Additive Main Effects and Multiplicative Interactions Analysis of Yield Performances in Bread Wheat Genotypes across Environments

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Abstract: This study was carried out to determine the yield performances of 20 bread wheat genotypes across six environments in Central Anatolia, Turkey, in the 2000-2001 growing season. The experimental layout was a randomized complete block design with four replications. Additive main effects and multiplicative interactions analysis (AMMI) indicated that the yield performances of genotypes were under the major environmental effects of genotype by environmental interactions. The first two principal component axes (PCA 1 and 2) were significant (p < 0.01) and cumulatively contributed to 78.64% of the total genotype by environment interaction. A biplot generated using genotypic and environmental scores of the first two AMMI components also showed that genotypes with larger PCA 1 and lower PCA 2 scores gave high yields (stable genotypes), and genotypes with lower PCA 1 and larger PCA 2 scores had low yields (unstable genotypes), as in the sites tested.

Key Words: Bread Wheat, Yield, AMMI Analysis, Biplot

Ekmeklik Buğday Genotiplerinde Çevreler Üzerinden Verim Performanslarının Eklemeli Ana Etkiler ve Çarpımsal İnteraksiyonlar Analizi

Özet: Bu çalışma, 20 ekmeklik buğday genotipinin 6 çevrede verim performanslarını belirlemek amacıyla 2000-2001 yılı yetiştirme sezonunda yürütülmüştür. Denemeler, tesadüf blokları deneme deseninde 4 tekerrürlü olarak kurulmuştur. Eklemeli ana etkiler ve çarpımsal interaksiyonlar analizi (AMMI), genotip x çevre interaksiyonunda genotiplerin verim performansları üzerine çevresel etkilerin baskın olduğunu göstermiştir. İlk iki ana bileşen ekseni (PCA 1 ve 2), istatistiksel olarak önemli (p<0.01) bulunmuş ve genotip x çevre interaksiyonunun % 78.64'ünü açıklamıştır. İlk iki AMMI ögesinin genotip ve çevresel skorlarından oluşturulan biplot analizi, yüksek PCA 1 ve düşük PCA 2 skorlarına sahip genotiplerin yüksek verim (stabil genotip), yüksek PCA 2 ve düşük PCA 1 skorlarına sahip genotiplerin ise düşük verim (stabil olmayan genotip) verdiklerini ve denemeye ait çevrelerin de aynı durumu gösterdiğini ortaya koymuştur.

Anahtar Sözcükler: Ekmeklik Buğday, Verim, AMMI analizi, Biplot

Introduction

Plant breeders invariably encounter genotype x environment interactions (GEIs) when testing varieties across a number of environments. Depending upon the magnitude of the interactions or the differential genotypic responses to environments, the varietal rankings can differ greatly across environments. A combined analysis of variance can quantify the interactions, and describe the main effects. However, analysis of variance is uninformative for explaining GEI. Other statistical models for describing GEI such as the additive main effects and multiplicative interaction (AMMI) model are useful for understanding GEI.

The AMMI model is a hybrid analysis that incorporates both the additive and multiplicative components of the two-way data structure. AMMI biplot analysis is considered to be an effective tool to diagnose GEI patterns graphically. In AMMI, the additive portion is separated from interaction by analysis of variance (ANOVA). Then the principal components analysis (PCA), which provides a multiplicative model, is applied to analyze the interaction effect from the additive ANOVA model. The biplot display of PCA scores plotted against each other provides visual inspection and interpretation of the GEI components. Integrating biplot display and genotypic stability statistics enables genotypes to be grouped based on similarity of performance across diverse environments (Thillainathan and Fernandez, 2001).

Concerning the use of AMMI in multi-environmental trials (MET) data analysis, which partitions the GEI matrix into individual genotypic and environmental scores, an

example was provided by Zobel et al. (1988), who studied the GEI of a soybean MET. Another example was provided by Annicchiarico and Perenzin (1994), who showed that earliness x cold stress and plant height x drought interactions for wheat were responsible for the observed GEIs. Yan et al. (2000) applied AMMI analysis to the yield data of Ontario Winter Wheat performance trials, and suggested two winter wheat mega-environments in Ontario. Yan et al. (2001) compared the merits of two types of genotype main effect plus GEI biplots in MET data analysis and indicated that both sites' regression model and Man-del's solution for sites regression model (SREG) were equally effective in displaying the 'which-won-where' pattern of the MET, although the SREG model's biplot explained slightly more genotype main effect plus GEI. Yan and Rajcan (2002) applied to genotype by trait biplot analysis soybean multiple trait and MET data and found that selection for seed yield alone was not only the simplest, but also the most effective strategy in the early stages of soybean breeding.

The objectives of this study were to (i) interpret GEI obtained by AMMI analysis of yield performances of 20 bread wheat genotypes over six environments, (ii) visually assess how to vary yield performances across environments based on the biplot, and (iii) determine genotypes with high yields, depending on the differential genotypic responses to environments.

Materials and Methods

This study was carried out to determine the yield performances of 20 bread wheat genotypes across six environments, including three rain-fed environments undertaken in Konya-Center, Konya-Cumra and Karaman-Kazimkarabekir, and also three irrigated environments conducted in Konya-Center, Konya-Cumra and Aksaray-Kocas, during the 2000-2001 growing season. Of the 20 advanced lines used, 16 were from the National Bread Wheat Improvement Program, Turkey, and four from the International Winter Wheat Improvement Program based on a joint project between Turkey, CIMMYT and ICARDA (Table 1). The

Table 1.   Origin and Pedigree of Genotypes

Genotypic Code	Pedigree of Genotypes	Origin
1	Hawk/Agri	RBWYT[1]
2	Atlas 66//Hys/7c	RBWYT
3	Hn7/Orofen//Bjn8/3/Seri 82/4/74cb462/Tapper//Von Ewt	RBWYT
4	Bolal 2973/Thunderbird	RBWYT
5	Lnd/Swo791o95a/4/Ym/Tob//Mcd/3/Lira	RBWYT
6	Tx73v203*3/Amt/5/C126.13/Cofn//Co59287/3/P101/4/Bl.Sel/Au/6/1d13	RBWYT
7	Es85-19/3/Jcam/Emu "S"//Dove "S"	RBWYT
8	Ferrugineum (Azer) 1986/4/Au//Yt 54/N10b/3/Grk	RBWYT
9	Ks2142/4/Krc 66/3/Tt-50-18/P 101//11-50-18/Vgdwvf	RBWYT
10	Plk 70/Lira "S"//86zhonk 205 (Dryland)	RBWYT
11	Es85-19/3/Jcam/Emu "S"//Dow "S"	RBWYT
12	Unknown	RBWYT
13	Bl.Sel/Kkz//8393/P 243-24/3/Co 693591/Ctk	RBWYT
14	63-122-66-2/No//Lov2f$_1$/3/F$_1$kvz/Hys/4/Tjb916.46/Cb306//2*Mhb/3/Buc	RBWYT
15	Plk 70/Lira "S"//86-Zhonk 205 (Dryland)	RBWYT
16	IWWIP-9032	CIT[2]
17	IWWIP-9537	CIT
18	EBVD 99-9	RBWYT
19	Ji5418/Maras	CIT
20	Id800994.W/Falke	CIT

[1] Regional Bread Wheat Yield Trial-Turkey
[2] CIMMYT/ICARDA/TURKEY Wheat Improvement Program

experimental layout was a randomized complete block design with four replications. Sowing was done by an experimental drill in 1.2 m x 7 m plots, consisting of six rows with 20 cm left between the rows. The seeding rate was 450 seeds m^{-2} for irrigated and 550 seeds m^{-2} for rain-fed environments. Fertilizer application was 27 kg N ha^{-1} and 69 kg P2O5 ha^{-1} at planting and 40 kg N ha^{-1} at stem elongation stage. Harvesting was done in 1.2 m x 5 m plots by experimental combine. Details of soil properties, date of planting, date of harvesting and status of rainfall and/or irrigation for the six environments are given in Table 2. Yield (kg ha^{-1}) was obtained by converting the grain yields obtained from plots to hectares.

SAS software (1996) was used to perform analysis of AMMI on the values of grain yield obtained per plot across environments. PROC GLM of SAS was run to calculate genotype by environment interactions. For each genotype and environment, genotypic and environmental scores were obtained by PROC IML of SAS. In addition, principal component axes (PCAs) were extracted and statistically tested by Gollob's (1968) F-test procedure (Vargas and Crossa, 2000). These components were used to obtain a biplot by SAS GPLOT procedure (Burgueno et al., 2001). To assess fitting AMMI model, predictive and postdictive approaches offered by Zobel et al. (1988) were applied to the data.

Results and Discussion

The AMMI analysis of variance of grain yield (kg ha^{-1}) of the 20 genotypes tested in six environments showed that 90.76% of the total sum of squares was attributable to environmental effects, only 2.5% to genotypic effects, and 7.12% to GEI effects (Table 3). A large sum of

Table 2.   Code, soil properties, date of planting, date of harvesting, status of rainfall + irrigation for each environment

Environment	Code	Soil properties	Date of Planting	Date of Harvesting	Rainfall + (Irrigation) (mm)
Karaman-Kazimkarabekir	E1*	pH = 8.2, clayey, red brown	05.11.00	16.07.01	255
Konya-Cumra	E2*	pH = 7.8, clayey loam, hydro-morphic alluvial	28.10.00	15.07.01	240
Konya-Center	E3*	pH = 8.2, clayey, alluvial	21.10.00	10.07.01	210
Konya-Cumra	E4**	pH = 7.8, clayey loam, hydro-morphic alluvial	27.10.00	24.07.01	240 + 100
Konya-Center	E5**	pH = 8.3, clayey, alluvial	22.10.00	23.07.01	210 + 100
Aksaray-Kocas	E6**	pH = 8.3, silty, brown	08.11.00	25.07.01	265 + 100

*,** rain-fed and irrigated, respectively.

Source	d.f.	Sum of Square	Mean Square	Explained (%)
Model	122	828725807.0	6792834.5**	
Environment (E)	5	751732304.0	1503464.8**	90.76
Genotype (G)	19	17366646.2	914034.0**	2.05
E x G	95	59102019.8	622126.5**	7.12
Interaction PCA 1	23	30012884.1	1304908.1**	50.78
Interaction PCA 2	21	16470383.7	784303.9**	27.86
Interaction PCA 3	19	6355565.6	334503.5	10.75
Interaction PCA 4	17	4380428.3	257672.2	7.41
Interaction PCA 5	15	1882757.8	125517.2	3.78
Interaction PCA 6	13	0.0	0.0	0.00
Pooled error	357	92380186.0	258768.0	
CV = 15.21		R^2 = 0.899		

Table 3.   Additive main effects and multiplicative interactions analysis of variance for grain yield (kg ha^{-1}) of the genotypes across environments

** Significant at the 0.01 probability level.

squares for environments indicated that the environments were diverse, with large differences among environmental means causing most of the variation in grain yield. The magnitude of the GEI sum of squares was 3.4 times larger than that for genotypes, indicating that there were substantial differences in genotypic response across environments.

Results from AMMI analysis (Table 3) also showed that the first principal component axis (PCA 1) of the interaction captured 50.78% of the interaction sum of squares in 24.21% of the interaction degrees of freedom. Similarly, the second principal component axis (PCA 2) explained a further 27.86% of the GEI sum of squares. Furthermore, PCA 1 and PCA 2 had sums of squares greater than that of genotypes. The mean squares for the PCA 1 and PCA 2 were significant at P = 0.01 and cumulatively contributed to 78.64% of the total GEI. Therefore, the post-dictive evaluation using an F-test at P = 0.01 suggested that two principal component axes of the interaction were significant for the model with 44 degrees of freedom. However, the prediction assessment indicated that AMMI with only two interaction principal component axes was the best predictive model (Zobel et al., 1988). This model (AMMI 1 and AMMI 2) had 44 degrees of freedom. Further interaction principal component axes captured mostly noise and therefore did not help to predict validation observations. Thus, the interaction of the 20 genotypes with six environments was best predicted by the first two principal components of genotypes and environments.

The most accurate model for AMMI can be predicted by using the first two PCAs (Gauch and Zobel, 1996; Yan et al., 2002). Conversely, Sivapalan et al. (2000) recommended a predictive AMMI model with the first four PCAs. These results indicate that the number of the terms to be included in an AMMI model cannot be specified a priori without first trying AMMI predictive assessment. In general, factors like type of crop, diversity of the germplasm, and range of environmental conditions will affect the degree of complexity of the best predictive model (Crossa et al., 1990).

A biplot is generated using genotypic and environmental scores of the first two AMMI components (Vargas and Crossa, 2000). A biplot has four sections, depending upon signs of the genotypic and environmental

scores. In the Figure 1, the sites fell into four sectors: the best genotype with respect to site E3 was genotype 2. Genotype 19 was best for site E5; genotypes 20, 14 and 8 were best for sites E2 and E4; and for E6 and E1 the best genotypes were 11 and 7. Genotypes located near the plot origin were less responsive than the vertex genotypes. Genotypes 2 and 19 gave the highest average yield (largest PCA 1 scores), but were stable over the sites, due to the fact that they did not give small absolute PCA 2 scores. In contrast, the non-adapted genotypes 9 and 15 yielded poorly at all sites, as indicated by their small PCA 1 scores (low yielding) and relatively small PCA 2 scores (relatively stable). The average yield of genotypes 20, 14, 13, 11, 8 and 7 were below average (PCA 1 scores < 0) and highly unstable (large absolute PCA 2 scores). The biplot shows not only the average yield of a genotype (PCA 1 effects), but also how it is achieved. That is, the biplot also shows the yield of a genotype at individual sites. For example, genotype 19 had the highest average yield because it yielded the highest at sites E3 and E5, and yielded above average at all other sites. On the other hand, the average yield of genotypes 8 and 7 were below average, because they yielded below average at sites in pairs, E2-E4 and E1-E6, respectively.

With respect to the test sites, E5 was most discriminating as indicated by the longest distance between its marker and the origin. However, due to its
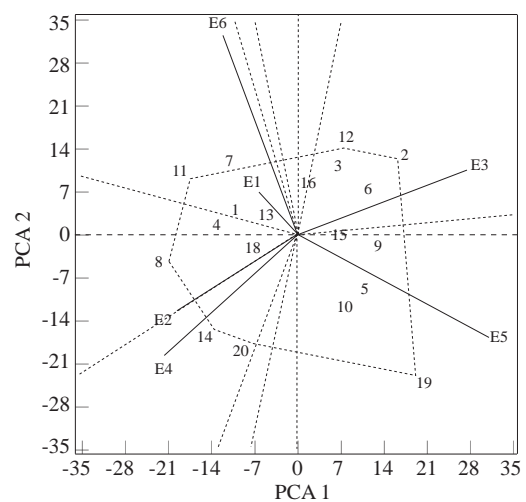

Figure 1.   Biplot of 20 genotypes and six environments for grain yield using genotypic and environmental scores

large PCA 2 score, genotypic differences observed at E5 may not exactly reflect the genotypes in average yield over all sites. Site E3 was not the most discriminating, but genotypic differences at E3 should be highly consistent with those averaged over sites, because it had near-zero PCA 2 scores compared to the others except that the PCA 2 score for E1 was smaller than that of E1 and that PCA 1 score for E3 was larger than that of E1. At a site with a near-zero PCA 2 score, genotypes are essentially ranged according to their PCA 1 scores. In the present study, PCA 2 scores for environments were far from zero, in spite of having larger PCA1 scores.

Conclusion

AMMI analysis should provide (i) an enhanced understanding of GEIs in METs, (ii) increasingly accurate yield estimates using means for multiplicative interaction effects, and (iii) the increased probability of identifying the next royalty-paying genotype. The interaction of the 20 genotypes with six environments was best predicted by the first 2 principal components of genotypes and environments. Consequently, biplots generated using genotypic and environmental scores of the first two AMMI components can help breeders have an overall picture of the behavior of the genotypes, the environments and GEIs.

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