

GGE-Biplot Analysis of Multi-Environment Yield Trials in Bread Wheat

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Abstract: Yield data of 25 bread wheat genotypes tested across 9 rain-fed environments during the 2002-2003 growing season were analyzed using the GGE (i.e. G, genotype + GEI, genotype-by-environment interaction) biplot method. E (environment) explained 81% of the total (G + E + GE) variation, whereas G and GEI captured 7.3% and 11.7%, respectively. The first 2 principal components (PC1 and PC2) were used to create a 2-dimensional GGE-biplot and explained 46.2% and 15.8% of GGE sum of squares (SS), respectively. Genotypic PC1 scores >0 detected the adaptable and/or higher-yielding genotypes, while PC1 scores <0 discriminated the non-adaptable and/or lower-yielding ones. Unlike genotypic PC1 scores, near-zero PC2 scores identified stable genotypes, whereas absolute larger PC2 scores detected the unstable ones. On the other hand, environmental PC1 scores were related to non-crossover type GEIs and the PC2 scores to the crossover type. Of the tested genotypes, G7, G19 and G24 were desirable in terms of higher yielding ability and stability. Nine test environments were sampled from the Central Anatolian Plateau and constituted 2 mega-environments (ME1 and ME2). The former included environments E1 (Konya), E3 (Obruk), E5 (Haymana) and E8 (Uşak), and the latter included E2 (Çumra), E4 (Ereğli), E6 (Ulaş), E7 (Eskişehir) and E9 (Altıntaş). On the other hand, E2 (Çumra) was the best representative of the overall environments and the most powerful to discriminate genotypes.

Key Words: Bread wheat (*T. aestivum* L.), multi-environment yield trials, GGE-biplot analysis

Abbreviations: GEI, Genotype-by-Environment Interaction; MEYTs, Multi-Environment Yield Trials; ME, Mega-Environment; PC, Principal Component

Ekmeklik Buğdayda Çok Çevreli Verim Denemelerinin GGE-Biplot Analizi

Özet: 2002-2003 yılı yetiştirme döneminde, 9 çevrede denenen 25 ekmeklik buğday genotipinin tane verimi değerlerine, GGE-biplot analizi (G, genotip + GEI, genotip çevre interaksyonu) uygulanmıştır. Toplam varyasyonun (G + E + GEI) % 81'ini E, % 7.3'ünü G ve % 11.7'sini ise GEI açıklamıştır. Biplotu oluşturmak için kullanılan ilk iki ana bileşen (PC1 ve PC2), GGE kareler toplamının % 46.2 ve % 15.8'ini oluşturmuştur. PC1 değerleri >0 olan genotipler yüksek verimli ve/veya uyumlu iken, PC1 değerleri <0 olan genotipler ise düşük verimli ve/veya uyum sağlayamayanlar olarak belirlenmiştir. Genotiplerin PC1 değerlerinden farklı olarak, sıfıra yakın PC2 değerleri stabil genotiplerle ilgili iken, mutlak değerleri büyük olan PC2 değerleri ise stabilitesi düşük genotiplerle ilgili olmuştur. Diğer taraftan çevrelerin PC1 değerleri, çapraz olmayan GEI, PC2 değerleri ise çapraz GEI'ne işaret etmiştir. Denemede G7, G19 ve G24 genotiplerinin yüksek verimli ve stabil oldukları belirlenmiştir. Orta Anadolu Platosundan örneklenen deneme çevreleri iki büyük çevreye (ME1 ve ME2) ayrılmış, E1 (Konya), E3 (Obruk), E5 (Haymana) ve E8 (Uşak) ilk büyük çevreyi (ME1), E2 (Çumra), E4 (Ereğli), E6 (Ulaş), E7 (Eskişehir) ve E9 (Altıntaş) ise ikinci büyük çevreyi (ME2) oluşturmuştur. Diğer taraftan E2 (Çumra) ise tüm deneme çevrelerini temsil etme ve denenen genotipleri en güçlü ayırma özelliğine sahip olmuştur.

Anahtar Sözcükler: Ekmeklik buğday (*T. aestivum* L.), çok çevreli verim denemeleri, GGE-biplot analizi

Introduction

Multi-environment yield trials (MEYTs) are used in the final selection cycles to identify superior genotypes in plant breeding programs. This task is not generally easy due to the frequent presence of GEI. It attenuates the

association between phenotype and genotype, reducing genetic progress in plant breeding programs. Means across environments are adequate indicators of genotypic performance only in the absence of GEI. If it is present, the use of means across environments ignores the fact

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that genotypes differ in relative performance over environments (Voltas et al., 2002). A significant GEI may be either (i) a non-crossover type where the ranking of genotypes remains constant across environments and the interaction is significant because of changes in the magnitude of the response, or (ii) a crossover type where a significant change in rank occurs from one environment to another. When selecting genotypes across a number of environments, plant breeders look for a non-crossover type of GEI or preferably the absence of a GEI for general adaptation (Matus-Cadiz et al., 2003), and a crossover type of GEI for specific adaptation.

ANOVA is an additive model that describes the main effects effectively and determines if GEI is a significant source of variation, but it does not provide insight into the genotypes or environments that give rise to the interaction (Samonte et al., 2005). Yan et al. (2000) proposed a method, namely GGE-biplot, which allows visual examination of the GEI pattern of MEYT data. The GGE-biplot emphasizes 2 concepts. First, although the measured yield is the combined effect of G, E, and GEI, only G and GEI are relevant to, and must be considered simultaneously, in genotype evaluation, hence the term GGE. Second, the biplot technique, developed by Gabriel (1971), is employed to approximate and display the GGE of a MEYT, hence the term GGE biplot. This GGE-biplot is constructed by the first 2 principal components (PC1 and PC2, also referred to as primary and secondary effects, respectively) derived from subjecting environment-centered yield data, i.e. the yield variation due to GGE, to singular value decomposition. This GGE-biplot is shown to effectively identify the GEI pattern of the data. It clearly shows which genotype won in which environments, and thus facilitates ME identification (Yan et al., 2000).

MEYTs aim not only to identify superior genotypes for the target region, but also to determine if the target region can be subdivided into different MEs. Investigation of ME is a prerequisite for meaningful cultivar evaluation and recommendation (Yan et al., 2000). CIMMYT has introduced the concept of ME, defined as "a broad, not necessarily contiguous area, occurring in more than one country and frequently transcontinental, defined by similar biotic and abiotic stresses, cropping system requirements, consumer preferences, and, for convenience, by volume of production" (Braun et al., 1996). Based on this definition, the winter wheat production area of Turkey has been classified as a unique ME, particularly the Central Anatolian Plateau.

Plant breeding programs should take GEI into consideration as well as an estimate of its magnitude, relative to the magnitude of G and E effects, which affects grain yield. Furthermore, the identification of genotypes that yield best across a number of environments would be useful to breeders and producers. Using the GGE-biplot methodology, this study targeted (i) to interpret magnitude and causes of G, E, GEI on yield performances of 25 bread wheat genotypes tested across 9 environments, (ii) to facilitate visual comparison among genotypes and environments (iii) and to determine if Central Anatolian Plateau might be divided into distinct MEs.

Materials and Methods

Twenty-five bread wheat genotypes were grown in 9 rain-fed environments, viz. Konya, Çumra, Obruk, Ereğli, Haymana, Ulaş, Eskişehir, Uşak and Altıntaş, during the 2002-2003 growing season at the Central Anatolian Plateau in Turkey. The 25 genotypes comprised 5 registered cultivars, 7 advanced lines from NBWIP (National Bread Wheat Improvement Program, Turkey) and 13 advanced lines from IWWIP (International Winter Wheat Improvement Program), a joint program involving Turkey, CIMMYT and ICARDA. The experimental layout was a randomized complete block design with 4 replications. Sowing was done with an experimental drill in 1.2 m x 7 m plots, consisting of 6 rows spaced 20 cm apart. The seeding rate was 550 seeds m⁻². Fertilizer application was 27 kg N ha⁻¹ and 69 kg P₂O₅ ha⁻¹ at the planting and 50 kg N ha⁻¹ at the stem elongation stage. Harvesting was done with an experimental combine in 1.2 m x 5 m plots. Grain yield was obtained by expressing plot grain yields on a hectare basis (t ha⁻¹). Details of the 25 genotypes and 9 environments are given in Tables 1 and 2.

GGE-biplot methodology, which is composed of 2 concepts, the biplot concept (Gabriel 1971) and the GGE concept (Yan et al., 2000), was used to visually analyze the MEYTs data. This methodology uses a biplot to show the factors (G and GE) that are important in genotype evaluation and that are also the sources of variation in GEI analysis of MEYTs data (Yan et al., 2000, 2001). The GGE-biplot shows the first 2 principal components (PC1 and PC2, also referred to as primary and secondary effects, respectively) derived from subjecting environment-centered yield data (yield variation due to

Table 1. Code, origin, pedigree, selection history and mean yield (t ha⁻¹) of genotypes.

Code	Pedigree and selection history	Origin	Mean Yield (t ha ⁻¹)
G1	TJB916.46/CB306//2*MHB/3/BUC/4/WEAVER2 SWM940349*-1H-1P-1P-5YK-OYK	IWWIP ¹	2.182
G2	F12.71/ANZA/V763-153/3/PLK70/LIRA EWT 89093-SE-3T-1T-2T-2T-1T-0T	IWWIP	2.492
G3	86HONG205/207W12.11//HATUSHA CIT937077 -OSE-1YC-1YC-OYC-1YC-OYC	IWWIP	2.717
G4	FRTL//AGRI/NAC CMSW93WM0071 -OAP-OYC-8YE-OYC-3YC-OYC	IWWIP	2.575
G5	KARAHAN-99 = C126-15/COFN"S"/3/N10B11/P14//SEL101/4/KRC YE 2957-4E-1E-1E-0E	NBWIP ²	2.961
G6	1D13.1/MLT//RSK/NAC CIT932043 -OSE-OYC-6YE-OYC-1YC-OYC	IWWIP	2.370
G7	RECITAL/TIA.2//TRK13 CIT937239 -OSE-OYC-4YE-OYC-02YC-OYC	IWWIP	3.063
G8	KS82W418/SPN//KS82W418/SPN/3/RMN F12-71/JUP WHQ941070*-1H-1P-2P-3YK-OYK	IWWIP	2.559
G9	UNKNOWN	NBWIP	2.664
G10	BAĞCI-02 = HN7/OROFEN/BJN8/3/SERI82/4/74CB462/TRAPPER//VONA EWT 8913-SE-OYC	IWWIP	2.803
G11	WRM/4/.../ATR71/6/PF8215 SWM 940117 *-1H-12P-1P-3YK-OYK	IWWIP	2.630
G12	HYS//R37/GHL121/3/PASA SWM 940335 -1P*-1H-12P-1YK-OYK	IWWIP	2.584
G13	TJB916.46/CB306//2*MHB/3/BUC/4/WEAVER2 SWM 940349 *-1H-1P13YK-OYK	IWWIP	2.448
G14	TAM200/KAUZ 960686 CMSW91M 00414S - OSE-OYC-2YC-OYC	IWWIP	2.459
G15	YAKAR-99 = LOV21, F1/FL, KVZ/HYS	NBWIP	2.750
G16	TX71A1039-VI*3/AMI(TX81V6603)//MVR16-85 BDKE 920008 -2F5 BD-OBD	NBWIP	2.475
G17	PLK70/LIRA"S//30-KZ-1 BDKE 920012 -2F5 BD-OBD	NBWIP	2.906
G18	ES 14/FLAMURA 85 YE 7907 6F5 BD OBD	NBWIP	3.054
G19	SDY/ALD/3/NAI60/HN7//BUC/4/KEA/TOW/5/YAN7578.128 CMWW91M00067T 3F5 BD OBD	IWWIP	3.003
G20	GEREK-79 = MENK"S"/MY-48//4-14/3/YAYLA-305	NBWIP	2.981
G21	KS2142/4/KRÇ66/3/TT-50-18/P101//11-50-18/VGDWVF BDKE 910010 1F5 BD OBD	NBWIP	2.904
G22	TAM200/KAUZ 960686 CMSW91M 00414S -OSE-OYC-1YC-OYC	IWWIP	2.668
G23	UNKNOWN	NBWIP	2.799
G24	J15418/MARAS TCI 922142 -OSE-OYC-3YC-OYC	NBWIP	3.116
G25	ALTAY-00 = ES-14//YKT/BLUEBOY2	NBWIP	2.862

¹ International Winter Wheat Improvement Program-Turkey/CIMMYT/ICARDA² National Bread Wheat Improvement Program-Turkey

Table 2. Code, soil property, amounts of precipitation (mm) and mean yield (t ha⁻¹) of environments.

Environment	Code	Soil property	Precipitation (mm)	Mean Yield (t ha ⁻¹)
Konya	E1	pH = 8.2, clayey, alluvial	326	3.092
Çumra	E2	pH = 7.8, clayey, loam, hydromorphic alluvial	430	3.791
Obruk	E3	pH = 8.0 clayey, loam, brown	NA*	1.523
Ereğli	E4	pH = 7.9, silty, brown	370	1.938
Haymana	E5	pH = 7.8, silty, loam	376	2.590
Ulaş	E6	pH = 8.2 clayey, brown	360	1.801
Eskişehir	E7	pH = 7.8, red brown	375	3.931
Uşak	E8	pH = NA, red clayey	443	3.118
Altıntaş	E9	pH = NA, red clayey	NA	2.703

*, data not available

GGE) to singular value decomposition (Yan et al., 2000). In the present study, genotype-focused scaling was used in visualizing for genotypic comparison, with environment-focused scaling for environmental comparison. Furthermore, the symmetric scaling was preferred in visualizing the which-won-where pattern of the MEYTs yield data (Yan, 2002).

Results and Discussion

The combined ANOVA showed that bread wheat grain yields were significantly affected by E, which explained 81% of the total (G + E + GEI) variation, whereas G and GEI, which were significant ($P < 0.0001$), accounted for 7.3% and 11.7%, respectively (Table 3). Gauch and

Zobel (1997) reported that, in normal MEYTs, E accounts for about 80% of the total variation, while G and GE each account for about 10%. The partitioning of GGE through GGE-biplot analysis showed that PC1 and PC2 were significant factors, explaining 46.2% and 15.8% of GGESS, respectively. Together, they accounted for 62% of GGESS (Table 4).

It is very common for MEYTs data to embody a mixture of crossover and non-crossover types of GEI. In this study, different genotypes produced the highest grain yield in different environments. Genotypes G7, G17 and G20 (Gerek-79) possessed the highest yield in environments E4 (Ereğli), E8 (Uşak) and E3 (Obruk), respectively (Table 5). These differential rankings of genotypes across test environments revealed that there

Table 3. Combined analysis of variance of yield data of 25 bread wheat genotypes tested across 9 environments.

Source	DF	SS	MS	F	P	Model	SS (%) [‡]
Environment (E)	8	581.178	72.647	45.37	0.0001	Random	81
Rep(E)	27	43.228	1.601				
Genotype (G)	24	51.806	2.158	5.03	0.0001	Fixed	7.3
GEI	192	82.412	0.429	2.22	0.0001	Random	11.7
Error	648	125.149	0.193				
Total	899	883.776					
CV(%): 16.15		R ² : 0.86		H: 0.16 ± 0.05 [‡]			

[‡], Total sum of squares of G, E and GEI

[‡], Broad sense heritability ± standard error on plot basis

Table 4. GGE-biplot analysis of yield data of 25 bread wheat genotypes tested across 9 environments.

Principal component	Singular values	Eigen values	% of total eigen values	Cumulative % of eigen values
PC1	7.871	61.956	46.2	46.2
PC2	4.609	21.246	15.8	62.1
PC3	4.276	18.280	13.6	75.7
PC4	3.384	11.453	8.5	84.3
Residual		21.111	15.9	15.9
Total		134.045 [§]	100	100

[§], Total eigen values equal total sum of squares of G and GEI

Table 5. Mean yield of 25 bread wheat genotypes tested across 9 environments.

Code	E1 [†]	E2	E3	E4	E5	E6	E7	E8	E9	Mean Yield (t ha ⁻¹)
G1 [†]	2.213	3.100	1.315	1.583	2.238	1.209	3.248	2.713	2.023	2.182
G2	2.650	3.080	1.418	1.808	2.115	1.795	3.895	2.370	3.295	2.492
G3	2.840	3.753	1.708	2.425	2.153	2.010	3.940	2.870	2.750	2.717
G4	2.730	3.543	1.620	1.805	2.360	1.643	3.988	2.973	2.513	2.575
G5	3.203	4.113	1.598	2.235	3.430	2.480	3.735	3.083	2.775	2.961
G6	2.990	2.973	1.333	1.357	1.925	2.043	3.658	2.895	2.160	2.370
G7	3.585	3.878	1.698	2.735	3.130	2.093	3.953	3.290	3.203	3.063
G8	2.655	3.583	1.358	1.498	2.670	1.563	4.160	2.580	2.965	2.559
G9	3.443	4.000	1.593	2.098	2.388	1.635	3.635	2.780	2.403	2.664
G10	3.013	4.015	1.565	1.585	3.318	1.485	4.348	3.543	2.355	2.803
G11	3.703	3.813	1.523	1.858	1.860	1.548	3.755	2.933	2.675	2.630
G12	2.740	3.410	1.628	1.985	2.765	1.575	3.148	3.123	2.880	2.584
G13	2.900	3.335	1.263	2.003	1.808	2.070	3.540	2.550	2.563	2.448
G14	3.170	3.033	1.498	2.078	2.078	1.670	3.525	2.718	2.363	2.459
G15	3.355	4.350	1.588	1.685	2.368	1.855	4.025	3.145	2.383	2.750
G16	2.563	3.353	1.268	1.838	2.293	1.598	3.570	3.243	2.547	2.475
G17	3.398	3.940	1.470	1.620	3.035	1.940	4.170	3.983	2.595	2.906
G18	4.100	4.643	1.583	1.983	3.278	1.930	4.185	3.398	2.383	3.054
G19	2.940	4.510	1.605	1.783	2.918	2.165	4.353	3.400	3.350	3.003
G20	3.808	4.005	1.913	2.200	3.228	2.028	3.763	3.608	2.275	2.981
G21	3.020	4.275	1.520	2.345	2.373	1.658	3.928	3.725	3.288	2.904
G22	3.185	3.703	1.540	1.548	2.878	1.169	4.303	3.245	2.443	2.668
G23	3.053	4.065	1.320	1.820	2.933	1.910	4.470	2.935	2.685	2.799
G24	2.900	4.188	1.645	2.368	3.403	1.685	4.815	3.570	3.470	3.116
G25	3.140	4.126	1.513	2.200	1.806	2.270	4.175	3.280	3.245	2.862
Mean	3.092	3.791	1.523	1.938	2.590	1.801	3.931	3.118	2.703	2.721

[†]; [‡] represent genotypes and environments given in Tables 1 and 2, respectively.

exists possible crossover GEI. However, crossover GEI is not always the case. Genotype G5 (Karahan-99) was the highest yielding in environments E5 (Haymana) and E6 (Ulaş). Moreover, genotype G18 exhibited the highest yield potential in environments E1 (Konya) and E2 (Çumra), whereas genotype 24 was the highest in environments E7 (Eskişehir) and E9 (Altıntaş). These results in differential change of yield mean but not of ranking of genotypes showed that GEI may also have a non-crossover nature.

A GGE-biplot based on genotype-focused scaling was depicted in order to detect the locations of genotypes. Genotypes that had PC1 scores >0 were identified as higher yielding (except genotype G22) and those that had PC1 scores <0 were identified as lower yielding (except genotype G3) (Figure 1 and Table 1). In other words, due to the near-perfect correlation ($r = 0.974$; $P < 0.001$) between the genotypic PC1 scores and genotypic yield means, PC1 scores >0 detected the genotypes of interest (i.e. adaptable or higher yielding), while PC1 scores <0 discriminated the non-adaptable ones. Unlike the PC1, PC2, which was related to genotypic stability or instability, divided the genotypes of interest into 2 groups based on their scores. Group 1 consisted of 4 stable

genotypes (G7, G23, G5 and G15) that were higher yielding, since near-zero PC2 scores showed genotypic stability. As for Group 2, it consisted of 9 unstable genotypes (G25, G24, G21, G19, G17, G18, G20, G10 and G22) that were higher yielding, as absolute larger PC2 scores were associated with genotypic instability.

Another GGE-biplot, which was based on environment-focused scaling, was portrayed to estimate the pattern of environments (Figure 2). Environment PC1 had only positive scores. This suggests that PC1 represents proportional genotype yield differences across environments, which leads to a non-crossover GEI. That is to say, genotypes with greater PC1 scores can be easily identified in environments with larger PC1 scores (Yan et al., 2000). In contrast to environmental PC1, PC2 had both positive and negative scores (Figure 2). It gives rise to the crossover GEI, leading to disproportionate genotype yield differences across environments (Yan et al., 2000). A genotype may, on the one hand, have large positive interactions with some environments; it may, on the other hand, have large negative interactions with some other environments. Under limited resources and the need to conduct MEYTs in a limited number of environments, E2, E7 and E8 (also including E3) may be better test

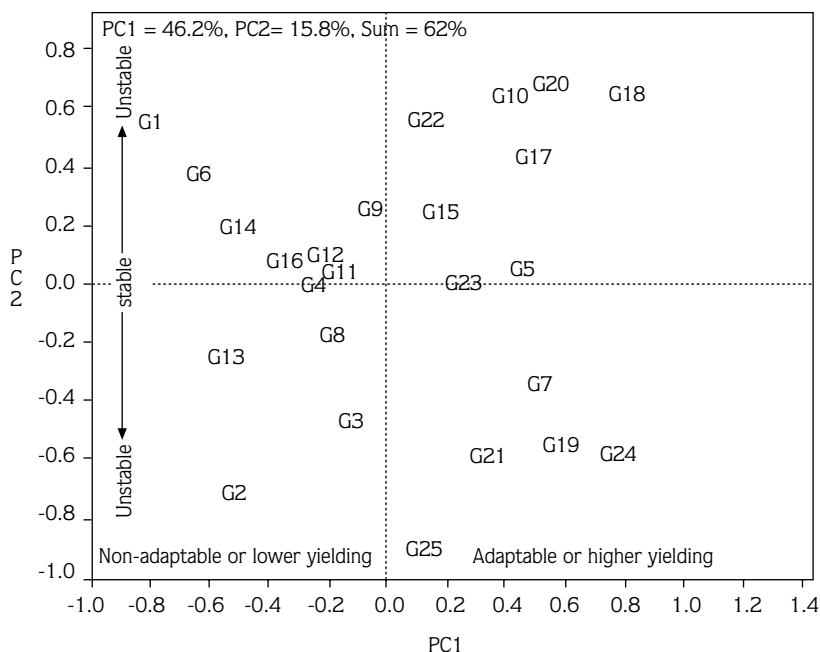


Figure 1. GGE-biplot based on genotype-focused scaling for genotypes. PC and G stand for principal component and genotypes, respectively. Details of genotypes are given in Table 1.

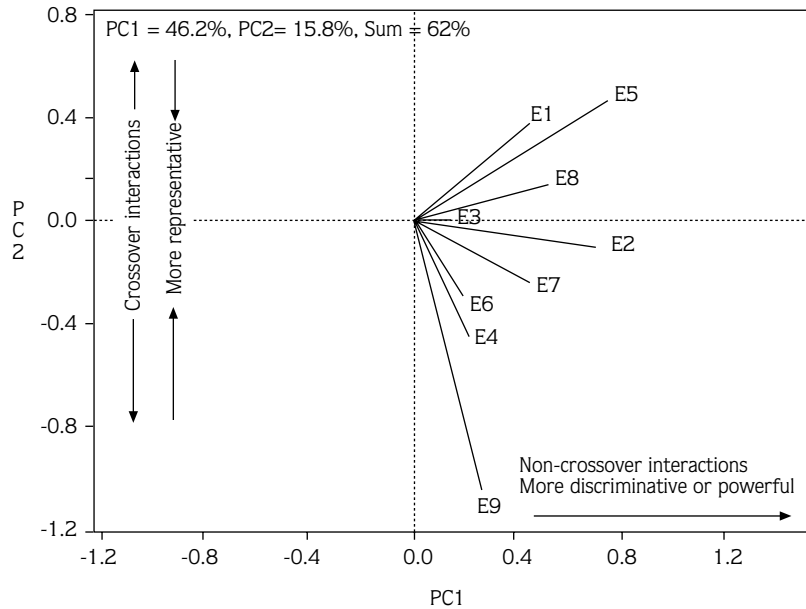


Figure 2. GGE-biplot based on environment-focused scaling for environments. PC and E stand for principal component and environments, respectively. Details of environments are given in Table 2.

environments. Favorable test environments should have large PC1 scores (more discriminating of the genotypes) and near-zero PC2 scores (more representative of an average environment) (Yan et al., 2001).

Environment PC1 scores correlated with environment yield means ($r = 0.695$; $P < 0.05$; Table 2). Taking into account such a correlation, the test environments could not be discriminated sufficiently, because of the lack of ancillary environmental data, corresponding geographic characteristics (longitude, latitude etc.), soil properties (soil type, soil fertility etc.) and unpredictable climatic features (distribution and amount of precipitation, high and low temperatures etc.).

The correlation coefficients among the 9 test environments are presented in Table 6. The vector view of the GGE-biplot (Figure 2) provides a succinct summary of the interrelationships among the environments. The lines that connect the biplot origin and the markers of the environments are called environment vectors. The angle between the vectors of 2 environments is related to the correlation coefficient between them. Table 3 contained 36 correlation coefficients, 16 of which were significant. All environments were positively correlated because all angles among them were smaller than 90° , except that

environment E1 negatively correlated with E9. The angle between environments E5 and E9 was only slightly smaller than 90° ; therefore, the correlation between them should be close to 0. In Table 6, it was 0.117. The loose association of E9 with E3 and E8 was also well reflected in Figure 2. There were inconsistencies, however. For example, Figure 2 suggested that E6 and E4 were the most closely correlated environments, but the largest correlation coefficient was actually between E8 and E2 (Table 6). Some inconsistencies were expected because the biplot did not explain 100% of the GGE variation (Yan, 2002).

Indirect selection can be applied in the case where the same character is measured on the same genotypes in different environments. Where there are no correlations of error effects among environments, the phenotypic correlation between environments may be used to investigate indirect response to selection (Cooper and DeLacy, 1994). Test environment E1 correlated significantly with E2, E3 and E8, while E7 correlated well with E2, E5, E8 and E9. In addition, E5 correlated significantly with E2, E3 and E8; E2 with E3 and E8; E8 with E3; E3 with E4; and E4 with E6 and E9 (Table 6). Such significant correlation coefficients among test

Table 6. Correlation coefficients among test environments.

Environment		E1	E2	E3	E4	E5	E6	E7	E8	E9
E1	Konya	1.000								
E2	Çumra	0.567**	1.000							
E3	Obruk	0.516**	0.492**	1.000						
E4	Ereğli	0.294	0.312	0.543**	1.000					
E5	Haymana	0.320	0.552**	0.472*	0.159	1.000				
E6	Ulaş	0.329	0.335	0.215	0.417*	0.099	1.000			
E7	Eskişehir	0.203	0.615**	0.177	0.011	0.477*	0.115	1.000		
E8	Uşak	0.405*	0.633**	0.447*	0.191	0.585**	0.123	0.430*	1.000	
E9	Altıntaş	-0.124	0.310	0.150	0.482*	0.117	0.299	0.424*	0.156	1.000

* ; ** indicate significance at $P < 0.05$ and $P < 0.01$, respectively.

environments suggest that indirect selection for grain yield can be practical across the test environments. For instance, the genotypes adaptable or higher yielding in environment E1 may also show similar responses to E2, E3 and E8 as well. However, indirect selection from one environment to another may not be sufficiently successful, considering that 16 out of 36 environmental pairwise correlations were significant.

Visualization of the which-won-where pattern of MEYTs data is important for studying the possible existence of different mega-environments (ME) in a region (Gauch and Zobel, 1997; Yan et al., 2000, 2001). The polygon view of a GGE-biplot explicitly displays the which-won-where pattern, and hence is a succinct summary of the GEI pattern of a MEYT data set (Figure 3). The polygon is formed by connecting the markers of the genotypes that are further away from the biplot origin such that all other genotypes are contained in the polygon. The rays in Figure 3 are lines that are perpendicular to the sides of the polygon or their extensions. For example, Ray 1 is perpendicular to the side that connects genotypes G20 and G18 (the G18-G20 side); Ray 2 is perpendicular to side G18-G24; similarly, Ray 3 is perpendicular to side G24-G25, Ray 4 to side G25-G2, Ray 5 to side G2-G1, and Ray 6 to side G1-G20.

These 6 rays divide the biplot into 6 sectors, and the environments fall into 3 of them (Figure 3). An interesting feature of this view of a GGE biplot is that the vertex genotype(s) for each sector has higher (some times the highest) yield than the others in all environments that fall in the sector (Yan, 2002). Thus, 4 environments, E1

(Konya), E3 (Obruk), E5 (Haymana) and E8 (Uşak), fell into sector 1 delineated by Rays 1 and 2, and the vertex genotypes for this sector were G18 and G20 (Gerek-79), suggesting that higher-yielding genotypes for these 4 environments were G18 and G20. Similarly, 4 environments, E2 (Çumra), E4 (Ereğli), E6 (Ulaş) and E7 (Eskişehir), fell into sector 2 delineated by Rays 2 and 3, and the vertex genotype for this sector was G24, suggesting that the higher-yielding genotype for these 4 environments was G24. A single environment, E9 (Altıntaş), fell into sector 3 delineated by Rays 3 and 4. The vertex genotype for this sector was G25 (Altay-00). Figure 3 suggests that there exist 2 possible winter wheat MEs in the Central Anatolian Plateau: one (ME-1) represented by genotypes G18 and G20, and the other (ME-2) by G24 and G25. ME-1 corresponded to environments and genotypes falling into sector 1, and ME-2 to those in sectors 2 and 3. To better understand the pattern of environments, sector 3 was intentionally combined with sector 2 to constitute ME-2. However, this ME pattern needs verifying through multi-year and -environment trials to be carried out in the target region. Such ME classification was merely set up with MEYTs data, without considering the ME definition of the CIMMYT wheat breeding program (Braun et al., 1996). Taking into account the fact that a winter wheat growing area, especially Central Anatolian Plateau, is quite similar in terms of climatic and soil characteristics (Çakmak et al., 1999), that registered winter wheat cultivars are widely adaptable to that area, and that the ME-12 introduced by CIMMYT for that area is still valid (Braun et al., 1996), it may not be divided into sub-areas in order to establish more than one ME.

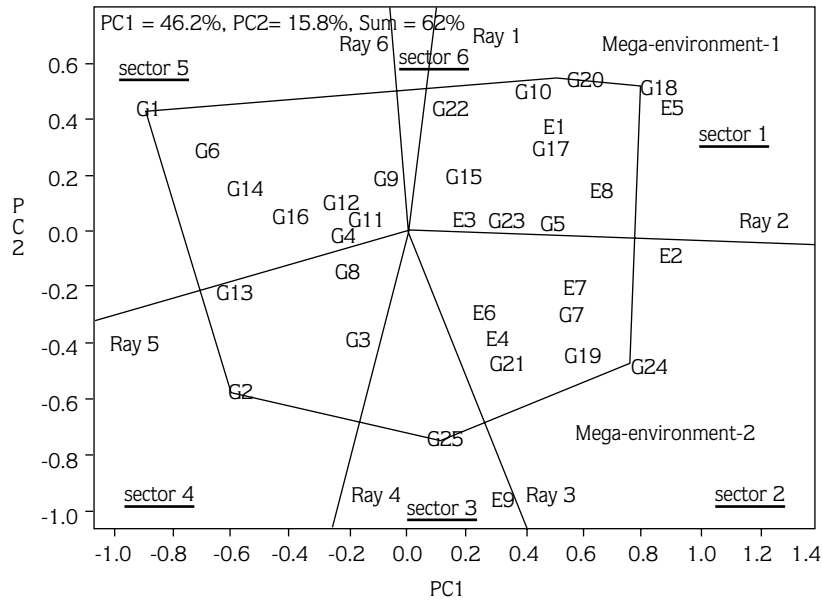


Figure 3. Polygon views of the GGE-biplot based on symmetrical scaling for the which-where pattern for genotypes and environments. PC, G and E stand for principal component, genotypes and environments, respectively. Details of genotypes and environments are given in Tables 1 and 2.

Yield performance and stability of genotypes were evaluated by an average environment coordination (AEC) method (Yan, 2001; Yan and Hunt, 2002; Yan, 2002). In this method, an average environment is defined by the average PC1 and PC2 scores of all environments, represented by a small circle (Figure 4). A line is then drawn to pass through this average environment and the biplot origin; this line is called the average environment axis and serves as the abscissa of the AEC. The ordinate of the AEC is the line that passes through the origin and is perpendicular to the AEC abscissa (Figure 4). Unlike the AEC abscissa, which has one direction, with the arrow pointing to greater genotype main effect, the AEC ordinate is indicated by double arrows, and either direction away from the biplot origin indicates greater GEI effect and reduced stability. The AEC ordinate separates genotypes with below-average means from those with above-average means. Furthermore, the average yield of genotypes is approximated by the projections of their markers to the AEC abscissa. To illustrate, genotypes with above-average means were from G24 to G15, while genotypes below-average means were from G22 to G1. The length of the average environment vector (the distance from biplot origin and

the average environment marker), relative to the biplot size, is a measure of the relative importance of genotype main effect vs. GEI. The longer it is, the more important is the genotype main effect, and the more meaningful the selection based on mean performance. For this study, the length of the average environment vector was sufficient to select genotypes based on yield mean performances. Genotypes with above-average means (i.e. from G24 to G15) could be selected, whereas the rest were discarded. On the other hand, genotypic stability is quite crucial, in addition to genotype yield mean. A longer projection to the AEC ordinate, regardless of the direction, represents a greater tendency of the GEI of a genotype, which means it is more variable and less stable across environments or vice versa. For instance, genotypes G23, G7 and G24 were more stable as well as high yielding. Conversely, G18, G25 and G20 were more variable, but high yielding.

An ideal genotype should have the highest mean performance and be absolutely stable (i.e. perform the best in all environments). Such an ideal genotype is defined by having the greatest vector length of the high-yielding genotypes and with zero GEI, as represented by an arrow pointing to it (Figure 5). Although such an ideal genotype may not exist in reality, it can be used as a

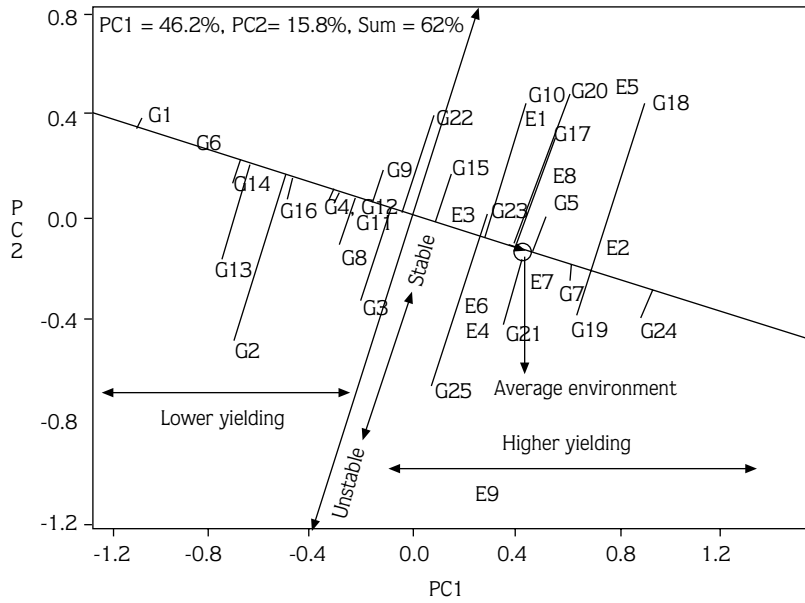


Figure 4. Average environment coordination (AEC) views of the GGE-biplot based on environment-focused scaling for the means performance and stability of genotypes. PC, G and E stand for principal component, genotypes and environments, respectively. Details of genotypes and environments are given in Tables 1 and 2.

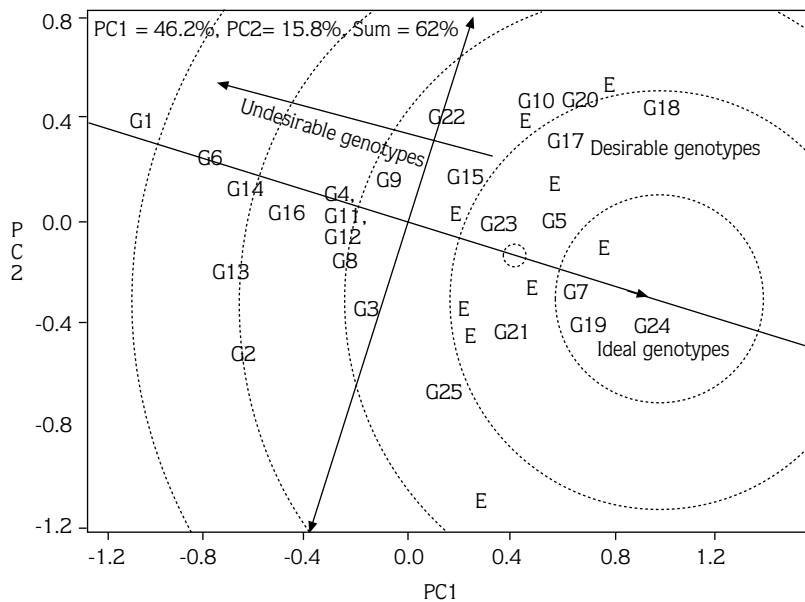


Figure 5. GGE-biplot based on genotype-focused scaling for comparison the genotypes with the ideal genotype. PC, G and E stand for principal component, genotypes and environments, respectively. Details of genotypes and environments are given in Tables 1 and 2.

reference for genotype evaluation. A genotype is more desirable if it is located closer to the ideal genotype. Thus, using the ideal genotype as the center, concentric circles were drawn to help visualize the distance between each genotype and the ideal genotype. Because the units of both PC1 and PC2 for the genotypes are the original unit of yield in the genotype-focused scaling (Figure 5), the units of the AEC abscissa (mean yield) and ordinate (stability) should also be the original unit of yield. The unit of the distance between genotypes and the ideal genotype, in turn, is the original unit of yield as well. Therefore, the ranking based on the genotype-focused scaling assumes that stability and mean yield are equally important (Yan, 2002). Figure 5 revealed that G24, G7 and G19, which fell into the center of concentric circles, were ideal genotypes in terms of higher yielding ability and stability, compared with the rest of the genotypes. In addition, G21, G23, G5 (Karahan-99), G17 and G18, located on the next concentric circle, may be regarded as desirable genotypes. Surprisingly, the other registered higher-yielding cultivars G10 (Bağcı-02), G15 (Yakar-99), G20 (Gerek-79) and G25 (Altay-00), together with the unstable and lower yielding genotypes G3, G9 and G22, were situated at the third concentric circle.

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). Such an ideal environment is represented by an arrow pointing to it (Figure 6). Although such an ideal environment may not exist in reality, it can be used as a reference for genotype selection in the MEYTs. An environment is more desirable if it is located closer to the ideal environment. Thus, using the ideal environment as the center, concentric circles were drawn to help visualize the distance between each environment and the ideal environment (Yan et al., 2000; Yan and Rajcan, 2002). Figure 6 indicated that E2 (Çumra), which fell into the center of concentric circles, was an ideal test environment in terms of being the most representative of the overall environments and the most powerful to discriminate genotypes. Favorable environments were E7 (Eskişehir), E8 (Uşak), E5 (Haymana) and E1 (Konya). On the other hand, the unfavorable ones were E3 (Obruk), E6 (Ulaş), E4 (Ereğli) and E9 (Altıntaş). The favorable environments, together with E2, showed high yield potential ($> 3.00 \text{ t ha}^{-1}$, except E5), and the unfavorable ones low yield potential ($< 2.00 \text{ t ha}^{-1}$, except E9) (Table 2).

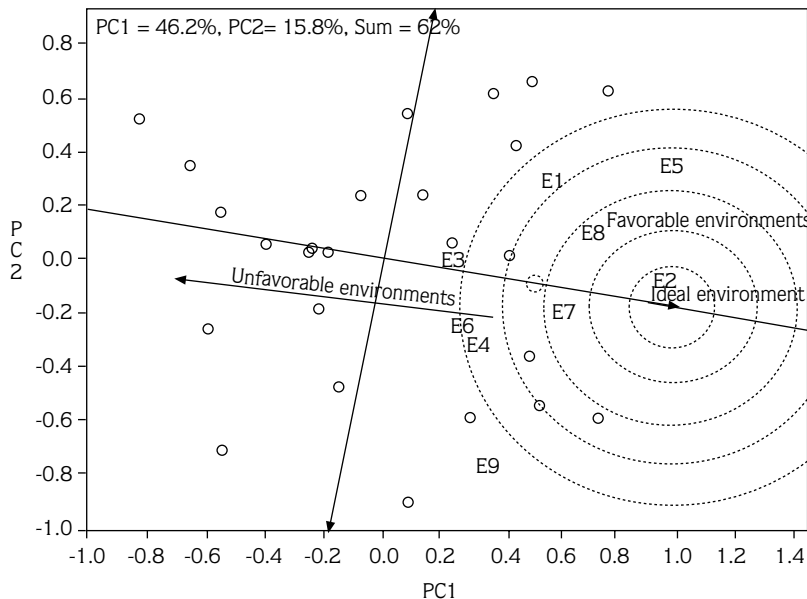


Figure 6. GGE-biplot based on environment-focused scaling for comparison the environments with the ideal environment. PC, o and E stand for principal component, genotypes and environments, respectively. Details of genotypes and environments are given in Tables 1 and 2.

Cooper et al. (1997) reported that yield under low-stress environments was an effective predictor of yield under similar low-stress target environments. However, the value of the low-stress environments as a predictor of yield in the water-limited target environments decreased with increasing water stress. Yield in the stress environments was a poor predictor of yield in the target environments. They also suggested that yield improvement can best be achieved by selection for a combination of yield potential in favorable environments and yield in on-farm trials that sample the range of water-limited environments of the target population of environments. The findings of this study were in accordance with those reported by Cooper et al. (1997), given that favorable environments were more representative of the overall environments and more powerful to discriminate genotypes than the unfavorable ones. In addition, one of the essential parameters to select high yielding genotypes adaptable to target environments is value of heritability for grain yield per se. For this study, broad sense heritability (H) on a plot basis for grain yield of 25 bread wheat genotypes tested over 9 rain-fed environments was low ($H = 0.16 \pm 0.05$, Table 3). This result was confirmed by Braun et al. (1992), who indicated that H for grain yield was low in low-yielding environments. On the other hand, Cooper et al. (1993) stated that the term repeatability (R) should be used in preference to H as the genotypes are considered fixed (as were they in this study) and they also concluded that R was low in stressful environments.

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Conclusion

The magnitude of genotype-by-environment interaction (GEI) for grain yield of 25 bread wheat genotypes tested across 9 rain-fed environments sampled from the Central Anatolian Plateau was larger than that of genotype main effect, but smaller than that of environment main effect. The genotypes studied exhibited both crossover and non-crossover types of GEI. The former substantially led to differential rankings of genotypes across test environments, thereby making genotypic selection difficult for the rain-fed conditions of the Central Anatolian Plateau.

In spite of the fact that improving a rain-fed wheat variety is a persistent challenge considering long-running CIMMYT, ICARDA and Turkish rain-fed wheat breeding program efforts, among the genotypes studied there were desirable ones in terms of both stability and high-yielding ability or adaptability. As for the test environments, there existed 2 possible rain-fed MEs (i.e. ME1 and ME2) in the Central Anatolian Plateau. Therefore, rain-fed wheat improvement programs will surely focus on them (ME1 and ME2) in order to foster yield-based selection gain in MEYTs.

Indirect selection among test environments might also be employed to reduce the number of test environments by eliminating those that are highly correlated with each other, thereby economizing and optimizing the conduct of MEYTs. On the other hand, a low H value might suggest that genotype performance trials should be conducted in a number of populations of environments sampled from the target region (e.g., the Central Anatolian Plateau).

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