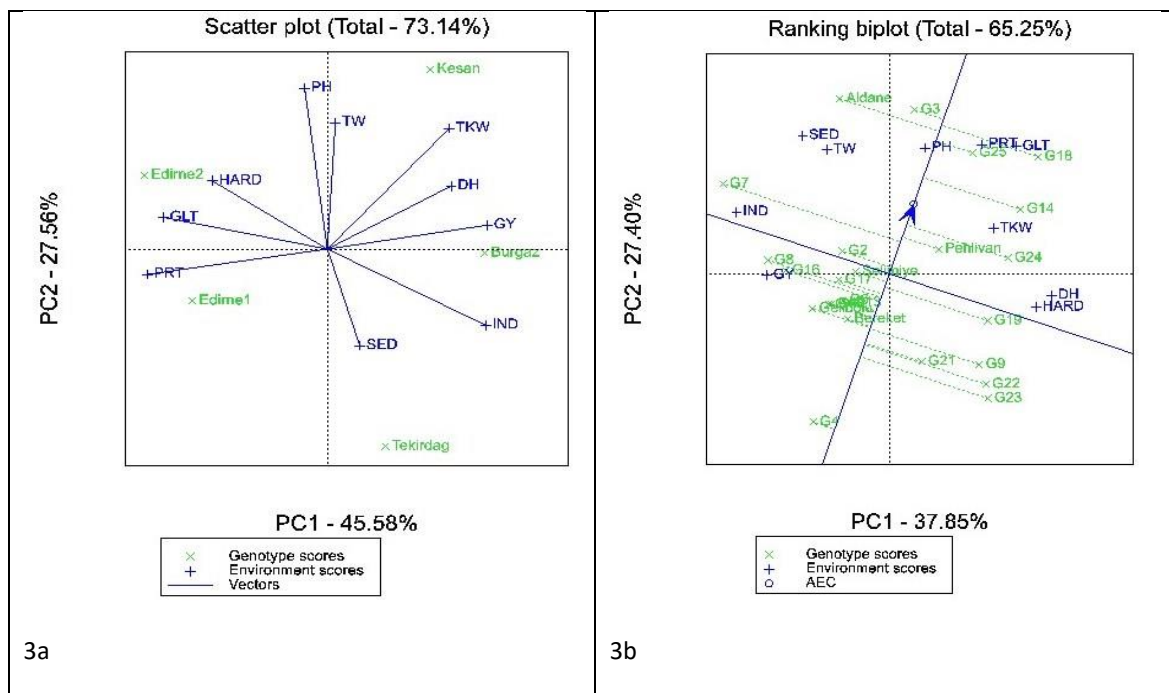
The relationships among locations and parameters in Figures 2a and 2b are visualized by genotype profiles. A biplot illustrated as a graph can be bi-directionally interpreted in different ways (Yan and Rajcan, 2002; Yan and Tinker, 2006). The cosine of the angle between the vectors of the two properties approaches the Pearson correlation between them. Therefore, an angle < 90° shows a positive correlation, an angle > 90° shows a negative correlation, and an angle of 90° shows a zero correlation.



The length of the vector is an approximation of trait variation. The angle between the vector of any genotype and any trait gives information about the state of the genotypes. If the angle is quite acute or if the angle is too large, this indicates that the genotype is below the mean for that trait. The vector length of a genotype indicates its strength or weakness for all trait profiles. According to these principles described in the GT biplot technique, the following observations can be made about Figure 2b. Grain yield was positively and highly correlated with gluten index, and positively correlated with test weight and sedimentation, but it was negatively correlated with other parameters investigated in this research (PH, PRT, GLT, TKW, DH and HARD). On the other hand, there was a positively highly association between sedimentation and test weight, protein content, gluten value, days of heading, and hardness (Figure 2b).



**Figure 2.** Ranking genotypes based on mean performance in five environments (2a). The GGE biplot to show which genotypes performed best in which environments and a genotype by trait biplot representing 25 winter wheat genotypes measured for parameters (2b).



**Figure 3.** Relationship among test environments and genotypes based parameters investigated (Figure 3a), and average environment coordination (AEC) views of the GGE-biplot based on environment-focused scaling for the means performance and stability of genotypes (3b).

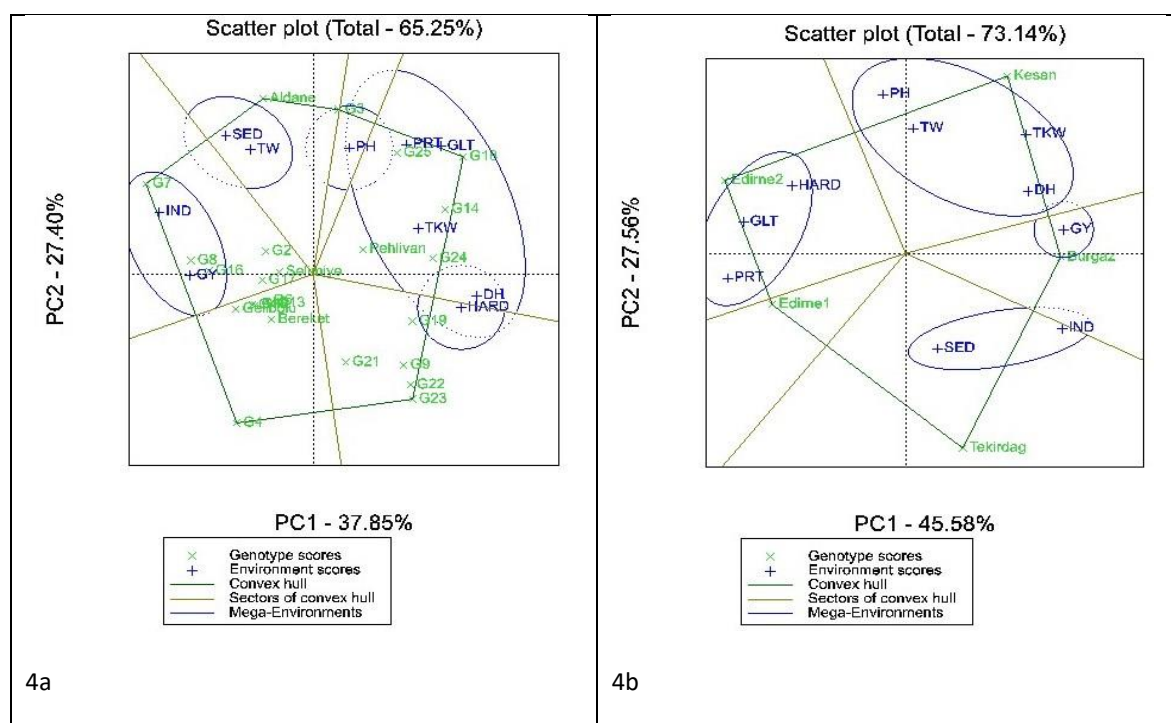
With the longest vectors from the origin, traits PH, IND and PRT were the most discriminating. TKW, GY, and GLT were moderately discriminating, while SED and HARD were least discriminating. Considering the angles between parameters vectors, parameters results in PH and TW were strongly correlated, similarly to those obtained in PRT and GLT (Figure 3a). Figure 3b shows a vertical mean axis and a horizontal stability axis based on trait values; genotypes are evaluated based on these two axes. If the genotypes are located below the vertical axis, they are undesirable. If they are located above the vertical axis, they are desirable genotypes. On the other hand, genotypes located near or at the center of the horizontal line are stable and unstable if they move away from the horizontal line (Kendal and Sayar, 2016). According to Figure 3b, G2 and Pehlivan are quite stable because they are located close to the center of the horizontal axis. Genotype G3 is very favourable because it is located near the center of the horizontal axis and on all traits. G23, G22 and G9 are undesirable genotypes because they are located under the vertical axis line. G7, G24 and Aldane are located above the axis vertical genotypes are desirable based on parameters profiles (Figure 3b).

The polygon of the which-won-where/what of the GT biplot based on data across environments is shown in Figure 4a. The polygon view of the GGE-biplot analysis helps one detect cross-over and non-crossover genotype-by-environment interaction and possible mega environments in multi-location yield trials (Yan et al. 2007). If the genotypes and properties are located in the same sector when starting from the lower right part of the graph, they are closely related (Yan and Tinker, 2006). According to this description different traits are associated with different cultivars in each sector. Genotypes G18 won

in one sector and G25, G14, G24 and Pehlivan were located in same sector, they are correlated with PRT, GLT and TKW. G7 won in other sector (G8, G16, G2, G17 and Selimiye are located in this sector) and it was correlated with IND and GY. Cultivar Aldane won in other sector, it was correlated with SED and TW (Figure 4a).

G18, Aldane (G1), G7, G4 and G23 were vertex genotypes (Figure 4a). They are best in the environment lying within their respective sector in the polygon view of the GGE-biplot (Yan and Tinker 2006); thus these genotypes are considered specifically adapted. Genotypes close to the origin of axes have wider adaptation.

When the locations and parameters are examined different traits have been found to be associated with a different environment. One of the vertex locations Keşan was correlated with TKW, TW, DH and PH. Edirne2 location was correlated with HARD, GLT and PRT. Location Burgaz was in another sector it was correlated with GY. Location Tekirdağ was the other sector, it was correlated with SED and IND. (Figure 4b).



**Figure 4.** Grouping of the genotypes and traits by GGE Biplot analysis method in terms of observed traits and relationships of genotypes with these traits (4a). Polygon view of the GGE biplot using symmetrical scaling of bread wheat genotypes across five environments (4b)

## **Conclusion**

There were significant difference among genotypes and environment. Genotypes when tested across different environmental conditions often show significant variation in grain yield. The highest grain yield was performed by genotypes G7 and followed by G12. Considering simultaneously mean yield and stability, G7 and G12 were the best genotypes. G3 is more ideal genotype because it is located in the ideal center, followed by G25 because it is the nearest genotypes to the ideal center. So these genotypes can thus be used as for the evaluation of bread wheat genotypes in the region. According to location, Burgaz is a more ideal environment because it is located in an ideal center, followed by Keşan because of the nearest genotypes to the ideal center. With the longest vectors from the origin, environments Edirne1 and Edirne2 were the most discriminating location. Considering the angles between environmental vectors, yield results in Keşan and Burgaz were strongly correlated, similarly to those obtained in Burgaz and Edirne1. Grain yield was positively and highly correlated with gluten index, test weight and sedimentation. On the other hand, there was a positively highly association between sedimentation and test weight, protein ratio, wet gluten content, days to heading, and hardness. With the longest vectors from the origin, traits plant height, gluten index and protein ratio was the most discriminating parameters. Considering the angles between parameters vectors, parameters results in plant height and test weight were strongly correlated, similarly to those obtained in protein ratio and wet gluten content. In the evaluation of genotypes, G2 and Pehlivan are quite stable because they are located close to the center of the horizontal axis. Genotype G3 is very favourable because it is located near the center of the horizontal axis and on all traits. G7, G24 and Aldane are located above the axis vertical genotypes are desirable based on parameters profiles.

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