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ANALYSIS OF GENOTYPE BY ENVIRONMENT INTERACTION FOR SPIKE TRAITS IN WINTER SIX-ROW BARLEY

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Abstract: This research was conducted with some spike traits of twenty winter six-row barley genotypes in six environments. The aim of this study was to determine the significance and take advantage useful genotype by environment interacton (GEI) by applying AMMI-1 model. High statistical significance GEI was determined. Wide adaptability genotypes were J-29, J-33, J-9 and J-21 for spike length (SL) as Grand and Ozren for grain number per spike (GNS). The winner genotypes in all environments were Ozren and Grand for SL as Ozren for GNS. All the examined environments can be considered as one megaenvironment, which indicates that unpredictable interactions dominate in this research.

Keywords: barley, spike traits, GE interaction, AMMI model, stability

Introduction

Barley (*Hordeum vulgare* L.) is one of the most important cereal crops in the world. Based on number of grains row per spike there are two different forms of barley spike. Six-row spikes show fertile lateral spikelets compared with two-row spikes with sterile lateral spikelets (Ullrich, 2011). Spike length and grain number per spike are one of the most important components of grain yield of barley. Six-row barley per unit of spike length contains a greater number of grains compared to two-row barley, so even a small increase in spike length is followed by a significant increase in the grain number per spike. That is why increasing the spike length of the six-row form of barley is one of the main goals in breeding (Dodig, 2000). An increase in grain number per spike affects

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the increase in grain yield, and its increase can compensate for the reduced number of spikes and plants per unit area (Barczak and Majcherczak, 2009).

Genotypes have different expression depending on environmental conditions (Bocianowski et al., 2019). In this way, they form genotype by environment interaction (GEI) whose presence complicates the effectiveness of selection (Pržulj et al., 2015). A special group of models for analysis of GEI are linear-bilinear statistical models that have the ability to model complex interactions in multiple dimensions. The additive main effects and multiplicative interaction (AMMI) analysis are widely used (Alake and Ariyo, 2012).

Materials and methods

The data set in this paper represents spike traits as spike length and grain number per spike of 20 winter barley genotypes, 11 recognized cultivars and 9 advanced breeding lines of F7 and F8 generation (marked with J). Genotypes were origin from Republic of Serbia and according to type of spike belong to six-row barley (*Hordeum sativum, ssp. vulgare).*

Field trials were conducted over a two growing seasons (2008/2009 and 2009/2010) at three locations in Serbia under dry farming conditions: Kragujevac (KG)-central Serbia (44º02′N 20º56′E, altitude 185 m, Smonitza type soil), Zemun Polje (ZP)-north Serbia (44º49′N, 20º17′E, altitude 96 m, calcareous Chernozem) and Zaječar (ZA)-eastern Serbia (43º53′N, 22º17′E, altitude 144 m, non-carbonate Smonitza). The first season was moderately humid (based on precipitation) with warm and sunny spring (stem elongation, anthesis and grain filling stage) while the second season was humid with colder and cloudly spring. Combinations year and locality there were six environments were labeled as follows: KG09, ZP09, ZA09 represent locations KG, ZP and ZA in the first growing season, while KG10, ZP10 and ZA10 represent the same locations in the second growing season, respectively. The experiments were set up according to Fisher's plan of randomized blocks with four replications and 5 m^2 plots. Sowing was machine in mid-October. At full maturity, from each plot 20 primary spikes were analyzed according the length (cm) and number of grains.

Spike traits data were analyzed using linear mixed model with homogeneous residual error variances. The choice between models is based on the value of the Akaike Information Criterion (AIC). The interaction and assessment of genotype stability in different environmental conditions was analyzed using a linear-bilinear model Additive Main effects and Multiplicative

Interaction (Gauch and Zobel, 1996). The statistical significance of individual AMMI models was tested, and the AMMI-1 view was applied, taking into account all the advantages of the applied approach (Yan and Tinker, 2006). In the biplot graph, AMMI parameters on the ordinate are the values of the interaction principal components (IPC-1), while on the abscissa are the mean values of the genotypes and the environments. AMMI-1 model had its estimated value for interaction and equal IPC-1g x IPC-1e. This estimated interaction is part the AMMI-1 expected values of traits for any genotype and environment combination. The rest is the additive AMMI-0 part of the AMMI model is simply the genotype average plus the environment average minus the general average (Zobel et al., 1988). Statistical data processing was performed using R software, version 3.1.2 (R Development Core Team, 2014).

Results and discussion

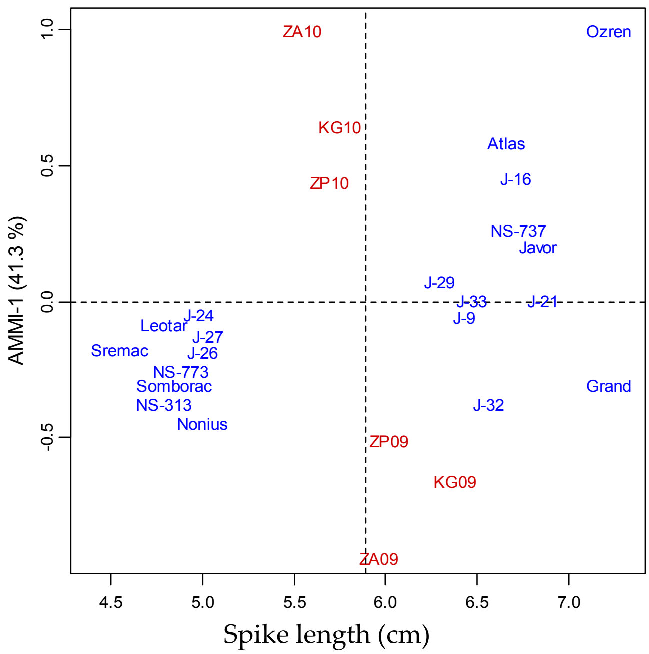
To explain the variation for spike length (SL) and grain number per spike (GNS), using Akaike's information criterion (–583.6, 1391.8, respectively), it was determined that the most suitable mixed model with homogeneous error variances environments (Table 1). For both traits, the effect of genotype and the interaction of genotype with the external environment stand out as a highly significant factor ($P < 0.01$) for explaining the variation, while the environment in which the research was conducted did not show significance ($P > 0.05$). Therefore, the application of the AMMI model is justified because, based on Shaft and Price (1998), this model has an advantage in a situation of significant interaction and nonsignificant main effects.

Table 1. Mixed model with homogeneous variances of environmental errors of spike length (SL) and grain number per spike (GNS) of twenty six-row barley across six environments

Source variation	SL		GNS	
	Fixed effect			
	F	*P*	*F*	*P*
Genotype (G)	63.35	<0.0001	12.66	<0.0001
	Random effect			
	Z	*P*	*Z*	*P*
Environment(E)	1.50	0.0670	1.57	0.0588
Interaction(G×E)	6.79	<0.0001	6.80	<.0001
Residual σ^2	13.08	<0.0001	13.08	<.0001

$P < 0.01$ – highly significant; $P < 0.05$ – significant; $P > 0.05$ not significant

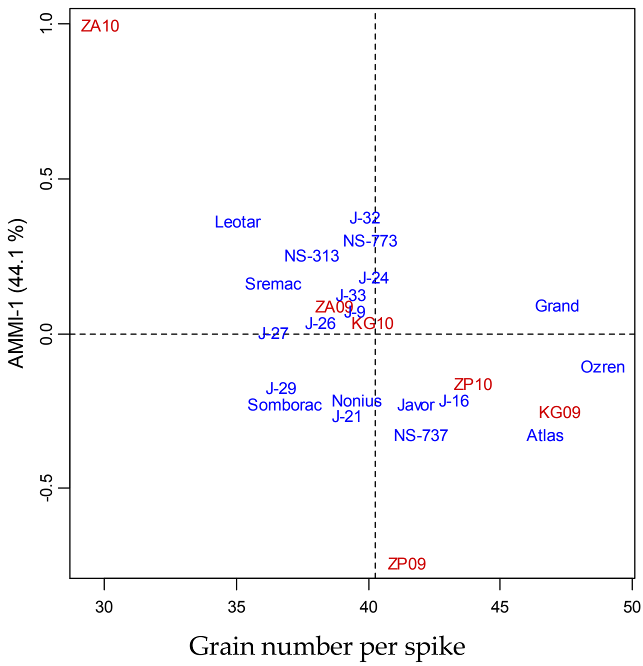
AMMI-1 analysis for SL of six-row barley showed that the first principal component explained 41.3 % of the genotype by environment interaction (Graph 1). Regarding the SL low interaction values indicating a high stability were observed for genotypes J-24, Leotar and J-27 with below average of spike length (5.89 cm). In case breeding lines J-29, J-33, J-9, J-21 the highest stability was associated with high values of this trait. These genotypes maintain the yield level in all environments and are less sensitive to changes in external conditions. The stability of certain above average genotypes can generally be considered as the ability to be well adapted to unfavorable climate conditions (Ciulca et al., 2018). Elakhdar et al. (2017) such genotypes are considered widely adaptable and important in the use of beneficial interaction effects. Genotype Ozren was the lowest stability and the highest values of lenght which in accordance with Mohhamed et al. (2009) which indicate that it is more difficult to achieve stability at high values of properties.



Graph 1. AMMI1 biplot for spike length of twenty six-row barley genotypes across six environments

Based on the results of the AMMI-1 model for the GNS of six-row barley (Graph 2), we observe that the first principal component explained 44.1 % of the sum of squares of the interaction between genotype and external environment.

The highest stability was recorded by genotypes J-27, J-26, J-9, J-33, Grand and Ozren which showed high variaton of this trait over the environments. Regarding wide adaptation, genotypes Grand and Ozren stood out. They were very stable and with a significantly higher number of grains compared to the general average (40.2). None of the genotypes showed significant unstability. For the GNS, higher values of the trait were not associated with unstability as for the SL. Only genotypes J-33 and J-9 showed stability in both traits, while Ozren was the most unstable in SL and among the most stable in GNS.



Graph 2. AMMI1 biplot for grain number per spike of twenty six-row barley genotypes across six environments

AMMI model provides an agronomically meaningful interpretation of the data which is usually desirable in order to make reliable traits estimations. They are given in Table 2 AMMI-1 estimates for SL and GNS. These estimated values are used for prediction and recommendation, and their values depend on the characteristics of the investigated environments. In such cases when the environments are location-year combinations, Zobel et al. (1988) points out that a locality suitable for prediction and recommendation is one whose interaction effects differ slightly from year to year. The environments of each locality in SL differ significantly in the interaction effect. Gauch and Zobel (1997) suggest yes large unpredictable interactions and diference between years require other access so the best predictive strategy is not to try to exploit interactions (only AMMI-0). For the GNS, this approach was not applied.

It is noticed that they were Grand and Ozren in SL as Ozren in GNS winner and recommended genotypes in all environments (Table 2). AMMI-1 model data compared to unadjusted data in our research (results not shown) has a smaller number of winning genotypes. We had three winners for both traits (Grand, Ozren and NS-737 for SL; Grand, Ozren and Atlas for GNS). This is in agreement with the results obtained by Egesi et al. (2002) indicating that AMMI-1 model ignoring irrelevant interaction noise and error thus reducing the number of winner genotypes. These were also the genotypes with the highest average trait values in our research because AMMI-1 estimates interaction has low values (GNS) or is ignored in case of differences in effects of environments (SL), so values estimates were based mainly on the main effect (AMMI-0).

Table 2. AMMI-1 estimated values for SL (cm) and GNS (in brackets) twenty six-row barley genotypes across six environments

Genotypes	KG09	ZP09	ZA09	KG10	ZP10	ZA10
Grand	**7.71**(54.2)	**7.35**(48.5)	**7.29**(45.7)	**7.08**(47.2)	**7.02**(51.0)	**6.88**(37.0)
NS-313	5.28(44.8)	4.92(39.0)	4.86(36.3)	4.65(37.8)	4.59(41.6)	4.45(27.7)
Ozren	**7.71(55.9)**	**7.35(50.3)**	**7.29(47.4)**	**7.08(48.9)**	**7.02(52.7)**	**6.88(38.5)**
Sombor	5.34(43.8)	4.98(38.2)	4.92(35.3)	4.71(36.8)	4.65(40.6)	4.51(26.4)
Sremac	5.04(43.4)	4.68(37.8)	4.62(34.9)	4.41(36.4)	4.35(40.2)	4.21(26.2)
Atlas	7.16(53.8)	6.80(48.2)	6.74(45.2)	6.53(46.7)	6.47(50.5)	6.33(36.2)
Leotar	5.28(42.0)	4.92(36.7)	4.86(33.6)	4.65(35.1)	4.59(38.9)	4.45(24.5)
NS-773	5.37(47.0)	5.01(41.2)	4.95(38.6)	4.74(40.1)	4.68(43.9)	4.54(30.0)
Nonius	5.49(46.4)	5.13(41.0)	5.07(38.1)	4.86(39.6)	4.80(43.4)	4.66(29.1)
NS-737	7.21(49.1)	6.85(43.5)	6.79(40.5)	6.58(42.0)	6.52(45.8)	6.38(31.5)
Javor	7.32(48.8)	6.96(43.2)	6.90(40.3)	6.69(41.8)	6.63(45.6)	6.49(31.3)
J-26	5.49(45.2)	5.13(39.5)	5.07(36.7)	4.86(38.2)	4.80(42.0)	4.66(27.9)
J-32	7.05(46.8)	6.69(41.0)	6.63(38.4)	6.42(39.9)	6.36(43.7)	6.22(29.9)
J-24	5.47(47.2)	5.11(41.4)	5.05(38.7)	4.84(40.2)	4.78(44.0)	4.64(30.2)
J-9	6.92(46.5)	6.56(40.8)	6.50(38.0)	6.29(39.5)	6.23(43.3)	6.09(29.2)
J-33	6.96(46.3)	6.60(40.5)	6.54(37.8)	6.33(39.3)	6.27(43.1)	6.13(29.1)
J-27	5.52(43.4)	5.16(37.7)	5.10(34.9)	4.89(36.4)	4.83(40.2)	4.69(26.1)
J-29	6.78(43.7)	6.42(38.1)	6.36(35.2)	6.15(36.7)	6.09(40.5)	5.95(26.2)
J-16	7.20(50.2)	6.84(44.6)	6.78(41.7)	6.57(43.2)	6.51(47.0)	6.37(32.8)
J-21	7.35(46.3)	7.48(40.6)	6.93(37.7)	6.72(39.2)	6.66(43.0)	6.52(28.7)

Since the existence of one winner genotype is observed in all localities, which is according to the winner-method proposed by Gauch (2013) za AMMI-1 model, the data suggest considering all environments as a single mega-environment for spike traits of barley. Our trial is clearly dominated by unpredictable interactions over predictable ones which acording Gauch and Zobel (1997) indicates that they are typically associated with years and make mega-environments less numerous and less advantage can be taken of specific adaptations. This is the main reason for the existence of only one such environment in this paper and the reason why specific adaptations do not significant.

Conclusion

Genotype by environment interaction (GEI) is complex problem which complicates the selection process field crops. Our study showed complex and importance investigate of interaction. Variable climatic conditions require barley breeders to select adaptability genotypes and therefore the AMMI model is very suitable. Only genotypes J-33 and J-9 showed stability in both traits while stability not associated with average values of genotypes. Genotypes with wide adaptation and suitable for growing in different agroecological conditions were J-29, J-33, J-9 and J-21 for spike length (SL) as Grand and Ozren for grains number per spike (GNS). However, based AMMI-1 estimated values, the winner genotypes in all environments were Ozren and Grand for SL as Ozren for GNS. This genotypes had the highest values of spike traits. Therefore all the examined environments can be considered as one megaenvironment, which indicates that unpredictable interactions dominate in this research, due to which specific adaptations were not of high importance. All this information could be use in barley breeding in order to increase the genetic gain for grain yield.

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