



## Environment by Genotype Interaction and Stability of Bread Wheat (*Triticum aestivum* L.) Genotypes under Rainfed Conditions in Trakia Region

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### ABSTRACT

The study was conducted in the Trakya region, Turkey at five environments during the 2015-2016 growing cycles. Grain yield were subjected to analysis of variance (ANOVA), the additive main effect and multiplicative interaction (AMMI) and genotype and genotype-by-environment (GGE) biplot analyses. ANOVA and AMMI analysis showed highly significant ( $p < 0.01$ ) differences among environments (E). Environment was responsible for the greatest part of the variation, followed by genotype and its interaction effects. Average yield across five environments varied from the highest 6673 kg ha<sup>-1</sup> to the lowest 5008 kg ha<sup>-1</sup>. Across five environment Genotypes G7 and G12 had highest grain yield. Burgaz was found near the ideal test environment of the average environment coordination. Therefore, this location should be used as the most suitable to select widely adapted genotypes. For grain yield, cultivars Gelibolu, and G17, G8, and G12 lines were well adaptable to all environmental conditions. The graphical result showed that the first principal component PC1 explained 44.71% of the interaction sum of the square while the second principal component, PC2 explained 22.57% of some of the square interaction. The result of PCA revealed that the 2 principal components contributed 67.27% of the total variability. In the study, genotypes G12 and G17 selected in 2016 and then were released in 2019 named Anafarta and Abide, respectively.

**Keywords:** Bread wheat, GE interaction, GGE biplot, yield, stability

### Introduction

Bread wheat is a widely cultivated crop throughout the Trakya region of Turkey. Because of the various environmental conditions yield and quality in wheat varies in the region and GGE biplot analysis provides an easy and comprehensive solution to genotype by environment interaction (Öztürk and Korkut 2018; Öztürk 2021). The basic aim of plant breeding research is to improve genotypes for a given environment. Genotype (G) and environment (E) are thus the two explicit components that define a plant breeding research program and that also determine the potential for technology spillovers (Maredia et al. 1999). Evaluation of genotypes across various environments and several years is needed in order to identify stable genotypes that could be recommended for release as new cultivars and/or for use in the breeding programs (Sharma et al. 2010).

Environmental factors play a main role in the expression of genotype characteristics (Peterson et al. 1998). The highly variable wheat growing environments provide ample opportunity for differentiation of target environments and the manifestation of genotype-environment interactions. The multiplication trials used in plant breeding are subject to two main sources of variation genotypes, location and their interaction (Petersen 1994). Genotype performance changes due to environmental stresses and differences in their ability to adapt to the stress factors. Due to various environmental conditions, abiotic stress factors can cause a reduction in yield and yield components in bread wheat genotypes (Öztürk and Korkut, 2020). Numerous methods have been developed to reveal patterns of G × E interaction, additive main effects and multiplicative interaction (AMMI) (Gauch 1992).

The AMMI stability parameters allow examining yield stability after reducing the noise from the GE interaction effect (Ajay et al. 2020). Genotype environment ( $G \times E$ ) interactions are of major importance because they provide information about the effect of different environments on cultivar performance and have a key role in the 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 the performance of elite materials (Solomon et al. 2018). Performance trials have to be conducted in multiple environments because of the presence of GE. Variety trials provide essential information for selecting and recommending cultivars. Although data may be collected for many traits, an analysis may be limited to a single trait usually yield and information on other traits is often left unexplored (Yan and Tinker 2006). The success of crop improvement activities largely genotype evaluation by eliminating unnecessary testing depends on the identification of superior genotypes for sites (Letta 2009). 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). 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 selection of relatively high and stable yielding genotypes is a key component in wheat breeding programs to improve yield performance under various environmental conditions. Environmental variations are important in determining the performance of wheat genotypes. A variety of statistical procedures are in fact available to analyze and determine the results of multi-location trials and genotype  $\times$  environmental interaction (GEI) data. In this study, two multivariate analyses such as AMMI and GGE biplot have been performed. Finlay and Wilkinson's joint regression model (1963) and Eberhart and Russel's method (1966) were applied and the regression coefficient ( $b$ ), determination coefficients of the regression equations ( $R^2$ ) were calculated (Finlay and Wilkinson 1963; Eberhart and Russell 1966 and 1969; Tai 1971).

The most important goal in all crop breeding programs is to increase yield, and yield improvement requires the use of efficient statistical methods to identify superior genotypes. In determining the superiority of genotype, in addition to high yield, yield stability in different environments must also be considered. AMMI and biplot analyses are good tools for selecting superior genotypes and to increase efficiency in selection (Naik et al. 2022). Therefore, the aim of this research was to assess the yield and the performance of the advanced bread wheat genotypes and to investigate their yield stability and genotype-by-environment interactions across various environmental conditions.

### Materials and Methods

The experiments were carried out at five locations in the Trakya region, Turkey, in the 2015-2016 growing seasons on winter wheat (*Triticum aestivum* L.) under rainfed conditions. Each location was considered as a single environment. Twenty-five winter wheat genotypes, 5 of them were local checks and 20 advanced lines, were examined in randomized complete block design (RCBD) with four replications. Each plot was comprised of 6 rows of 6 m, spaced 0.17 meters apart. The seeds were sown at the rate of 500 seeds per square meter.

The AMMI method combines the traditional analysis of variance (ANOVA) and principal component analysis (PCA) into a single analysis with both additive and multiplicative parameters (Gauch, 1992). The first part of AMMI uses the standard ANOVA procedures to estimate the genotype and environment main effects. The second part involves the PCA of the interaction residuals. Genotype and genotype  $\times$  environment (GGE) biplot analyses were conducted using GGE biplot software (Yan and Kang, 2002) to determine the performance and stability of grain yield. The biplot analysis was used to identify genotypes superior for individuals and multiple traits. GGE biplot analysis has been widely used to determine performance stability in multiplications trials when identifying superior genotypes (Yan et al. 2007; Sharma et al. 2010). Data were analyzed statistically for analysis of variance with 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.

### Results and Discussion

The results of the variance analysis of the research are listed in Table 1. The combined analysis of variance (ANOVA) revealed significant differences among genotypes and environments for grain yield ( $p < 0.01$ ) (Table 1). Average grain yield across five locations

varied from the highest 6673 kg ha<sup>-1</sup> to the lowest 5008 kg ha<sup>-1</sup>. The highest grain yield was performed by genotypes G7 followed by G12 (Table 4). The result of the AMMI model for grain yield is presented in Table 2. The data of twenty-five bread wheat genotypes in multi-location year trials were analyzed to determine whether the effect of the Genotype × Environment (GE) interaction. Data were also graphically analysed by the genotype × trait biplot method as recommended by Yan and Tinker (2005). The analysis of variance showed that the GEI was not significant. The multiplicative variance of the treatment sum of squares due to GEI was further partitioned by principal component analysis. The ordination technique revealed significant differences for IPC1 and IPC2. The factors explained, showed that wheat genotypes grain yield was affected by environment (9.11%), genotype (5.52%) and GEI (21.02%). GEI effect was responsible for the greatest part of the variation, followed by environment and then genotype.

When looking for a link between traits that could potentially help the yield breeding, it is imperative that the data be analyzed by various statistical methods (Tsenov et al. 2020). 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 (Yan and Tinker 2006). To visually display relations of observed traits and genotypes multivariate biplot analysis, described by Yan and Rajcan, (2002), Yan and Tinker (2006) are used. Environmental variations are important in determining the performance of wheat genotypes. So, to develop cultivars for various environments, very necessary for breeders to evaluate their genotypes based on many years and several locations. The observed G×E interactions in the AMMI model have been partitioned among the first and second IPCA accounting for 44.71% and 22.57%, respectively. The result of principal component analysis revealed that the two principal components (PC1, PC2) contributed 67.27% of the total variability. In the graphic analysis, the first principal component (IPCA1) represents genotype productivity and the second principal component (IPCA2) represents genotype stability (Yan et al. 2000).

In the GGE biplot (Figure 1a), the vectors from the biplot centre divided the graph into seven distinct sectors. The highest yielding genotypes were identified for each sector. The wheat genotypes located on vertices of polygon performed either best or poorest in one or more environments. The G7 was the highest yielding

genotype in environment E1 (Edirne1). Genotype G6 and G12 was the best performer in environment E5 (Keşan) (Table 3, Figure 1a).

Discriminating ability is an important measure of a test environment. Another equally important measure of a test environment is its representativeness of a target environment. An ideal environment should be highly differentiating of the genotypes and at the same time representative of the target environment (Dehghani et al. 2006). The discrimination and representativeness of wheat genotypes according to traits are displayed in Figure 1b. 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). Similarly to the ideal genotype, the ideal environment is located in the first concentric circle in the environment-focused biplot, and desirable environments are close to the ideal environment. The ideal environment is representative and has the highest discriminating power (Yan and Tinker, 2006). The most ideal genotypes are located in the centre, whereas genotypes located on the mean vertical axis, but far from the centre, are ideal; genotypes located below the vertical axis are undesirable. According to this statement, placed near to the first concentric circle, G7 was the ideal genotype position and it can be used as a reference for genotype evaluation in breeding study (Figure 1b).

The GGE biplot in Figure 1b shows the relative ranking of the environments relative to the ideal. The ideal environment represented by the small circle with an arrow pointing to it (Figure 1b) is the most discriminating of genotypes and yet representative of the other test environments. The environment closest to the center of the concentric circles is the most representative of the environments. An ideal genotype should have high mean performance and be absolutely stable across environments. In Figure 1b, the arrow direction of the single-arrowed line indicates the ideal genotype. Therefore, E1 (Edirne1) is a more desirable test environment than others, which had a greater value for IPC1, showing a greater power of discrimination among the genotypes in related to the other environments (Figure 1b). Therefore, the E1 location can be regarded as the most favourable environment to select extensive adapted genotypes.

The average yield performance and stability of genotypes were assessed by an average environment coordination (AEC) method (Yan 2002). In the average environmental coordinate (AEC) system, the AEC X-axis (PC1) passes through the biplot origin with an arrow indicating the positive end of the axis and indicates the mean performance axis of genotypes.

GGE Biplot graph in Figure 2a showed that the mean performance based on environments and stability of wheat genotypes in grain yield. The results in Figure 2a showed that genotypes G7, G19, and G21 were found stable. Among the stable genotypes, performances of G7, G19, and G21 were above average in generally all the environments. Based on Figure 2a, genotypes with above-average yield were from G11 to G12 and located on the right side of the biplot origin, while genotypes with below average yield were from G10 to G3 and located on the left side of the biplot origin. Genotypes G11, G24, G10 (Bereket), and G6 were unstable. The yield performances of these genotypes significantly altered based on environmental conditions. According to results, genotypes G12 and G6 had adaptive to favorable (ideal) environments (Figure 2a).

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 (Figure 2b). The angle between the environment vectors provides further information on the correlation between environments, where an acute angle indicates a positive correlation, an obtuse angle indicates a negative correlation and a right angle indicates no correlation (Figure 2b). According to, all environments were positively correlated except E2 as all of the angles among them were smaller than  $90^\circ$  suggesting that indirect selection for yield can be practical across these test environments. There is also strong positive correlation between environment E3, E4 and E5 (Figure 2b). A genotype adaptable or with good performance in one environment may exhibit a similar response in another environment. With the longest vectors from the origin, environments E1 (Edirne1) and E2 (Edirne2) were the most discriminating. E5 (Keşan) was moderately discriminating, while E4 (Tekirdağ) was least discriminating (Figure 2b).

In Figure 3a, X-coordinate indicates the main effects (means) and the y-coordinate indicates the effects of the interaction (IPCA1). In the biplot, ten bread wheat genotypes (G2, G6, G7, G11, G12, G16, G17, G19, G20 and G21) and two environments (E3 and E5) located on the right side of the graph. These were considered high yielding genotypes and environments. Due to the lowest IPCA scores, genotypes G1 and G10 were least involved with the interaction, and are therefore the most stable. Furthermore, the genotypes G21 and G22 were the most unstable, G4 with the highest average yield. The most ideal genotype should combine high yield and stable performance across a range of production environments. Among the high yielding genotypes, G8 and G2 genotypes can be

best evaluated based on stability and grain yield with a combined low absolute PC1 score and high yield (Figure 3a).

A stable genotype should have around unit regression coefficient over environments ( $b_i \approx 1$ ) and minimum deviation from the regression ( $S^2d=0$ ) in addition to higher grain yield than the population mean. The coefficient of regression for grain yield is presented in Figure 3b. According to grain yield, it was determined that genotypes Gelibolu, G17, G8 and G12 were well adaptable to all environmental conditions. Genotype G7 had higher grain yield under unfavourable conditions. Genotypes G16, G18 and G25 were medium adaptable to all environments and genotypes G2 and G6 were well adaptable to well fertile environmental conditions (Figure 3b). The adaptability of a genotype to diverse environments is usually tested by the degree of its interaction with different environments under which it is grown. A genotype is considered to be more adaptive or stable if it has a high mean yield but a low degree of fluctuation in yielding ability when grown over diverse environments.

The development of high yielding genotypes in all environmental conditions is an important result for the success of breeding studies. The stability parameters of the wheat genotypes are given in Table 5. Genotypes G7 and G12 had higher yield potential across four environments. Genotypes G4 and G2 were very stable due to their highest determinations coefficient ( $R^2$ ). The regression coefficients (b) values of the wheat genotypes varied from 0.02 to 1.63. The b value showed great variation between genotypes. This result indicated that twenty-five wheat genotypes showed different performances across five environments. Cultivar Gelibolu and G12, G18, and G22 lines had optimum b value. The highest positive intercept values (a) were determined in genotypes G21, G7, G13, G19, and Aldane (Table 5). This result explained that all these genotypes were higher yields both under well fertile and unfertile environmental conditions.

The cultivar Gelibolu surpassed the average grain yield, showed minimum deviation from linear regression ( $S^2d=214.05$ ), positive intercept value ( $a=29.51$ ), and its coefficient of regression ( $b=1.01$ ) was almost one. Therefore it would be well adapted to a better environment. The genotype G7 yielded the highest grain yield followed by cultivar Anafarta (G12) and G6, all these genotypes showed a lower coefficient of determinations and the highest deviation from linear regression. Among these, genotype G7 was well adapted to the poor environment and has above average stability; while genotypes G8 and G12 had almost unit regression coefficient, and both were well adapted to all the environments.

The cultivar, Gelibolu had a mean value higher than the general mean, regression coefficient around unity, and minimum deviation from regression, thereby it was identified as a stable genotype across the environments (Table 5).

### Conclusions

The result of the research revealed the importance of genotype-environment interaction. Therefore, genotypes reacted differently in different environments. There was a significant difference among genotypes and environment due to various environmental conditions. Genotype  $\times$  environment interaction effect was responsible for the greatest part of the variation, and then followed by environment and genotype. Genotype G7 had the highest grain yield and then followed by G12. G7 was the ideal genotype and it can be used as a reference for genotype evaluation. Among locations, E1 (Edirne1) is a more desirable test environment than others, which had a greater value for IPC1, showing a greater power of discrimination between the genotypes in regards to the other environments. Therefore, the location E1 should be regarded as the most suitable to select widely adapted genotypes. Among the stable genotypes, performances of G7, G19, and G21 were above average in all the environments. The yield performances of these genotypes significantly

varied based on environmental conditions. According to results, genotypes G12 and G6 had adaptive to favourable (ideal) environments. E1 (Edirne1) and E2 (Edirne2) were the most discriminating environments due to the longest vectors from the origin. Environment E5 (Keşan) was moderately discriminating, while environment E4 (Tekirdağ) was least discriminating. Among the high yielding genotypes, genotypes G8 and G2 can be best evaluated based on stability and grain yield with a combined low absolute PC1 score and high yield. For grain yield, it was determined that genotypes Gelibolu, G17, G8 and G12 were well adaptable to all environmental conditions. Under unfavourable environment condition G7 had higher grain yield. Genotypes G2 and G6 were well adaptable to well fertile environment conditions across five environments. In the research, genotypes G12 and G17 selected in 2016 and were released in 2019 named Anafarta and Abide.

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Table 1. Analysis of variance for grain yield in twenty-five wheat genotypes grown across five environments.

| Source of variation | DF  | SS         | MS        | F Ratio |
|---------------------|-----|------------|-----------|---------|
| Environment (E)     | 4   | 640801.51  | 160200.37 | 34.67** |
| Genotypes (G)       | 24  | 257483.29  | 10728.47  | 2.32**  |
| Error               | 96  | 443530.30  | 4620.10   |         |
| C. Total            | 124 | 1341815.10 |           |         |

\* and \*\* indicate significances, at  $p < 0.05$  and  $p < 0.01$ , respectively. DF: Degree of freedom, SS: Sum of square, MS: Mean of square.

Table 2. The variance of AMMI analysis of bread wheat genotypes on yield.

| Source of variation         | DF  | SS       | MS     | F       | SST%  |
|-----------------------------|-----|----------|--------|---------|-------|
| Treatments                  | 124 | 12213361 | 98495  | 1.69**  |       |
| Genotypes (G)               | 24  | 1891870  | 78828  | 1.35ns  | 5.52  |
| Environments (E)            | 4   | 3122716  | 780679 | 11.72** | 9.11  |
| Block                       | 15  | 999083   | 66606  | 1.14    |       |
| Interactions (G $\times$ E) | 96  | 7198775  | 74987  | 1.28    | 21.02 |
| IPCA1                       | 27  | 6329646  | 234431 | 4.01**  |       |
| IPCA2                       | 25  | 491435   | 19657  | 0.34    |       |
| Residuals                   | 44  | 377695   | 8584   | 0.15    |       |
| Error                       | 360 | 21032233 | 58423  |         |       |
| Total                       | 499 | 34244676 | 68627  |         |       |

\* and \*\* indicate significances, at  $p < 0.05$  and  $p < 0.01$ , respectively. SST%: Percentage relative to the sum of squares total, DF: Degree of freedom, SS: Sum of square, MS: Mean of square, IPCA: Interaction Principal Components Axes.

Table 3. Based on AMMI selections the first four genotypes for the per environment and IPCA scores.

| Environment | Mean yield<br>(kg ha <sup>-1</sup> ) | 1  | 2   | 3   | 4   | IPCA[1] | IPCA[2] |
|-------------|--------------------------------------|----|-----|-----|-----|---------|---------|
| E1          | 4796                                 | G7 | G12 | G17 | G6  | 9.61    | -10.71  |
| E2          | 5273                                 | G7 | G12 | G17 | G6  | 9.12    | -6.25   |
| E3          | 6942                                 | G7 | G12 | G25 | G2  | 8.69    | 6.31    |
| E4          | 5752                                 | G2 | G4  | G25 | G7  | 4.04    | 12.40   |
| E5          | 6540                                 | G9 | G6  | G12 | G11 | -31.47  | -1.75   |

E1: Edirne 1, E2: Edirne 2, E3: Lüleburgaz, E4: Tekirdağ, E5: Keşan, IPCA: Interaction Principal Components Axes.

Table 4. Yield response across five environments and standard deviation in genotypes.

| G No       | Genotypes      | E1   | E2   | E3   | E4   | E5   | Mean                     |
|------------|----------------|------|------|------|------|------|--------------------------|
| 1          | G1 (Aldane)    | 4922 | 5393 | 7136 | 5621 | 5080 | 5951±1051 <sup>a-e</sup> |
| 2          | G2             | 4892 | 5599 | 7633 | 6167 | 6635 | 6144±1071 <sup>abc</sup> |
| 3          | G3             | 4310 | 5336 | 5834 | 4173 | 5125 | 5008±747 <sup>f</sup>    |
| 4          | G4             | 4368 | 4793 | 7512 | 6090 | 6314 | 5924±1169 <sup>a-e</sup> |
| 5          | G5 (Selimiye)  | 3947 | 5053 | 7062 | 5503 | 5116 | 5284±1147 <sup>def</sup> |
| 6          | G6             | 5670 | 6047 | 7609 | 5741 | 7737 | 6362±1227 <sup>ab</sup>  |
| 7          | G7             | 6852 | 6994 | 7512 | 6602 | 6352 | 6673±556 <sup>a</sup>    |
| 8          | G8             | 4956 | 4733 | 7453 | 5632 | 6339 | 6275±1008 <sup>ab</sup>  |
| 9          | G9             | 3282 | 3941 | 5818 | 6105 | 5809 | 5149±1168 <sup>ef</sup>  |
| 10         | G10 (Bereket)  | 4254 | 4454 | 6965 | 4831 | 5335 | 5065±1189 <sup>f</sup>   |
| 11         | G11            | 4555 | 5112 | 7055 | 6300 | 6844 | 5842±1252 <sup>a-f</sup> |
| 12         | G12            | 6196 | 6670 | 7735 | 6164 | 7697 | 6581±1124 <sup>a</sup>   |
| 13         | G13            | 4782 | 5450 | 6228 | 5740 | 6222 | 5928±720 <sup>a-e</sup>  |
| 14         | G14            | 4075 | 4687 | 6243 | 5483 | 5307 | 5312±782 <sup>c-f</sup>  |
| 15         | G15 (Pehlivan) | 3821 | 4634 | 7408 | 5470 | 5341 | 5345±1325 <sup>c-f</sup> |
| 16         | G16            | 5532 | 4960 | 7362 | 5584 | 6688 | 5960±1070 <sup>a-e</sup> |
| 17         | G17            | 5839 | 6139 | 7307 | 5412 | 6760 | 6056±965 <sup>a-d</sup>  |
| 18         | G18            | 4850 | 5337 | 7300 | 4326 | 5715 | 5666±1157 <sup>b-f</sup> |
| 19         | G19            | 5442 | 5799 | 6721 | 5719 | 6026 | 5849±556 <sup>a-f</sup>  |
| 20         | G20 (Gelibolu) | 5327 | 5503 | 7617 | 6000 | 5768 | 6102±882 <sup>a-d</sup>  |
| 21         | G21            | 5935 | 5830 | 5686 | 6056 | 6573 | 5951±409 <sup>a-e</sup>  |
| 22         | G22            | 3372 | 4844 | 5945 | 6454 | 6072 | 5535±1232 <sup>b-f</sup> |
| 23         | G23            | 3709 | 4182 | 6030 | 6223 | 5959 | 5353±1066 <sup>c-f</sup> |
| 24         | G24            | 4097 | 5179 | 7180 | 5908 | 5043 | 5282±1291 <sup>def</sup> |
| 25         | G25            | 4912 | 5152 | 7210 | 6498 | 4518 | 5663±1140 <sup>b-f</sup> |
| Mean       |                | 4796 | 5273 | 6942 | 5752 | 6015 | 5770                     |
| CV (%)     |                | 8.2  | 10.1 | 8.3  | 9.7  | 8.7  | 11.7                     |
| LSD (0.05) |                | 55.8 | 75.1 | 81.6 | 78.8 | 74.1 | 83.30                    |

Table 5. The stability parameters and IPCA parameters of AMMI model of the genotypes across five environments.

| G No | Genotypes      | X    | R <sup>2</sup> | S <sup>2</sup> d | a       | b    | IPCAg[1] | IPCAg[2] |
|------|----------------|------|----------------|------------------|---------|------|----------|----------|
| 1    | G1 (Aldane)    | 5951 | 0.27           | 1347.43          | 202.77  | 0.68 | 3.93     | 0.01     |
| 2    | G2             | 6144 | 0.98           | 29.82            | -151.76 | 1.33 | 0.68     | 1.79     |
| 3    | G3             | 5008 | 0.36           | 591.15           | 176.25  | 0.56 | 1.94     | -5.50    |
| 4    | G4             | 5924 | 0.99           | 29.96            | -244.87 | 1.45 | 0.39     | 4.50     |
| 5    | G5 (Selimiye)  | 5284 | 0.93           | 145.78           | -270.73 | 1.38 | 2.76     | 3.03     |
| 6    | G6             | 6362 | 0.60           | 1009.08          | -47.83  | 1.19 | -1.31    | -3.49    |
| 7    | G7             | 6673 | 0.31           | 353.37           | 442.84  | 0.39 | 3.96     | -5.23    |
| 8    | G8             | 6275 | 0.55           | 764.93           | 89.72   | 0.93 | 0.55     | 1.07     |
| 9    | G9             | 5149 | 0.61           | 883.65           | -143.27 | 1.14 | -33.79   | 0.04     |
| 10   | G10 (Bereket)  | 5065 | 0.88           | 293.02           | -295.82 | 1.39 | 1.73     | 0.50     |
| 11   | G11            | 5842 | 0.76           | 619.30           | -203.98 | 1.37 | -0.81    | 3.01     |
| 12   | G12            | 6581 | 0.53           | 981.93           | 65.78   | 1.03 | -0.13    | -4.47    |
| 13   | G13            | 5928 | 0.28           | 619.23           | 316.11  | 0.48 | 0.42     | -1.44    |
| 14   | G14            | 5312 | 0.80           | 207.71           | 28.28   | 0.87 | 1.54     | 1.65     |
| 15   | G15 (Pehlivan) | 5345 | 0.97           | 89.44            | -406.19 | 1.63 | 2.02     | 4.56     |
| 16   | G16            | 5960 | 0.67           | 626.56           | -35.99  | 1.10 | 0.20     | -1.61    |
| 17   | G17            | 6056 | 0.57           | 671.85           | 81.86   | 0.91 | 1.02     | -5.39    |
| 18   | G18            | 5666 | 0.47           | 1178.30          | -6.65   | 0.99 | 1.94     | -4.27    |
| 19   | G19            | 5849 | 0.89           | 55.63            | 206.39  | 0.66 | 2.00     | -3.17    |
| 20   | G20 (Gelibolu) | 6102 | 0.83           | 214.05           | 29.51   | 1.01 | 3.05     | 0.44     |
| 21   | G21            | 5951 | 0.01           | 278.46           | 584.90  | 0.02 | 0.42     | -5.68    |
| 22   | G22            | 5535 | 0.43           | 1447.48          | -26.88  | 1.01 | -0.69    | 6.04     |
| 23   | G23            | 5353 | 0.65           | 669.81           | -82.36  | 1.07 | -0.65    | 5.58     |
| 24   | G24            | 5282 | 0.83           | 459.97           | -321.79 | 1.47 | 3.36     | 4.03     |
| 25   | G25            | 5663 | 0.45           | 1186.97          | 13.71   | 0.96 | 5.48     | 3.99     |

X: Mean yield, R<sup>2</sup>: Coefficient of determinations, S<sup>2</sup>d: Deviation from regression, a: Intercept value, b: Coefficient of regression.

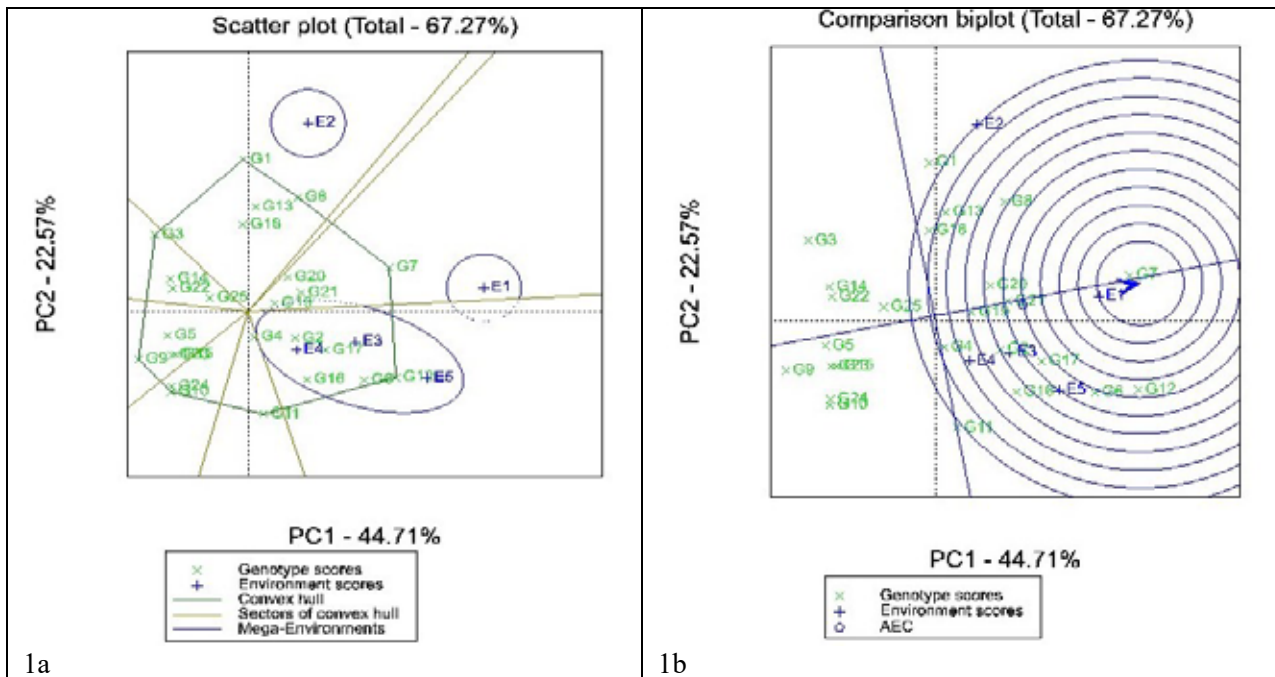


Figure 1. Polygon views of the GGE graph demonstrated that the mega-environments and the which-won-where view of the genotype according to grain yield (1a) and, GGE biplot according to genotype-focused scaling for comparison of the genotypes with the ideal genotype (Figure 1b).

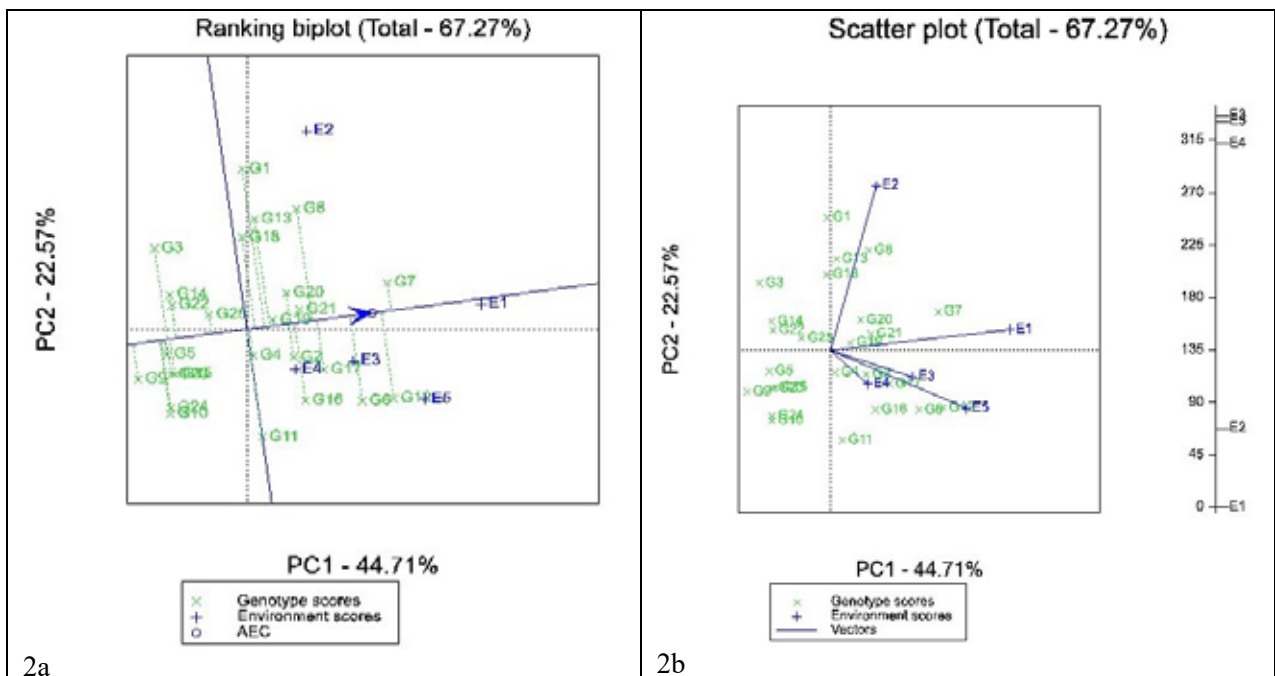


Figure 2. GGE biplot graph demonstrated ranking of the twenty-five genotypes according to mean yield and stability in yield (2a), and GGE biplot the evaluation of the relationship among environments (Figure 2b).



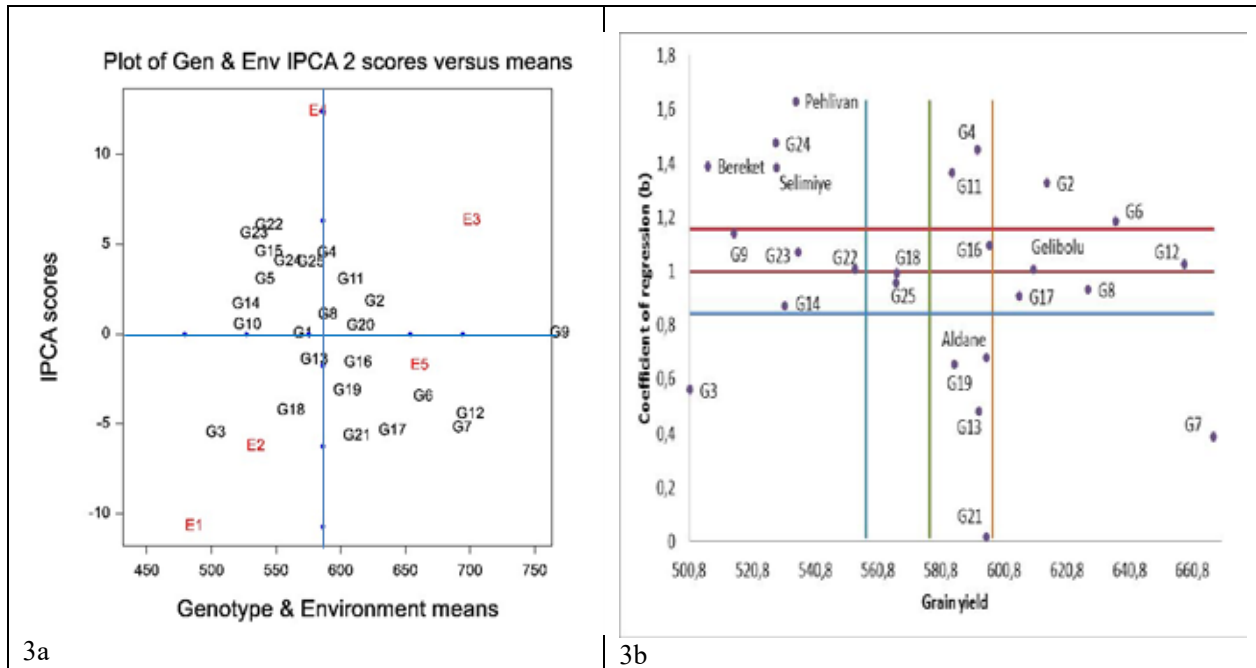


Figure 3. Genotypes environmental means and IPCA scores for twenty-five genotypes across five environments, and scatter plot of regression coefficient of 25 wheat genotypes yield (3b).

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