Pavel SOLONECHNYI, Mikhail KOZACHENKO, Nataliya VASKO,
Vladimir GUDZENKO, Vitaliy ISHENKO, Galina KOZELETS,
Nadezhda USOVA, Yuriy LOGVINENKO, Aleksandr VINYUKOV[1]

AMMI AND GGE BIPLOT ANALYSIS OF YIELD PERFORMANCE OF SPRING BARLEY (*Hordeum vulgare L.*) VARIETIES IN MULTI ENVIRONMENT TRIALS

SUMMARY

We evaluated the phenotypic stability and adaptability of spring barley varieties using the additive main effect and multiplicative interaction (AMMI) and genotype main effect (G) plus genotype-environment (GE) interaction (G+GE) biplot models. The research was conducted in five locations by randomized complete block design with three replications in each location in 2015-2016. The grain yields of all nine barley genotypes were significantly affected by environment, which accounted for 90.5% of the total variation, whereas genotype and genotype-environment interaction accounted for 4.0% and 5.5%, respectively. The AMMI and GGE biplot models reflected most of the variation caused by genotype and genotype-environment interaction effects in the first two principal components – 78.8% and 79.3%, respectively. The AMMI stability value (ASV) revealed that varieties Khors (G4) and Poduv (G5) were stable. GGE-biplot "which-won-where" showed that 9 environments used for the study belonged to 3 mega-environments with wining varieties Vzirets (G1), Inkliuziv (G6) and Dokaz (G9). According to the ideal genotype biplot, varieties Dokaz (G9), Inkliuziv (G6) and Khors (G4) were the best genotypes demonstrating high average yields and high stability of performance across the test locations. The results finally indicated that AMMI and GGE biplot were informative methods to explore stability and adaptation patterns of genotypes in practical plant breeding and in subsequent variety recommendations.

Keywords: Spring barley, GGE biplot, AMMI analysis, yield

INTRODUCTION

Barley breeding is a time consuming process, which in many cases lasts over a decade. Selection of superior genotypes is one of the most important goal

[1]Pavel Solonechnyi (corresponding author: pashabarley86@gmail.com), Mikhail Kozachenko, Nataliya Vasko, Plant Production Institute nd. a V. Ya. Yuriev NAAS, Kharkov, UKRAINE; Vladimir Gudzenko, The V.M. Remeslo Myronivka Institute of Weat NAAS, Mironovka, UKRAINE; Vitaliy Ishenko, Galina Kozelets, Kirovograd State Agricultural Experimental Station of NAAS, Kropivnitskiy, UKRAINE; Nadezhda Usova, Institute of oilseeds crops of NAAS, Zaporozhzhye, UKRAINE; Yuriy Logvinenko, Aleksandr Vinyukov, Donetsk State Agricultural Experimental Station of NAAS, Krasnoarmeysk, UKRAINE

in barley breeding. In order to evaluate the performance of these genotypes, plant breeders conduct field trials in different locations. These tests enable collecting data on genotype stability and adaptability (Mirosavljević, 2014).

When genotypes are tested for performance in several environments, the rankings usually differ as differences in environment may produce different effect on genotypes. Such inconsistent phenotypic performance of genotypes across environments is called genotype-environment interaction (Asfaw et al., 2009). Genotype-environment interaction (GEI) is differential phenotypic performance of genetically uniform genotypes across test environments. It occurs because different genotypes have different genetic potentials to adjust them selves to variable environments and causes one genotype to not win every where and always (Zeleke and Berhanu, 2016).

In this context, Multi Environment Trials (METs) are important for studying yield stability, adaptation and as well for prediction of yield performance of genotypes across environments (Solonechnyi at al., 2015). Typically, environment causes most of the total yield variations, while genotype and genotype-environment interaction (GEI) are usually less effective (Yan and Kang, 2003; Dehghani et al., 2010). A large GEI variation usually hinders the accuracy of yield estimation and reduces correlation between genotypic and phenotypic values. GEI is a universal phenomenon when different genotypes are tested in a number of environments, and is an important issue for plant breeders and agronomists to predict cultivar behavior in different locations across different years prior to any recommendation concerning varieties (Kang, 1998; Annicchiarico, 2002; Karimizadeh et al., 2012; Yan et al., 2007; Mortazavian, 2014).

Different methods are presented for statistical analysis of MET data, including parametric and non-parametric, to estimate the nature of genotype interactions with the environment and their control, but a method that would be approved by everyone has not still been introduced (Kaya et al., 2006).

Two frequently used statistical analyses are the additive main effects and multiplicative interaction (AMMI) model and the genotype main effects and genotype-environment interaction effects (GGE) model (Gauch, 2006). These two statistical analyses (AMMI and GGE) have broader relevance for agricultural researchers because they pertain to any two-way data matrices, and such data emerge from many kinds of experiments.

The AMMI model is a hybrid model involving both additive and multiplicative components of two way data structure which enables a breeder to precisely predict genotypic potentiality and environmental influences on it. AMMI uses ordinary ANOVA to analyze the main effects (additive part) and principal component analysis (PCA) to analyze the non additive residual left after ANOVA (Gauch, 1988; Zobel at al., 1988). Concerning the use of AMMI in METs data analysis, which partitions the GEI matrix into individual genotypic and environmental scores, an example was provided by Zobel et al. (1988).

Purchase et al. (2000) developed a quantitative stability value to rank genotypes through the AMMI model, namely the AMMI Stability Value (ASV).

Yan et al. (2000) proposed a modification of the conventional AMMI analysis called GGE (genotype and genotype-environment interaction) which is used for GEI analysis. The GGE analysis pools the genotype effect (G) with GE (multiplicative effect) and submits these effects to principal component analysis. According to Yan et al. (2000), this biplot is identified as a GGE biplot. GGE biplot has some graphical visualization function such as visualization of genotypes performance in a specific environment, visualization of relative adaptability of a genotype in a varying environment, visualization of comparison of two genotypes in different environment, visualization of identifying the best genotypes in every environment, visualization of an environmental group for a specific genotpe(s), visualization of genotype average performance and stability, and visualization of discrimination and representation of environment (Yan and Hunt, 2001). These aspects make GGE biplot a most comprehensive tool in quantitative genetics and plant breeding (Mousavi at al., 2016).

This objective of our study was to evaluate the adaptability and yield stability of spring barley varieties using GGE biplot and AMMI analysis to select varieties that have both high performance and phenotypic stability.

MATERIAL AND METHODS

Trials. Nine spring barley varieties bred at the Plant Production Institute nd. a V.Ya. Yuryev of NAAS were tested in nine environments, including five different locations, in 2015 and 2016. The locations were: Kharkov in the northeast of Ukraine; Mironovka in the north of Ukraine; Kropivnitskiy in the central part of Ukraine; Krasnoarmeysk and Zaporozhzhye in southeast of Ukraine (Table 1). The genotypes were grown by a randomized complete block design with three replications in each site.

Table 1. Code and name of 9 spring barley and 5 testing locations

Variety	Code	Location	Year	Code	Latitude	Longitude	Altitude (m)
Vzirets	G1	Kharkov	2015	E1	50°00' N	36°13' E	117
Agrariy	G2		2016	E2			
Alegro	G3	Mironovka	2015	E3	49°39' N	31°00' E	128
Khors	G4		2016	E4			
Poduv	G5	Zaporozhzhye	2015	E5	47°50' N	35°08' E	86
Inkliuziv	G6		2016	E6			
Modern	G7	Kropivnitskiy	2015	E7	48°30' N	32°16' E	113
Kozvan	G8		2016	E8			
Dokaz	G9	Krasnoarmeysk	2016	E9	48°16' N	37°10' E	181

ANOVA. Combined analysis of variance was performed for all the environments and included five locations and two years (data of Krasnoarmeysk were for one year). The treatment sum of squares was partitioned into its three

components: genotype (G), environment (E) and genotype-environment interaction (GEI).

GGE biplot analysis. The 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 multi-environment yield trials (METs) data. This methodology uses a biplot to show the factors (G and GE) that are important in genotype evaluation and that are also sources of variation in GEI analysis of METs data (Yan et al., 2000, 2001).

AMMI analisys. Stability (AMMI stability value (ASV) was calculated according to the formula, as described by Purchase et al. (2000).

The data on yields were mathematically processed using Genstat12 software.

RESULTS AND DISCUSSION

ANOVA and AMMI analysis. Combined analysis of variance showed that there were highly significant differences for environment, genotype and their interactions. Combined analysis of variance and AMMI analysis are shown in Table 2. In our study, spring barley grain yields were significantly affected by the environment, which accounted for 90.5% of the total (G + E + GE) variation, whereas genotype and genotype-environment interaction accounted for 4.0% and 5.5%, respectively. A large sum of squares for environments indicated that the environments were diverse, with large differences between environmental means causing variation in the grain yields.

Table 2. Combined and AMMI analyses of variance and contributions of the first four principal components to the grain yield of 9 spring barley genotypes in 9 environments

Source	DF	SS	MS	G+E+GE SS (%)	GE SS (%)
Genotypes (G)	8	19.6	2.450**	4.0	
Environments (E)	8	442.5	55.228**	90.5	
Interactions (GE)	64	27.4	0.428**	5.5	
IPCA1	15	13.1	0.873		47.8
IPCA2	13	8.5	0.652		31.0
IPCA3	11	2.3	0.206		8.4
IPCA4	9	1.7	0.193		6.2
Residuals	16	1.8	0.115		
Error	144	4.5	0.031		
Total	242	494.0	2.041		

DF = degree of freedom; SS = sum of squares; MS = mean square; IPCA = interaction principal component axis; **significant at 1 %.

In most multi-environment trials the environment accountes for over 80% of the total variation (Yan, 2002; Yan and Kang, 2003; Gauch at al., 2008).

Combined ANOVA determines whether GEI is a significant source of variation or not and estimates it, but does not provide insight into the patterns of genotypes or environments that give rise to the interaction (Samonte et al., 2005). Therefore, the combined data were also analyzed using the AMMI model that further partitions GEI into IPCA (Interaction Principal Components Axes) components. The results from AMMI analysis also show that the first and second principal component axis accounted for 78.8% of the interaction variability, enabling us to evaluate the stability of genotypes for these two components.

Table 3 shows the AMMI model IPCA1 and IPCA2 scores of the grain yield for 9 spring barley genotypes in 9 environments and the AMMI stability value (ASV) for each genotype. Purchase et al. (2000) developed a quantitative stability value to rank genotypes through the AMMI model, named the AMMI Stability Value (ASV). According to ASV ranking, varieties Khors (G4) and Poduv (G5) were the most stable genotypes, while genotype Vzirets (G1) was unstable.

Table 3. Mean grain yield (tha^{-1}), first and second principal component axis (IPCA) and AMMI stability values (ASV) for the grain yield of 9 spring barley genotypes in 9 environments

Code	Mean	IPCA1	IPCA2	ASV
G1	4.68	-1.217	0.067	2.284
G2	4.46	0.335	0.626	0.504
G3	4.60	0.330	-0.620	0.553
G4	4.95	0.143	0.020	0.031
G5	4.78	-0.022	0.028	0.002
G6	4.98	0.281	-0.173	0.152
G7	4.12	0.481	0.264	0.425
G8	4.33	-0.195	0.517	0.326
G9	4.99	-0.136	-0.728	0.558
Mean	4.65			
LSD$_{05}$	0.09			

GGE biplot analisys. The first two principal components of GGE biplot model obtained by singular value decomposition of the centered data of grain yield accounted for 79.3% of the total variability caused by G + GE effects. Out of these variations, PC1 and PC2 accounted 52.2% and 27.1% variability, respectively.

Visualization of the "which-won-where" pattern of MET data is important for studying 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 MET data set (Figure 1). By connecting the genotype markers and the rays as depicted, the rays in Figure 1 are lines that are perpendicular to the sides of the polygon or their extensions. These 6 rays divide the biplot into 7 sectors, but environments fall into three of them, so the genotypes vertex in these sectors may indicate higher or the highest yield compared to other parts in all environments (Yan, 2002).

PC1 = 52.20%; PC2 = 27.12%; Sum =
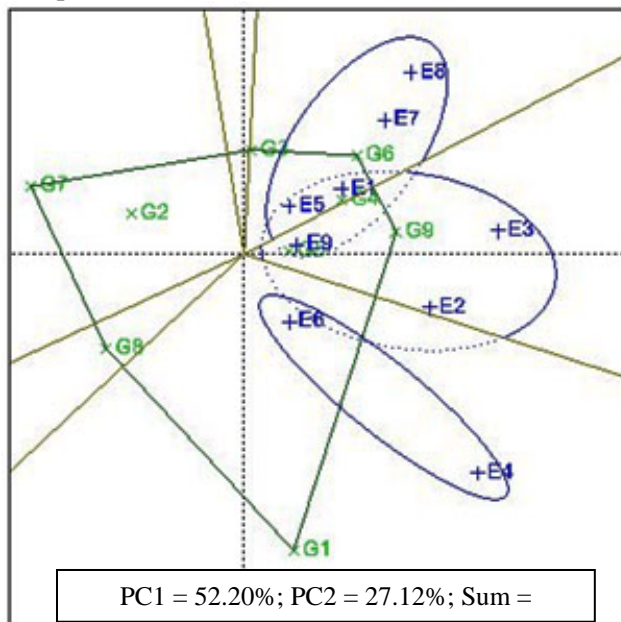
Figure 1. Polygon views of the GGE biplot based on symmetrical scaling for the «which-won where» pattern for genotypes and environments.

Another important feature of this biplot is that it indicates environmental groupings, which suggests a possible existence of different mega-environments. Thus, in our studies the first mega-environment consists of environments E8, E7, E5 and E1 with variety Inkliuziv (G6) being the winner. The environments E3, E2 and E9 makes up the second mega-environment, where variety Dokaz (G9) is winner. The last mega-environment consists of environments E4 and E6, where variety Vzirets (G1) has the highest yield capacity.

The yield stability of genotypes was evaluated by the average environment coordination (AEC) method (Yan, 2001; Yan and Hunt, 2001; Yan, 2002). In this method, the average principal components will be used in all environments, as depicted in Figure 2. A line is then drawn through this average environment and the biplot origin; this line is called the average environment axis and serves as the abscissa of the AEC. Unlike the AEC abscissa, this has one direction, with the arrow pointing to a greater genotype main effect; the AEC ordinate in either direction away from the biplot origin indicates a greater GEI effect and reduced

stability. The AEC ordinate separates genotypes with below-average means from those with above-average means. Varieties Dokaz (G9), Khors (G4) and Inkliuziv (G6) had the highest mean yields, varieties Modern (G7) and Kozvan (G8) – the lowest mean yields. The yield of variety Vzirets (G1) was the most variable, while varieties Khors (G4), Poduv (G5) and Dokaz (G9) were noticeable for their high stability.
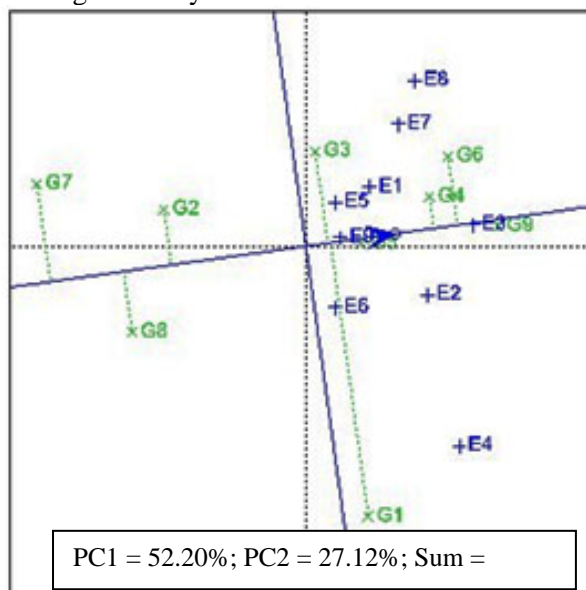

PC1 = 52.20%; PC2 = 27.12%; Sum =

Figure 2. Average environment coordination (AEC) views of the GGE biplot based on environment-focused scaling for the mean performance and stability of genotypes

Stability in itself, however, is not the only parameter of genotype evaluation, because the most stable genotypes do not necessarily have high performance (Mohammadi at al., 2007; Mohammadi and Amri, 2008). An ideal genotype is one that has both high mean yield performance and high stability. The centre of concentric circles (Figure 3) represents the position of an ideal genotype, which is defined by a projection onto the mean-environment axis that equals the longest vector of the genotypes that had above-average mean yields and by a zero projection onto the perpendicular line (zero variability across all environments). The closer a genotype to the ideal one is the more valuable it is. Although such an ideal genotype may not exist in reality, it can be used as a reference for genotype evaluation (Yan and Tinker, 2006). Thus, varieties G7, G2, and G8 which had fell below the AEC ordinate, showed below average seed yield performance, whereas varieties G1, G3, G8, G4, G6 and G9, which fell above the AEC ordinate, performed above average. Varieties Dokaz (G9), Inkliuziv (G6) and Khors (G4) which had performed above average and had relatively shortest projection vectors from AEC line, were both high yielding and widely adapted.
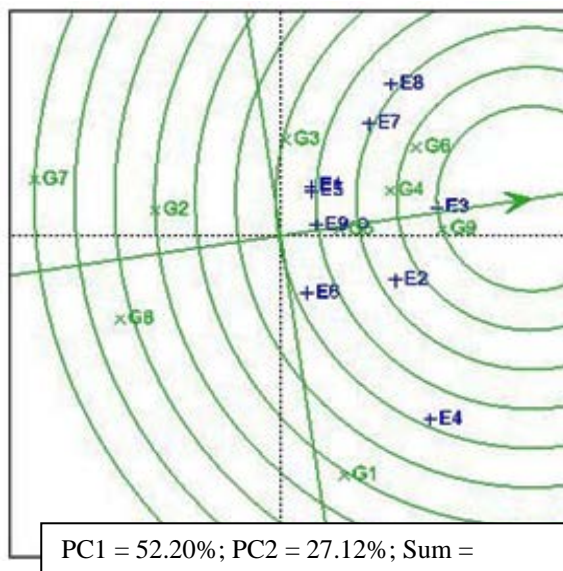
PC1 = 52.20%; PC2 = 27.12%; Sum =

Figure 3. GGE biplot based on genotype-focused scaling for comparison
the genotypes with the ideal genotype.

GEI reflects differences in adaptation and can be exploited by selecting for
specific adaptation if the trend in specific adaptability of genotypes is repeatable
over years (Annicchiarico, 2002; Yan et al., 2007). However, in this study, the
specific adaptability trend was not repeated over years as different environments
were grouped differently in the two years. Therefore, GEI couldn't be exploited
and should be minimized by selecting for broad adaptation. Thus, broadly
adapted varieties, G9, G6, G4 and G7, were recommended for verification and
release.

**Discriminating ability, representativeness and relationships of the test
environments.** According to Yan et al. (2007), due to the discriminative ability
and representativeness of GGE view, the biplot was an effective tool for
environment evaluation, which was not possible with the AMMI model. In
environment focusing scaled vector view of GGE biplot, the cosine of the angles
between environment vectors show relationships between test environments: with
acute angles indicating strong positive correlation, obtuse angles – strong
negative correlation or cross over GEI of genotypes, and right angle showing no
correlation (Yan and Tinker, 2006). Hence, highly correlated environments E9
with E3, E6 with E4, E5 with E7 and E8 (Figure 4).

Discriminating ability and representativeness of the testing environments
are an important measure in the GGE biplot. An environment is more desirable if
it is located closer to the ideal environment. Thus, using the ideal environment as
the centre, concentric circles were drawn to help visualize the distance between
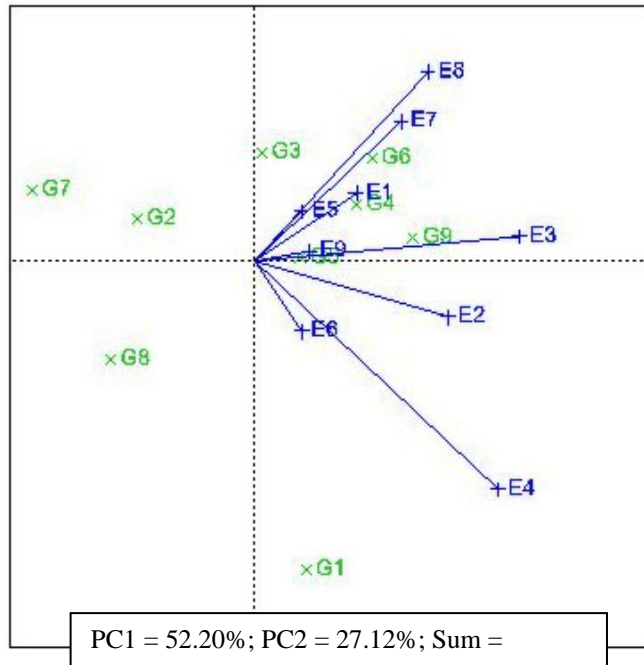each environment and the ideal environment (Yan et al., 2000; Yan and Rajcan,
2002).

PC1 = 52.20%; PC2 = 27.12%; Sum =

Figure 4. GGE biplot showing relationships among the test environments
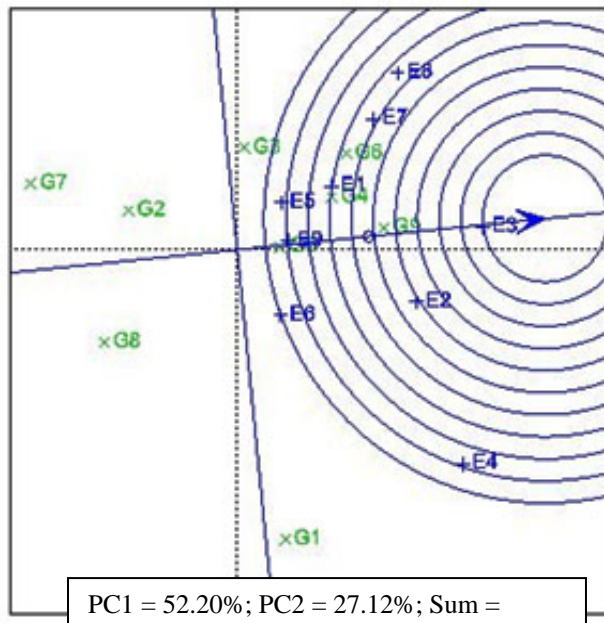

PC1 = 52.20%; PC2 = 27.12%; Sum =

Figure 5. Ranking of environments based on discriminating ability and representativeness

Figure 5 shows that environment E3 was the ideal test environment in terms of being the most representative of the overall environment and was chosen to select superior genotypes. Environments E6, E5 and E9, closer to the biplot origin, are characterized by similar performance of all genotypes; hence they provide little or no information about the genotypic differences, therefore, similar test environments should not be considered as test environment for yield trials. E8 and E4 have long vectors and large angles with the abscissa, hence, should not be used for selecting superior genotypes, but useful for culling unsuitable genotypes.

CONCLUSIONS

The result showed that the magnitude of the environmental effect was by far higher than the genotype effect and genotype-environment interaction effect. Spring barley varieties evaluated in this study had highly significant genetic differences in the grain yield performance across the environments.

Varieties Dokaz, Inkliuziv, Khors and Poduv are characterised by the highest mean yield and high stability and are expected to have the greatest commercial success. In terms of the regional distribution, it should be emphasized that it has a predictive character and requires continued multi-year testing.

The results finally indicated that AMMI and GGE biplot were informative methods to explore stability and adaptation of genotypes in practical plant breeding and in subsequent variety recommendations.

ABREVIATION

AMMI – additive main effects and multiplicative interaction; GGE – genotype main effects and genotype-environment interaction effects; AEC – average environment coordinate; PCA – principal components analysis; SVD – singular value decomposition; GEI – genotype-environment interaction.

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