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Evaluation of bread wheat genotypes under irrigated multi-environment conditions using GGE biplot analyses

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Abstract

This research was carried out to determine stable genotypes, and investigate genotype environment interaction (GEI) effects on the grain yields of 9 bread wheat genotypes (5 cultivars, 4 advanced lines) across eight irrigated environments in the Central Anatolian Region, in 2002–2003 and 2003–2004 growing seasons. The experimental layout was a randomized complete block design with four replications. GGE biplot methodology was used to evaluate phenotypic stability in genotypes. GGE biplot analysis indicated that the effects of environments, genotypes and genotype environment (GE) were highly significant ($P < 0.01$). The first two principle component axes (PC1 and PC2) were significant ($P < 0.01$) and cumulatively contributed to 76.14% of the total genotype by environment interactions. The biplot (PC1 versus mean grain yield) showed five groupings of genotypes: ‘Line-1’ generally low yielding and unstable (high negative PC1 score); and ‘Line-3’ was low yielding and moderately stable across environments (low positive PC1 score); ‘Katea-1’, ‘Yıldız-98’ and ‘Line-2’ were high yielding, and stable (had low positive PC1 scores). ‘Konya-2002’ was high yielding and moderately stable across environments (low negative PC1 score). For irrigated bread wheat genotypes grain yields were relatively stable at Haymana and Çumra, while grain yields obtained at Konya were unstable across both years. Besides, superior bread wheat genotypes selections with specific or broad adaptation were identified by a biplot generated using genotypic and environmental scores of the first two GGE biplot components (PCA1 and PCA2).

Key words: bread wheat, *Triticum aestivum* L., multi environment trials, GGE biplot.

Introduction

Cultivars grown in multi-environment trials (MET) react differently to environmental changes. This differential response of cultivars from one environment to another is called genotype environment interaction (GEI). GEIs are an important issue facing plant breeders and agronomists. A significant GEI for a quantitative trait such as grain yield can seriously limit progress in selection. The study of the GEI may assist understanding of stability concept. Information on the structure and nature of GEI is particularly useful to breeders because it can help determine if they need to develop cultivars for all environments of interest or if they should develop specific cultivars for specific target environments.

Several methods have been proposed for statistical analysis of GEI and to predict the phe-

notypic response to changes in the environment (Eeuwijk, 1995). The success of identifying high yielding genotypes from yield trials depends on the effectiveness of the statistical analysis used to evaluate patterns in the data and estimated yields (Yan, Kang, 2003).

The biplot method originated with Gabriel (1971), and its use was subsequently expanded by Kempton (1984) and Zobel et al. (1988). The extensive usefulness of GGE biplot, where G = genotype effect and GE = genotype-by-environment effect, has only recently been elucidated (Yan et al., 2001). The GGE biplot approach has strongly captured the imagination of plant breeders and production agronomists.

Biplot analysis is a multivariate analytical technique that graphically displays the two-way

data and allows visualization of the interrelationship among environments, and the interrelationship between GEs. Biplots are useful for summarizing and approximating patterns of response that exist in the original data (Gabriel, 1971). Two types of biplots, GE biplot (Zobel et al., 1988) and GGE biplot (Yan et al., 2000), were used to visualize the GE two-way data but each had its unique functions. The GE biplot refers to graph of the GEI obtained from the Additive Main Effects and Multiplicative Interactions (AMMI) model. The "GGE" refers to the genotype main effect (G) plus the GE interaction, which are the two sources of variation of the Site Regression (SREG) model (Burgueno et al., 2001). The measured yield of each cultivar in each test environment is a measure of environment main effect (E), genotype main effect, and GEI (Yan, Kang, 2003).

The GGE biplot graphically displays G and GE of a MET in a way that facilitates visual cultivar

evaluation and mega-environment identification. The GGE biplot software was chosen to facilitate the application of the GGE biplot methodology in MET data analysis and the analyses of two-way data.

The aim of this study was (i) to identify the structure of GEI in grain yield of irrigated bread wheat genotypes (ii) to identify the genotypes, which could have wide or specific adaptation in irrigated environments of Central Anatolian Region using GGE biplot analysis method.

Materials and methods

The experiment was carried out in 2002 and 2003 at four locations in Turkey. The locations included Konya, Çumra, Haymana and Eskisehir. The agro-ecological characteristics of the locations are shown in Table 1.

Table 1. Environment description, agronomic details and grain yield (t ha⁻¹) for environments

Code	Growing season	Environment	Soil properties	Fertilization kg ha ⁻¹		Rainfall + irrigation mm	Sowing date	Harvesting date
				N	P ₂ O ₅			
K02	2002–2003	Konya	pH = 8.2 clayey, alluvial	36 ^a + 80 ^b	92 ^a	330 + 100	19 10 2002	18 07 2003
C02	2002–2003	Çumra	pH = 8.2 clayey loam, hydro-morphic alluvial	36 + 80	92	430 + 100	16 10 2002	16 07 2003
E02	2002–2003	Eskisehir	pH = 7.8 clayey, red brown	36 + 80	92	375 + 100	10 10 2002	18 07 2003
H02	2002–2003	Haymana	pH = 7.8 clayey, brown	36 + 80	92	252 + 100	11 10 2002	15 07 2003
K03	2003–2004	Konya	pH = 8.2 clayey, alluvial	36 + 80	92	354 + 100	18 10 2003	18 07 2004
C03	2003–2004	Çumra	pH = 8.2 clayey loam, hydro-morphic alluvial	36 + 80	92	280 + 100	16 10 2003	10 07 2004
E03	2003–2004	Eskisehir	pH = 7.8 clayey, red brown	36 + 80	92	265 + 100	10 10 2003	10 07 2004
H03	2003–2004	Haymana	pH = 7.8 clayey, brown	36 + 80	92	181 + 100	11 10 2003	10 07 2004

Note. ^a – seed-bed, ^b – tillering + stem elongation.

Nine bread wheat genotypes (5 cultivars, 4 advanced lines) from the working collection of National bread wheat breeding unit were used in this study, and pedigrees are given in Table 2.

Experimental layout was a randomized complete block design with four replications. Sowing was done by an experimental drill in 1.2 x 7 m plots, consisting of six rows with 20 cm left between the rows. Seeding rate was 450 seeds m⁻² for all environments. Fertilizer application was 36 kg N ha⁻¹ and 69 kg P₂O₅ ha⁻¹ at planting and 40 kg N ha⁻¹ at the tillering stage and at the stem elongation stage. Trials conducted in Konya and Cumra were irrigated at stem elongation and flowering stages, whereas

those in Haymana and Eskisehir were irrigated at pre flowering stage. Harvesting was done in 1.2 x 5 m plots by experimental combine. Grain yield was obtained by converting the grain yields obtained from plots to hectares.

Analysis of variance was conducted by SAS (SAS/STAT User's Guide, 1999) to determine the effect of genotype (G) and GEI among these factors on grain yield. In addition, principal component axes (PCAs) were extracted and statistically tested by Gollob's (1968) F-test procedure (Vargas, Crossa, 2000). The first two components were used to obtain a biplot by GGE biplot (Burgueno et al., 2001), which is a SAS application of MET's data.

Table 2. Code, pedigree, selection history of nine irrigated bread wheat genotypes

Code / cultivars	Pedigree and selection history
Kınacı-97*	Kınacı-97
Konya-2002	Konya-2002
Katea-1	Katea-1
Bezostaja-1	Bezostaja-1
Yıldız-98	Yıldız-98
Line-1	KS82W422/SWM754308//KS831182/KS821422/3/OR7946/HILL//HILL WHQ941891*-1H-1P1P-1YK-0YK
Line-2	AGRI/NAC//ATTILA CMSW92WM00232S-0SE-0YC-4YC-0YC-2YC-0YC
Line-3	FRTL//AGRI/NAC CMSW93WM0071-0AP-0YC-17YE-0YC-1YC-0YC
Line-4	UNKNOWN 96.7 F2.96.7-0SE-4YA-4YC-0YC

* – cultivars

Results and discussion

Genotypes (G), environments (E) and genotype x environment interactions (GEI) were highly significant ($P < 0.01$) on yield and accounted for 2.71%, 83.78% and 10.08% of the total sum of squares, respectively (Table 3).

The constrictive success for GGE biplot using all data (all four replications), indicated that the

GEI sum of squares was partitioned into two components: 76.14% due to PCA1 (52.37%) and PCA2 (23.77%) with 26 degrees of freedom; and 23.86% residual or random variation (noise) with 30 degrees of freedom. The model-validation procedure, therefore, identifies that the 23.86% of the GEI sum of squares as allocated to the residual term was not of predictive value.

Table 3. Combined analysis for grain yield (t ha⁻¹) of nine irrigated bread wheat genotypes across eighth environments

Source	DF	SS	MS	Explained %
Model	95	637.095	6.706**	
Environment (E)	7	533.758	76.251**	83.78
Replication (E)	24	21.868	0.911**	3.43
Genotype (G)	8	17.236	2.154**	2.71
E x G	56	64.233	1.147**	10.08
PC1	14	33.638	2.403**	52.37
PC2	12	15.271	1.273**	23.77
Residual	30	15.324	1.945	23.86
Pooled error	192	61.071	0.318	
Corrected total	287	698.166		
		R ² – 0.91	CV – 11.32	

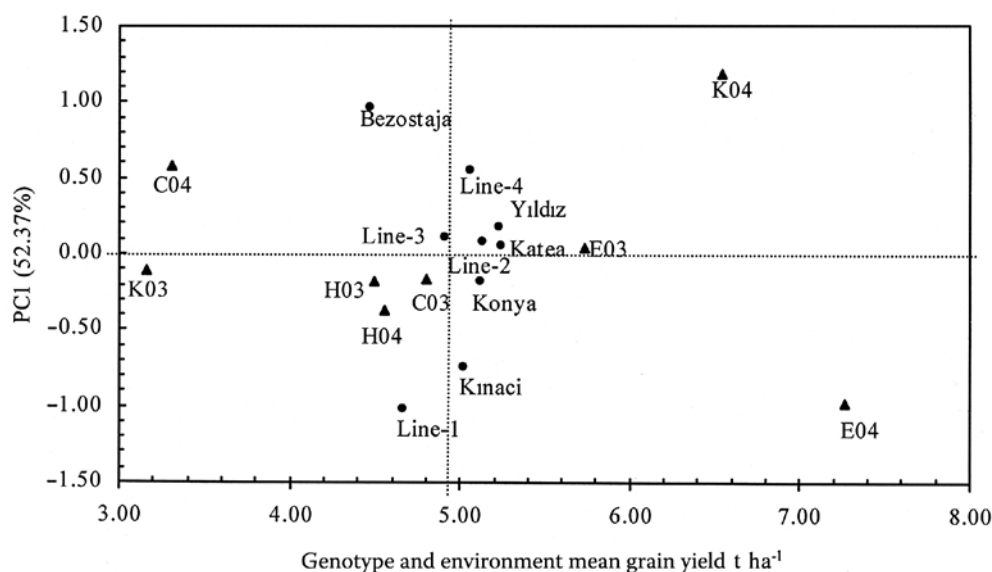
** – significant at 0.01 probability level

The biplot analysis provides a graphical representation (Figure 1) to summarize information on the GE main effects and the first principal component scores of the interactions (PCA1) of both genotypes and environments simultaneously (Kempton, 1984). Displacement along the abscissa reflected differences in main effects, whereas displacement along the ordinate exhibited differences in interaction effects.

Genotypes or environments on the same parallel line, relative to the ordinate, have similar yields (Figure 1), and a genotype or environment on the right side of the midpoint of this axis has higher yields than those on the left hand side. Consequently, genotypes 'Konya-2002', 'Katea-1', 'Yıldız-98' and 'Line-2' were generally high yielding, with 'Katea-1' being the overall best. In contrast, 'Bezostaja-1', 'Line-1' and 'Line-3' were generally low

yielding genotypes. Four groupings were evident from the biplot (Figure 1): 'Line-1' generally low yielding, and unstable (high negative PC1 score); and 'Line-3' were low yielding and moderately stable across environments (low positive PC1 scores);

'Katea-1', 'Yıldız-98' and 'Line-2' were high yielding, and stable (had low positive PC1 scores). 'Line-4' was high yielding and very unstable across environments (high positive PC1 score).



Notes. ● – genotypes, ▲ – environments; K03 – 'Konya-03', K04 – 'Konya-04', E03 – 'Eskişehir-03', E04 – 'Eskişehir-04', H03 – 'Haymana-03', H04 – 'Haymana-04', C03 – 'Cumra-03', C04 – 'Cumra-04'. The vertical and horizontal lines represent the grand mean yield (4.90 t ha⁻¹) and PC1 (first principal component axes) = 0, respectively.

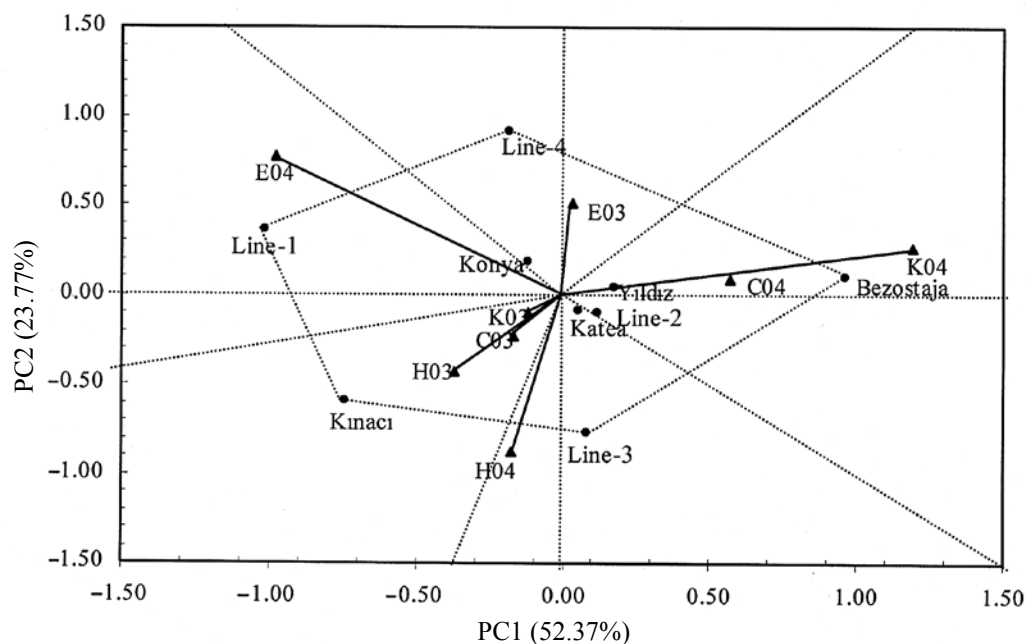
Figure 1. Biplot for grain yield of irrigated wheat genotypes and environment in Turkey

Genotypes with PC1 scores near zero had little interaction across environments and *vice versa* for environments (Crossa et al., 1991). For such genotypes, overall mean ranking is a reliable measure. Genotype and environment combinations with PC1 scores of the same sign produced positive specific interaction effects, whereas combinations of opposite signs had negative specific interactions. Four genotypes 'Katea-1', 'Yıldız-98', 'Line-2', and 'Konya-2002' had negligible interactions with the environments, indicating their broad adaptations with 'Katea-1' being the most stable genotype across environments (Figure 1). Genotypes, 'Line-4', 'Kınacı-97' and 'Line-1' were highly unstable and were generally poorly adapted to the environments.

In 2002–2003 growing season, GEI was generally low compared to 2003–2004. Discriminating ability is an important measure of a test location. A test location's lack of discriminating ability provides no information about the cultivars and, therefore the test location is useless. Another equally important measure of a test location is its representativeness of the target location. If a test location is not representative of the targets location, it is not only useless but also misleading since it may provide biased information about the tested cultivars. An ideal location should be highly differentiating of the genotypes and at the same time representative of

the target location. The GGE biplot way of measuring representativeness is to define an average location and use it as a reference or benchmark (Yan, Kang, 2003). Overall, Eskişehir had lower PCA1 scores than the other locations. Generally, Çumra and Haymana environments had moderate GE interaction effects (average PCA1 scores), while Konya had the highest PCA1 values and exhibited the most unstable yields. Thus, Konya would be a good selection site for bread wheat improvement when targeting a wide range of environments.

The GGE biplot graphically displays G plus GE of a MET in a way that facilitates visual cultivar evaluation (Yan et al., 2000). Only two PC (PC1 and PC2) are retained in the model because such a model tends to be the best model for extracting patterns and rejecting noise from the data. In addition, PC1 and PC2 can be readily displayed in a two-dimensional biplot so that the interaction between each genotype and each environment can be visualized (Yan, Hunt, 2002). The convex hull in (first two significant PC axes) Figure 2 is drawn on genotypes relatively remote from the biplot origin so that all other genotypes are contained within the convex hull. Figure 2 also contains a set of lines, perpendicular line does not necessarily intersect the convex-hull side; it may only intersect extension of the convex-hull side, e.g. the convex-



Note. ● – genotypes, ▲ – environments; K03 – ‘Konya-03’, K04 – ‘Konya-04’, E03 – ‘Eskişehir-03’, E04 – ‘Eskişehir-04’, H03 – ‘Haymana-03’, H04 – ‘Haymana-04’, C03 – ‘Çumra-03’, C04 – ‘Çumra-04’.

Figure 2. Biplot representation for the yield data for nine irrigated bread wheat genotypes grown in eight environments in Turkey, showing the first two principal axes

hull side that connects ‘Line-3’ and ‘Kinacı-97’. These perpendiculars divide the biplot into several sectors, and the environments inevitably fall into the sectors (Yan, 2001). There are five sectors in Figure 2, with genotypes ‘Bezostaja-1’, ‘Line-1’, ‘Kinacı-97’, ‘Line-3’ and ‘Line-4’ as the corner or vertex genotypes. Environments K04 (‘Konya-04’) and C04 (‘Çumra-04’) fell in the sector in which ‘Bezostaja-1’ was the vertex genotype. This means that ‘Bezostaja-1’ was the best genotype for K04 and C04. H04 (‘Haymana-04’) fell in the sector in which ‘Line-3’ was the vertex genotype, ‘Line-3’ was the best for H04, K03 (‘Konya-03’), C03 (‘Çumra-03’), H03 (‘Haymana-03’) fell in the sector in which ‘Kinacı-97’ was the vertex genotype, ‘Kinacı-97’ was the best for K03, C03, H03, E04 (‘Eskişehir-04’) fell in the sector in which ‘Line-1’ was the vertex genotype, ‘Line-1’ was the best for E04; E03 (‘Eskişehir-03’) fell in the sector in which ‘Line-4’ was the vertex genotype, ‘Line-4’ was the best for E03. Cultivars ‘Katea-1’, ‘Yıldız-98’, ‘Line-2’ and ‘Konya-2002’ had above-average yield in all environments except K04, E04 and H04. Another application of the GGE biplot geometry is to visually identify the mean performance and stability of genotypes. The mean yield of the genotypes can then be approximated by nominal yields of the genotypes in that mean location. The performance of genotypes ‘Line-4’, ‘Kinacı-97’ and ‘Line-1’ are highly variable (less stable), whereas genotypes ‘Katea-1’, ‘Yıldız-98’ and ‘Line-2’ are highly

stable. An ideal genotype is one that has both high mean yield and high stability. Both ‘Bezostaja-1’ and ‘Konya-2002’ has red grains and same quality characters. ‘Bezostaja-1’ is still growing under most of irrigated areas of Central Anatolian region, so we need to compare ‘Konya-2002’ and ‘Bezostaja-1’ indicating that ‘Bezostaja-1’ had higher yield in only C04 and K04, whereas ‘Konya-2002’ had higher yield in all the environments. According to these results ‘Konya-2002’ is better than ‘Bezostaja-1’ thus, can be recommended for farmers in this region. In addition, the ideal test environment should have large PC1 scores (more power to discriminate genotypes in terms of the genotypic main effect) and small (absolute) PC2 scores (more representative of the overall environments) (Yan, Kang, 2003; Kaya et al., 2006). Thus, Konya location can be evaluated as an ideal test environment.

Conclusion

The GGE biplot analysis is an important tool for selecting high yielding, stable genotype. The genotypes ‘Katea-1’, ‘Yıldız-98’, ‘Line-2’ and ‘Konya-2002’ were hardly affected by the GEI effects and thus would perform well across a wide range of environments. In conclusion, Konya location can be regarded as a good selection site for irrigated bread wheat improvement programs.

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Duoninio kviečio genotipų vertinimas įvairiomis drėkinamos aplinkos sąlygomis taikant *GGE biplot* analizę

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Santrauka

Tyrimai atlikti aštuoniuose drėkinamos aplinkos variantuose, siekiant nustatyti stabilius genotipus ir iširti genotipo bei aplinkos sąveikos įtaką duoninio kviečio 9 genotipų (5 veislių ir 4 perspektyvių linijų) grūdų derliui Centrinės Anatolijos regione vegetacijos laikotarpiu 2002–2003 ir 2003–2004 m. Tyrimų laukeliai išdėstyti atsitiktinai keturiais pakartojimų blokais. Taikant *GGE biplot* analizę vertintas genotipų fenotipinis stabilumas. *GGE biplot* analizė parodė, kad aplinkos, genotipų ir genotipo bei aplinkos sąveikos įtaka buvo esminė ($P < 0.01$). Pirmosios dvi pagrindinės komponentų ašys (PC1 ir PC2) taip pat buvo esminės ($P < 0.01$) ir apėmė 76,14 % visų genotipo bei aplinkos sąveikų. *Biplot* metodu (lyginant PC1 ir grūdų vidutinį derlių) genotipai skirstyti į tokias grupes: 'Line-1' buvo nederlinga ir nestabili, 'Line-3' taip pat buvo nederlinga, tačiau vidutiniškai stabili skirtingose aplinkose, 'Katea-1', 'Yıldız-98' bei 'Line-2' buvo labai derlingos ir stabilios, 'Konya-2002' buvo derlinga ir vidutiniškai stabili. Drėkinant duoninio kviečio genotipų grūdų derlius buvo gana stabilus Haymana ir Çumra vietovėse, o Konya vietovėje gautas grūdų derlius abiem metais buvo nestabilus. Be to, pranašesni specifiniai arba gerai prisitaikę duoninio kviečio genotipai nustatyti taikant *biplot* metodą, sukurtą panaudojus pirmų dviejų *GGE biplot* komponentų (PCA1 ir PCA2) genotipų ir aplinkos balus.

Reikšminiai žodžiai: duoninis kvietys, *Triticum aestivum* L., tyrimai įvairiose aplinkose, *GGE biplot* analizė.