



Identification of the Most Desirable Maize Testing Environments in Northern Serbia

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Summary: One of the final stages in the process of maize breeding is testing the potential hybrids in pre-registration multi-location trials. The aim of this study was to evaluate six locations (Pančevo, Sremska Mitrovica, Ruma, Srbobran, Rimski Šančevi and Sombor) in the northern Serbia for testing yields of maize seed hybrid by GGE (Genotype and Genotype by Environment Interaction) biplot method in the period from 2007 to 2011. This study comprised 24 maize hybrids tested across 6 environments. Different sets of hybrid were used every year. Hybrids served as "a random" factor for the evaluation of locations. The ANOVA indicated significant effects of genotypes (G) and environments (E) every year, while their interaction (GE) was significant in 2007, 2009 and 2011. On average, the SO location provided the smallest amount of information and therefore can be excluded from further trials and analysis. The sites SM and RU were the most similar locations and only one of these two locations should be included in further trials. The location RŠ presented the smallest repeatability. For analysis that is more detailed it is necessary to include more locations in trials and analysis.

Key words: analysis, environment, GE interactivity, grain yield, hybrids, maize, Zea mays L.

Introduction

Maize is one of the three most important agricultural species worldwide and according to FAO, it was grown on about 170 million hectares in 2011 (FAOSTAT 2011). It is used mainly as a food staple, livestock feed, as feedstock for food processing and in chemical industry. Maize is the most widespread field crop in Serbia, and it is cultivated in various agro-climatic conditions on approximately 1.2 million hectares. Maize breeding has been carried out for decades at the Institute of Field and Vegetable Crops. One of the final stages in the process of maize breeding is testing the potential hybrids in pre-registration trials. These trials are conducted annually on several different locations and their objective is to select hybrids with the best performance and to acquire information about hybrids responses to different environmental conditions (Mitrović et

al. 2011). Hybrids in trials are potential candidates for official examination by the state commission for plant varieties and species.

The evaluation of hybrids is a difficult process because of the interaction between genotype and environment (GEI). It is a phenomenon that involves different genotypes, cultivars or hybrids reacting in various environments (Kang 2004). Interaction, therefore, interferes in the selection process and makes it more complicated. It diminishes correlation between genotypic and phenotypic parameters and reduces the progress in plant breeding. The importance of understanding this factor lies in the identification of optimal conditions for hybrid evaluation and recommendation for better performing and more adaptable hybrids (Yan et al. 2000).

Several methods have been created to assess the interaction of genotype by environment. The analysis of variance, linear regression, nonlinear

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analysis, multivariate analysis and non-parametrical statistics are the base on which these methods were developed (Balestre et al. 2009, Crossa 1990, Eberhart & Russel 1966, Gauch & Zobel 1997, Yan et al. 2000). Additive model such as Analysis of Variance (ANOVA) estimates the effects of main factors and defines if GEI is an important factor for variation. However, ANOVA does not provide access into genotypes and environments that are involved in interaction (Samonte et al. 2005).

GGE (Genotype and Genotype by Environment Interaction) biplot is commonly used for the interpretation of GEI. Two essential parts of this method are biplot concept (Gabriel 1971) and GGE concept (Yan et al. 2000). It is created for visual analysis of data from multi-environmental trials (MET) and uses biplot to present two factors - genotype and GEI, which are of the highest importance for assessment of genotypes in various climatic and soil conditions. This model displays two first main components - PC1 and PC2 - which are the two most important sources of variance. These components were obtained by singular values decomposition of GGE data.

The main objective of this article is to examine the possibility of acquiring reliable information from smaller number of locations. In addition, the aim of this paper is to identify groups of locations with similar characteristics among examined sites that will allow the elimination of highly correlated sites from further analysis. The third objective is detection of poor environment, which offers unreliable information about hybrid performance.

Materials and Methods

Data used in this work are from pre-registration trials that consist of 24 experimental hybrids from the FAO 600 group. These trials are conducted on six locations in the northern Serbia: Sombor (SO), Srbobran (SRB), Rimski Šančevi (RŠ), Pančevo (PA), Ruma (RU) and Sremska Mitrovica (SM) (Tab. 1). GGE biplot analysis was performed on data from five-year period (2007-2011). Different sets of hybrid were used every year but within year on each of the six locations was the same set of hybrids. Hybrids served as a random factor for the evaluation of locations. The trials were arranged in a randomized complete block design with three replications. The experimental plot size for each hybrid was 9.75 m² (6.5 m long with two rows). The distance between rows was 0.75 m, and 0.22 m within rows, with density of 60,606 plants/ha. The planting and the harvesting were performed by machine. The standard agro-technical practice was applied in accordance to local agro-ecological

Table 1. Geographic position and soil characteristic of test environments Tabela 1. Geografske koordinate i tip zemljišta test lokacija

	Ge Geo		Soil type/ Tip zemljišta	
Location Lokaliteti	Latitude Geografska širina	Longitude Geografska dužina	Altitude (m)/ Nadmorska visina (m)	
Rimski Šančevi (RŠ)	45°20′N	19°51′E	82	Non-carbonate chernozem, Bezkarbonatni černozem
Sombor (SO)	45°46′N	19°06′E	87	Carbonate chernozem/ Karbonatni černozem
Srbobran (SRB)	45°32′N	19°44′E	79	Chernozem/ Černozem
Pančevo (PA)	44°52′N	20°39′E	82	Carbonate chernozem/ Karbonatni černozem
Ruma (RU)	45°00′N	19°49′E	111	Chernozem/ Černozem
remska Mitrovica (SM)	44°58′N	19°36′E	100	Chernozem/ Černozem

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conditions. The grain yield in t/ha was calculated to 14% grain moisture.

The analysis of variance has been done for each year and each region, which is shown in Table 2. GGE biplot was used for the evaluation of locations. This method combines the analysis of variance and PCA (Principal Components Analysis) in form

 $Y_{ij} - \mu - E_j = \lambda_1 \varepsilon_{i1} \eta_{1j} + \lambda_2 \varepsilon_{i2} \eta_{2j} + e_{ij}$ where Y_{ij} is the corresponding variable of the *i*-th genotype in *j*-th environment, μ is the total mean, E_j is the main environment effect of j-th, λ_1 and λ_2 are singular values of principal components PC1 and PC2; ε_{i1} and ε_{i2} are eigenvectors in *j*-th environment (location) for PC1 and PC2 of i genotype in j environment.

All data analyses were performed within R computing environment (R Development Core Team 2011).

Results and Discussion

The results show that maize grain yield was significantly influenced by environment effects, which accounted for 68%, 80%, 84%, 50% and 78% of total yield variation in 2007, 2008, 2009, 2010 and 2011, respectively (Table 2). Based on ANOVA results, it is evident that GEI was significant in 2007, 2009 and 2011 and insignificant in 2008 and 2010. Although GEI has agronomically and genetically important effect and the sum of squares accounts a large proportion of the total variation, ANOVA test of GEI is often not significant due to high degree of freedom (Crossa 1990.) The percentage of GEI in the total variation was usually about 10% except in 2007 and 2010 when its value was 25% and 36% respectively. Our results are similar with the findings of Kaya et al. (2006), who

Table 2. The analysis of variance for 24 maize hybrids grain yield across 6 environments in the northern

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Year/ Godina	Source of variation/ Izvori varijacije	Degrees of freedom/ Stepeni slobode	Sum of squares/ Sume kvadrata	Means of squares/ Sredine kvadrata	F values/ F vrednosti	%SS/ % Suma kvadrata
2007	G	23	93,552	4,067	3.07**	6.9
	E	5	914,145	182,829	137.77**	68
	GxE	115	335,881	2,921	2.2**	25.1
2008	G	23	349,113	15,179	11.77**	12.8
	E	5	2194,574	438,915	340.45**	80.5
	GxE	115	182,187	1,584	1,23	6.7
2009	G	23	145,224	6,3141	6.4**	5.3
	E	5	2315,9806	463,1961	469.84**	84.1
	GxE	115	291,1383	2,5316	2.57**	10.6
2010	G	23	230,06	10,003	1.86*	13.6
	E	5	846,506	169,301	31.48**	50.1
	GxE	115	613,012	5,331	0,99	36.3
2011	G	23	215,425	9,366	6.09**	10.4
	E	5	1619,765	323,953	210.73**	78.4
	GxE	115	230,722	2,006	1.31*	11.2

^{** -} significant at 0.01 level of probability / značajno na nivou 0.01

^{* -} significant at 0.05 level of probability / značajno na nivou 0.05

showed that E explained for about 81% of the total variation, while G explained 7% and GE explained for about 13%. Fan et al. (2007) reported that the effects of environment and genotype explained 69% and 8.5% of total treatment variance respectively, whereas the interaction explained 16% of the total treatment variance. Gauch and Zobel (1996) showed that 80% of the total sum of treatments is environment effect and 10% the effect of genotype and interaction in standard multi-location trials.

At GGE biplot, lines that connect the origin of biplot with the environments coordinate are termed vectors (Yan et al. 2006). The angle between vectors represents correlation between them, but not completely, because biplot does not explain the total variance of data (Yan 2002). PC1 and PC2 captured approximately 68%, 83%, 75%, 78% and 71% of total variation, in 2007, 2008, 2009, 2010 and 2011, respectively. If two environment vectors form acute angle, environments are positively correlated, if angle is obtuse environments are negatively correlated and if angle is 90° environments are not correlated.

GGE biplot enables environment evaluation for their discriminative ability and representativeness (Yan et al. 2006). The length of vector describes the discriminative ability of location. Greater length of vectors means larger standard deviation and therefore better discrimination, while environments points with shorter vector length has less discriminative ability. An environment that has the smallest angle with average environment axis (AEA) is the most representative test location. AEA passes through the biplot origin and average values of PC1 and PC2 for the all environments (Yan et al. 2001). Average coordinate values for environment are marked with open circle, while arrows on AEA represent an "ideal" environment that would be the most representative and discriminative location for conducted trial (Fig. 1, 2, 3, 4 and 5).

In 2007 trial (Fig. 1), the most discriminative locations were SM and RU. RU is more representative because it forms smaller angle with AEA axis. The least information is acquired from the location SO which is represented by the shortest vector. The angle between vectors for location PA and locations RŠ, SO, SRB and RU is higher than 90 degrees, which indicates that in 2007 these four locations were negatively correlated with PA.

Environment SRB forms the smallest angle with AEA, and it is closest to the arrow on AEA axis in

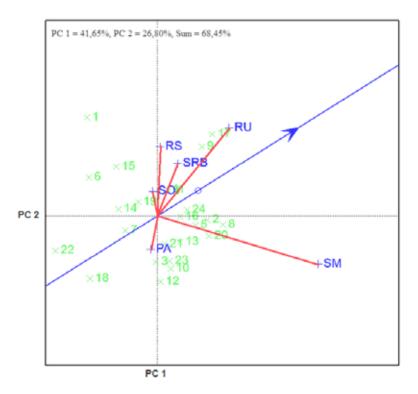


Fig. 1. GGE biplot of 24 maize hybrids grain yield across 6 environments in 2007. Graf. 1. GGE biplot za prinos zrna 24 hibrida kukuruza na 6 lokacija u 2007.

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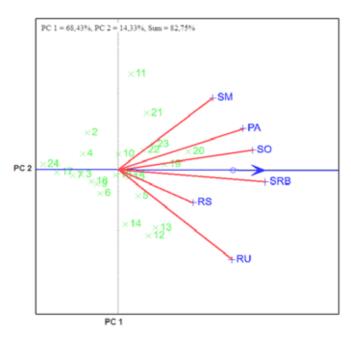


Fig. 2. GGE biplot of 24 maize hybrids grain yield across 6 environments in 2008. Graf. 2. GGE biplot za prinos zrna 24 hibrida kukuruza na 6 lokacija u 2008.

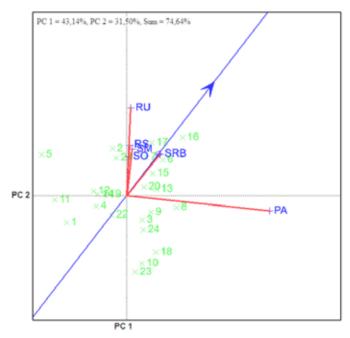


Fig. 3. GGE biplot of 24 maize hybrids grain yield across 6 environments in 2009. Graf. 3. GGE biplot za prinos zrna 24 hibrida kukuruza na 6 lokacija u 2009.

2008 (Fig. 2). Therefore, SRB could be identified as a good test environment for selecting generally adapted genotypes. Angles between all locations are acute, which indicates that examined locations in this year are positively correlated.

In 2009, the most discriminative was location PA and the most representative was again SRB. RS, SM, SO and RU were positively correlated environments (Fig. 3); close associations between testing environments shows that

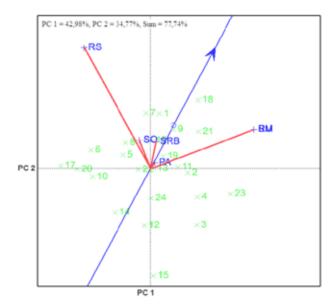


Fig.4. GGE biplot of 24 maize hybrids grain yield across 6 environments in 2010. Graf. 4. GGE biplot za prinos zrna 24 hibrida kukuruza na 6 lokacija u 2010.

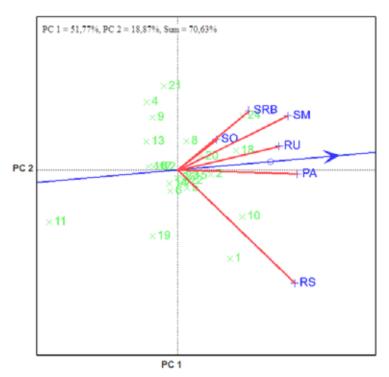


Fig. 5. GGE biplot of 24 maize hybrids grain yield across 6 environments in 2011. Graf. 5. GGE biplot za prinos zrna 24 hibrida kukuruza na 6 lokacija u 2011.

similar information about the genotype performance could be obtained from fewer test environments (Yan et al. 2006). The location SO was again the least discriminating environment.

In 2010, the longest vector length had location RS, and it was the most discriminative location (Fig. 4). Two most similar locations were SM and RU. PA was the site with the shortest vector that makes it the least discriminative location.

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In 2011, all environments were positively correlated as in 2008. The year 2011 marked RS as the most discriminative, while SO had the shortest vector length (Fig. 5). The sites SM and RU were placed closest and the most representative was location PA.

In three of five years of conducted trial location SO provided the least amount of information and thus can be excluded from further trials and analysis. The inconsistency of representativeness and discriminative ability of examined environments are probably the result of different climatic conditions during different years in which hybrid and location were tested. The location RS has presented the smallest repeatability year by year and as such, the site can be successfully used as the replacement of certain locations. In 2008, 2009 and 2010, SRB was the most representative location in conducted trials, and could be identified as a good location for further maize hybrid tests. In three of five years, sites SM and RU were the most similar locations, which suggest that they had similar genotype performance. High correlation between these two locations can be explained by small physical distance. Therefore, resources and time could be saved by including only one of these two locations in further analysis. The exclusion of similar or less representative sites allows the incorporation of other locations in the MET using similar resources. According to Stojaković et al. (2010), all locations, at which the experiments were carried out, are located in first two regions for maize production in Serbia, and because of that it would be preferable to include some other trial locations from the third or the fourth production region with lower maize yield performance and in stressful condition. This would allow recommendations of locations for testing hybrids with larger agro-ecological plasticity.

Conclusions

Genotype by environment interaction is a phenomenon that involves different genotypes, cultivars or hybrids reacting in various environments and it interferes in the selection process and makes it more complicated. GGE biplot (Genotype and Genotype by Environment Interaction) is commonly used for the interpretation of GEI. The aim of this study was to evaluate examined test locations in northern Serbia by GGE biplot. The location SO provided the smallest amount of information and therefore can be excluded from further trials and analysis. SM and RU were the most similar locations, which suggest that they had similar genotype performance. SRB was the most representative location in conducted trials. For more detailed analysis it is necessary to include more locations in trails and analysis.

References

- Balestre, M., de Souza, C.J., von Garcia, P.R., de Lunzzo, O.R., & Valente, M.P.J. (2009). Yield stability and adaptability of maize hybrids based on GGE biplot analysis characteristics. Crop Breed. Appl. Biotechnol, 9, 219-228.
- Crossa, J. (1990). Statistical analyses of multilocation trials. Adv. Agron., 45, 55-85. doi:10.1016/S0065-2113-(08)60818-4
- Eberhart, S.A., & Russell, W.A. (1966). Stability parameters for comparing varieties. *Crop Sci.*, 6, 36-40. doi:10.2135/cropsci1 966.0011183X000600010011x
- Fan, X., Kang, M.S., Chen, H., Zhang, Y., Tan, J., & Xu, C. (2007). Yield Stability of Maize Hybrids Evaluated in Multi-Environment Trials in Yunnan, China. *Agronomy Journal*, 99(1), 220-228. doi:10.2134/agronj2006.0144
- FAOSTAT. (2011). Food and Agriculture Organization of the United Nations, FAOSTAT database. Retrieved from http://faostat.fao.org/site/567/DesktopDefault.aspx?PageID=567#ancor
- Gabriel, K.R. (1971). The biplot graphic display of matrices with application to principal component analysis. *Biometrika*, 58(3), 453-467. doi:10.1093/biomet/58.3.453
- Gauch, H.G., & Zobel, R.W. (1996). AMMI analysis of yield trials. In M.S. Kang & H.G. Gauch (Eds.), Genotype by Environment Interactions. (pp. 85-122). Boca Rataon, Florida, USA: CRS Press.
- Gauch, H.G., & Zobel, R.W. (1997). Identifying mega-environments and targeting genotypes. Crop Sci., 37, 311-326.
- Kang, M.S. (2004). Breeding: Genotype-by-environment interaction. In R.M. Goodman (Ed.), Encyclopedia of Plant and Crop Science. (pp. 218-221). New York: Marcel Decker.
- Kaya, Y., Akcura, M., & Taner, S. (2006). GGE-Biplot analysis of multi-environment yield trials in bread wheat. *Turk J. Agric*, 30, 325-337.
- Mitrović, B., Stanisavljević, D., Treskić, S., Stojaković, M., Bekavac, G., Nastasić, A., & Ivanović, M. (2011). GGE biplot analysis of multi-environment trials of NS maize hybrids. Field Veg. Field Veg. Crop Res, 48(1), 77-82. doi:10.5937/ratpov1101077M
- R Development Core Team. (2011). A language and environment for statistical computing. Retrieved from www.Rproject.org

- Samonte, S.O.P.B., Wilson, L.T., Mcclung, A.M., & Medley, J.C. (2005). Targeting cultivars onto rize growing environments using AMMI and SREG GGE biplot analysis. *Crop Sci.*, 45(6), 2414-2424. doi:10.2135/cropsci2004.0627
- Stojaković, M., Ivanović, M., Jočković, D., Bekavac, G., Purar, B., Nastasić, A., . . . Laišić, R. (2010). NS hibridi kukuruza u proizvodnim rejonima Srbije. *Ratar. Povrt.*, 47(1), 93-102.
- Yan, W. (2002). Singular-value partitioning in biplot analysis of multienvironment trial data. Agron. J., 94, 990-996.
- Yan, W., Hunt, L.A., Sheng, Q., & Szlavnics, Z. (2000). Cultivar evaluation and megaenvironment investigation based on the GGE biplot. Crop Sci., 40, 597-605.
- Yan, W., Cornelius, P.L., Crossa, J., & Hunt, L.A. (2001). Two types GGE biplots for analyzing multi-environment trial data. Crop Sci., 41, 656-663.
- Yan, W., & Tinker, N.A. (2006). Biplot analysis of multi-environment trial data: Principles and applications. *Can. J. Plant Sci.*, 86(3), 623-645. doi:10.4141/P05-169
- Yan, W., Frégeau-Reid, J., Pageau, D., Martin, R., Mitchell-Fetch, J., Etienne, M., . . . Sparry, E. (2010). Identifying essential testlocations for oat breeding in eastern Canada. *Crop Sci.*, 50, 504-515.

Identifikacija najpoželjnijih lokaliteta za testiranje hibrida kukuruza u severnoj Srbiji

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Sažetak: Jedna od krajnjih faza u procesu oplemenjivanja kukuruza je testiranje potencijalnih hibrida u više-lokacijskim pretkomisijskim ogledima. Cilj ovog istraživanja bila je procena šest lokaliteta (Pančevo, Sremska Mitrovica, Ruma, Srbobran, Rimski Šančevi i Sombor) u severnoj Srbiji za testiranje prinosa zrna hibrida kukuruza GGE biplot metodom u periodu od 2007 do 2011. god. Ovo istraživanje je obuhvatilo 24 hibrida kukuruza testirana na šest lokaliteta. Različiti setovi hibrida su korišćeni svake godine. Hibridi su služili kao "random" faktor za procenu test lokaliteta. ANOVA test je pokazao značajne efekte genotipa (G) i životne sredine (E) svake godine, dok je njihova interakcija (GE) bila značajna u 2007, 2009. i 2011. U proseku, lokalitet SO je pružio najmanje informacija, pa se stoga može isključiti iz daljih ogleda i analiza. Lokaliteti SM i RU su bili najsličniji, tako da samo jedan od njih treba da se uključi u dalja testiranja. Lokalitet RŠ je imao najmanju ponovljivost. Takođe trebalo bi uključiti, druge, do sada nekorišćene lokalitete u budućim višelokacijskim ogledima.

Ključne reči: analiza, GE interakcija, hibridi, kukuruz, prinos zrna, Zea mays L., životna sredina