ASSESSMENT STABILITY OF MAIZE LINES YIELD BY GGE-BIPLOT ANALYSIS

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Maize genotypes have varied reactions in different localities, years, treatments or the combination of these factors, due to genotype x year interaction. The objective of this study was to estimate genotype by locality, by year, by treatments (G×L×Y×T) interaction using AMMI model, to identify maize genotypes with stable and high yield performance in different growing seasons. The trials with seven maize lines/genotypes were conducted during two years (2010–2011) at the four treatments and two locations: Pančevo and Zemun Polje. The results showed that the influence of: genotype (G), locality (L), treatment (T) and G×L, G×T, Y×L, Y×T, L×T, G×Y×T, G×L×T, Y×L×T, G×Y×L×T interaction, on maize yield were significant (p<0.01). The share of genotype for maize grain yield in the total phenotypic variance was 21.16%, the aggregate share of the years and the locality was 6.10%, the treatment was 18.22%, and the total interaction was 54.52%. The AMMI analysis of the main components of IPCA1 and IPCA2 for the interaction of G×L and G×T shows that the first major component, IPCA1, comprises 100% of the sum of the squared interaction G×L and showed a statistically significant effect. The results also show that the sums of the squares of the first and second major components (PC1 and PC2) constitute 100% of the sum of the squared interaction G×L. The IPCA1 share in the G×T interaction was 47.39% and the IPC2 was 37.94%. IPC1 and IPC2 for this interaction was 85.33%. A high level of IPC2

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indicates a significant treatment effect. The results of AMI analysis show that there is a significant difference between the genotype reactions to different ecological conditions for investigated factors. It also provided better insight in specific association between maize grain yield, locality, treatment and meteorological variables. Among the tested maize lines/genotypes, L-5, L-4 and L-6 could be separated as highest yielding genotypes, however L-5 could be recommended for further breeding program and in large-scale seed production due to its stable and high yielding performance.

Key worlds: Zea mays L., lines, AMMI analysis, G×Y×L×T interaction, yield

INTRODUCTION

Maize (*Zea mays* L.) is one of the biggest profits in 20th-century agriculture. Strategically, it is important agricultural species that occupies the third place in the world's widespread distribution (143 mil. ha), after wheat (215 mil. ha) and rice (151 mil. ha) and in Serbia it is at first place. In the last few years' average, areas under maize in Serbia were about 1.2 million hectares and they were recorded oscillations. Hybrid is just one of the many, but also the most important factor of production, whose effect, fortunately, can be controlled. For successful production it is necessary to select several hybrids, most suitable for a certain agro-ecological area (POPOVIĆ, 2010; 2015). Average maize yield in the world is 5.6 t ha^{-1} (ŽIVANOVIĆ and POPOVIĆ, 2016; ZRAKIĆ *et al.,* 2017; MAKSIMOVIĆ *et al.,* 2018). The world's total production of maize is about 1,000 million tones. The world's largest producers of maize are USA, China and Brazil with a total of two-thirds of world production. According to the harvested areas, Serbia is the fourth in Europe (POPOVIĆ, 2010).

There are many definitions of stability and adaptability but the following ones prevail. Stability is the ability of a genotype to have always the uniform yield regardless of environmental effects (HILL *et al.,* 1998 Citate: BECKER, 1981). Adaptability is the ability of aa variety to provide stable and high yield under different environmental conditions (HILL *et al.,* 1998 Citate: FINLY and WILKINSON, 1963).

Maize breeding programs depend on the understanding and knowledge of genetic diversity and relationship among inbred lines and breeding material. This is crucial in terms of the yield, as the major objective in all breeding programs as well as in all other targeted traits (MLADENOVIĆ DRINIĆ *et al.,* 2004; MILIVOJEVIĆ *et al.,* 2017). Stability and adaptability of genotypes are best assessed by evaluating the cultivars in different environments and ecological regions. Changes in environments affect both crop growth and grain yield due to significant genotype × environment interactions (GEI) (POPOVIĆ *et al.,* 2012; 2016). Results of multi-environment trials (MET) have demonstrated the existence of GEI (BADU-APRAKU *et al.,* 2011; 2013; STOJAKOVIĆ *et al.,* 2015; PRŽULJ *et al.,* 2015). The presence of a significant GEI complicates the selection of superior cultivars and the best testing sites for identifying superior and stable genotypes. This necessitates extensive testing of cultivars in multiple environments over several years before cultivars are recommended for release. Grain yield being a complex trait routinely exhibit GEI, thus requires genotype evaluation in MET in the advanced stages of selection (FAN *et al.,* 2007). Analysis of MET data revealed that some cultivars are well adapted to specific ecological regions (YAN, 2010). Therefore, selection of suitable genotypes and testing sites is crucial to the success of a plant breeding program.

Climate change can alter the arable farming with reducing yields in maize belts, at the same time (LEE and TOLLENAAR, 2007; POPOVIC, 2010). For a more successful breeding work knowledge of the value of the interaction of the genotype and the external environment is of great importance. Choosing of superior maize hybrids for production is difficult, due to the presence of genotype interaction and environmental factors (GEI). The stability and adaptability of the genotype under different conditions is due to its genetic structure, but it is known a little about the components that determine stability more closely and a relationship between them, as well as the effect of breeding system on them (LEE and TOLLENAAR, 2007). By using statistical methods, it is possible to exclude the consequences of interaction of genotype and external environment and to isolate stable and high yield genotypes. Such a method of selecting maize hybrids in literature is known as a dynamic concept of stability and accepted in maize breeding programs. The most commonly used statistical analysis for the interpretation of GEI is based on the use of biplots of the AMMI model. This model is distinguished because it interprets the effects of genotype (G) and the location (E) as additive, and on the GEI, as a multiplicative non-adaptive component, an analysis of the main components is applied (DUARTE and VENCOVSKY, 1999). With this analysis, one or more statistically significant components (PCA axes) are generated from the sum of the squares. A biplot graph is used for interpreting the results, and it combines the mean values of the genotype properties and some of the main components of the interaction.

Several stability statistics used to partition GEI include regression analysis, multivariate analysis, cluster analysis, genotype main effect plus genotype × environment (GGE) biplot (YAN, 2001) and additive main effect and multiplicative interaction (AMMI). However, both GGE and AMMI analyses are the most frequently used in analyzing GEI pattern of multi-environment data set. AMMI analysis is capable of detecting GEI in a multi-dimensional space and presents the interaction visually using a biplot. AMMI has been used to analyze GEI in wheat (CHANG and CHAI, 2006), barley (MIROSAVLJEVIC *et al.*, 2015), sugar beet (ĆIRIĆ *et al.*, 2017) and maize (BADU-APRAKU *et al.,* 2011; 2013; STOJAKOVIĆ *et al.,* 2015; OYEKUNLE *et al.,* 2017). Therefore, understanding the GEI between intermediate maturing maize genotypes and testing locality for evaluating regional trials in Serbia is very important for evaluating the stability and suitability of the genotypes and environments.

The aim of this research is to determine the influence of genotype, year, locality and treatment (sulfonylurea) on the stability of yield of tested maize lines and to identify superior and stable genotypes across environments and assess relationships among test environments. This work should be useful for maize selectors to understand the interaction of the genotype × environment, as well as the agricultural producers in selecting maize hybrids.

MATERIALS AND METHODS

The research was carried out at two sites: in Zemun Polje (in the Maize Research Institute) and in Pančevo (in the Institute Tamiš), in two variant with treatments, during 2010 and 2011, the basic plant material consists of six maize lines (L-1, L-2, L-3, L-4, L-5 and L-6). Examines were based on a completely random block system, in three reps, with 20 plants in each repetition. Each genotype was planted in one row with ten houses with two plants each, so that the size of the elementary plot was 2.8 m^2 (0.7m x 0.4m). The density of crops was 74,280 plants

per hectare. Sowing and harvesting were done manually and, in the experiment, standard maize cultivation technology was applied except for variants with treatment. The experiments were four sub-treatments with Sulfonylurea herbicides: 1. T_1 - Control was without herbicide, treatment was done only with water - treatment 1; 2. T_2 - active substance Nicosulfuron, and the Motivell preparation in the amount of 1.25 l ha^{-1} (6.3 ml per treatment) - treatment 2; 3. T_3 - active substance Rimsulfuron, and the Tarot preparation in the amount of 60 g ha^{-1} (0.3 g per treatment) - treatment 3; 4. T_4 - active substance Forasulfuron, and the Ekvip preparation in the amount of 2.5 l ha^{-1} (12.6 mL per treatment) - treatment 4. Herbicides were applied when corn was in the phase of 9-10 developed leaves (15-16 per BBCH scale) with a Solo spiral type with Tee Jet KSR11003, with a water consumption of 250 l ha^{-1}. At the time of the technological maturity, at both localities, from each tested genotype, 10 plants from three reps were taken in order to obtain data on the following grain yield. Biometric data processing is based on repetition for grain yield.

Data analysis

The AMMI model (The Additive Main Effects and Multiplicative Interaction) was used to assess the G×E interaction, and it can be represented by the following formula (GAUCH *et al.,* 2008):

$$Y_{ger}= \mu + \alpha_g + \beta_e + \Sigma_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge} + \varepsilon_{ger}$$

Where: Y_{ger} is the yield for the genotype g in the environment e the replication r. The additive parameters are: m – the grand mean, α_g – a/the genotypic mean deviation from the grand mean, β_e – the environmental mean deviation. The multiplicative parameters are: λ_n– a singular value for n interaction principal component axis n, γ_{gn} – the genotypic eigenvector for IPCA axis n, δ_{en} – the eigenvector of the environment for IPCA axis n, ρ_{ge} – a residue when not all PCA axis are included and e_{ger} - the error. Statistical data analysis was performed using the GenStat 12th computer statistical program (GenStat for Windows 12th Edition, VSN International, Hemel Hempstead). AMMI analyses were performed in Excel Biplot Macros. Among multivariate analysis models, the additive main effects and multiplicative interaction (AMMI) biplot and the genotype main effect and genotype × environment interaction (GGE) biplot have been frequently used to visualize G×E interaction. The main differences of the two methods, AMMI analysis is referred to double-centered principal component analysis (PCA), whereas GGE biplot analysis is based on environment-centered PCA (RAO *et al.,* 2011). The AMMI model incorporates analysis of variance (ANOVA) and PCA in a single statistical model (GAUCH *et al.,* 2008). In AMMI models, using ANOVA additive effect is separated from interaction, and then PCA is applied to analyze interaction effect (KAYA *et al.,* 2002). The biplot graphic presentation shows both main and interaction effects for genotypes and environments simultaneously and provides a more in-depth analysis of G×E interaction (ZOBEL *et al.,* 1988). Authors state that it is high-value genotypes of the PC1 component are distinguished above the average expression of the tested trait. In contrast, the second interaction component (PC2) indicates genotype stability. Zero value shows highest stability and when the value goes from zero, it shows instability. We have theoretically and practically observed four different combinations of these two components: the

first consists of over average and stable genotypes (high value PC1, low PC2 value), the second group of over average and unstable genotypes (high value PC1, high value of PC2), third sub average and stable (low PC1 value, low PC2 value), and fourth sub average and unstable genotypes (low PC1 value, high PC2 value).

Meteorological data

Meteorological data, especially precipitation and temperature, varied significantly trough the growing seasons (POPOVIĆ *et al.,* 2015; 2016; ŽIVANOVIĆ *et al*., 2017). Monthly precipitation and average temperature were collected from the weather station located near the experimental fields, in Pančevo and Zemun Polje, Serbia. Total amount of precipitation during crop growth cycle was 480 mm (2010) and 369 mm (2011) in Pančevo and 497 mm (2010) and 328 mm (2011) in Zemun Polje, figure 1. Average monthly temperature was 18.4ºC (2010) and 19.5ºC (2011) in Pančevo and 18.5ºC (2010) and 19.6ºC (2011) in Zemun Polje, fig. 1.
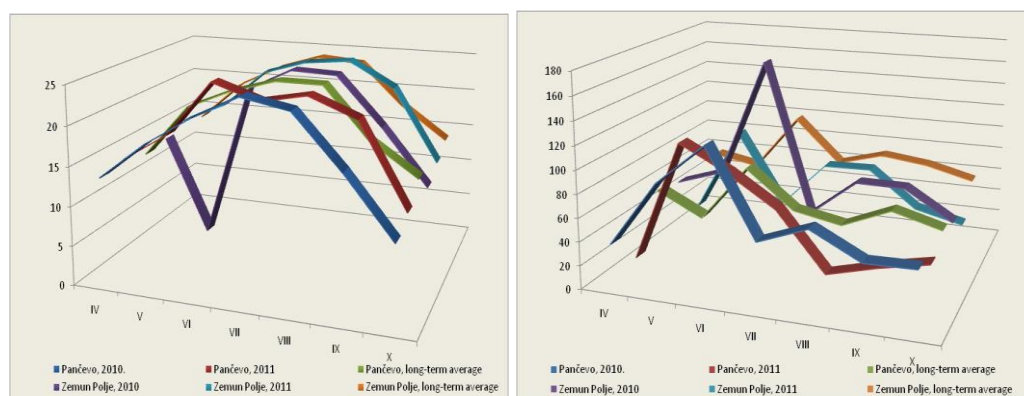
a.   b.

Figure 1. Average temperature (ºC), a., and total precipitation (mm), b., 2010-2011

Meteorological conditions are very variable in our country and significantly affect the yield (POPOVIĆ *et al.,* 2012; 2015; 2016; JANKOVIĆ *et al.,* 2018).

RESULTS AND DISCUSSION

Maize grain yield is one of the most important parameters for estimating maize hybrid value, in almost all programs of selection and breeding of standard grain quality. The analysis of variance (ANOVA) separates the overall variability on the main - additive effects of environment (E), genotype (G), and non-additive genotype $\times$ environment interaction (GE).

In Table 1, the total sum of the squares was divided into the additive (genetic) and non-additive (ecological) component by analyzing the variance for the mass of the grains yield of the tested maize inbred lines. A statistically significant influence of the genotype, location and

treatment, as well as all forms and levels of interactions for the grain yield (G×L, G×T, L×T, Y×L, G×Y×T, G×L×T, Y×L×T and G×Y×L×T) were recorded, Table 1.

Table 1. Analysis of variance of AMMI model for grain yield (kg ha^{-1})

Sources of variation	DF	Yield (kg ha^{-1})		
		SS	SS (%)	MS
Genotype (G)	5	15955	21.16	3190**
Year (Y)	1	2065	2.72	2065 ^{ns}
Location (L)	1	2564	3.38	2564**
Treatment (T)	3	13775	18.22	4592**
G×Y	5	3083	4.07	617 ^{ns}
G×L	5	4725	6.25	945**
IPCA1	5	4725	6.25	945**
IPCA2	3	0,00	4.62	000 ^{ns}
G×T	15	3492	4.62	233**
IPCA1	7	1655	2.30	236 ^{ns}
IPCA2	5	1325	1.60	265 ^{ns}
Y×L	1	1224	1.62	1224**
Y×T	3	4467	5.91	1489**
L×T	3	1309	1.73	436**
G×Y×L	5	4503	5.96	901 ^{ns}
G×Y×T	15	3050	4.04	203**
G×L×T	15	4221	5.59	281**
Y×L×T	3	1051	1.39	350**
G×Y×L×T	15	8748	11.58	583**
Error	192	1328	1.76	6.92 ^{ns}
Sum	287	75560	100.00	-

*, ** - significant at the probability level 0.05 and 0.01

The sum of squares of genotype was about eight times higher than the sum of squares of year and about six times higher than squares of the locality, Table 1. The share of sum of squares of genotype in the total variation is for 2.94% higher than the share of the sum of the squares of the treatment. The genotype share in the total phenotypic variance was 21.16%, the aggregate share of the years and the localities was 6.10%, the treatment was 18.22%, and the total interaction was 54.52%.

There was a significant difference between the reaction of genotypes to different ecological conditions and on different treatments in experiment. Different reaction of inbred lines to environmental factors caused high sum of the squares of individual interactions and their significant effect on total phenotypic variability which is reflected by high interaction in the overall variation of grain yield. The large sum of squares of genotype and the high value of the share of treatment variance in the total phenotypic variability indicate a great divergence between the observed inbred lines and their reaction on applied treatments when it comes to this

trait. Considering the existence of a significant share of the interaction of the genotype with other sources of variation (localities and treatments), an AMMI analysis of its main components IPCA1 and IPCA2 for interaction G×L and G×T was done. The first major component, IPCA1, comprised 100% of the sum of the squares of the interaction G×L and showed a statistically significant effect. The results also show that the sums of the squares of the first and second major components (PC1 and PC2) constitute 100% of the sum of the squares of the interaction G×L. Also, the first PC1 axis has extremely high proportion in the total interaction, which points to the significance of the genotype in the overall variation and significance of the genotype for total interaction. The share of IPCA1 in terms of G×T interaction is 47.39%, and IPC2 makes 37.94%. IPC1 and IPC2 in this interaction together comprise 85.33% of the interaction. A high level of IPC2 refers shows high impact of treatment.

BABIĆ *et al.* (2006) in their researches state that many authors showed the possibility of developing highly yielding and stable hybrids. The assumption was that commercial maize hybrids were characterized not only by the level of average yield bat also by their stability. The authors state that there are significant differences in yields and some yield components between genotypes, environments and interactions G×L, and that there was a significant share of the genotype and interaction G×L and G×Y in total phenotypic variation for yield and some of the components of the yield. In addition to the effect of the main factors, their interactions (G×Y, G×L, Y×L, G×Y×L) were high significant for all investigation trait (JOVOVIC *et al.,* 2012).

The IPCA values of interaction components for the grain yield of studied lines of maize are shown in Table 2. According to the IPCAg1 values in the interaction G×L, the lines L-3 and L-4 are characterized by a high level of stability while the other lines deviate significantly either positively or negatively. It should be noted that these lines also had a relatively high yield. The L-5 and L-6 lines has the highest average yield while far less stability have the inbred lines L-3 and L-4. L-4, L-5 and L-6 lines had an average yield of over 4 tons, and could be considered desirable for further processing.

Table 2. IPCA component of interaction and AMMI value of stability for maize grain yield

Genotype	Yield				
	Average	Genotype x Locality		Genotype x Treatment	
		IPCAg1	IPCAg2	IPCAg1	IPCAg2
L-1	2910	-7.984	0.000	-10.752	6.965
L-2	2764	-12.488	0.000	12.446	6.708
L-3	3830	1.107	0.000	-8.993	-2.884
L-4	4345	-1.471	0.000	3.182	1.636
L-5	4665	9.033	0.000	2.875	-14.892
L-6	4445	11.797	0.000	1.243	2.465

When it comes to the first components of interaction G×T, the most stable is the L-6 genotype both for IPCAg1 and IPCAg2, and the least stable is L-2 lines are based on IPCAg1

and L-5 based on IPCAg2. It should be noted that line L-2 is characterized by the lowest average grain yield and low stability, which is confirmed by IPCAg1 values.

Herbicides from the group of Sulphonylureas caused stress in the line of maize, which is best reflected in the reduction in yield. Although they achieved the highest yields, the hybrids of the FAO group 600 were mostly affected by these climatic conditions. Forasulfuron is a herbicide from the group of sulfonylurea which caused stress to the greatest extent while Nicosulfuron was the most effective.

Genotypes with a minimum variance, as well as the minimum value of the PC1 axis or when this value tends to be zero in different external environments, are considered stable (SABAGHNIAA *et al.,* 2006).

Stability of grain yield for maize lines

The variability and stability of the grain yield of maize lines is shown in figure 2 using the GGE-biplot method (Figure 2a). The highest stability in terms of grain yield expression was exhibited by the genotype L-3, whose average value for the tested property almost coincides with the overall average for all the genotypes involved in the study. The L-5 and L-6 genotypes, which has the best expression, is also characterized by high stability. The lowest stability was demonstrated by L-6 and L-4 genotypes, but they are characterized by good expression of this trait in the investigated localities, while the genotypes L-2 and L-1 are not important for further selection in terms of the trait as they had the expression below average.
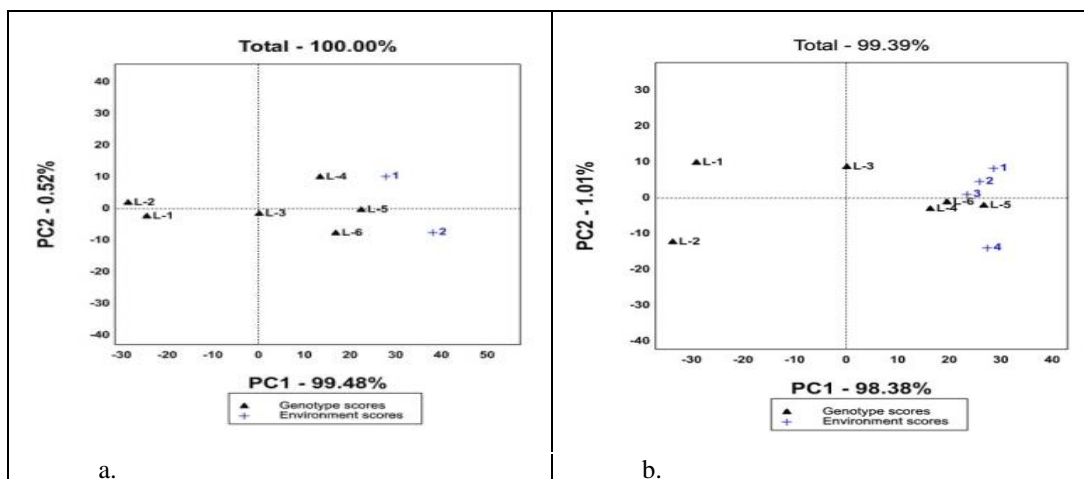

Figure 2. GGE biplot demonstrates the stability of expression for the yield of lines based on the locality (a), and the treatment (b).

The highest stability in terms of grain yield expression was revealed by the genotype L-5, followed by the genotypes L-4, L-6 and L-3 in different treatments (Figure 2b). The lowest stability was demonstrated by the genotypes L-2 and L-1, which again confirmed that these genotypes are not important for further selection for grain yield. It can be concluded that the

constant stability of grain yield expression was demonstrated by the genotype L-5, both in terms of the tested localities and the applied treatments. A similar conclusion can also be made for the genotype L-3, for which it can be said that it does not represents anything new in the selection, considering the yield level, achieved at the localities by different treatments.

Figure 3a shows a graphic arrangement and a comparison of genotypes and locality according to the expression of grain yield, and in graph 3b, a comparison of genotypes and treatments was performed to express the same trait. The graphic representation is a complement to the previous graphs, that relate to stability, where genotypes that are farthest from the coordinative start are linked, so that a multi-legged geometric body is obtained, within which other genotypes are found. Genotypes which are at the corners of this body are genotypes with the best or the weakest expression of grain yield.

With the with drawal of the axis from the coordinate start, which encloses the angle of 90 degrees with the sides of the multi-legged geometric body or the imaginary extension of those sides, the biplot is divided into several sectors on the basis of which the tested genotypes are grouped.
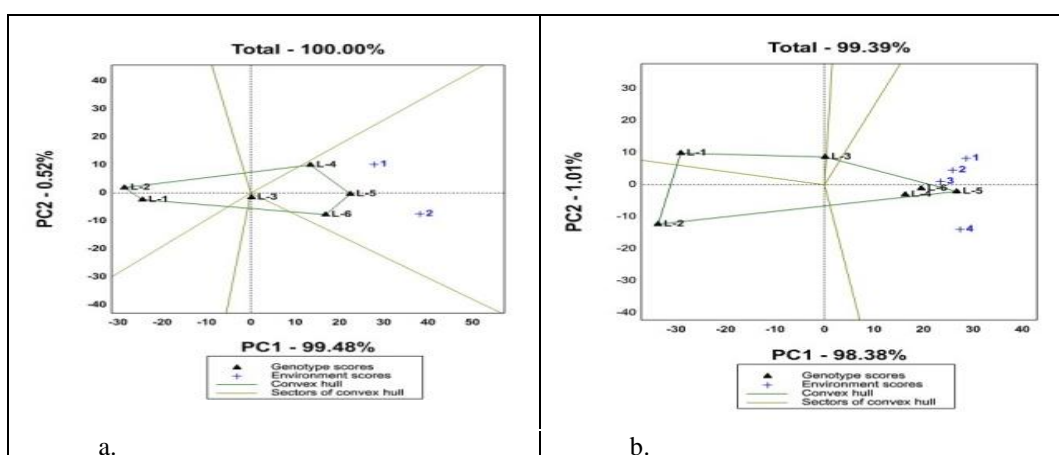

Figure 3.GGE-biplot view for line yields according to the "wich-won-where" model, based on the locality (a), and the treatment (b).

The axis from the coordinate start divides biplots into five sectors (Figure 3a). Both localities belong to the same sector. The best expression and maximum stability in the first locality was achieved by the L-5 line. The L-4 line had somewhat lower expression and a lower level of stability at the first locality. As the value of the second locality is in the same sector, the expression of this feature in the L-6 line was more expressed in this locality, but with somewhat lower stability. The expression of grain yield at L-3 is matches with a general average, and the value of PC2 tends to be zero, and this line is stable, but it does not pose a challenge for the selectors. The other three genotypes did not show any significance in any of the observed localities.

Figure 3b shows that the coordinate system is divided into four sectors. All treatments are in the same sector. Based on the phenotypic expression for grain yields, the genotypes L-5, L-6 and L-4 occupy the same sector on biplot. The mentioned genotypes showed the best values in the examined treatments, which, according to their average values, are also located in the same sector. Genotypes L-1, L-2, and L-3 did not show a good result in terms of applied treatments.

On the Figure 4a, the formation of the coordinates of the average locality was made, which allowed the comparison of the tested genotypes with an ideal genotype. The position of the ideal genotype is represented by the smallest circle and arrow within it, and defined by the average values of PC1 and PC2 of the tested localities. It is a genotype that has achieved the best expression of the trait in all localities. The tested genotypes are compared to it and the ranking is carried out based on the distance indicated by the concentric circles. In this graph, we can see that the line L-5 tends to be an ideal genotype and that the L-4 and L-6 lines are somewhat distant.
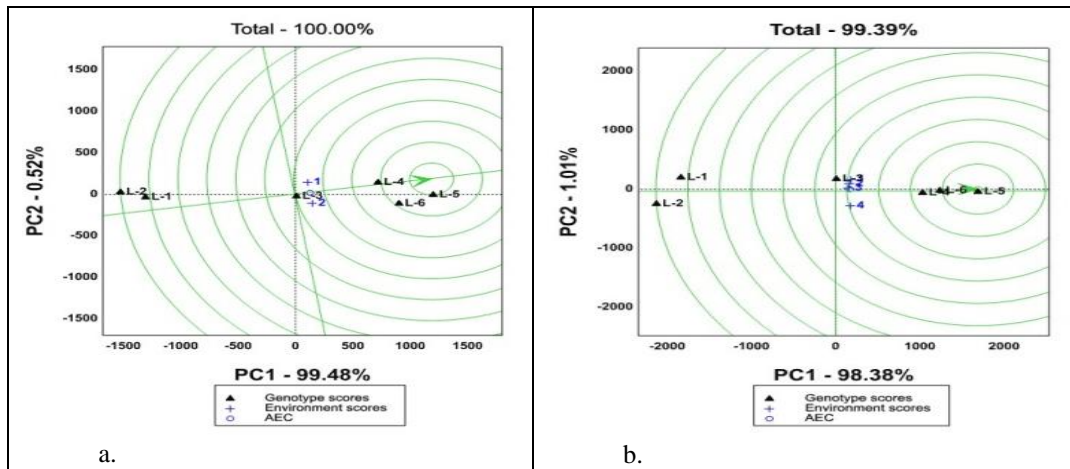

Figure 4. GGE biplot presentation for line yield according to the ideal genotype model, based on the locality (a) and the treatment (b).

In the coordinate system, it appears that the sites of the locality almost match with the expression of this characteristic in line L-3, but the expression of grain yield at this line is far from ideal. The other lines are at the opposite end of an ideal genotype and are not of interest to the further process of breeding.

At applied treatments, L-5 and L-6 are in the smallest circle, while L-4 is at the very edge of the circle, and these lines are closest to the ideal genotype, both in terms of stability and in terms of featured expression (Figure 4b). Similar to the tested localities, it appears that the coordinate system, the treatment sites almost corresponds to with the expression of this property in the L-3 line, but the grain yield expression at this line is far from ideal. The other lines are at the opposite end of the ideal genotype and are not interesting for breeding work.

Genotypes of interest in production are genotypes with high values of the PC1 component when it comes to the properties in which the plus variants, i.e. the higher the average value of the tested property and the lower the value of the PC2 component, i.e. close to zero. In the properties in which the minus variants are preferred in the selection process (for example, the height of the stem, etc.), genotypes with a lower PC1 value and a PC2 value tend to be zero, are desirable. Low-grade genotypes PC2 are characterized by broad adaptability, as opposed to specific adaptive genotypes that are located far from the coordinative start. Therefore, the high value of PC1 indicates that the best expression of the trait is in specific agro-ecological conditions.

Based on the phenotypic grain yield expression, the hybrid H-4 had the highest expression and high level of stability, and the hybrid H-5 had the highest level of stability and high phenotypic expression in the conditions of different treatments. Based on this analysis, it can be concluded that maize hybrids achieve different yields of grains in different environments, and that the reorientation of the production area and the identification of genotypes with higher phenotypic stability can contribute to the improvement of the overall corn production. Technology which will achieve the yield level almost the same as its genetic potential should be used and in that way it would be easier to avoid expensive mistake in production process.

BRANKOV's results (2016) are similar to our research. The author states that from the applied herbicides, sulfonylurea significantly influenced the changes in the content of biochemical parameters in the leaves of corn lines. The average world loss of corn yield, caused by weeds is around 10% (OERKE, 2006). According to SPASOJEVIC *et al.* (2014), without the application of herbicides, maize yield can be reduced by more than 50%. As the level of coagulation significantly influences yield, weed control is a basic component in almost every plant production system. Today, it is recommended that weed control, as well as other harmful organisms, be carried out with an integrated approach (IWM - Integrated Weed Management) (SIMIC *et al.*, 2013).

The GGE biplot figure for grain yield was more practical than AMMI1, and its interpretation provided a greater wealth of information. Our results are consistent with the results authors OLIVEIRA *et al.* (2010) where the authors they say it is the GGE biplot method performed better than AMMI1 in retaining a greater portion of the sums of squares (G + GE) and (GE), whereas the models AMMI1 and AMMI1.2 tend to be more accurate than model GGE2. However, the GGE biplot graph was more practical and its interpretation provided a greater wealth of information (OLIVEIRA *et al.,* 2010).

The results of AMI analysis show that there is a significant difference between the genotype reactions to different ecological conditions for investigated factors. The first PC1 axis had an extremely high proportion in overall interaction, which points to the significance of the genotype in overall variation and the significance of the genotype for overall interaction.

BALESTRE *et al.* (2009) in this study is evaluated these genotypes at locations within the same state, unlike in this study, where very different sites in terms of soil and climatic features were used, resulting in a more complex pattern of GE interaction. Thus, when aiming to evaluate genotypes for regional programs (similar environments) the performance of the GGE biplot method is slightly superior. While on the contrary, in breeding programs on a nationwide seed scale, the performance of the AMMI method tends to be better.

CONCLUSION

Results from this study have suggested that AMMI analysis is very applicable for the analysis of maize lines and different years, locality and treatment interaction. The share of genotype for maize grain yield in the total phenotypic variance was 21.16%, the aggregate share of the years and the locality was 6.10%, the treatment 18.22%, and 54.52% for the total interaction. The share of IPCA1 for maize grain yield in G×T interaction was 47.39%, while IPC2 was 37.94%. IPC1 and IPC2 for this interaction is 85.33%. A high level of IPC2 indicates a significant treatment effect. The share of sum of squares of genotype in the total variation is for 2.94% higher than the share of the sum of the squares of the treatment. The genotype share in the total phenotypic variance was 21.16%, the aggregate share of the years and the localities was 6.10%, the treatment was 18.22%, and the total interaction was 54.52%. The IPCA1 share in the G×T interaction was 47.39% and the IPC2 was 37.94%. IPC1 and IPC2 for this interaction was 85.33%. A high level of IPC2 indicates a significant treatment effect. Among the tested maize lines/genotypes, L-5, L-4 and L-6 could be marked as highest yielding genotypes. Line L-5 could be recommended for further breeding program and large-scale production due to its stable and high yielding performance. It also provided better insight in the specific association between maize grain yield, locality, year and treatment.

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OCENA STABILNOSTI PRINOSA LINIJA KUKURUZA POMOĆU GGE-BIPLOT ANALIZE

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Izvod

Genotipovi kukuruza imaju drugačiju reakciju pri različitim: lokalitetima, godinama, tretmanima ili njihovoj kombinaciji, usled prisustva interakcije genotipa i sredine. Cilj ove studije bio je da se proceni uticaj interakcije genotip x lokalitet x godina x tretman (G×L×Y×T) pomoću AMMI modela, kako bi se identifikovali genotipovi kukuruza sa stabilnim i visokim prinosima u različitim vegetacionim sezonama. Ispitivanja sa sedam linija/genotipova kukuruza sprovedena su tokom dve godine (2010-2011), četiritretmana i na dve lokacije: Pančevo i Zemun Polje. Rezultati pokazuju da je uticaj: genotipa (G), lokaliteta (L), tretmana (T) i interakcije G × L, G × T, Y × L, Y × T, L × T, G × Y × T, G × L × T, Y × L × T, G × Y × L × T, na prinos kukuruza bio značajan (p <0.01). AMMI analiza glavnih komponenti IPCA1 i IPCA2 za interakciju G×L i G×T pokazuje da prva glavna komponenta, IPCA1, obuhvata 100% od sume kvadrata interakcije G×L i pokazala je statistički značajan uticaj. Rezultati pokazuju da sume kvadrata prve i druge glavne komponente (PC1 i PC2) čine 100% sume kvadrata interakcije G×L. Udeo IPCA1 kada je u pitanju interakcija G×T iznosila je 47,39%, a IPC2 37,94%. IPC1 i IPC2 kod ove interakcije iznosila je 85,33%. Visok nivo IPC2 ukazuje na značajan uticaj tretmana. Rezultati AMI analize pokazuju da postoji značajna razlika između reakcije genotipova na različite ekološke uslove za ispitivane faktore. Takođe su omogućili, bolji uvid u specifičnu povezanost prinosa zrna kukuruza, lokaliteta, tretmana i meteoroloških varijabli. Među testiranim linijama/genotipovima kukuruza, linije L-5, L-4 i L6 mogu se izdvojiti kao genotipovi sa najvecim prinosima, međutim linija L-5 se može preporučiti za dalje programe oplemenjivanja u proizvodnju velikih razmera zbog stabilnih i visokih prinosa.