

Multi-environmental Evaluation of Triticale, Wheat and Barley Genotypes by GGE Biplot Analysis

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Abstract: The research was carried out with 9 triticale, 3 bread wheat, 3 durum wheat and 3 barley varieties and advanced lines in Tekirdağ, Edirne and Silivri locations during three years. In the study, the data obtained from combined variance analysis were performed and the significance of the differences between the averages was determined by LSD multiple comparison test. GGE biplot analysis and graphics were made by using the statistical package program. The genotypes G2 and G3 for thousand kernel weight, genotype G1 for the heading time and test weight, genotypes G14 and G15 for the maturation time, number of spikelets per spike and grain weight per spike and G13 for the plant height, spike length and grain yield per hectare decare revealed the highest values. The genotypes G6, G5, G4, G14, G9, G8 and G7 gave lower values than the average in terms of grain yield, whereas the other genotypes gave higher values than the general average. According to biplot graphical results, while locations 1 and 8 were closely related, locations 9, 2 and 7 were positively related to these environments. Although the location 7 is slightly different from the other 4 locations, these 5 locations can be seen as a mega environment. Genotypes G12, G2, G3 and G10 for this mega-environment showed the best performances. According to the results of grain yields obtained from 9 different locations, the location 5 was the most discriminating area while the location 1 was the least discriminating. Location 2 was the best representative location, while locations 4 and 7 were with the lowest representation capability. The locations that are both descriptive and representative are good test locations for the selection of adapted genotypes. Test environments, such as location 8, with low ability to represent are useful for selecting genotypes that perform well in specific regions if the target environments can be subdivided into sub-environments.

Key words: GGE biplot, genotype, mega-environment, descriptive location and representative.

1. Introduction

The most important criterion for crop yield per unit is the potential of genotypic genetic efficiency, and the effect of the environment on which these genotypes are cultivated is also very important. When genotypes are grown in different environmental conditions, there may be changes in their characteristics.

The most important criterion for high grain yield is the genotypic potential of plants and the effect of the environment in which the genotypes are grown is also very important. The performance of the genotypes in different environmental conditions allows revealing the characteristics of the genotypes better. The data obtained from the analysis of variance in experiments

conducted in different environments show that genotype x environment interaction is important as a result of different genotypes reacting to different environmental conditions. Several statistical parameters have been developed by some researchers such as [1] regression coefficient (b_i) and regression deviation squared averages (S^2_{di}) [2], equivalence value (Wi_2) [3], variance of stability [4] coefficient of variation (CV_i) and genotypic variance (S^2_i) [5] environmental effects (α_i), deviation from linear response (λ_i) and [6], the expression coefficient (R^2).

The introduction of genotypes at different locations and years of experimentation and the establishment of their stability provides a more detailed description of the yield and yield characteristics of genotypes. If there is no genotype environmental intervention in experiments conducted at different years and locations,

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genotypes can be considered as reliable in any environment. This is rarely seen except for some characteristics under simple genetic control. Quantitative characteristics such as grain yield are highly influenced by the environments in which the genotypes grow, which means that there is a high level of genotype environmental interactions. This indicates genotype environment interactions are important. In case of the importance of the genotype environmental interactions, performance ranking of genotypes causes changes in different environments. Genotypes with both high yield and high stability are revealed by different analysis methods developed by different researchers. The different areas in which the experiments are conducted are evaluated both in terms of discrimination and representation.

In recent years, multivariate techniques such as AMMI and GGE biplot have been widely used to reveal the genotype environmental interaction and the stability of genotypes. Ref. [7] reported that AMMI and GGE-biplot analyses are effective methods for describing the genotype environmental interaction. Low PCA and ASV genotypes are considered to be stable in the AMMI method. However, it appears that AMMI does not have the internal product feature that forms the basis of biplot analysis [8]. For this reason, GGE biplot analysis is used more often to determine the best genotypes effectively among test environments. It was created by the first two major components (PC1 and PC2) consisting of environment, genotype and GEI variations. Genotypes with high PC1 and small PC2 (near-zero) scores are considered as stable genotypes [9].

Many researchers have been using GGE biplot technique to identify the association between genotypes and environments, in order to determine the adaptation and/or magnitude of the G×E interaction, or to identify mega-environments and suitable wheat genotypes for specific regions [10, 11]. Multiple environment trials are used in order to identify and analyze the major factors that are responsible for

genotype adaptation and final selection [12, 13]. GEI is important for plant breeders and agronomists and the stability is mostly used to characterize a genotype, which specified a comparatively stable yield and is not affected by changing environmental conditions. In plant improvement activities and in many aspects of barley research, the analysis of GEI is of primary importance, as it is also for other crops [14, 15]. Grain yield, stability, and adaptability are highly influenced by environment [16]. Wheat genotypes must be tested in MEYTs (multi-environment yield trials) to determine grain yield, stability, GEI (genotype by environment interaction), adaptability, and to identify a potential candidate to release for commercial cultivation [17]. The effectiveness of AMMI procedure has been widely applied by many authors [18].

In our study, a total of 18 genotypes, including 9 triticale, 3 bread wheat, 3 durum wheat and 3 barley varieties, were tested at 3 different locations during 3 years. According to the results of variance analysis, the genotype environment interaction was found to be important for the number of heading days, the number of seeds per spike, the grain weight per spike, the thousand kernel weight, the test weight, the plant height, the number of maturing days. Average performance and stability levels of the genotypes were determined by GGE biplot analysis. Triticale genotypes were compared in terms of average performance and stability with bread wheat, durum wheat and barley varieties

2. Materials and Methods

2.1 Material

This study was carried out in Tekirdağ (40°59' N, 27°34' E, elev. 10 m), Edirne (41°38' N, 26°35' E, Elevation 32 m) and Silivri (41°4' N, 28°14' E, elevation 14 m) locations during 2004-2006 years. In the study, 9 triticale genotypes, 3 bread wheat varieties, 3 durum wheat varieties and 3 barley varieties were used as material (Table 1).

Table 1 List of genetic material used in the research.

Entry No.	Genotype/variety	
1	Katea I	Bread wheat
2	Pehlivan	Bread wheat
3	Flamura 85	Bread wheat
4	Tunca 79	Durum wheat
5	Epidur	Durum wheat
6	Gediz 75	Durum wheat
7	Balkan 96	2-rowed barley
8	Barberousse	6-rowed barley
9	Sladoran	2-rowed barley
10	Tacetinbey	Triticale
11	Presto 2000	Triticale
12	Tatlıcak 97	Triticale
13	Karma 2000	Triticale
14	Melez 2001	Triticale
15	Mikham 2002	Triticale
16	Ar/Snp6//Tarasca	Triticale
17	Rhino.1RS	Triticale
18	Lira/Buc	Triticale

2.2 Soil and Climate Characteristics of the Trial Areas

According to the results of the soil analysis, the pH of the trial soil was 7, 10, salty, phosphorus content (P_2O_5) was 8.42 kg da^{-1} , the potassium content (K_2O) was 55.80 kg da^{-1} and the organic matter content was 1.21% in Tekirdağ. In Edirne location, silty clay, pH 5.89, salted, available phosphorus content (P_2O_5) 21.98 kg da^{-1} , available potassium content (K_2O) 70.45 kg da^{-1} , and organic matter content is 1.16%. In the Silivri location, pH 7.68, unsalted phosphorus content (P_2O_5) was 1.45 kg da^{-1} , available potassium content (K_2O) was $290.67 \text{ kg da}^{-1}$ and organic matter content was 1.96%.

The climate data for the locations are given in Table 2. Tekirdağ location (493.4 mm) in the first year, Edirne location (481.7 mm and 532.7 mm) in the second and third showed higher total rainfall than other locations (Table 2). When the total precipitation of the plants in the grain filling periods (April, May, June) is examined, in the first year, in the Tekirdağ location (163.6 mm), Edirne location (169.4 mm), Silivri location (116.3 mm); in the second year, Tekirdağ location (103.9 mm), Edirne location (88.1

mm), Silivri location (132.4 mm); in the third year, Tekirdağ location (52.6 mm), Edirne location (118.3 mm) and Silivri location (95.6 mm) have been exposed to rainfall at varying rates (Table 2). Raining at varying levels in the grain filling periods caused significant differences in terms of the characteristics investigated between the years and locations. In Table 2, it is seen that the mean temperature values in locations are close to each other.

2.3 Establishment of Field Experiment

Field trials were conducted in randomized block design with 3 replicated at each location and year. Plants were sown in plots consisting of 6 rows with 5 m length and 17 cm length apart by sowing machine. Sowing density was 500 seeds per m^{-2} . A total of 140 kg ha^{-1} pure nitrogen was applied in the sowing, tillering and booting period. In addition, 40 kg ha^{-1} P_2O_5 was applied in the plantation and herbicide was applied against weeds. It is seen in Table 2 that the average temperature values of the locations are close to each other.

2.4 Statistical Analyses

The data obtained from the combined variance analysis were performed according to randomized blocks experimental design by using MSTAT version 3.00/EM computer package program. The significance of differences between the averages was determined by LSD ($p \leq 0.05$) multiple comparison test [19]. GGE biplot analysis and graphics was made by using the Genstat-14.0 statistical package program according to Refs. [17, 20].

The value of PC1 (1st major component) in GGE Biplot graph refers to the average of the genotypes in terms of the characters studied and it takes place in the horizontal plane of the graph. PC2 (2nd major component) value is the stability of character and is located in the vertical plane of the graph. As the value of PC2 approaches the mean value of zero, the stability value increases and the stability decreases as

Table 2 Climatic data of locations for three years.

Climatic data	Location	Year	November	December	January	February	March	April	May	June	Total
Precipitation, mm	Tekirdağ	1 st year	19.8	61.9	148.3	37.2	62.4	30.5	26.8	106.3	493.2
		2 nd year	27.7	45.5	62.7	74.9	20.9	12.7	78.2	13.0	335.6
		3 rd year	105.2	91.2	26.2	76.9	101.6	9.5	14.1	29.0	453.7
	Edirne	1 st year	8.7	49.4	61.2	9.4	34.1	14.6	59.6	95.2	332.2
		2 nd year	27.8	107.1	84.3	144.7	29.7	17.6	55.4	15.1	481.7
		3 rd year	90.2	89.3	56.4	55.7	122.8	24.0	36.5	57.8	532.7
	Silivri	1 st year	30.6	50.1	93.5	33.1	60.1	21.9	30.2	64.2	383.7
		2 nd year	21.0	49.2	58.4	61.7	20.5	15.3	87.1	30.0	343.2
		3 rd year	97.5	87.3	43.2	40.7	97.0	8.7	25.2	61.7	461.3
Mean											
Avg. Temperature, °C	Tekirdağ	1 st year	10.6	6.4	4.0	5.7	8.3	12.0	16.3	21.0	10.5
		2 nd year	11.4	7.7	6.1	4.2	7.6	12.2	16.9	20.5	10.8
		3 rd year	9.7	7.3	2.4	4.4	8.0	12.4	17.2	21.6	10.4
	Edirne	1 st year	9.1	3.5	2.2	4.9	8.6	13.2	17.1	22.1	10.1
		2 nd year	9.8	5.5	4.4	3.4	8.0	13.4	18.6	21.5	10.6
		3 rd year	8.4	4.7	0.3	3.3	8.5	14.0	18.4	22.4	10.0
	Silivri	1 st year	9.5	5.2	2.5	4.6	7.6	11.4	15.6	20.5	9.6
		2 nd year	10.1	6.2	4.8	3.5	6.9	12.1	16.5	19.2	9.9
		3 rd year	8.2	5.7	1.2	3.5	7.5	12.2	16.7	21.1	9.5

the value increases from zero [17]. It is expected that the GGE biplot graphs have at least 50% or more of the sum of the % PC1 and % PC2 values. The high value of the total value of the investigated characters indicates that the importance of the interaction is high [21].

3. Results and Discussion

In the study, the mean values and significance groups obtained in 9 triticale genotype, 3 bread wheat varieties, 3 durum wheat varieties and 3 barley varieties are given in Table 3.

The differences between locations and years due to the examined characteristics were statistically significant. The averages of genotypes changed between 227.07-211.89 days for the maturation period, 117.83-77.21 cm for plant height, 13.18-8.40 cm for spike length 54-85-33.19 unit for number of grain per spike, 2.31-1.74 g for grain weight per spike, 51.77-40.26 g for thousand kernel weight, 80.26-58.89 kg/hl for test weight and 5.91-4.61 tons for grain weight per hectare.

GGE biplot analysis results were given separately for the study conducted with 18 genotypes including

triticale, bread wheat, durum wheat and barley in 3 years and 3 different locations. In GGE biplot analysis, the average of the genotypes with high PC1 score is high. Genotypes with low PC2 scores have stable yields among the environments. According to the biplot graph showing the correlation between the genotypes and the characteristics examined over the year and location averages, the total variation is represented by 53.1% PC1 (Principal component 1) and 19.51% PC2.

Fig. 1 shows which genotypes have the best performance in terms of the relation between the trial triticale, barley, bread and durum wheat genotypes and the investigated characters, and there are 4 different groups in terms of the characters examined. The TKW (thousand kernel weight) in single group, HD (heading time) and TW (test weight) in the same group, MD (maturation time), GN (number of grains) per spike and GW (grain weight) per spike in a separate group, and PH (plant height), SL (spike length) and GY (grain yield) per hectare took place in a separate group (Fig. 1). [8], who interpreted the relationship between examined characters and environments, revealed that the characters in biplot

Table 3 Mean values and significance groups for the characters.

Mean values	Heading (days)	Maturing (days)	Plant height (cm)	Spike length (cm)	Grain number	Grain weight (g)	Thousand kernel wt. (g)	Test wt. (kg/hl)	Grain yield (t/ha)
Locations									
Tekirdağ	170.03 a*	219.67 c	104.42 a	9.70 a	45.74 a	2.24 a	47.25 a	75.06 a	5.64 a
Edirne	169.64 b	224.24 a	98.03 c	9.53 b	42.38 b	2.08 b	45.14 b	72.75 c	5.53 b
Silivri	169.48 b	221.60 b	101.70 b	9.73 a	42.48 b	2.00 c	45.14 b	73.54 b	4.76 c
Years									
1 st year	170.26 b	223.23 b	96.97 c	9.85 a	39.69 c	1.89 c	46.08 b	73.30 c	5.00 b
2 nd year	163.52 c	214.32 c	100.61 b	9.52 b	47.20 a	2.38 a	47.46 b	75.04 a	5.47 a
3 rd year	175.38 a	227.98 a	106.57 a	9.52 b	43.70 b	2.04 b	43.00 c	73.96 b	5.46 a
MSE	0.827	22.173	21.623	0.487	22.81	0.079	6.20	3.61	0.213
Genotypes									
12	171.89 abc	225.67 abc	120.49 a	11.23 c	44.22 cde	2.09 abc	40.93 fg	74.67 de	5.91 a
11	171.41 bc	225.37 a-d	116.80 ab	10.17 d	44.74 cd	2.18 ab	45.59 def	75.85 bc	5.89 a
18	167.11 cde	223.26 a-e	112.84 ab	10.19 d	45.85 cd	2.30 ab	47.96 bcd	74.52 de	5.76 a
17	165.56 de	224.00 a-e	114.89 ab	11.96 b	43.41 cde	2.20 ab	47.52 bcd	77.19 bc	5.67 ab
10	165.33 de	227.07 a	109.20 bc	11.56 bc	44.44 cde	2.31 a	51.77 a	75.74 bcd	5.65 ab
15	173.15 ab	226.82 ab	117.83 a	11.49 bc	46.11 cd	2.14 abc	40.26 g	74.52 de	5.65 ab
2	173.79 a	221.11 de	92.53 e	8.40 e	35.82 fg	1.89 de	49.48 abc	79.07 ab	5.58 abc
13	168.26 bcd	224.22 a-e	118.54 a	11.98 b	53.96 ab	2.35 a	43.44 ef	74.19 de	5.55 a-d
1	173.74 a	220.74 e	102.34 cd	9.84 d	45.81 cd	2.07 de	41.00 fg	78.89 ab	5.43 a-e
16	163.52 de	222.26 b-e	101.24 d	11.11 c	44.30 cde	2.13 abc	50.19 ab	75.00 d	5.36 a-e
3	172.59 ab	220.96 de	85.82 ef	8.42 e	39.11 efg	2.02 bcd	47.59 bcd	80.26 a	5.24 a-e
7	164.19 de	212.74 f	84.34 fg	7.75 fg	34.92 gh	1.89 de	47.67 bcd	63.26 f	5.17 a-e
8	162.74 e	211.96 fg	84.89 fg	6.88 h	38.92 efg	1.91 cde	41.70 fg	62.59 fg	5.02 a-e
14	172.19 abc	225.22 a-e	120.02 a	13.18 a	54.85 a	2.33 a	42.11 fg	72.41 e	5.00 a-e
4	175.56 a	224.44 a-e	88.19 ef	8.11 ef	44.78 cd	2.07 de	45.67 de	78.19 bc	4.77 b-e
6	174.56 a	221.82 cde	85.56 ef	7.100 gh	48.55 bc	2.18 ab	46.78 cde	79.41 ab	4.67 cde
9	163.67 de	211.89 g	77.21 g	6.93 h	33.19 h	1.74 e	47.56 bcd	58.89 g	4.65 de
5	175.70 a	223.56 a-e	92.16 e	7.44 fgh	40.59 def	2.04 bcd	47.96 bcd	79.30 ab	4.61 e
LSD ($p \leq 0.05$)	0.7072	5.5562	0.2894	3.1115	4.615	0.714	2.4237	0.91717	5.417
CV (%)	3.6057	6.2804	6.7733	3.3397	1.024	3.744	1.6093	8.49899	1.570

* Within columns, means with the same letter are not significantly different ($p \leq 0.05$).

diagonal have the best or worst performance in the surrounding circles and there is a strong correlation or relationship between the characters in the same sector. At the same time, it is reported that genotypes that have localized in the same sector have similar character potency in terms of the characteristics studied (discriminative potential), in other words there is a similarity between these locations. When the performance of the genotypes is based on the characteristics, genotype 2 and genotype 3 for thousand kernel weights, genotype 1 for duration of

heading and test weight, the maturation period, the number of grain per spike and genotype 14 and 15 for the grain weight characters, G13 for the plant height, spike length and hectare yield characteristics show the best characters (Fig. 2).

In the analysis of the demonstration of the relationship between the characteristics examined and the locations, the total variation was determined as 70.89%, while 39.37% of this variation was represented or explained by PC1 (Principal component 1) and 31.55% PC2.

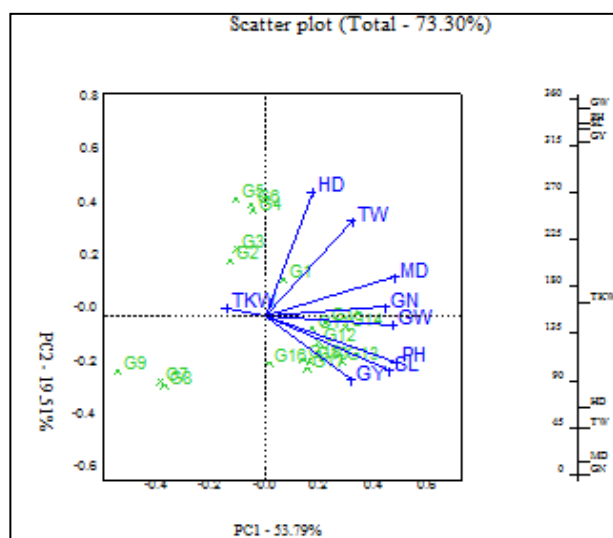


Fig. 1 Biplot graph showing the correlation between genotypes and characters.

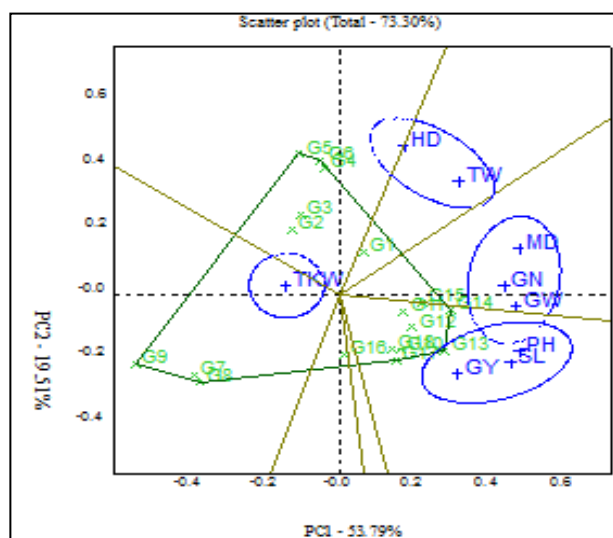


Fig. 2 Biplot graph showing the relationship between genotypes and characters.

Biplot analysis shows that the high genotypic effect in the appearance of the characters is with high PC1 value. However, the high PC2 value indicates that genotypic effects as well as genotypic environmental effects are important, i.e. genotype \times environment interaction is important. The PC2 values between the studied environments and the character are close to the PC1 value, indicating the significant genotype \times environmental interaction effect in the formation of the characters.

When the biplot graph (Fig. 3) showing the relationship between locations and the character is

examined, there are 3 different groups in terms of characters. While locations 4 and 7 on the same axis of the locations have similar characters, location 4 obtained lower values, and in location 7 lower stability values were observed. Compared with locations 7 and 9 on the same axis, low stability values were obtained at both locations. The number 9 location has been very low. Locations 4, 5, 1 and 9 on the same axis on the biplot graph gave the highest values among the locations, whereas location 1 gave more stable values. Locations from 4, 5, 1 and 9 on the same axis on the biplot graph gave the highest values while location 1 gave more stable values. When the characters studied are considered, heading time, maturing time, plant height, grain yield, number of seeds in the plant and spike length characters formed a similar group, and the number 8 location was selected as the most suitable for these characters.

Thousand weight and spike weight characters were collected in another group with the previous close group. In terms of these characters, location 6 gives the most suitable values. The hectoliter weight alone constituted a separate group and the location 5 for this character was determined as being the most appropriate (Fig. 3).

According to biplot graph showing the relation between locations and genotypes in terms of grain

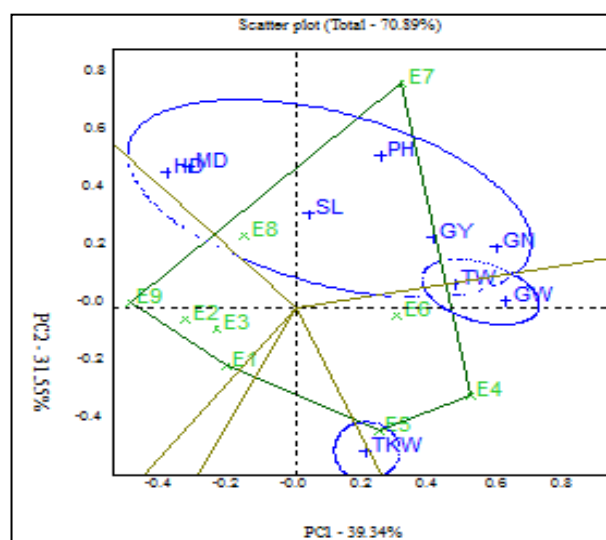


Fig. 3 Biplot graph showing the relationship between locations and the characters.

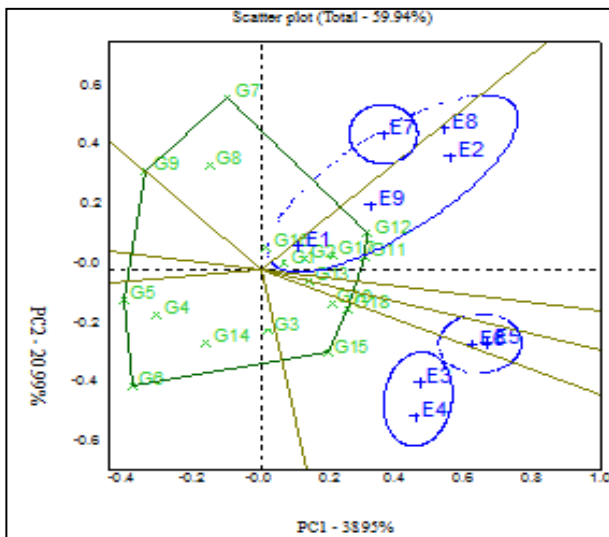


Fig. 4 Biplot showing the relationship between location and genotypes for grain yield.

yield, 59.94% of the total variation is revealed (PC1% 38.95% and PC2% 20.99%) (Fig. 4). In the examination of which genotype and which environment has the best performance in terms of grain yield, genotypes 6, 5, 4, 14, 9, 8 and 7 had lower grain yields than the average, while the other genotypes had higher values than the general average. According to biplot graph, locations 1 and 8 are closely related, while locations 9, 2 and 7 are positively related to these locations. Although the number 7 location is slightly different from the other 4 locations, these 5 locations are seen as mega environments. For this environment, genotypes 12, 2, 3, 7 and 10 showed the best performance.

Locations 6 and 5 have a very close positive relationship and they form another environment. Genotype 18 has the best feature for this environment. Locations 3 and 4, which are closely related positively, constitute the third environment. For this environment, genotype 15 shows the best yield. The closest location to the biplot origin is the area where the most stable values are obtained from the location 1. Locations 8, 2 and 5 gave low values of stability because they are quite distant from the biplot origin. These locations are highly discriminating. These locations can provide beneficial results in the selection of genotypes for

specific regions and in the elimination of low-stability genotypes.

The place of the test locations next to each other on the biplot shows that these locations have similar characteristics when the genotypes are characterized in terms of grain yield. This demonstrates that it is enough to carry out experiments at only one locality from these locations, so that the breeding programs can be carried out with less labor and cost. According to the results obtained, it seems to be sufficient to carry out the trial of 3 different locations instead of 9 locations for grain yield. These results show that the genotypes 15 and 12 are higher than the average yield but the genotype 12 is better than the genotype 15 in terms of yield and stability. Among genotypes 7 and 12, genotype 12 is above general average and more stable than genotype 7. From genotypes 15 and 6, genotype 6 is below the general average and stability is low, while number 15 is above the general average and high stability. In experiment, genotype 16 is the most stable genotype in all the experiments, while the average grain yield is close to the general average, which reduces the importance of this genotype. Genotypes 3, 1, 2 and 6, which are located on the general average and which are closest to the center, have been identified as the most stable genotype for all regions and these genotypes should be considered as priority in the selection studies to be made for future years (Fig. 4).

The discriminatory and representativeness of the trial environments from the grain yield results obtained at 9 different locations where the yield experiments of the triticale genotypes are carried out are given in Fig. 5. The concentric circles on the biplot help to visualize the length of the vectors. This relates to the standard deviation in the relevant environment and is an indication of the distinctive features of the environment. According to the obtained data, the location number 5 is the most discriminating whereas the location number 1 shows the least discriminating characteristic. The average environment axis

(represented by the small circle at the end of the arrow) has the average coordinates of all test environments. Environmental coordination passes through the environment average and biplot origin. A test location with a smaller environmental angle than the average environmental coordinate has the ability to represent more than other test locations. Location 2 is the most representative environment, while locations 4 and 7 have the lowest representation. Test locations, both discriminatory and representative, are good test environments in the selection of genetically adapted genetics (such as environment 1). Test environments with low representation capabilities, such as location 8, are useful in selecting genotypes that are well-adapted to particular areas, especially if the target environments can be subdivided into sub-environments. Locations with high discriminability, such as environment 8, are useful for screening unstable genotypes, but only in a mega medium with low representativeness.

In the analysis of the stability of genotypes in terms of grain yield for GGE-biplot analysis, the total variation was 59.94%, which was represented or explained by 38.1% PC1 (Principal component 1) and 20.99% PC2.

In Fig. 6, the G7, G8, G9, G4, G5 and G6 genotypes on the left of the mid-cut line according to the mean environment coordinate (AEC) method have genotypes with lower average grain yields whereas the other genotypes have higher average values.

G12 and G11 are the genotypes with the highest grain yield (highest PC1 value) according to the location average and at the same time, the line that cuts the origin horizontally shows that the vectorial angles are low (there is no longer the distance that the line intersects horizontally). G9, G5, and G6 genotypes with grain yield below the average of locations have shown characteristics that are appropriate for specific areas (high rainfall areas, or genotypes suitable for low rainfall areas) due to the large distance of the line horizontally intersecting the origin.

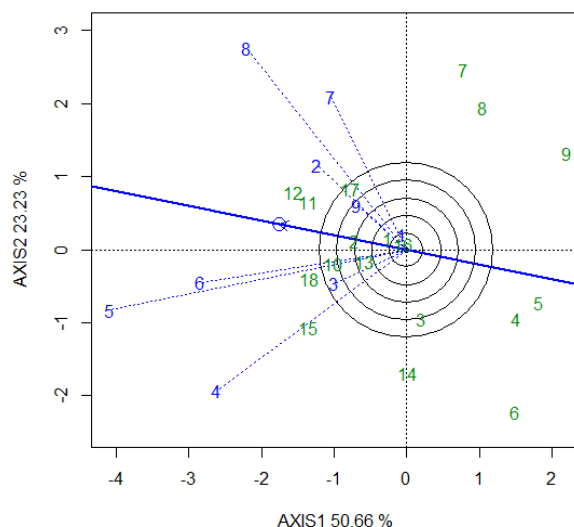


Fig. 5 Differentiation and representativeness of experiment sites in terms of grain yield.

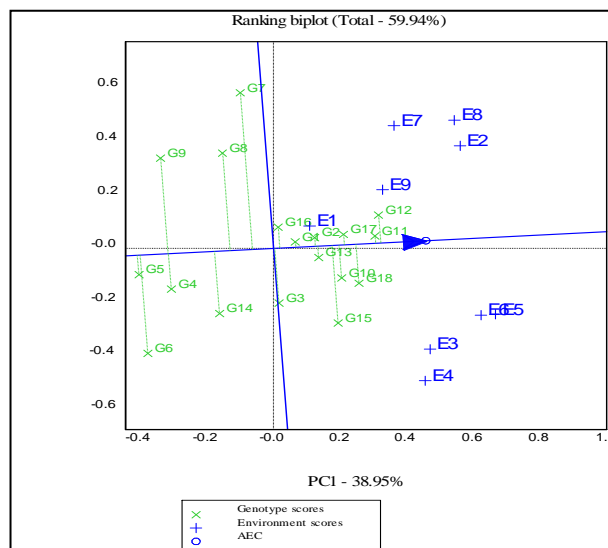


Fig. 6 Biplot graph showing stability of genotypes in terms of grain yield.

The G4 and G5 genotypes are located near the left of the line that cuts the origin to the left and the line that horizontally crosses were the low values in terms of stability and grain yield among the genotypes. The G16 and G1, G13 and G2 genotypes, showing the biplot to the right of the vertical origin, above the horizontal line and nearest to the origin, showed good stability to all locations. The G3 genotype, which is very close to the general population but below it, is good in terms of stability but low in importance due to its value lower than average. The biplot graph

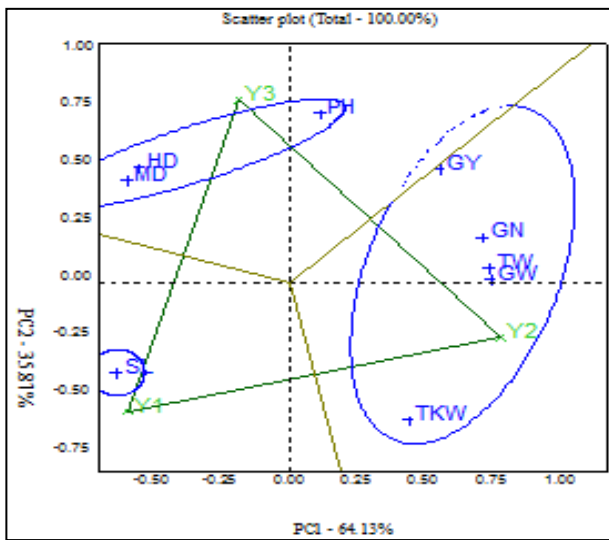


Fig. 7 Biplot graph showing the relationship between years and characters.

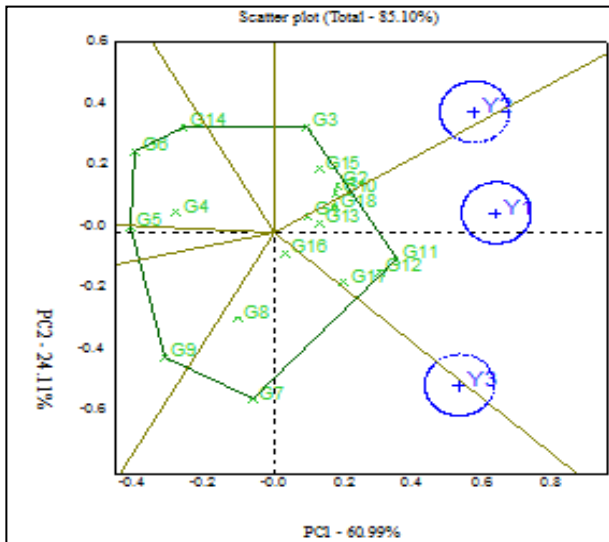


Fig. 8 Biplot graph showing the relationship between years and genotypes for grain yield.

between the years and the characteristics examined in the yield values of the genotypes taken for the experiment show different features for each year. In the first year when lower data were obtained in the trial, better spike values were obtained, and below the general average and near average values were obtained in the 3rd year. In the third year, the number of days to maturity and the plant height were obtained from the characteristics examined (Fig. 7).

In the second year when the values above the general average were weighed, for grain yield, number

of grain per spike, thousand kernel weight, grain weight per spike and test weight were obtained with better results. The difference between the characters analyzed according to years suggests that the ecological differences in years caused significant changes in characters. If the differences between years can be explained in detail, selection criteria should be arranged according to these changes.

When the changes in genotypes according to years in terms of grain yield are examined, the first and second year property values are closer, while there is a significant difference between the second and third year. There is also a difference between the first year and the third year (Fig. 8). Genotype 12 and 13 were the best genotypes in the first year of experiment, whereas in the second trial, genotypes 10, 2 and 18 were the best genotypes among them. In the 3rd trial, the genotypes showed the most favorable value in terms of yield. Genotypes 13 and 2 were the most stable genotypes in all years, giving the genotype number 16 which is closest to the biplot origin and is valued above the general average.

4. Conclusion

When the correlations between genotypes of triticale, barley, bread, and durum wheat genotypes are examined, G2 and G3 for thousand kernel weight, G1 for heading time and test weight, G14 and G15 for the number of grains per spike, number of spikelet per spike and grain weight per spike, and G13 for plant height showed better performances. G16 and G1 are genotypes that give the most stable values for all the closest points to the biplot origin. G1 and G3 for a thousand kernel weight, G1 for the heading time and test weight, G14 and G15 for the grain numbers per spike, G13 for spike length showed the most superior features. G16 and G1, which are closest to the biplot origin, are the genotypes showing the highest stability in terms of the observed characters.

When the biplot graph showing the relation between the features and the locations is examined, it

is seen that there are 3 different groups according to the characters. Environments 4 and 7 on the same axis exhibit similar properties, while higher values are obtained in the environment 4 and the value of stability in the environment 7 is lower. When 7 and 9 environments on the same axis were compared, low stability values were obtained in both areas, and location number 9 gave very low values. While the highest values were obtained from the environment 5, 1 and 9 on the same axis in the biplot graphic, the most stable values are obtained from environment 1. When the characters were evaluated, the heading time, maturation time, plant height, grain yield, number of grain per spike and spike length were collected in the same group. The environment 8 is the most appropriate for these characters. The heading time, the maturation time, and the number of grains per spike the biplot has been used, plant height, grain yield, number of grain per spike and spike length were collected in the same group. The environment 8 is the most appropriate for these characters. Thousand kernel weight and spike weight are collected in another group with the previous close group. Environment 6 gave the best values for these characters. Test weight constituted a separate group and environment 5 gave the best values for this character.

Biplot graph of the relationship between locations and genotypes shows which genotype has the best performance in which environment. Genotypes 6, 5, 4, 14, 9, 8 and 7 had lower grain yields than the average, whereas the other genotypes had higher values than the general average. According to the biplot graph, environments 1 and 8 are closely related, while locations 9, 2 and 7 are positively related to this environment. Although the location 7 differs slightly from the other 4, these 5 environments are located in a mega environment. Genotypes 12, 2, 3 and 10 for this mega-environment have shown the best performance.

According to the grain yield results obtained in the 9 different regions where the yield experiments are carried out, the number 5 environment is the most

discriminating, whereas the environment 1 is the least discriminating. According to the results, environment 2 is the most representative environment, while environments 4 and 7 are the lowest. The test circles, both discriminatory and representative, are good test environments for the selection of adapted genotypes. Test environments with low ability to represent, such as environment number 8, are useful in selecting genotypes customized to specific regions, if the target environments can be divided into sub-environments.

As a summary of the results obtained, the lowest values for stability were obtained in barley and durum wheat genotypes. Triticale genotypes and bread wheat genotypes in the 9 different locations show the highest adaptability to all the locations, while wheat genotypes of bread wheat genotypes followed by triticale. The lowest values were in barley and durum wheat genotypes.

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