



GGE-BIPLLOT ANALYSIS OF DURUM WHEAT YIELD TRIALS

Yüksel KAYA^{1*}


¹Department of Crop Science, Faculty of Agriculture, Siirt University, 56800, Siirt, Turkey

Abstract: Durum wheat (*Triticum durum* L.) is a vital crop in the rain-fed areas of Turkey. In this study, the grain yield of twenty durum wheat genotypes (sixteen advanced lines with four checks) tested across 8 rain-fed environments during the 2008-2009 cropping season was evaluated using GGE (Genotype (G) Main Effect + Genotype by Environment Interaction (GEI)) Biplot Approach. Environment (E) captured most (83 %) of the grain yield (GY) variation, while the portions attributed to G and GEI were only 6 and 11 %, respectively. In addition, most of the testing Es were highly correlated. According to GGE-Biplot analysis, 'Which won where' pattern partitioned the testing Es into three mega-environments (ME): the first ME with six Es with G13 (the highest yielder) as the winning genotype; the second ME encompassed one environment (E1, Konya) with G4 (the lowest yielder) as the winning genotype, and the last ME represented by one location (E6, Altintas) with G10 (the higher yielder) as the winning genotype. GGE-Biplot analysis showed that although the Durum Wheat Yield Trials were conducted in many environments, outcomes alike can be obtained from one or two representatives of each ME. On the other hand, no correlation of these MEs with their geographic location was observed. In conclusion, the presence of cross-over GEI underscores that efforts should be given to identify specifically adapted genotypes rather than broadly adapted ones tested on multi-environment trials (METs).

Keywords: Durum wheat, Genotype by environment interaction, GGE-Biplot, Grain yield

*Corresponding author: Department of Crop Science, Faculty of Agriculture, Siirt University, 56800, Siirt, Turkey

E mail: y.kaya@siirt.edu.tr (Y. KAYA)

Yüksel KAYA  <https://orcid.org/0000-0003-3969-3097>

Received: February 07, 2022

Accepted: February 18, 2022

Published: April 01, 2022

Cite as: Kaya Y. 2022. GGE-Biplot analysis of durum wheat yield trials. BSA Agri, 5(2): 104-109.

1. Introduction

Multi-environment trial (MET) plays an essential role in plant breeding. The main goal in plant breeding is to select new cultivars agronomically superior (i.e., high grain yield) over commonly grown cultivars (Rakshit et al., 2012; Li and He, 2021). However, little attention is given to the interaction of genotypes with unpredictable target environments. In this context, METs can help understand genotypes' performance in various environments by measuring the stability of genotypes (Gs) across environments (Es) (Tekdal et al., 2017; Scapim et al., 2000). But, MET data are rarely used to their full potential, even though data on most plant traits have been collected. Furthermore, in the analysis of such data, primarily genotypes are selected based on G main effects, while GEI (genotype by environment interaction) is ignored (Yan and Tinker, 2006; Kendal, 2019).

Various statistical models have been suggested to analyze the complexity of the GEI (Yan and Kang, 2003). One of those models, the biplot methodology, depicts the complex GEI in a simple, graphical fashion (Gabriel, 1971). Two types of Biplot, AMMI (Additive Main-effect and Multiplicative Interaction) Biplot (Crossa, 1990; Gauch, 1992) and GGE (Genotype + Genotype by Environment Interaction) Biplot (Yan et al., 2000; Yan and Kang, 2003), are the most commonly used to understand GEI comprehensively. Both G and GEI should simultaneously be included in a model to evaluate

genotypes (Yan and Tinker, 2006; Sabaghnia et al., 2008). The G + GEI (GGE) biplot discards E main effects and merges G main effects with the GEI dataset (Yan et al., 2000). It dissects the GEI pattern in the data and delineates 'which-won-where' and mega-environments (Yan et al., 2007; Yan, 2019; Yan et al., 2021).

So far, GGE-biplot analysis has been applied to many crops such as soybean (Yan and Rajcan, 2002), rice (Samonte et al., 2005), bread wheat (Kaya et al., 2006; Roozeboom et al., 2008; Akcura et al., 2011; Nehe et al., 2019), barley (Dehghani et al., 2006; Mohammadi et al., 2009), peanuts (Putto et al., 2008), lentils (Sabaghnia et al., 2008), corn (İlker et al., 2009), oats (Yan et al., 2010) and sorghum (Rao et al., 2011). However, despite reports on GGE-biplot analysis in selecting superior genotypes or test environments in such crops, its application to durum wheat METs in Turkey is insufficient (Tekdal et al., 2017; Kendal, 2019; Mohammadi et al., 2021). Genotypes (i.e., breeding lines) are routinely tested to select ones adaptable to Turkey's Winter Durum Wheat Zone. The target environments (i.e., Winter Durum Wheat Zone) are distributed across latitudes and altitudes with various climatic conditions, representing durum wheat-growing areas in the Central Anatolian Region and Transition Regions of Turkey. Therefore, to show the usefulness of the GGE-Biplot method in dissecting the complex GEI in MET data, we analyzed the GYs of 16 improved lines with four checks tested in eight rainfed environments.



2. Material and Methods

2.1. Field Trials

During the 2008-2009 cropping season, 20 winter durum wheat genotypes were tested in eight rainfed sites (Konya, Çumra, Eskişehir, Ulaş, Emirdağ, Altındaş, Esenboğa, and Malya), representing the Central Anatolia Region (CAR) and Transition Regions (TZs) of Turkey (Tables 1 and 2). The experiment was set up in a randomized block design with three replications. Sowing was done with an experiment drill in 1.2 m × 7 m plots (6 rows with 20 cm spacing apart). The sowing rate was 550 seeds m⁻². Fertilizers were applied as 27 kg N ha⁻¹ and 69 kg P₂O₅ ha⁻¹ during planting and 50 kg N ha⁻¹ just before the stem elongation stage (Zadoks Stage 30). Harvest was done by a plot-combine in 1.2 m × 5 m plots. Grain yield (GY) was expressed as tonnes per hectare (t

ha⁻¹).

2.2. Statistical Analysis

In the analysis of variance (ANOVA), the E and blocking effects were accepted as random, while the G effect was accepted as fixed. ANOVA was applied to GY data combined over the years. Gs and Es were descending ranged based on LSD (Least Significant Difference) test. Gs performances, their stabilities, and the ideal G were determined by the GGE-Biplot analysis method. Also, following the same process, the distinctive and representative abilities of the Es and the ideal E were determined. Again, thanks to the related procedure, ME and which-won-where patterns were determined for Es and Gs. ANOVA, LSD test and GGE-biplot analysis were conducted using GENSTAT 12 (Yan et al., 2000; Yan et al., 2001; Yan, 2002).

Table 1. Genotypes

Code	Pedigree	Yield (t ha ⁻¹)
G1	1-KOBAK2916*61-130/3/GOKALA//BR180/WLS/4/ B24SYRIAN-2	3.02 ^{eg}
G2	2-KOBAK2916*61-130/3/GOKALA//BR180/WLS/4/ B24SYRIAN-2	2.75 ^j
G3	KND1149//68111/WARD/3/RICCYA(WINTER)/BERK	3.01 ^{eg}
G4	1-ALTINTAS/3/ZF/LDS//185-1/3/61-130/LDS	2.58 ^k
G5	KIZILTAN	2.81 ^{ij}
G6	2-ALTINTAS/3/ZF/LDS//185-1/3/61-130/LDS	2.86 ^{gh}
G7	3-ALTINTAS/3/ZF/LDS//185-1/3/61-130/LDS	3.00 ^{gh}
G8	073-44/BERKMEN 469 WINTER	2.83 ^{hj}
G9	TA=TRANSVAAL AFRIKCA/BERK469/GERARDO516	2.97 ^{gh}
G10	KUNDURU	3.25 ^{bd}
G11	AKBUG."S"/RUGBY NEW.N.DURUM/BD2777//SARI BUG.	2.97 ^{gh}
G12	1-61-130/UVY162/64140/WARD	3.10 ^{cf}
G13	HARA456/4/61-130/414-44//68111/WARD/3/69T02/69T11/ ZF7113	3.75 ^a
G14	2-61-130/UVY162/64140/WARD	3.29 ^b
G15	MIRZABEY	3.26 ^{bc}
G16	3-61-130/UVY162/64140/WARD	3.32 ^b
G17	CKM79/KOBAK/LEEDS//6783	3.18 ^{be}
G18	WALNOVA GE 598(ITALIA)//YUMA/FATO"S"/3/ TWWOH84-32	3.08 ^{df}
G19	BERK469//68140/WARD/CKM79"S"	3.06 ^{ef}
G20	ALTINTAS	3.09 ^{cf}
	Mean	3.06
	LSD (0.05)	0.17

Genotypes were descending ranged based on LSD (Least Significant Difference) test.

Table 2. Environments

Code	Environment	Yield (t ha ⁻¹)	Precipitation (mm)	Latitude	Longitude	Altitude (m)
E1	Konya	1.86 ^h	320	37°51' N	32°33' E	1029
E2	Cumra	4.47 ^a	285	37°35' N	32°38' E	1012
E3	Eskisehir	2.91 ^e	371	39°48' N	30°27' E	813
E4	Ulas	2.23 ^f	353	39°16' N	36°46' E	1472
E5	Emirdag	4.29 ^b	416	39° 4' N	31°21' E	959
E6	Altindas	3.47 ^c	560	39° 3' N	30° 6' E	1019
E7	Esenboga	2.11 ^g	402	40° 7' N	32°59' E	942
E8	Malya	3.16 ^d	310	39°16' N	34°18' E	1157
	Mean	3.06				
	LSD (0.05)	0.11				

Environments were descending ranged based on LSD (Least Significant Difference) test.

3. Results

3.1. Analysis of Variance

Analysis of variance (ANOVA) revealed that E and G main effects and GEI were significant ($P < 0.001$, Table 3). As is typical of most METs, GY was significantly affected by E, accounting for 83% of the total variation (G+E+GEI). However, the effect of GEI was greater than that of Gs. The Gs ratio of 17% over (G+GEI) suggested the possible

presence of multiple durum wheat mega-environments (MEs) in the CAR and TZs of Turkey, where the genotype rank was different from other MEs. Partitioning the G + GEI by GGE biplot analysis showed that the first two principal components (PC1 and PC2) were factors, accounting for 70% of the total sum of squares of G+GEI (Figure 1).

Table 3. Analysis of variance for grain yield

Source	df	SS	MS	F	Model	Explained (%)
Environment (E)	7	404.19	57.74	184.04***	Random	83
Replication (E)	16	5.02	0.31			
Genotype (G)	19	28.30	1.49	3.86***	Fixed	6
G x E Interaction	133	51.29	0.39	4.00***	Random	11
Error	304	29.28	0.10			
Total	479	518.08				100

CV(%) = 10.14 R² = 0.94 Mean = 3.06 t ha⁻¹

***= significant at the 0.001 probability level.

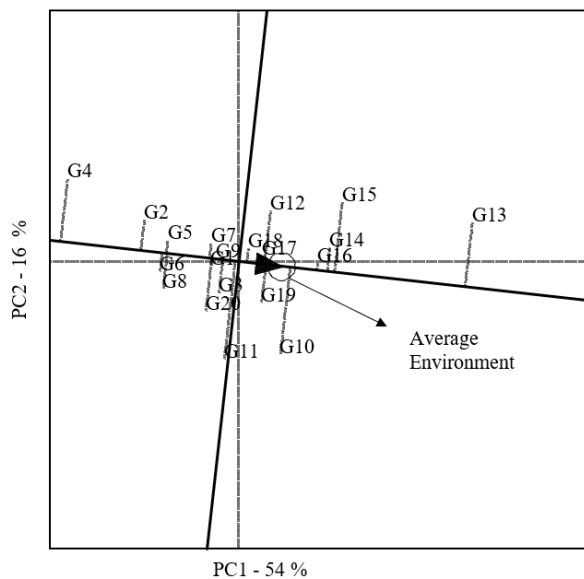


Figure 1. Comparing genotype performance vs. stability. G stands for genotypes.

3.2. Genotype and Environment Means

The average GYs of genotypes over environments ranged from 2.58 t ha⁻¹ for G4 to 3.75 t ha⁻¹ for G13, with an overall average of 3.06 t ha⁻¹ (Table 1), whereas the average GYs for environments varied between 1.86 t ha⁻¹ in E1 (Konya) and 4.47 t ha⁻¹ in E2 (Çumra) (Table 2). Average GY in the GEI data matrix (data not given) ranged from 1.40 t ha⁻¹ for the G4 genotype in E7 (Esenboğa) to 5.74 t ha⁻¹ for G13 in E5 (Emirdağ). The lowest and highest yielding genotypes were originated from Turkey's Winter Durum Wheat Breeding Program.

3.3. Genotype Performance and Stability

The genotype performance and stability were depicted by the GGE biplot (Figure 1). Also, it can be evaluated together with the average environmental coordination (AEC) method (Yan, 2001; Yan, 2002). Accordingly, G16

and G14 were the best performers in terms of GY, followed by G17 and G18 (Figure 1). On the other hand, G2 and G4 were the worst yielders. It can be observed that G15, G12, G19, and G10 were the least stable for GY with higher projections from the AEC abscissa. In contrast, G1 and G9 were relatively stable, if not higher grain yielders. G13 was the highest grain yielder but not stable.

Furthermore, Figure 2 showed the genotype ranking for GY in terms of the 'ideal genotype', indicating the best performer with stability across environments (Yan and Tinker, 2006). Our study revealed that G13 followed by G16, G14, and G15 was close to the ideal genotype. Those were high yielders within all genotypes tested, but G13 and G15 were not stable (Table 1).

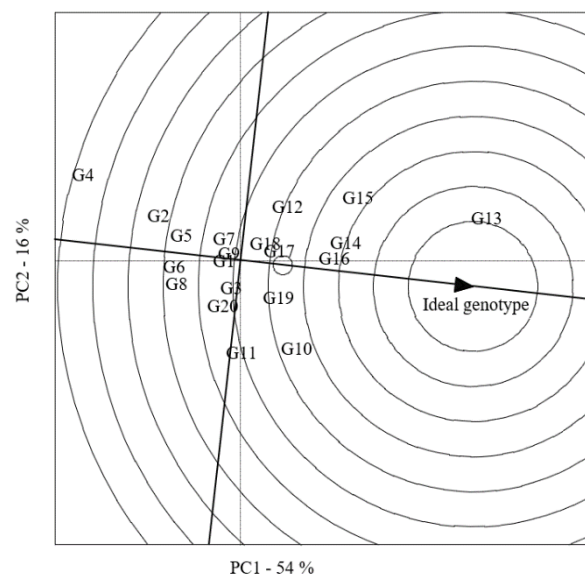


Figure 2. Detecting ideal genotype. G stands for genotypes.

3.4. Comparison of Environments

Most environments were highly correlated for GY, except E1 and E6 (Figure 3). E1 consistently showed inverse relationships with the remaining environments, as the vector showed wide-angle. However, E2, E3, E5, and E8 were not associated with close right angles to E6 and E4 (Yan and Tinker, 2006).

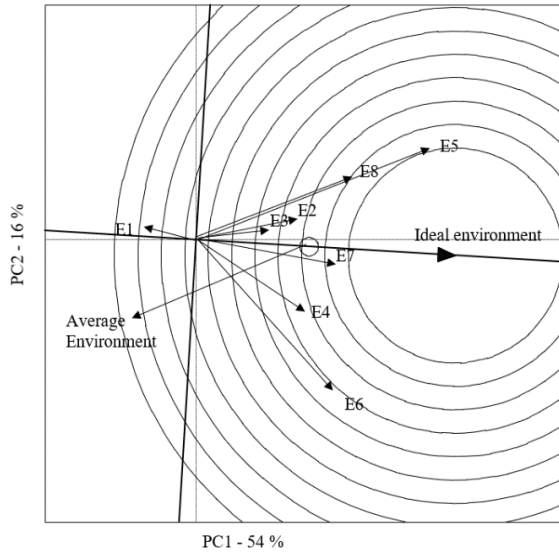


Figure 3. Detecting environment representativeness, its discriminative ability, and ideal environment. E stands for environments.

The vector length of an environment represents its discrimination ability (Yan et al., 2000). Therefore, E5 and E6 were the most discriminatory environments. The angle between an environment and AEC represents the representativeness of the environment: the larger the angle, the less representative the environment (Yan et al., 2000). Therefore, E7 was the most representative while E6 was the least representative. An ideal environment should both distinguish genotypes and represent the average environment. According to the definition of an ideal environment, there was no ideal environment between them (Figure 3). However, E7 as the most representative environment and E5 as the most discriminatory environment could be considered ideal if combined.

3.5. Which-Won-Where Pattern and Mega-Environment Detection

The which-won-where biplot is established by combining the furthest (i.e., vertex) genotypes that form a polygon (Yan, 2001). Genotypes at the polygon's vertices are either the best or the poorest in one or more environments. The genotype at the vertex of the polygon performs best in the environment entering the sectors. The which-won-where biplot for GY is presented in Figure 4. Biplot demonstrated the presence of the cross-over GEI and mega-environments (MEs) for GY. The biplot (Figure 4) was substantially illustrative as it could distinguish environments more effectively and the polygon (trapezoid) was well distributed (Yan, 2002; Yan

and Tinker, 2006). The trapezoidal polygon had four genotypes, namely G13, G4, G11, and G10 (Figure 4). G13 genotype performed best in 1E2 (Cumra), E3 (Eskişehir), E4 (Ulas), E5 (Emirdağ), E7 (Esenboğa) and E8 (Malya), while G4 performed best in E1 (Konya) and G10 in E6 (Altıntaş). The vertex genotype G11 did not perform well in any test environments. The equality lines effectively divided the biplot into four sectors, holding all environments. Thus, the test environments were divided into three MEs: the first ME1 with 1E2 (Cumra), E3 (Eskişehir), E4 (Ulas), E5 (Emirdağ), E7 (Esenboğa), and E8 (Malya), with G13 as the winning genotype. The second ME included E1 (Konya) with G4 as the winning genotype, while the last ME was represented by E6 (Altıntaş) with G10 as the winner. Sector 4 did not have any ME as none of the test environments were engaged. On the other hand, there was no correlation between environments in an ME in terms of geographic location, precipitation pattern, and altitude (Table 2 and Figure 4).

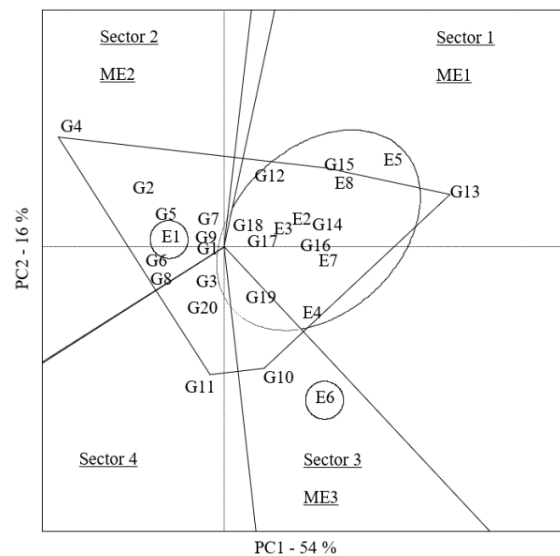


Figure 4. Detecting mega-environments and which-won-where pattern. G and E stand for genotypes and environments.

4. Discussion

The GGE biplot has been used in only a few studies to analyze the MET data of durum wheat in Turkey (Tekdal et al., 2017; Kendal, 2019). In our research, E contributed 83% of the total variation in the data, whereas G and GEI contributed less. Gauch and Zobel (1997) reported that E usually accounted for approximately 80% of the total variation in MET data. In the MET data of bread wheat, Kaya et al. (2006) reported that the variation described by E was as high as 81%. A similar trend was reported by Dehghani et al. (2006) for barley MET in Iran. Putto et al. (2008) revealed that 50-80% of the total variation attributed to E, while the main effect of G contributed 15-46% of the total variation. In our study, GEI explained a higher proportion of variation than G alone. Compared with G, the higher ratio of GEI indicated the possible presence of different MEs in the test Es (Yan and Hunt,

2002; Mohammadi et al., 2009; Akcura et al., 2011; Rakshit et al., 2012; Kendal, 2019).

In our study, the first two PC explained 70% of the variability for the GY data of durum wheat METs. Also, G, together with GEI, accounted for 17% of the total variation for GY. Thus, the GGE-biplot can be interpreted as a useful visualization of variation in MET data (Gauch and Zobel, 1997). Furthermore, visual representation of PC1 and PC2 revealed the variation in the dataset. Thus, it was clear that five of the nine high grain yielders (G13, G15, G12, G10, and G19) were unstable, while eight of the eleven low yielders (G1, G3, G9, G7, G6, G5, G8, and G2) were stable. This can be explained by the fact that a different gene cluster governs the trait of interest, and the effect of E on the expression of that gene cluster varies significantly (Li and He, 2021).

The GGE-biplot allows the detection of genotypes close to the ideal genotype. Accordingly, a process alike can be applied to an ideal environment. G13 was most relative to the ideal genotype, followed by G16, G14, and G15. However, the G13 was the highest yielder but less stable. G13, which was closest to the ideal genotype, showed the best performance in E5 (Emirdağ), while it reached nearly the average yield in E6 (Altıntaş) and was behind the average yield at the E1 (Konya). In addition, G13 exhibited different GY values across test environments, indicating the cross-over GEIs (Nehe et al., 2019). A similar observation was reported in various crops (Dehghani et al., 2006; Kaya et al., 2006; Sabaghnia et al., 2008; Dehghani et al., 2008; İlker et al., 2009; Rakshit et al., 2012; Kendal, 2019).

Our study showed that all test environments except E1 and E6 were closely related, and most of them (i.e., E2, E3, E4, E7, and E8) were also close to the average environment. In other words, the discriminating ability and representativeness of test environments could be easily detected. Thus, E5 and E6 with higher vector lengths were more distinctive than E8 and E7. Therefore, environments close to the average environment, such as E7, E2, and E3, were the most representative and suitable test environments for selecting widely adapted genotypes. On the other hand, the distinctive and non-representative E6 helped determine specifically adapted genotypes. Therefore, a specifically adapted genotype to a particular environment could be conveniently described by employing this type of graphical representation (Plavsin et al., 2021).

Furthermore, closer relationships between test environments showed that the same information could be obtained from fewer environments. Thus, similar environments could be eliminated from the future METs for durum wheat in Turkey. It is vital in allocating scarce resources while setting up METs most appropriately (Yan et al., 2021). The presence of wide angles between environment vectors, indicating strong negative correlations between test environments, emphasizes the presence of solid crossover GEIs for GY in some environments (Yan and Tinker, 2006; Yan, 2019). They

noted that genotypes that perform better in one environment would underperform in another. At the same time, closer relationships between the test environments indicate the absence of crossover GEIs, suggesting genotype sequencing does not vary from one environment to another. A mixture of cross-over and non-cross-over GEI types is typical in MET data (Kaya et al., 2006; Fan et al., 2007; Sabaghnia et al., 2008; Rao et al., 2011; Rakshit et al., 2012; Yan, 2019; Yan et al., 2021). It could be possible because some genotypes were more sensitive to changes in the growing environment, while others would be stable in response to the environment.

The 'which-won-where' biplot model may be associated with cross-over GEI, ME differentiation, specific adaptation (Gauch and Zobel, 1997; Yan et al., 2000; Yan and Tinker, 2006; Putto et al., 2008; Rao et al., 2011; Nehe et al., 2019; Li and He, 2021; Plavsin et al., 2021). Based on the biplot analysis, test environments were divided into three MEs. It has been suggested that although testing genotypes has been conducted over many environments, a similar conclusion can be drawn from one or two representatives of ME. By doing so, the testing cost of genotypes over environments can be significantly reduced. However, the Biplot model needs to be validated in multi-year and environmental trials conducted on durum wheat (Yan et al., 2021).

5. Conclusion

The specific adaptation of the genotypes tested in this research suggests that it requires more emphasis than broader adaptation in durum wheat breeding (DWB). In this context, participatory DWB gains more importance than the current research station-oriented breeding program. 'Which-won-where' analysis has shown the existence of MEs, and most geographically different environments can produce similar outcome. Therefore, to effectively run ME with limited resources, discriminatory environments that cover representative environments can be included, rather than broadly expanding the trials onto relevant environments. Following a similar analysis, durum wheat breeders in other regions need to identify MEs and allocate test environments accordingly. The presence of cross-over GEI indicates that the current procedure does not realistically depict the actual situation. Instead, efforts are needed to identify environment-specific genotypes from multi-year and environmental data as this will take into account the stability parameter of the genotypes, so they should be taken into account for their release.

Author Contributions

All task made by single author and the author reviewed and approved the manuscript.

Conflict of Interest

The author declared that there is no conflict of interest.

Acknowledgments

This study was supported by the Ministry of Agriculture and Forestry, Republic of Turkey, Project No: TAGEM/TBAD/13/A12/P05/005.

References

- Akcura M, Taner S, Kaya Y. 2011. Evaluation of bread wheat genotypes under irrigated multi-environment conditions using GGE biplot analyses. *Zemdirbyste-Agri*, 98(1): 35-40.
- Casanoves F, Macchiavelli R, Balzarini M. 2005. Error variation in multi-environment peanut trials. *Crop Sci*, 45: 1927-1933.
- Crossa J. 1990. Statistical analyses of multi-location trials. *Adv Agron*, 44: 55-85.
- Dehghani H, Ebadi A, Yousefi. A. 2006. Biplot analysis of genotype by environment interaction for barley yield in Iran. *Agron J*, 98: 388-393.
- Dehghani H, Omidi H, Sabaghnia. N. 2008. Graphic analysis of trait relations of rapeseed using the biplot method. *Agron J*, 100: 1443-1449.
- Fan XM, Kang MS, Chen H, Zhang Y, Tan J, Xu C. 2007. Yield stability of maize hybrids evaluated in multi-environment trials in Yunnan, China *Agron J*, 99: 220-228.
- Gabriel KR. 1971. The biplot graphic display of matrices with application to principal component analysis. *Biometrika*, 58: 453-467.
- Gauch HG. 1992. AMMI analysis of yield trials. In: Kang MS, Gauch HG, editors. *Genotype-by-environment interaction*. CRC Press, Boca Raton, US, pp: 40.
- Gauch HG, Zobel RW. 1997. Identifying mega-environment and targeting genotypes. *Crop Sci*, 37: 381-385.
- Ilker E, Tonk FA, Caylak O, Tosun M, Ozmen I. 2009. Assessment of genotype x environment interactions for grain yield in maize hybrids using AMMI and GGE biplot analyses. *Turk J Field Crops*, 14(2): 123-135.
- Kaya Y, Akcura M, Taner S. 2006. GGE-biplot analysis of multi-environment yield trials in bread wheat. *Turk J Agric For*, 30: 325-337.
- Kendal E. 2019. Comparing durum wheat cultivars by genotype x yield x trait and genotype x trait biplot method. *Chil J Agr Res*, 79(4): 512-522.
- Li H, He Z. 2021. Warming climate challenges breeding. *Nat Plants*, 7: 1164-1165.
- Mohammadi R, Aghaee M, Haghparast R, Pourdad SS, Rostaii M, Ansari Y, Abdolahi A, Amri. A. 2009. Association among non-parametric measures of phenotypic stability in four annual crops. *Middle East-Russian J Plant Sci Biotec*, 3: 20-24.
- Mohammadi R, Sadeghzadeh B, Poursiahbidi, MM, Ahmadi, MM. 2021. Integrating univariate and multivariate statistical models to investigate genotype x environment interaction in durum wheat. *Ann Appl Biol*, 178: 450-465.
- Nehe A, Akin B, Sanal T, Evlice AK, Ünsal R, Dinçer N, Demir L, Geren H, Sevim I, Orhan Ş, Yaktubay S, Ezici A, Guzman C, Morgounov A. 2019. Genotype x environment interaction and genetic gain for grain yield and grain quality traits in Turkish spring wheat released between 1964 and 2010. *PLoS ONE*, 14(7): e0219432.
- Plavsin I, Gunjaca J, Simek R, Novoselovic D. 2021. Capturing GEI patterns for quality traits in biparental wheat populations. *Agronomy*, 11(6): 1022.
- Putto W, Patanothai A, Jogloy S, Hoogenboom S. 2008. Determination of mega-environments for peanut breeding using the CSM-CROPGRO-Peanut model. *Crop Sci*, 48: 973-982.
- Rakshit S, Ganapathy KN, Gomashe SS, Rathore A, Ghorade RB, Kumar MVN, Ganesmurthy K, Jain SK, Kamtar MY, Sachan JS, Ambekar SS, Ranwa BR, Kanawade DG, Balusamy M, Kadam D, Sarkar A, Tonapi VA, Patil JV. 2012. GGE biplot analysis to evaluate genotype, environment and their interactions in sorghum multi-location data. *Euphytica*, 185: 465-479.
- Rao PS, Reddy PS, Ratore A, Reddy BVS, Panwar S. 2011. Application GGE biplot and AMMI model to evaluate sweet sorghum (*Sorghum bicolor*) hybrids for genotype x environment interaction and seasonal adaptation. *Indian J Agric Sci*, 81: 438-444.
- Roozeboom K, Schapugh T, Tuinstra MR, Vanderlip R, Milliken GA. 2008. Testing wheat in variable environments: genotype, environment, interaction effects, and grouping test locations. *Crop Sci*, 48: 317-330.
- Sabaghnia N, Dehghani H, Sabaghpour SH. 2008. Graphic analysis of genotype by environment interaction for lentil yield in Iran. *Agron J*, 100: 760-764.
- Samonte SOPB, Wilson LT, Mcclung AM, Medley JC. 2005. Targeting cultivars onto rice growing environments using AMMI and SREG GGE biplot analysis. *Crop Sci*, 45: 2414-2424.
- Scapim CA, Oliveira VR, Braccini A, Cruz CD, Andrade CAB, Vidigal MCG. 2000. Yield stability in maize (*Zea mays* L.) and correlations among the parameters of the Eberhart and Russell, Lin and Binns and Huehn models. *Genet Mol Biol*, 23: 387-393.
- Tekdal S, Kendal E, Aktaş H, Karaman M, Doğan H, Bayram S, Düzgün M, Efe A. 2017. Biplot analiz yöntemi ile bazı makarnalık buğday hatlarının verim ve kalite özelliklerinin değerlendirilmesi. *TARM Derg*, 26: 68-73.
- Yan W. 2001. GGEbiplot-A Windows application for graphical analysis of multi-environment trial data and other types of two-way data. *Agron J*, 93: 1111-1118.
- Yan W. 2002. Singular value partitioning for biplot analysis of multi-environment trial data. *Agron J*, 4: 990-996.
- Yan W. 2019. LG biplot: a graphical method for mega-environment investigation using existing crop variety trial data. *Sci Rep*, 9: 7130.
- Yan W, Hunt LA. 2002. Biplot analysis of diallel data. *Crop Sci*, 42: 21-30.
- Yan W, Kang MS. 2003. GGE biplot analysis: a graphical tool for breeders, geneticists, and agronomists. CRC Press, Boca Raton, US, pp: 224.
- Yan W, Rajcan I. 2002. Biplot analysis of test sites and trait relations of soybean in Ontario. *Crop Sci*, 42: 11-20.
- Yan W, Tinker NA. 2006. Biplot analysis of multi-environment trial data: principles and applications. *Canadian J Plant Sci*, 86: 623-645.
- Yan W, Hunt LA, Sheng Q, Szlavnicz Z. 2000. Cultivar evaluation and mega-environment investigation based on GGE biplot. *Crop Sci*, 40: 597-605.
- Yan W, Kang MS, Ma BL, Woods S, Cornelius PL. 2007. GGE biplot vs. AMMI analysis of genotype-by-environment data. *Crop Sci*, 47: 643-653.
- Yan W, Fregeau-Reid J, Pageau D, Martin R, Mitchell-Fetch J, Etienne M, Rowsell J, Scott P, Price M, De Hann B, Cumiskey A, Lajeunesse J, Durand J, Sperry E. 2010. Identifying essential test location for oat breeding in eastern Canada. *Crop Sci*, 50: 504-515.
- Yan W, Mitchell-Fetch J, Beattie A, Nilsen KT, Pageau D, DeHaan B, Hayes M, Mountain N, Cumiskey A, MacEachern D. 2021. Oat mega-environments in Canada. *Crop Sci*, 61: 1141-1153.