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GGE BIPLLOT ANALYSIS OF WHEAT MEAN PERFORMANCE AND STABILITY AT DIVERSE LOCATIONS IN REPUBLIC OF MACEDONIA

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Abstract

Wheat is the most important cereal crop in Republic of Macedonia. Development of genotypes that will have high grain yield with stable performance in different growing conditions is of paramount importance. The objective of this research was to evaluate and to quantify the magnitude of the genotype x environment interaction effects on wheat grain yield and to determine the winning genotype for the test locations. Ten wheat genotypes were tested at three locations (Skopje, Strumica and Prilep) for two years (2006 and 2007). The grain yield data for each location were subjected to the GGE biplot analysis. This analysis depicted the adaptation pattern of genotypes at different locations and discrimination ability of testing locations. Out of the three locations, Prilep was identified as the most discriminative and representative location. The genotype Bt 04-073 had the highest overall mean yield, and an average stability over different locations. In each location, Radika and Bt 04-073 were the closest to the “ideal” genotype, followed by Bt 04-024. Those genotypes can be recommended for production in wheat growing regions in Republic of Macedonia.

Key words: wheat, genotype x environment interaction, GGE biplot, grain yield, stability analysis

Introduction

In the Republic of Macedonia, wheat is the most important cereal crop, grown on approximately 84181 ha in the last five years. Grain yield of cultivated genotypes in Macedonia is insignificantly higher (3056 kg ha⁻¹) than the global average yields (3010 kg ha⁻¹), but compared with the highest yield (7772 kg ha⁻¹), it is far below this value (FAOSTAT, 2011). In order to mitigate this, different improved cultivars are continually created or introduced. Those cultivars are being evaluated at different locations to test their performance and to identify the best genotypes in specific environments. The genotype × environment (GE) interaction usually complicates the selection for improved yield (Sabaghnia et al., 2013). According to Rodriguez et al. (2002) in the cases when the magnitude of GE is large it impedes the selection of stable genotypes and the selection advancement is slow.

Ceccarelli (1989) claimed that adaptation in crop plants corresponds to yield stability over time and environments. Considering this, when unpredictable GE interaction is present, cultivar evaluation must be carried out in multiple locations in order to fully test the target environment (Cooper et al., 2007). Consequently, for assessing genotypic value and cultivar's stability for yield performance, multi-environmental trial (MET) data are required. The main purpose of MET is to identify superior cultivars which could be recommended to farmers and to determine sites that best represent the target environment (Yan and Hunt, 2001).

The genotype performance across different environments could be difficult to determine without the help of graphical display of the data (Yan et al., 2001). Yan and Hunt (2001) proposed a GGE biplot that allows visual examination of the GE interaction pattern of the data. GGE biplot refers to the genotype main effect (G) and the genotype x environment interaction (GE), the main two sources of variation that are important to cultivar evaluation. It can be used to identify superior cultivars and test environments that facilitate identification of such cultivars. The detection of genotypes that have the highest yield across a number of environments could be useful to breeders and producers (Kaya et al., 2006). Thus, information on wheat cultivar stability in different environments, along with high yield may be helpful in selection of genotype(s) that have the best performance in favorable environments, but also maintain satisfactory yields under poor management.

The GGE-biplot methodology was used in this study (i) to graphically summarize the effects of genotypes (G) and genotype x environment (GE) interaction on yield performance of 10 bread wheat genotypes tested across 3 locations, (ii) to facilitate visual comparison among genotypes and environments and (iii) to determine if wheat growing regions in Macedonia might be divided into distinct MEs.

Materials and methods

The study was carried out in 2006 and 2007 in three different locations in Republic of Macedonia (Skopje, Prilep and Strumica). A set of 10 bread wheat genotypes (Radika, Bt 04-005, Bt 04-024, Bt 04-030, Bt 04-040, Bt 04-073, Bt 04-081, Bt 04-082, IJZK 16/99, MO 11/4) was used as experimental material (Table 1). Experimental layout was a randomized complete block design with five replications in each location. Each plot consisted of eight rows of 5 meter length. Between row distance was 12.5 cm. In order to eliminate side effects, data on grain yield were taken from the middle six rows of each plot. At harvest grain yield was determined for each genotype at each test location. The GGE biplot analysis was performed using R statistical software.

Results and discussion

GGE denotes genotype main effect (G) plus genotype by environment interaction (GE). For appropriate genotype evaluation (Yan, 2002), these two sources of variation that are relevant to genotype evaluation must be considered simultaneously, not alone or separately.

The vector view of the GGE biplot (Figure 1) presents a summary of the interrelationships among the locations. The test locations are connected to the biplot origin by lines, called environment vectors. The cosine of the angle between the vectors of two locations approximates the correlation between them (Kroonenberg, 1995; Yan, 2002). The distance between two locations represents their dissimilarity in discriminating the genotypes. Thus, the three locations fell into three different groups. The large angle between them implies poor correlation between these locations (Figure 1).

Table1. Genotype code and name of 10 bread wheat genotypes with their average grain yield across three locations

Genotype code	Genotype name	Grain yield (kg ha ⁻¹) per location			Average yield (kg ha ⁻¹)
		Skopje	Strumica	Prilep	
1	Radika	7.60	6.65	4.70	6.32
2	Bt 04-005	7.70	6.05	4.10	5.95
3	Bt 04-024	7.45	6.75	4.70	6.30
4	Bt 04-030	8.00	6.40	3.80	6.07
5	Bt 04-040	8.15	5.80	4.40	6.12
6	Bt 04-073	7.90	6.95	4.60	6.48
7	Bt 04-081	7.60	5.95	3.60	5.72
8	Bt 04-082	7.60	6.30	4.30	6.07
9	IJZK 16/99	7.50	6.85	4.60	6.32
10	MO 11/4	6.90	6.90	3.60	5.80

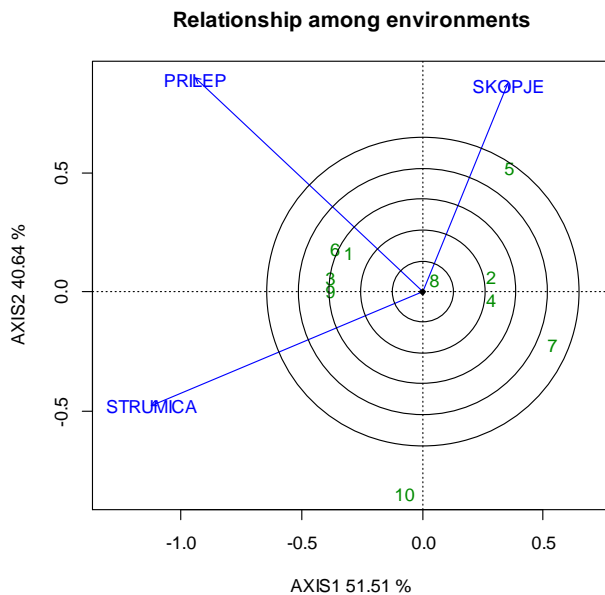


Figure 1. GGE biplot based on relationships among test environments.

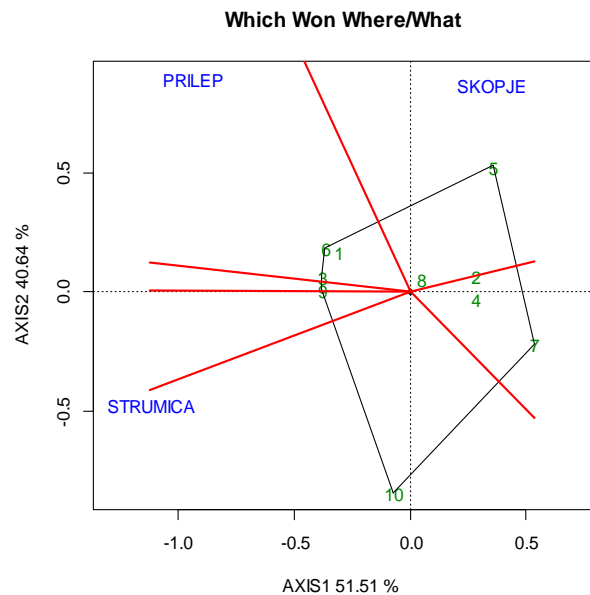


Figure 2. Which-won-where pattern of genotypes and environments.

One of the best possibilities that the GGE biplot methodology offers is showing the which-won-where pattern of a genotype by environment dataset (Figure 2). It graphically addresses important concepts such as crossover GE, mega environment differentiation, particular adaptation, etc (Yan and Tinker, 2005). The polygon is created by linking the markers of the genotypes that are the furthest away from the biplot origin such that all other genotypes are positioned in the polygon. Genotypes located on the vertices of the polygon performed either the best or the poorest in one or more environments. The vertex genotype(s) for each sector has higher (sometimes the highest) yield than the others in all environments that fall in that sector (Yan, 2002). The perpendicular lines are equality lines between adjacent genotypes on the polygon, which facilitate their visual comparison. Thus, all locations included in this

study fell into different sectors. The vertex genotype for the sector where Skopje was positioned was 5, for Prilep region was 6 and for Strumica region was genotype 10.

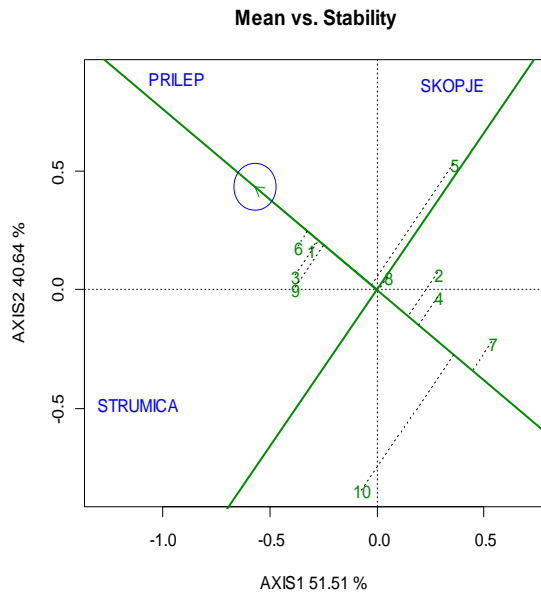


Figure 3. GGE biplot representing mean performance and genotypes stability

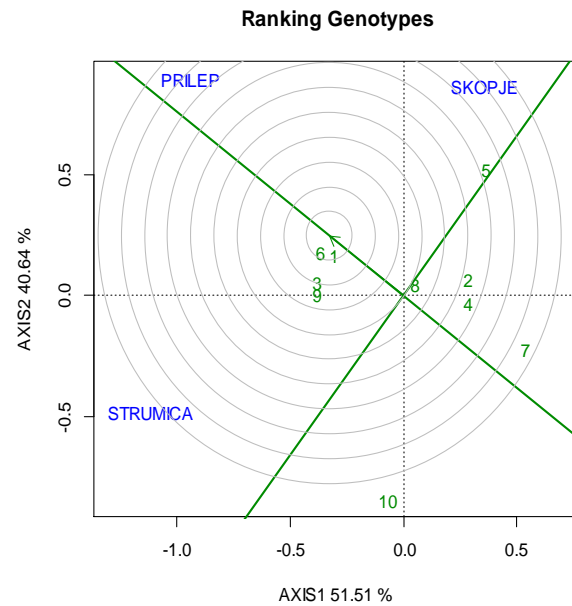


Figure 4. Genotype-focused scaling for comparison of the genotypes

The ranking of 10 genotypes based on their mean grain yield and yield stability for 3 locations is shown in Figure 3. It has been reported that when PC1 in a GGE biplot approximates the G (mean performance), PC2 must approximate the $G \times E$ associated with each genotype, which is a measure of instability (Yan et al., 2000; Yan, 2002). The line that passes through the biplot origin and the environmental average is known as the average environment coordinate (AEC) axis and is indicated by circle, which is defined by average PC1 and PC2 scores for all environments. Projection of genotype markers onto this axis represents the mean yield of the genotypes and the arrow points to higher mean yield across environments. Thus, genotypes 6, 1, 3 and 9 had higher grain yield than the other genotypes from this dataset. The line which passes through the origin but is perpendicular to the AEC represents the status of the genotypes stability. A position in either direction away from the biplot origin, on this axis, indicates greater $G \times E$ interaction and reduced stability (Yan, 2002). Therefore, genotypes 6, 1 and 8 were the most stable, while genotypes 5 and 10 showed more variable and the least stable performance (Figure 3). Similarly, when ranking genotypes (Figure 4), genotypes 6 and 1 and the closest to the "ideal" genotype.

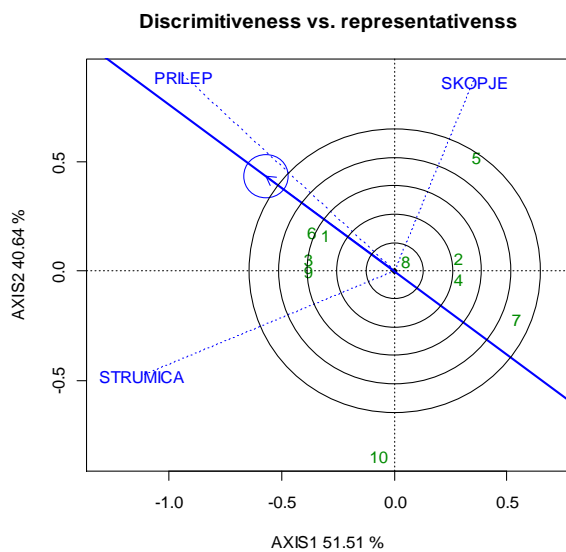


Figure 5. Discriminability and representativeness of the three locations

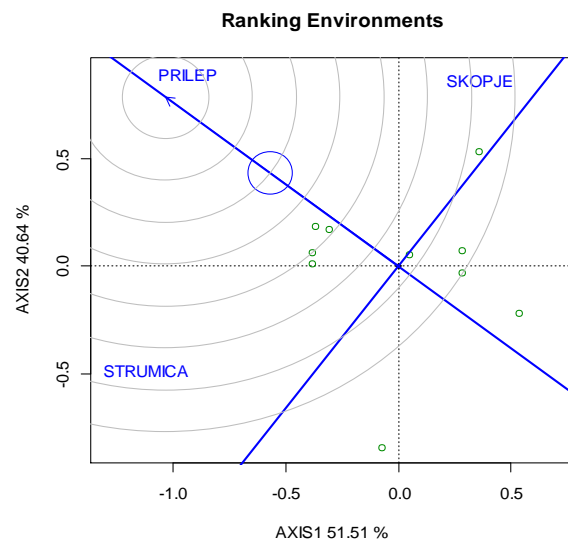


Figure 6. GGE biplot based on environment-focused scaling

The length of the environment vectors on the biplot approximates the standard deviation within each environment, which is a measure of its discriminating ability (Yan and Kang, 2003). Considering this, Prilep was the most discriminative location (Figure 5). When ranking the environments (Figure 6), Prilep was the closest to the “ideal” environment.

Conclusions

The analyzed ten bread wheat genotypes showed high variability for grain yield. The three locations included in this study could be considered as different mega-environments for wheat testing. Genotypes 6 (Bt 04-073) and 1 (Radika) had the highest average yield and were the most stable genotypes. Genotypes 5 (Bt 04-040) and 4 (Bt 04-030) had the best performance in Skopje region, 6 (Bt 04-073) and 10 (MO 11/4) in Strumica and 1 (Radika) and 3 (Bt 04-024) in Prilep. These genotypes should be recommended for growing in these specific locations.

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