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Araştırma Makalesi / Research Article

The Comparison Yield Performance of Chickpea Genotypes Grown in Different Locations by the GGE Biplot Method

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Abstract

G×E interaction is critical for understanding how genetic and environmental factors affect plant performance, and this interaction is essential for developing more efficient and adaptive genotypes in plant breeding. In study, The GGE biplot analysis played a crucial role in determining effects on the yield performance of genotype × environment (G×E) interactions and comparing the stability and adaptability of genotypes in Diyarbakir and Kiziltepe. Additionally, cluster analysis was performed using the Ward method, which grouped the genotypes based on yield similarities and identified distinct groups adapted to different environmental conditions. The experiments were arranged by the factorial experimental design with four replications in each environment during the summer seasons of 2015 and 2016.Consequently, the significant differences were determined between genotypes and locations and their interactions. GGE biplot analysis found that the variations in the yield performance of genotypes were caused by 81.24% by the first principal component (PC1) and 18.76% by the second principal component (PC2). FLIP98-206C and FLIP98-143C genotypes were shown high yield potential and stability. In contrast, genotypes D1-3 and Azkan exhibited lower stability and yield performance. Therefore, the high-yielding and broadly adapted genotypes must be prioritized for experiments in regions Diyarbakir and Kiziltepe. However, narrower target regions must be identified for low-performing genotypes and large-scale experiments in these regions should be conducted to understand the long-term yield and stability performance of high-yielding genotypes.

Keywords: Chickpea, GGE biplot, Genotype × Environment interaction, yield performance, cluster analysis

1.Introduction

Legumes (Leguminosae) are recognized as a key component of sustainable agriculture. This group of plants contributes to environmental sustainability by improving soil fertility and through their ability to biologically fix nitrogen, thus reducing the need for chemical fertilizers (Rufaioglu ve Tunc, 2024). Chickpea (*Cicer arietinum* L.) is a significant legume crops worldwide with high nutritional value and economic benefits particularly in arid and semi-arid climates (Varshney et al., 2019; Ipekesen ve Bicer, 2021). Chickpea plays a critical role in human nutrition due to its high protein content, richness in fiber and essential minerals (Jukanti et al., 2012). The increasing demand for food and the rapid decline in agricultural areas have required genetic improvement and the development of suitable cultivation strategies in strategic crops like chickpea to enhance agricultural productivity (Patel et al., 2021). However, global climate change is a threat for the sustainability and productivity of agricultural production. Therefore, the yield performance of genotypes should be identified, and the best genotypes should be selected having high yield under optimal environmental conditions (Yan and Tinker, 2014). This is particularly critical for identifying genotypes capable of providing high productivity in marginal agricultural areas and under changing climatic conditions (Upadhyaya et al., 2011).

GGE biplot analysis has been used as an effective method for evaluating genotype× environment interactions in many crops. GGE biplot was used to compare the yield performances of chickpea genotypes undergrown in different locations (Yan and Tinker, 2015). GGE biplot analysis is a technique developed to evaluate the yield performance of genotypes under specific environmental conditions and to visualize genotype×environment interactions (Yan and Kang, 2003). This analysis method, unlike other analytical techniques, highlights both the effects of genotype and environment, thus providing a more comprehensive evaluation (Mohammadi and Amri, 2013). It provides a graphical tool to better understand the performance of genotypes under different environments and to identify genotypes having the best yields (Yan and Tinker, 2006; Gauch, 2006). GGE biplot analysis simultaneously presents both yield and stability performance of genotypes under different environments (Yan and Tinker, 2006; Gauch, 2006). GGE biplot analysis facilitates decision-making processes in genetic breeding programs and cultivation strategies (Yan and Tinker, 2014). Moreover, GGE biplot analysis serves as a crucial tool for farmers and breeders by enabling a multidimensional assessment of environmental impacts on genotype performance particularly in ensuring sustainable productivity in agricultural production (Yan and Tinker, 2006; Dehghani et al., 2019). Thus, producers can predict which genotype will be more productive under specific conditions and design production (Yan et al., 2007; Gauch, 2013).

GGE biplot method has been widely employed to investigate genotype × environment interactions in many crops such as maize, wheat, and cotton (Blanche and Myers, 2006; Alwala et al., 2010; Yan et al., 2010). Besides simple analysis of variance and correlation analyses, the interpretation of graphs such as GGE biplot, which looks complex but offers a visual feast for multiple selections, provides a great advantage when determining genotype superiority (Bayhan, 2022). This method was also used to determine the yield and stability performance of chickpea genotypes under different locations and provides more effective and reliable results compared to alternative methods (Yan et al., 2007; Gauch, 2013). GGE biplot analysis, by revealing the sensitivity of genotypes to environmental conditions, facilitates the selection of the most suitable genotypes for cultivation in specific regions. Thus, it contributes to a better understanding of the impact of environmental variables on agricultural production and the development of genotypes capable of coping with these effects (Upadhyaya et al., 2011) and plays a significant role in selecting genotypes for yield and stability (Patel et al., 2021).

GGE biplot analysis can also identify specific adaptation abilities of genotypes by determining the adaptation abilities of genotypes to different environments and helps optimize local agricultural practices (Yan and Tinker, 2014).In another study, GGE biplot analysis was used to determine in which traits genotypes were superior and it was suggested that these genotypes could be used as parents in quality-oriented breeding programs (Karaman, 2020).Some studies have shown that GGE biplot analysis makes it possible to select chickpea genotypes that provide high yields in specific regions and exhibit stability against environmental variations (Mohammadi ve Amri, 2013). This case both provides higher profits to the producer and contributes to the sustainability of agriculture (Patel et al., 2021). Therefore, GGE biplot analysis is significant both in genetic breeding studies and for the sustainability of agricultural economics.

The aim of this study is to evaluate the yield performance of chickpea genotypes grown in different locations using the GGE biplot method and to reveal the responses of the genotypes to environmental variations.

2.Materials and Methods

2.1. Material

The experiments were carried out during the 2015 and 2016 summer season in two different environments in Türkiye. The locations consist of Diyarbakir province and Kiziltepe district of Mardin province located in the South-eastern Anatolia Region, Türkiye (Figure 1). Summer experiments were made in Kiziltepe on 15 February, in Diyarbakir on 18 February 2016. The experiments were set up based on the factorial experimental design with four replications in each environment. The plots consisted of six rows of 5 m length and 40 cm intervals. Sowings were made manually at a sowing density of 55 seeds/m2. In experiments, 30 kg ha^{-1} nitrogen and 50 kg ha^{-1} phosphorus fertilizers were used. Data on seed yield were obtained from 6.4 m2 of each plot. The name and origin of 19 chickpea genotypes were given in Table 1.

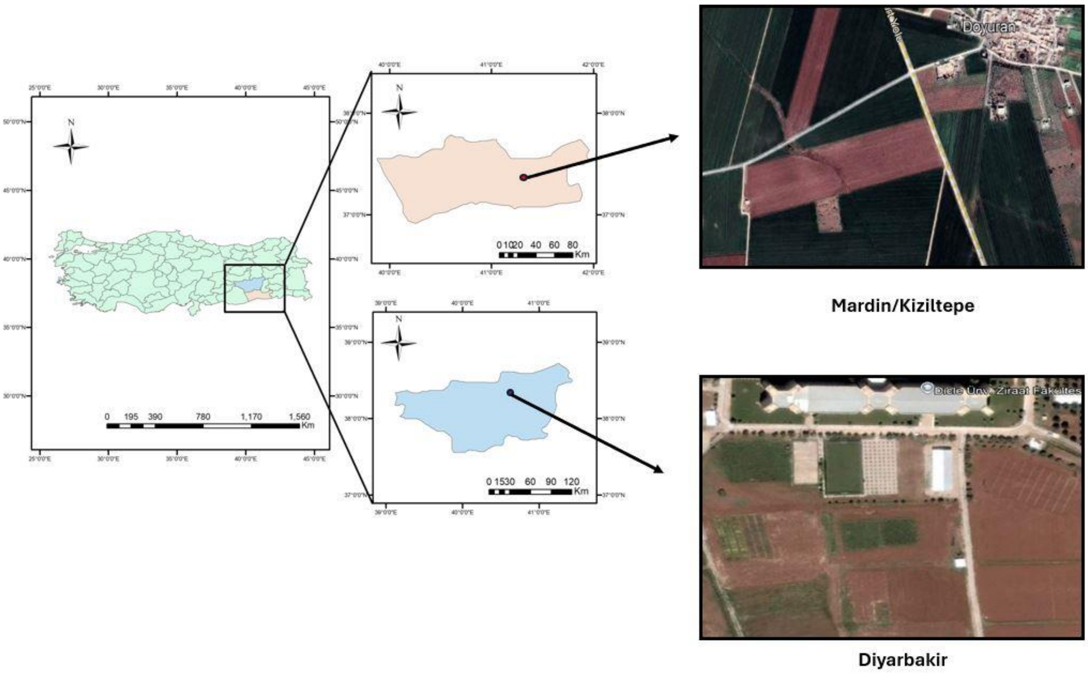

Figure 1. Study area map

Table 1. Name/Code and origin of 19 chickpea genotypes

Name/Code	Origin
D2-5	Konya × Balıkesir
D2-8(9)	Konya × Balıkesir
D1-3	Konya × Balıkesir
D2-6	Konya × Balıkesir
D1-13	Konya × ILC3279
D1-14	Diyar 95 × ILC 482
D1-28(9)	ILC3279 × Balıkesir
R4	Diyar 95 × ILC 482
R6	Diyar 95 × ILC 482
N5-5	Diyarbakir local variety
FLIP97-254C	Icarda
FLIP99-34C	Icarda
FLIP98-143C	Icarda
FLIP98-206C	Icarda
DIYAR	Türkiye
Arda	Türkiye
Azkan	Türkiye
Gokce	Türkiye
Cagatay	Türkiye

2.2. Soil properties

The soil texture of Diyarbakir experiment was clay loam, pH was between 7.19 and 7.24 and was poor for organic matter (0.79%). The soil texture of Kiziltepe experiment was clayey, pH was 7.59 and there was better organic matter (1.69%) than Diyarbakir experiment.

2.3. Climate data for locations

Figure 1 was presented the monthly average temperature (°C) and total rainfall (mm) data for Diyarbakir and Kiziltepe locations. Mean temperatures exhibited similar trends in both locations, however, Kiziltepe generally had higher temperature values than Diyarbakir.

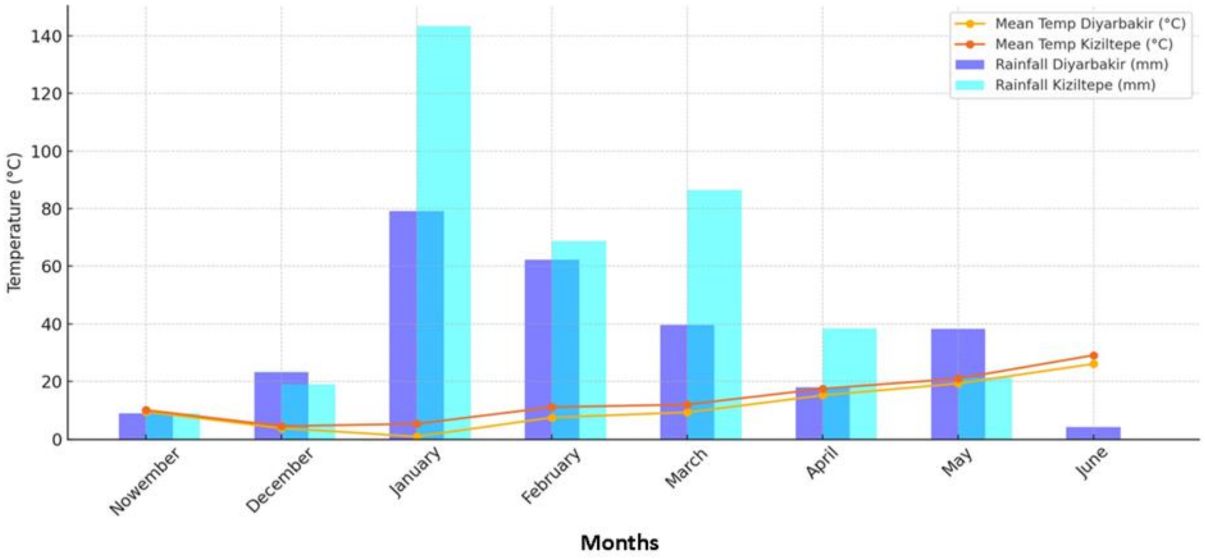

Figure 2. Climate data for two locations

When examining rainfall values, it was seen that seasonal variations in both Diyarbakir and Kiziltepe. Rainfall increased during the winter months

(November-February) and decreased significantly during the summer season (June-September). Particularly in January, rainfall was recorded as 79.2 mm in Diyarbakir and 143.4 mm in Kiziltepe, highlighting this period as one of the wettest seasons in both locations. Additionally, January was the coldest period in terms of temperature values. The average temperature was reduced to 0.9°C in Diyarbakir and 5.3°C in Kiziltepe. This difference showed that Kiziltepe had a relatively milder climate even during winter. Data was a crucial guide for developing location-specific strategies in agricultural practices and genotype selection (Figure 2).

2.4. Statistical analysis

Data were subjected to GGE biplot analysis to determine the effect of location, genotype and location × genotype interaction for yield in Genstat 12th Edition software. The cluster analysis realized to divide genotypes into groups based on similarity in yield by using Ward (Standardized by Column) method in JMP-Pro17 software. Graph analysis of the GGE biplot was realized by single-value decomposition according to the following formula reported by Yan et al. (2000).

Y_{ij}: the mean of ith genotype in jth environment,

μ mean of all genotypes

βj; main effect of jth environment

n; Singular value,

λ_1 and λ_2; the special quantities for the first and second components

ξ_{i1} and ξ_{i2}; the special vectors of genotypes

η_{i1} and η_{i2} ; Environment eigenvectors for nth interaction principal component,

εij; the remaining quantity for the ith genotype in jth environment

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1}\eta_{j1} + \lambda_2\xi_{i2}\eta_{j2} + \varepsilon_{ij}$$

(Yan, et al., 2000).

The GGE biplots were carried out to obtain the correlations among environments and genotypes using polygon, ranking and comparison techniques (Yan, 2002).

3. Result and Discussion

The results of the variance analysis showed that genotype (F=17.36**), location (F=60.78**), and genotype × location interaction (F=4.72**) were found to be statistically significant (p<0.01) (Table 1). All three factors had remarkable effects on the traits. The error variance was calculated as 149.55, and a coefficient of variation (CV) of 10.02% was observed (Table 2).

Table 2. Analysis of variance for 19 chickpea genotypes sown in the summer season at two environments

Variance Sources	DF	Mean Square	F Ratio
Genotype	18	2595.556	17.3556**
Location	1	9089.244	60.7766**
Genotype × Location	18	705.2157	4.7155**
Error	114	149.5518	
C. Total	151		
CV (%)	10.02		

**; significant level at P≤0.01.

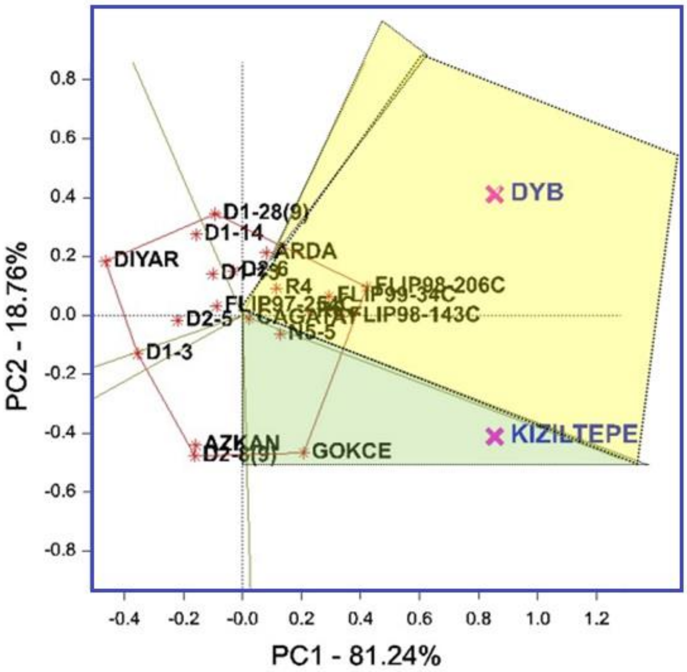

Figure 3. The determination of suitable genotypes in each environment by polygons

In the polygon graph, the first principal component (PC1) explained 81.24% of the total variance, while the second principal component (PC2) accounted for 18.76%. These components created new variables that reduced data complexity, making the similarities and differences between genotypes more comprehensible. In our study, the high explanatory values of PC1 and PC2 indicated that these two components effectively represented the genotype-environment interactions in the data. Each point in the graph represented a genotype, and the distance between genotypes reflected the degree of similarity or difference in their responses to environmental conditions. Genotypes positioned close to each other exhibited similar responses to environmental conditions for the traits analysed, whereas those farther apart showed different responses.

The polygons in the graph illustrated the range of environments in which each genotype performs well. The polygons divided into two major regions labelled Diyarbakir and Kiziltepe, represented the performance of genotypes in the experiment conducted in these two locations. The boundaries of the polygons highlighted which genotypes were most suitable for specific locations and under what conditions they achieved the highest yields. While the genotypes in the DYB region were better adapted to the environmental characteristics of Diyarbakir, the genotypes in the Kiziltepe region were adapted to the characteristics of Kiziltepe. Since these two locations had different climatic and environmental conditions, the responses of the genotypes varied under these conditions. This clustering of genotypes was highly useful in identifying regional adaptation differences and determining which genotypes were better suitable for specific regions. The clustering of genotypes such as Diyar, D1-3, D1-14, D1-28, and D2-96 under Diyarbakir location showed that these genotypes had a higher performance for yield compared to other genotypes in this location.

These genotypes were found to have a high adaptation structure to the soil and climate conditions of Diyarbakır. In the Kızıltepe region, Gökçe, Azkan, DZ-87 and FLIP98-143C were clustered. The temperature in Kızıltepe, climate and soil conditions of these genotypes showed that they were well suited to this region. The superior yield and stability of the FLIP98-143C and FLIP98-206C genotypes in this region showed that these genotypes could be recommended specifically for Kızıltepe. The closeness of FLIP98-206C and FLIP98-143C in the graph showed that these two genotypes responded similarly to environmental conditions and therefore showed comparable performance in both locations. There was a significant distance between genotypes located in different clusters such as Azkan and Diyar. This indicated that the responses of these two genotypes to environmental conditions considerably differed, and they performed better in different locations (Figure 3).

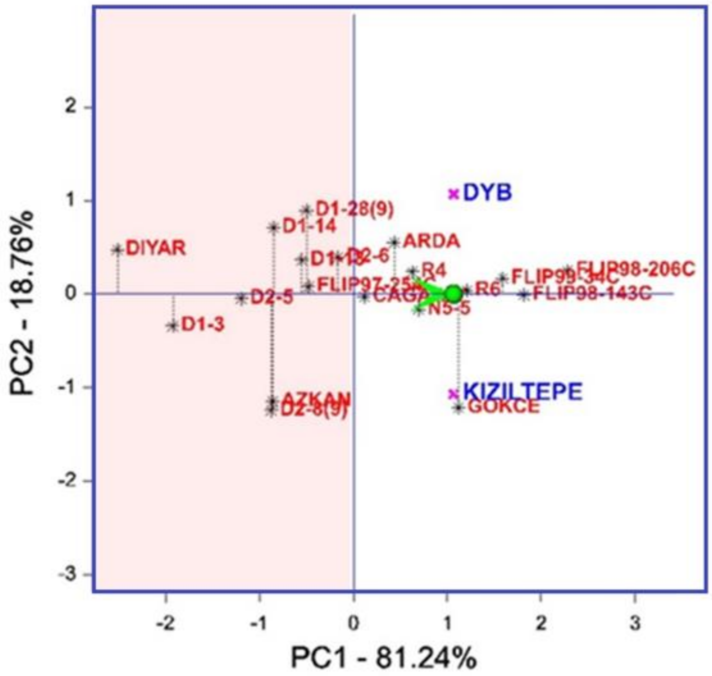

Figure 4. The determination of stability of genotypes based on average environment coordination (AEC) by ranking biplot analysis

Figure 4 represents a ranking biplot analysis based on the Average Environment Coordinate (AEC) method to determine the stability of chickpea genotypes. In this graph, the performance and stability of genotypes for yield were evaluated. The AEC line indicated whether the genotypes were close to the average yield and how well they adapted to environmental conditions. Genotypes located on or near the AEC line were considered closer to the average yield and generally stable, while those farther from the line were less stable and exhibited more variable performance under different environmental conditions.

The clustering of genotypes in two separate locations can be interpreted as an indication of their specific adaptation capabilities to environmental conditions. Genotypes located in the Kiziltepe region were more adapted to the environmental conditions of this region and exhibited higher yield performance. On the other hand, genotypes clustered in the Diyarbakir region were better adapted to its specific conditions. Diyar, Azkan, and D1-3 located near or along the AEC line in the graph suggested that these genotypes were more stable compared to others in terms of stability. In contrast, genotypes positioned farther from the AEC line (FLIP98-206C) were more sensitive to environmental conditions and exhibited variable performance for yield (Figure 4).

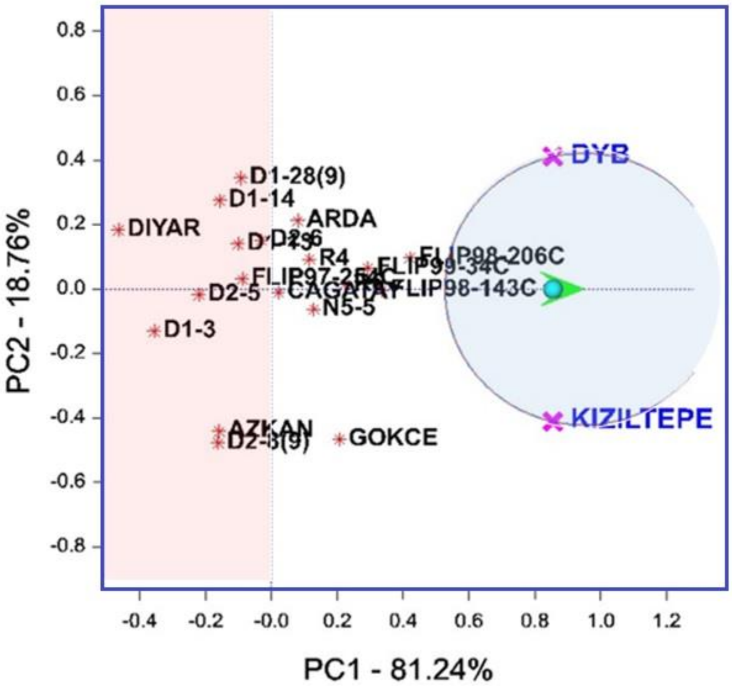

Figure 5. Ranking of genotypes according to ideal center by comparison biplot analysis

Figure 5 compares the yield performance and stability of chickpea genotypes in different locations with the ideal genotype. The ideal genotype represented the best characteristics for high yield and stability, and the proximity of genotypes to this center was used to assess their performance and adaptability. In the graph, the ideal genotype was positioned at a central location, and the distances of other genotypes from this center indicated their overall performance in yield and stability.

Genotypes located closest to the ideal centre were the most suitable for high-yield potential and environmental stability. In this graph, FLIP98-206C and FLIP98-143C were located closer to the ideal center, and these genotypes exhibited above-average performance in both locations. Genotypes located farther from the ideal center had a lower ideal performance for yield and stability. Especially, D1-3, Azkan, and DZ-87 located at a distance from the ideal genotype indicated lower adaptability for both yield and stability.

The clustering of genotypes based on Kiziltepe and Diyarbakir locations reflected the impact of environmental factors in these locations on the stability of the genotypes. The proximity of the Gokce genotype to the Kiziltepe cluster indicated that this genotype was better adapted to Kiziltepe and performs well under its environmental conditions. Evaluating genotypes based on such a biplot analysis was crucial for identifying genotypes that exhibited high yield and stability in both environments. Among genotypes, FLIP98-206C located near the ideal center demonstrated wide adaptability. Therefore this genotype could be used as parents in breeding programs. Conversely, genotypes with low environmental adaptability (D1-3) should be required to be reassessed for different environmental conditions or have their use in breeding programs limited (Figure 5).

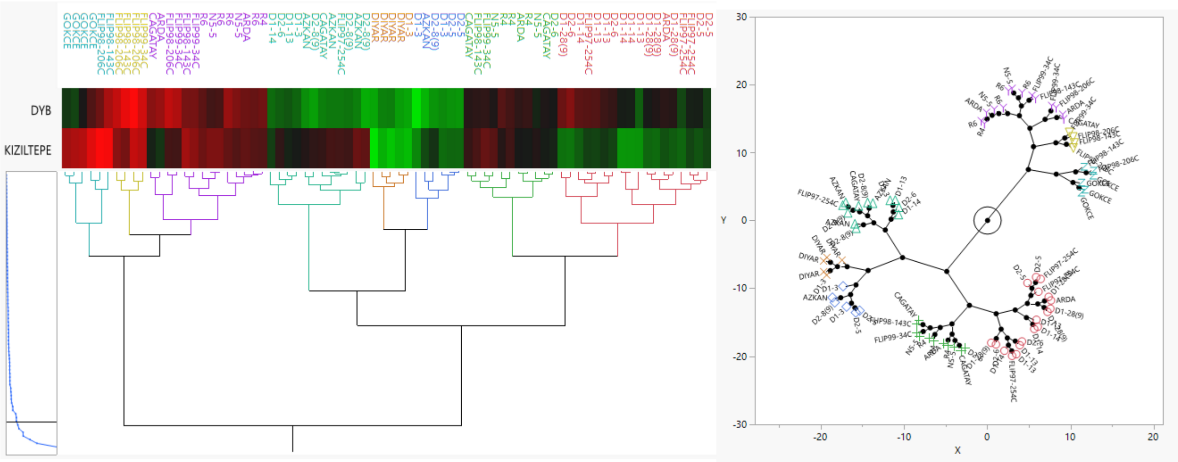

Figure 6. Clustering analysis by using Wards method for summer sowing

This graph represents the clustering analysis performed using the Ward method. On the left side of the graph, the dendrogram illustrated the clustering of genotypes, while on the right side, the visual representation of genotypes was shown using multidimensional scaling (MDS). This analysis aimed to group genotypes into similar clusters based on their yield performance and similarities. The Ward method clustered genotypes according to their degree of similarity, enabling a clearer observation of their responses to environmental conditions (Ward, 1963). The dendrogram in the graph showed how genotypes were grouped into clusters and how these clusters were organized based on yield and environmental responses.

In the graph, genotypes evaluated separately for Diyarbakir and Kiziltepe locations were placed in different clusters based on their responses to environmental conditions. This indicated that the environmental differences observed in these two locations affect the yield and stability performance of the genotypes. Genotypes within the same clusters demonstrated better adaptation to similar environmental conditions and exhibited high yield and stability characteristics (Figure 5). This suggested that these genotypes could be utilized in agricultural practices and breeding programs to ensure yield and stability under similar environmental conditions (Milligan and Cooper, 1987). This analysis was crucial for identifying which location genotypes achieved higher yields and where they maintained stable performance (Kaufman and Rousseeuw, 2005). The similarities identified in the clustering analysis of genotypes facilitated the selection of genotypes most suitable for varying environmental conditions. Utilizing these genotypes as parents in future breeding programs will contribute to the development of varieties with a broad adaptation capacity (Hair et al., 2014).

4.Conclusion

The GGE biplot analysis in the study demonstrated that genotypes respond differently to various environmental conditions and possess broad adaptation ability. The genotypes FLIP98-206C and FLIP98-143C, positioned close to the ideal center in the biplot analysis, were shown to have high yield potential and stability. In contrast, genotypes such as D1-3 and Azkan were found to exhibit lower stability and yield performance. It is recommended that high-yielding and broadly adapted genotypes like FLIP98-206C and FLIP98-143C be prioritized for trials in regions such as Diyarbakir and Kiziltepe. However, large-scale experiments in these regions will provide a more detailed understanding of the long-term yield and stability performance of these genotypes. Additionally, the adaptability of these genotypes should be tested in other arid and semi-arid regions to plan their widespread cultivation under suitable conditions. Additionally, for low-performing genotypes (D1-3 and Azkan), it is recommended to identify narrower target regions and focus more intensively on breeding efforts in these areas. Developing specific tolerances of these genotypes to certain environmental conditions and conducting improvement studies in this direction will provide a more strategic approach to their utilization.

Declaration of Author Contributions

The authors declare that they have contributed equally to the article. All authors declare that they have seen/read and approved the final version of the article ready for publication.

Declaration of Conflicts of Interest

All authors declare that there is no conflict of interest related to this article.

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