

PROFICIENCY OF BILOT METHODS (AMMI AND GGE) IN THE APPRAISAL OF TRITICALE GENOTYPES IN MULTIPLE ENVIRONMENTS

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Abstract. The AMMI (additive main effect and multiplicative interaction) and GGE (genotype, genotype x environment) biplot analyses were used to evaluate and identify stability and yield of Triticale genotypes at three different locations throughout two years (2014-15-2015-16). The AMMI analysis of variance showed significant genotype, environment and GE interaction and indicated 1.31, 98.40 and 0.28% of total variation, respectively. The GGE bi-plot analysis indicated 78.19% of the total variation (PC1 (principle component) 50.01%, and PC2 26.08%). This study has been useful to discriminate genotypes with superior and stable yield evaluated by the AMMI analysis and yield stability index incorporating the AMMI stability value and yield capacity in a single non-parametric index. The AMMI analysis indicated that G4, G8 (candidate) and G6 were found to be quite promising genotypes. In the GGE biplot analysis genotypes were investigated in two mega-environments, and the first mega-environment covered E3, E5 and E6, and the second mega-environment covered E1, E2 and E4. The genotypes G6, G8, G9 and G11 were the winning genotypes in ME (mega-environment) I, G3, G4 and G12 and in ME II. The GGE and AMMI biplot approaches let us to describe the best genotypes, and G8 to be stable and high yielding for both ME, G6 only for ME I, G4 only for ME II and can be recommended to release as a cultivar.

Keywords: *stability, interaction, yield, multi, approach*

Introduction

In order to ensure an adequate and balanced diet of the growing world population, food production should be increased in parallel. This is possible through the development and application of new cultivation techniques and also by the development of more efficient and high quality plant species. For this purpose, Triticale (*x Triticosecale Wittmack*), was developed as a new species, a hybrid of wheat and rye, used as an alternative cereal crop for growing in marginal areas (Kendal and Sayar, 2016). This new species is known that it is tolerant to diseases, pests, dry conditions, acid and problematic soils and it was determined that it could replace cereal forage crops. Triticale is mostly used in animal feeding and it is also evaluated as grain, roughage, silage and straw. The feed value of triticale is equivalent to corn, wheat, barley, rye and sorghum or better than them, while in feed rations, it can be preferred instead of corn, wheat, barley, rye and oats. Triticale is used primarily as animal feed,

and in recent years it has also been used in human food and ethanol production (Oral, 2018).

Triticale cultivation in the world has shown an increase of over 40% in the last a decade years. The area of cultivation of triticale is 3.8 million ha, and the production is around 14.7 million tons in the world, and this rate is increasing day by day (Anonymus 2; Ayalew et al., 2018). In Turkey, statistical data related to triticale production have started to be given after 2004, and in 2016, about 38.000 ha area was planted and about 125.000 tons of product was obtained from this area. However, in our country, Triticale is the highest yield in cereals and grain yields approximately 3360 kg per hectare (Anonymous 1; Kizilgeci, 2019). Therefore, triticale is gaining more and more attention both in the world and in our country.

The exploiting of heredity instability is one of the very significant issues in terms of breeding strategies and this situation can only be explained by phenotypically phrase (Rad et al., 2013). In order to explain the phenotypic variations, it is highly dependent on the effect of the environments. Explaining this diversity is upwards sophisticated by the fact that all genotypes don't react in the same way as change in circles and the two environments do not have exactly the same conditions (Neisse et al., 2018). If the performance of genotypes changes in different location, then the interaction of the genotype location is an important factor in plant breeding strategies. Therefore, analysis of any variance combined can measure GEI and identify main effectiveness, however it is not enough to declare the GEI effectiveness. A convenient analytic pattern like the additive main effects and multiplicative interaction (AMMI) can cure both the additive main effect and multiplicative interaction constituent utilize the ANOVA (analysis of variance) and IPCA (Interaction Principal Components), respectively (Kilic, 2014; Mohammadi et al., 2018). The GGE biplot exploits the PCA approach to investigate the multi environment data and allow the visual presentation of the relationship among genotypes, environments and interaction as well as.

The aim of this study were to (i) analyses the effect of GEI on grain yield of 12 triticale genotypes by two new biplot models (AMMI and GGE) (ii) identifying high yielding and stable triticale genotype(s) across locations and (iii) to detect appropriate genotype(s) for every location or environment.

Material and Methods

The ten spring triticale advanced lines and two local check were evaluated in three locations across two years (2014-2015 and 2015-2016 growing seasons). The information of genotypes showed in *Table 1*. The trials were planted following a randomized complete block design with four replications at each location. The information about test location is given in *Table 2*. Each parcel was set in a six row plot of 6 meter length and 1.2 m diameter with plant spacing of 20 cm. Sowing of trials were done in autumn and sowing density was used 500 seeds in per m⁻². The fertilization of planting time, 60 kg N ha⁻¹ and 60 kg P ha⁻¹ were used, and 60 kg N ha⁻¹ was used to each plots at tillering time for all plots. The grain yield was recorded from each plot after harvesting of the materials and measured extrapolated to ton/ha.

The described growing seasons 2014-2015

The rainfall was the same with long term in all location and it was enough for germination of plant after sowing time in October, the triticale had good weather in

winter days. Seasonal conditions were favorable for triticale cultivation in the development period in March and April in all location. Therefore, the expected high yield was obtained in all location of 2014-15 growing season. All location had good growing season, but in Ceylanpınar location the rainfall is very low than other location and it was partially heat stress during after heading time, in Adiyaman location during the spring period there was partially heat stress, In Diyarbakir location, conditions were more favorable than other locations.

Table 1. The code, name/pedigree of triticale genotypes

Code	Name of cultivar and pedigree of lines	Orijin
G1	LIRON_2/5/DIS B5/3/SPHD/PVN/YOGUI_6/4/ CTSS04Y00163S-102Y-06M-06Y-2M-3Y-0M-0SD-0SD-0SD	CIMMYT
G2	PRESTO//2*TESMO_1/MUSX 603/4/ARDI_1/... CTSS03Y00091T-050TOPY-5M-2Y-06Y-5M-1Y-0M-0SD-0SD-0SD	CIMMYT
G3	LIRON_2/5/DIS B5/3/SPHD/PVN/YOGUI_6/4/ CTSS03Y00033T-A-62M-1Y-06Y-2M-4Y-0M-0SD-0SD-0SD	CIMMYT
G4	TURACO/CENT.SARDEV/7/LIRON_2/5/DIS B5/3/... CTSS02B00186T-8Y-3M-3Y-4M-1Y-0M-0SD-0SD-0SD	CIMMYT
G5	Tacettinbey(check) -----Cukurova University	TURKEY
G6	DRIRA/2*CMH77A.1165/8/NIMIR_3/ERIZO_12/5/... CTSS02B0028T-6Y-3M-3Y-4M-2Y-0M-0SD-0SD-0SD	CIMMYT
G7	LIRON_2/5/DIS B5/3/SPHD/PVN/YOGUI_6/4/ CTSS02B00413S-22Y-2M-3Y-1M-2Y-0M-0SD-0SD-0SD	CIMMYT
G8	HX87-244/HX87-255/5/PRESTO//2*TESMO_1/... CTSS03SH00028S-25Y-2M-4Y-3M-1Y-0M-0SD-0SD-0SD	CIMMYT
G9	HX87-244/HX87-255/7/LIRON_2/5/DIS B5/3/SPHD/... CTSS03SH00030S-17Y-3M-4Y-3M-1Y-0M-0SD-0SD-SD	CIMMYT
G10	Presto(check) Transitional Zone Agricultural Research Institute	TURKEY
G11	LIRON_2/5/DIS B5/3/SPHD/PVN/YOGUI_6/4/... CTSS03Y00036T-A-1M-2Y-06Y-2M-4Y-0M-0SD-0SD-0SD	CIMMYT
G12	LIRON_2/5/DIS B5/3/SPHD/PVN/YOGUI_6/4/... CTSS03Y00036T-A-1M-4Y-06Y-4M-1Y-0M-0SD-0SD-0SD	CIMMYT

Table 2. Years, sites, codes and coordinate status of environments

Years	Code of Sites	Sites	Altitude (m)	Latitude	Longitude	Averag. of pers. (mm)
2014-2015	E1	Diyarbakır	612	37° 55' N	40° 14' E	584.2
	E2	Adiyaman	669	37° 76' N	38° 27' E	540.3
	E3	Ceylanpınar	366	36° 84' N	40° 05' E	306.0
2015-2016	E4	Diyarbakır	612	37° 55' N	40° 14' E	417.2
	E5	Adiyaman	669	37° 76' N	38° 27' E	402.4
	E6	Ceylanpınar	366	36° 84' N	40° 05' E	217.0

The described growing seasons 2015-2016

The rainfall of second season was late in planting time and it was low, in development of plant time, when we compare it with long term rainfall of locations. On the other hand; the temperature was high. Genotypes were exposed to drought in Ceylanpınar location. In the Adiyaman location, it was partially exposed to temperature stress. In Diyarbakır, heat stress was effective after heading period in April. Therefore, the grain yield of 2014-2015 season was suitable than 2015-16 growing season in all locations. The conditions of Ceylanpınar location is usually hard than other location, because the total of rainfall of seasons usually is low (Table 2).

Statistical analysis (AMMI and GGE)

The AMMI analysis was carried out using the adjusted mean values of grain yield to detect the relation among genotypes, locations and GEI over model designated by Zobel et al. (1988). The adopted method uses PCA to decompose the multiplicative effects of GEI into a number of IPCA. The two models (AMMI and GGE) analysis were carried out by Genstat software (version 12). The Additive mean effect and multiplicative interaction model analysis is based on the following formula; $Y_{ger} = \mu + \alpha_g + \beta_e + \sum_n \lambda_n \gamma_{gn} \delta_{en} + \epsilon_{ger} + \rho_{ge}$; where, Y_{ger} is the monitored grain yield of genotype (g) in environment (e) for replication (r); Additive parameters: μ is the grand mean; α_g is the deviation of genotype g from the grand mean, β_e is the deviation of the environment e; Multiplicative parameters: λ_n is the singular value for IPCA, γ_{gn} is the genotype eigenvector for axis n, and δ_{en} is the environment eigenvector; ϵ_{ger} is error term and ρ_{ge} is PCA residual.

AMMI Stability Value (ASV) is the space from the origin to the coordinate point in a two dimensional plot of to IPCA scores (Purchase, 1997). Because the IPCA1 score contributes to the sum of squares of GEI, a weighted value is needed. This weighted value was calculated for each genotype and each environment according to the relative contribution of IPCA1 to IPCA2 to the interaction sum of squares as follows:

$$ASV = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA1} + SS_{IPCA2}} (IPCA1Score)^2 \right] + (IPCA2Score)^2} \quad (Eq.1)$$

Where, SS_{IPCA1} / SS_{IPCA2} is the weight given to the IPCA1-value by dividing the IPCA1 sum of squares by the IPCA2 sum of squares (Purchase, 1997).

Genotypic stability index (GSI) incorporate mean and stability index in a single criteria and calculated as: $GSI = RASV + RY$ where, RASV is the rank of ASV and RY is the rank of mean yield of genotypes across environments. This index considered the rank of AMMI stability value to rank genotypes based on grain yield across environments.

On the other hand; data were graphically analyzed to interpret GEI to identify stable and adaptive genotypes using the GGE biplot described by Yan and Tinker (2006). The GGE biplot methodology (Yan et al., 2000) was applied for analysis of GE interaction of grain yield. The GGE biplot model is based on the following formula:

$$E(Y_{ij}) = \mu + \beta_j + K \sum_k \delta_k \gamma_{ik} \eta_{jk} \quad (Eq.2)$$

where $E(Y_{ij})$ is the expectation value of genotype i in environment j ; μ is the grand mean; β_j is the environment effect; K stand for the number of principal the environment effect; K stand for the number of principal components (PC) needed to provide an adequate explanation of G + GE; δ_k is singular value for the kth PC; and stands for the $\delta_k \gamma_{ik} \eta_{jk}$ ith genotype score and stands for the jth environmental score for the kth PC. Singular value η_{jk} partitioning is achieved by providing a scaling factor f to obtain alternative genotype ($c_{ik} = \delta_k^f$ and environment scores. The symmetric scaling ($f = 0.5$) was used in γ_{ik} ($d_{jk} = \delta_k^{1-f} \eta_{jk}$) visualizing which-wins-where pattern of MET data, due to its compliance with most of the features related to other benchmarking methods (Yan, 2002).

Result

The AMMI analysis

The variance of AMMI analysis showed that genotype, environment, GEI and IPCA (Interaction principle component analysis) had significant ($p < 0.01$) effect on triticale grain yield of 12 genotypes tested in six environments (*Table 3*). The environment main effect accounted for 98.40% of total variation, compared with 1.31% for genotype and 0.28% for GE interaction effects in the analysis of combined variance (*Table 3*). The quantity of genotypic effect was about two times greater than the GEI effect, which indicates different possible presence of MEs in the METs data. The major differences between the circles influenced the average of squares and caused the grain yield of each environment to change. The multiplicative variance of the treatment sum of squares due to interaction was partitioned into the fourth interaction principal components and the only one of them significant effect. The first PCs accounted for 56.75%, the second for 17.56%, the third for 17.11%, and the fourth only 8.55% of G+GE total variation for triticale data. Except the first IPCA-I, the remaining three IPC axes were non-significant and contributed 43.22% of the GEI (*Table 3*).

Table 3. *The analysis of variance for grain yield using AMMI model*

Source	df	SS	MS	F	G+E+GE SS explained (%)
Total	287.00	1091.60	3.80	-	-
Treatments	71.00	1024.40	14.43	55.80	-
Genotypes	11.00	28.40	2.58	9.98**	1.31
Environments	5.00	965.60	193.11	216.61**	98.40
Block	18.00	16.00	0.89	3.45	-
Interactions	55.00	30.40	0.55	2.14**	0.28
IPCA 1	15.00	19.00	1.26	4.89**	56.75
IPCA 2	13.00	5.00	0.39	1.50ns	17.56
IPCA 3	11.00	4.20	0.38	1.46ns	17.11
IPCA 4	9.00	1.80	0.19	0.75ns	8.55
Residuals	7.00	0.50	0.07	0.27	-
Error	198.00	51.20	0.26	-	-

df - degrees of freedom; SS - sum of squares; MS - mean square. **, $p < 0.01$; G - genotypes; E - environments

In the AMMI model, the figure interpret by two direction and x-axis represents the genotypes and environment main effect and y-axis represents the effects of interaction (*Fig. 1*). The genotypes and environment indicated much more variability in both main effect and interaction. The environment located above the y-axis mean that they are desirable and high-efficient, whereas the environments, which are located under of y-axis mean that they are unfavorable and low-yielding (Kendal and Tekdal, 2016). According to these definitions, in the AMMI (*Fig. 1*) indicated that grain yield of the first year (7.244 t/ha) is higher than in the second year (3.979 t/ha) in all locations (*Fig. 1 and Table 4*). When we evaluate the locations based on grain yield average, all locations were located above average (y axis) in the first crop season (2014-15), while all location were located under average (y axis) in the second crop season (2015-16). This implies that grain yield of first year in all locations were higher than the second year. On the other hand, when we evaluate the environments independently, the highest yield average is obtained from E1 and the lowest yield average is obtained from E6.

According to the location averages, Diyarbakir location (6.529 t/ha) is found to be more efficient than the other two locations in both years (Fig. 1 and Table 5). The AMMI (Fig. 1) also shows the stability of genotype based on mean grain yield of multiple environments. The genotypes located near the x-axis and on the right of the y-axis mean that they are stable and high-efficient, whereas the genotypes, which are located far from x-axis and left side of y-axis mean that they are unstable and low-yielding (Crossa et al., 1990). Accordingly, G7, G4 and G8 placement of near x axis and on the right of the y-axis, therefore it mean that these genotypes are quite stable and yielding. Moreover; G1, G3, G10 (check) and placement of far from x axis, so these genotypes are unstable across environments. The AMMI (Fig. 1) biplot showed that G4, G6 and G8 are quite yielding, while both of check used in the study (G5 and G10) are poorest genotypes across test environments (Table 4).

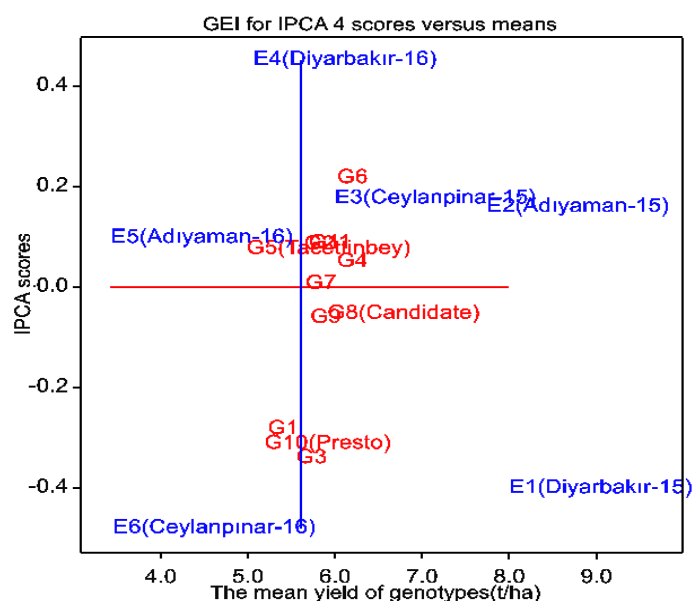


Figure 1. The AMMI shows the stability of genotype based on mean grain yield of multiple environments. The genotypes located near the x-axis and on the right of the y-axis mean that they are stable and high-efficient, whereas the genotypes, which are located far from x-axis and left side of y-axis mean that they are unstable and low-yielding. G1-G12 is the codes for the triticale disomic addition lines and G5 and G10 used as the control, respectively. E1- E3 are environment codes for 2014-15, E4-E6 for 2015-16 growing season

Table 4. The genotype means and IPCA scores based on six environments

Genotypes	Gen mean	IPCAg[1]	IPCAg[2]	IPCAg[3]	IPCAg[4]
G1	5.228	0.31884	0.21680	-0.37392	-0.28371
G2	5.644	0.35121	-0.47205	0.00288	0.08386
G3	5.553	-0.62687	-0.41001	0.10880	-0.34148
G4	6.022	-1.08531	0.33717	0.08051	0.04918
G5	4.984	0.34995	0.37082	0.64101	0.07483
G6	6.022	0.29643	0.34783	-0.12295	0.21614
G7	5.660	0.16724	-0.40324	0.39346	0.00543
G8	5.911	0.05858	-0.04726	-0.23521	-0.05409
G9	5.714	-0.03673	0.29583	-0.09229	-0.06228
G10	5.188	0.32915	0.08225	0.11694	-0.31300
G11	5.699	0.04626	-0.12553	-0.44469	0.08626
G12	5.713	-0.16875	-0.19261	-0.07455	0.53887

Table 5. AMMI-estimates per environment(yield(t/ha) across years and locations)

Geno- types	Diyarbakır				Adıyaman				Ceylanpınar			
	(E1) 2014-15		(E4) 2015-16		(E2) 2014-15		(E5) 2015-16		(E3) 2014-15		(E6) 2015-16	
	Yield	Rank	Yield	Rank	Yield	Rank	Yield	Rank	Yield	Rank	Yield	Rank
G1	7.324	G4	4.364	G12	7.348	G4	3.418	G6	5.485	G6	3.429	G6
G2	7.927	G3	5.337	G4	7.196	G6	3.797	G8	6.044	G7	3.563	G8
G3	8.766	G8	5.165	G8	7.776	G9	2.911	G11	5.572	G4	3.127	G9
G4	9.105	G7	5.471	G2	9.178	G8	2.978	G2	6.127	G8	3.272	G2
G5	6.991	G12	4.261	G6	6.910	G12	2.601	G12	6.105	G5	3.034	G7
G6	7.914	G9	5.333	G7	8.246	G11	4.072	G9	6.581	G9	3.986	G11
G7	8.147	G11	5.332	G11	7.256	G3	3.434	G7	6.277	G2	3.515	G1
G8	8.258	G2	5.339	G3	8.033	G1	3.910	G1	6.122	G12	3.806	G10
G9	8.008	G6	4.976	G9	8.097	G7	3.498	G10	6.093	G10	3.613	G4
G10	7.419	G10	4.414	G10	7.041	G2	3.117	G4	5.762	G11	3.376	G12
G11	8.003	G1	5.220	G1	7.867	G10	3.841	G3	5.752	G3	3.511	G3
G12	8.089	G5	5.529	G5	7.945	G5	3.543	G5	6.007	G1	3.165	G5
Mean	7.996		5.062		7.741		3.427		5.994		3.450	
Mean	6.529				5.584				4.722			
Mean	7.244						3.979					

The GGE Biplot analysis

The mean grain yield across two years (2014-15-2015-2016) in three location (Diyarbakır, Adıyaman, Ceylanpınar) of 12 triticale genotypes were showed in *Table 5*. These table data was used to generated a GGE biplot (*Fig. 2-Fig. 6*), although the genotype is compatible with biplot, it represents only 78.19% of the variation. In the present study, the first two IPCAS were used to portray genotype by environment interaction and placement on the (*Fig. 2-Fig. 6*). The GGE biplot provides good explanation of the pattern, regarding first two IPCs.

The relationships among and between genotypes and environments visualize in *Fig. 2*. A biplot such a graph to be interpreted bi-directionally has the following comments (Yan et al., 2000; Yan and Tinker, 2006). 1) The cosine of the angle between the vectors of the two environments approaches the Pearson correlation between them. Therefore, an angle of less than 90° shows a positive correlation, an angle greater than 90° shows a negative correlation and an angle of 90° shows zero correlation. 2) If the vector of a environment is longer than other vectors, the variation of this environment on genotypes is higher than the other environments, if the vector length of any environment is very short than other traits vector then the variation of this environment is very low. 3) The angle between the vector of any genotype and any environment gives information about the state of the genotypes to environments.

If the angle is quite sharp and narrow indicates that the genotype is desirable for that environment if the angle is too large then the genotype is undesirable for that environment. 4) The length of the vector of a genotype indicates the strength or weakness of the genotype for all environments. According to these explanations there are high correlation among E3, E5, E6 and G6 is desirable for these environment, while there are high correlation E1, E2 and E4 and G6 is desirable genotype for these

environments, and G8 (candidate) is desirable for all environments (*Fig. 2 and Table 6*). In *Fig. 3*, five sectors are created, with two sectors each of them consisting of three environments. These sectors stand for different MEs, because the winning genotypes for each sector are those positioned at the vertex we can say that G4 is winning genotype for sector II (E3, E5 and E6), G6 for sector I (E1, E2 and E4).

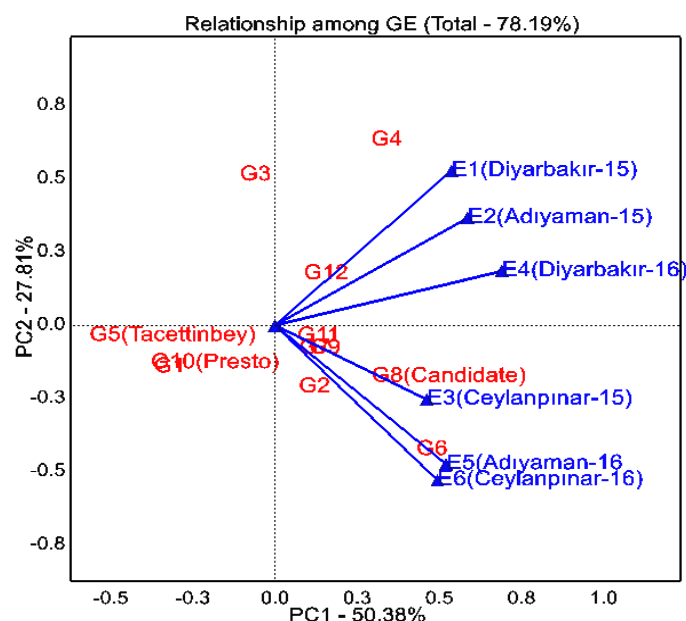


Figure 2. The GGE biplot which shows the relationships among test environments. The correlation coefficient between any two environments is approximated by the cosine of the angle between their vectors. Acute angles indicates a positive correlation, obtuse angles a negative correlation and right angles no correlation. G1-G12 is the codes for the triticales disomic addition lines and G5 and G10 used as the control, respectively. E1- E3 are environment codes for 2014-15, E4-E6 for 2015-16 growing season

Table 6. The first four AMMI selections for per environments, variance and IPCA scores

Env	Mean	Score	1	2	3	4	IPCAe[1]	IPCAe[2]	IPCAe[3]	IPCAe[4]	Variance
E1	7.996	-0.79	G4	G3	G8	G7	-0.78881	-0.44311	0.14583	-0.40141	0.6423
E2	7.741	-0.75	G4	G6	G9	G8	-0.74728	0.69354	-0.32960	0.15858	0.5670
E3	5.994	0.41	G6	G7	G4	G8	0.41209	0.30484	0.73113	0.17556	0.4741
E4	5.062	-0.14	G12	G4	G8	G2	-0.14082	-0.53822	0.06581	0.45130	0.4142
E5	3.427	0.70	G6	G8	G11	G2	0.69460	-0.18457	-0.59209	0.09693	0.3242
E6	3.450	0.57	G6	G8	G9	G2	0.57021	0.16753	-0.02109	-0.48096	0.2598

Similar situation (two mega- environment) occurred among environments presented in *Fig. 4*. The stability of genotypes also showed in *Fig. 5*, and generated by GGE biplot. The AEC is showing the stability genotypes based on across environment. The similar results indicated on *Fig. 6*, and G8 and G6 are favorable genotypes because they located near of center ideal center of biplot. The result showed that G8 (candidate) is quite stable and yielding, G6 and G4 are yielding as well as. The biplot showed that the selection of genotypes can be done both on specific and general goals.

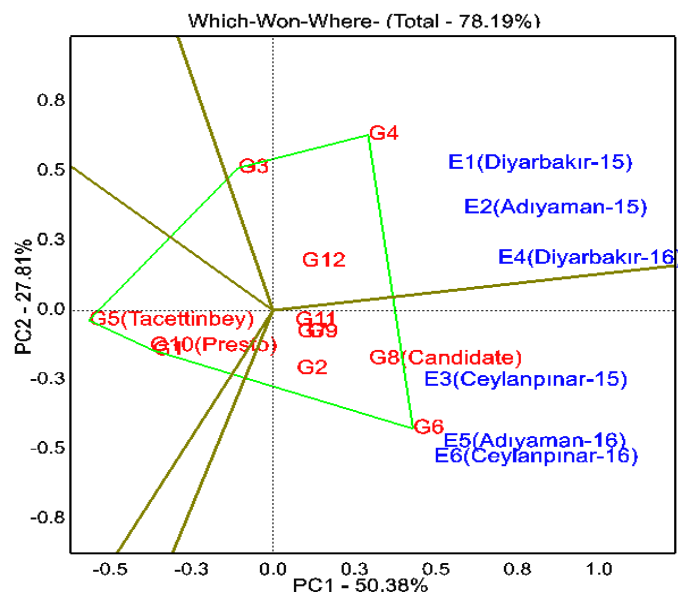


Figure 3. Which-won-where for genotypes and environments. The Polygon view of genotype-environment interaction for wheat-barley disomic addition lines over six test environments. The vertex genotype in each sector is the best genotype at environments whose markers fall into the respective sector. Environments within the same sector share the same winning genotype, and environments in different sectors have different winning genotypes. G1-G12 is the codes for the triticales disomic addition lines and G5 and G10 used as the control, respectively. E1- E3 are environment codes for 2014-15, E4-E6 for 2015-16 growing season

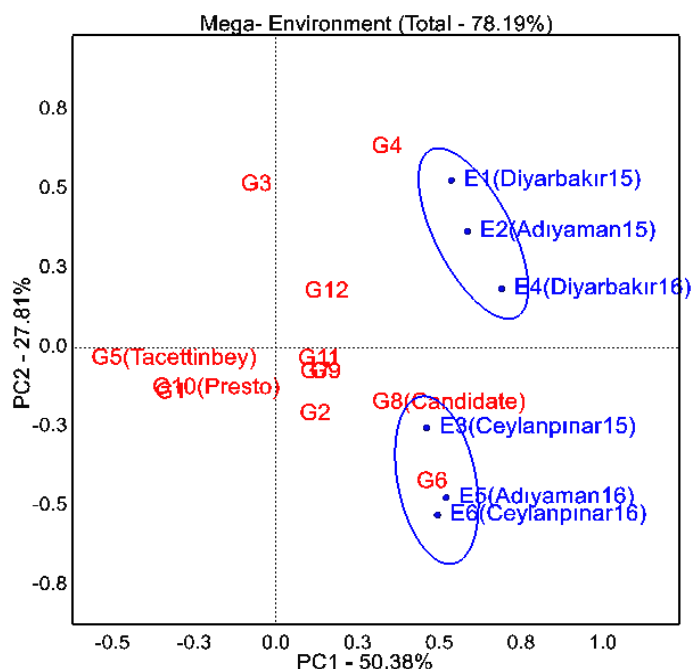


Figure 4. The potential mega-environments and ideal for mega environments. The environments which have same conditions located in the same mega-environment, and the genotypes which located in the center mega-center mean is desirable for this mega-environments. G1-G12 is the codes for the triticales disomic addition lines and G5 and G10 used as the control, respectively. E1- E3 are environment codes for 2014-15, E4-E6 for 2015-16 growing season

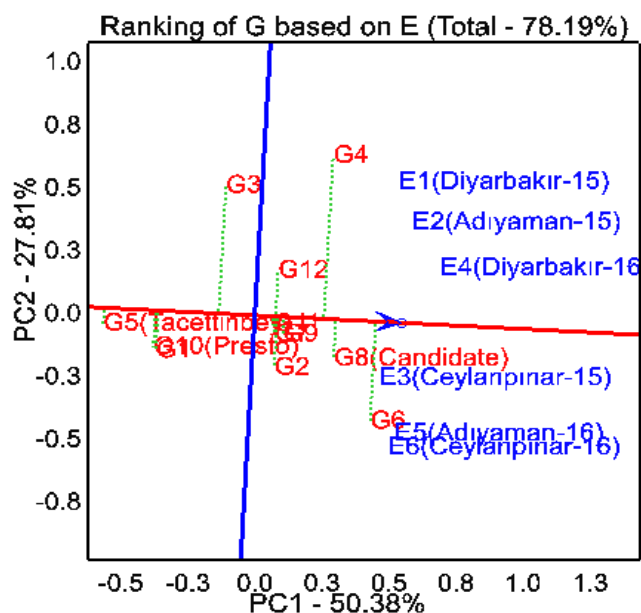


Figure 5. The GGE biplot showing the ranking of genotypes for both yield and stability performance over environments. The line passing through the biplot origin is called the average environment coordinate (AEC). More close to concentric circle indicates higher mean yield. The line which passes through the origin and is perpendicular to the AEC with arrows represents the stability of genotypes. Either direction away from the biplot origin, on this axis, indicates greater GE interaction and reduced stability. G1-G12 is the codes for the triticale disomic addition lines and G5 and G10 used as the control, respectively. E1- E3 are environment codes for 2014-15, E4-E6 for 2015-16 growing season

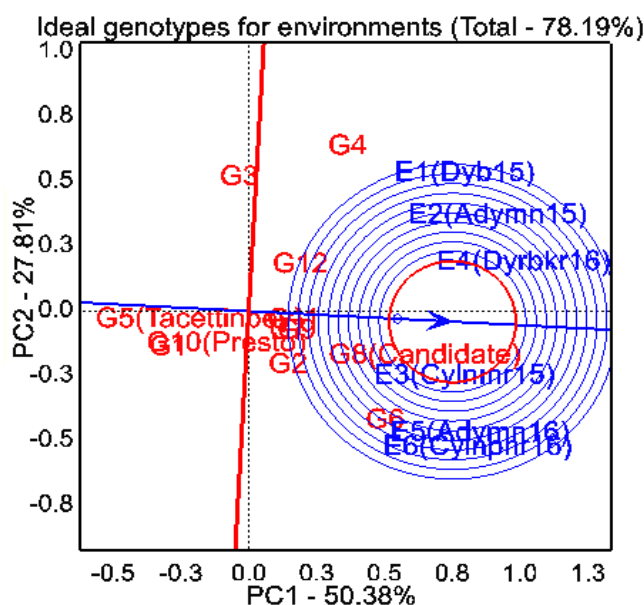


Figure 6. The comparison method rank the genotypes to an ideal genotype. The ideal genotype can be used as a reference for genotype evaluation. Thus, using the ideal genotype as the center, concentric circles were drawn to help visualize the distance between each genotype and the ideal genotype. G1-G12 is the codes for the triticale disomic addition lines and G5 and G10 used as the control, respectively. E1- E3 are environment codes for 2014-15, E4-E6 for 2015-16 growing season

Discussion

The multiple environments experiments aims to identify superior genotypes for different conditions. Due to the unpredictable environmental factors, different models (GE, GEI, GGE, AMMI) were developed to elucidate the effect of genotype, environment or interaction, and are still used in breeding studies (Kendal and Sayar, 2016; Kendal et al., 2016). In addition, The AMMI and GGE biplot techniques have been used for a long time by many researchers to understand the effect of genotype, environment and GEI based on grain yield (Yan and Tinker, 2006; Kendal and Dogan, 2015; Akcura et al., 2016; Oral et al., 2018). The AMMI analysis was used to identify the stability and superiority of genotypes, favorable and yielding environments based on multiple environments (Tekdal and Kendal, 2018). In the study AMMI analysis indicated that G4 and G6 were yielding genotypes, while G7 and G8 (candidate) were stable in tested environments. On the other hand, the study showed that the grain yield is fluctuation depend on factors of environmental and years. In addition, some locations (Diyarbakır) have proven to be highly yielding, some other locations (Ceylanpınar) have proven to be low-yielding even if the year conditions change. Some studies on AMMI commented that this model can be used to describe a two-way table of GE means. When the GE means are independent and homoscedastic, ordinary least squares (OLS) gives optimal estimates of the model (Gauch et al., 2008), this model could be used to evaluate genotypes at different locations over the years in breeding program (Sadeghzadeh et al., 2017). The magnitude of environment effect was higher than genotype effect (Rad et al., 2013). In triticale the locations that are both descriptive and representative are good test locations for the selection of adapted genotypes (Bilgin et al., 2018). According to GGE biplot showed that the selection of genotypes can be done both on specific and general goals. In the study, two mega-environment were occurred in the test environments and G4 was the best yielding in the poorest environments or years, and G6 for yielding crop seasons or environments, while G8 (candidate) is stable for general testing environments. According to results of a study indicated that an ideal genotype should have both high mean yield and high stability within a mega-environment (Yan and Tinker, 2006). In studies conducted in different years or environments, if there is no difference between two or more environments and within the same circle, this is called mega environment and it is recommended to work in one of these environmental groups in later studies. Fortunately, more than two mega-environments are often sufficient to allow GE to capture a sizeable portion of the interaction signal (Gauch, 2013; Hongyu et al., 2015). According to the results of the AMMI and GGE biplot models had similar results in view of specific adaptability to environmental conditions. Nevertheless, contrary results were obtained for environmental contribution to the stability of genotypes (Lule et al., 2014; Shahriari et al., 2018). Both AMMI and GGE were able to efficiently explore the variability present in MET data due to genotype-environment interaction and both models proved to be approximately equivalent, leading to substantially the same conclusions about the genotypes with the highest yield and stability (Neisse et al., 2018).

Conclusion

The results of study revealed that grain yield of triticale was highly influenced by environment effect followed by genotypic effects and GEI contributed the least. This study demonstrated that AMMI model was found effective for determining the yielding

and stabilize triticale genotypes and discriminating ability and representativeness of the test environments. According of the study, G4 and G6 showed specific ability, while G8 general adaptability in test environments. Moreover; G4 can be recommend for yielding (mega-env II), while G6 for low-yielding (Mega-env. I) seasons or environments. On the other hand, G8 can be registered as variety for study area, because this genotype is quite stable and yielding among genotypes in test environments. Both AMMI and GGE biplot model were proved to be approximately equivalent, leading to substantially the same conclusions about the genotypes with the highest yield and stability.

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APPENDIX



Picture 1. The locations of research was presented in Southeast Anatolia of Turkey