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Genotype by environment interaction for grain yield in winter oat

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Abstract

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The objective of this study was to examine the magnitude of genotype by environment interaction for grain yield and determine the adaptation of breeding lines of winter oat, grown in Southeast Bulgaria, using AMMI and GGE biplot methods. The study included 20 oat genotypes (18 breeding lines and 2 check varieties), analyzed in eight years through field trials arranged in a complete block design, with four replications. Grain yield of the tested genotypes varied from 1312 kg/ha to 8394 kg/ha throughout the eight growing seasons. In the AMMI analysis of variance, 67.23% of the total yield variation was explained by environment, 9.63% by differences between genotypes, and 23.13% by genotype by environment interaction. The first six interaction principal component axes were significant and cumulatively contributed to 98.53% of the total genotype by environmental interaction. AMMI and GGE biplots were powerful enough for visualizing the response patterns of genotypes. The line G3 ranked first in in grain yield and showed relative stability and can be selected for further evaluation for variety release. The line G13 and G16 are suggested for further inclusion in the breeding program of winter oat due to its high grain yield and intermediate stability.

Keywords: barley; AMMI analysis; GGE analysis; yield; stability; mutant

Introduction

Oat (*Avena sativa* L.) is an important cereal crop used for food, feed, and forage. The amount of oat used for human consumption has been increased, particularly because of health benefits related with content of dietary fibres, β-glucan, functional protein and lipids in the oat grain (Esposito et al., 2005).

Genotype by environment interaction (GEI) defined as the differential responses of genotypes across a range of environments (Kang, 2004). In breeding programs, GEI causes many difficulties, because it complicates the selection of superior genotypes, thereby reducing genetic progress (Romagosa & Fox, 1993). Breeders need to identify stable genotypes with the relatively consistent performance across a range of environments to ensure valid genotype recommendation.

Numerous statistical methods have been developed to investigate GE interaction, such as joint regression (Becker & Leon, 1988), sum of squared deviations from regression (Eberhart & Russel, 1966), stability variance (Shukla, 1972), coefficient of determination (Pinthus, 1973), coefficient of variability (Francis & Kanneberg, 1978), and type B genetic correlation (Burdon, 1977).

Among the various statistical procedures developed for the study of GE interaction, the additive main effect and multiplicative interaction (AMMI) and GGE biplot models are widely used, recently. AMMI model has been revealed to be efficient because it captures a large portion of the GE sum of squares and accurate separates main and interaction effects and provides the meaningful interpretation of the data (Ebdon & Gauch, 2002). When many genotypes are tested across several environments, it is often difficult to determine the pattern of genotypic response across environments without the help of the graphical display of the data. Biplot analysis is a multivariate analytical approach that graphically displays the 2-way data and allows visualization of the interrelations among genotypes, environments, and genotypes by environments interactions (Yan & Kang, 2003). A GGE biplot is formed by plotting the first principal component (PC) scores of the genotypes and the environments against their respective environment-centered or environment-standardized genotype-by-environment data. This analysis is used to identify high yielding and adapted genotypes as well as suitable test environments (Yan et al., 2000).

The objective of this study was to examine the magnitude of genotype by environment interaction for grain yield and determine the adaptation of breeding lines of winter oat,grown in Southeast Bulgaria, using AMMI and GGE biplot methods.

Material and Methods

This research was conducted during 8 growing seasons from 2003-04 to 2010-11 in the experimental field of the Institute of Agriculture – Karnobat.

The experimental area is located in Southeast Bulgaria. The climate is transitional continental, with long and relatively cool spring, dry and hot summer, long and rainy autumn, and little snow in winter, with large variations of temperature. The soil of experimental field is leached chernozem-smolniza, slightly acid (pH is 6.2).

The experiments were organized in a Complete Block Design with 4 replications on plots of 10 m^2. The plot yield was converted to t/ha. Standard agronomic and plant protection practices were used.

Eighteen advanced lines (from G3 to G20) of oat breeding program of the Institute of Agriculture – Karnobat were studied along with checks Dunav 1 (G1) and Resor 1 (G2) .

AMMI analysis was based on the model by Gauch (2006) and GGE was based on the model for two Principal Components according to Yan & Kang (2003). The statistical analysis was conducted using GenStat 12th edition (Genstat, 2010).

Results and Discussion

The AMMI analysis of variance for grain yield of the 20 oat genotypes tested for 8 growing seasons is presented in Table 1. The AMMI model revealed that oat grain yield was significantly affected by environment (growing season), genotype and genotype by environment interaction. The environment explained 67.23% of the total treatment (G+E+GEI) variation, whereas the G and GEI were accounted for 9.63% and 23.13%, respectively. A large variation explained by environments showed that the environments were diverse with large differences among environmental means causing most of the variation in grain yield (Shukla et al., 2015). The small portion of the total sum of square was attributed to genotypic (G) effect whereas, the magnitude of GE interaction sum of squares was higher than G effect revealed that there were considerable differences in genotypic response across environments (Shukla et al., 2015). Doehlert et al. (2001), Peterson et al. (2005) and Mut et al. (2018)also reported that oat grain yield was more strongly influenced by environment than by genotype. The contribution of GEI was more two times greater than that of the genotypes. The presence of significant GEI for grain yield of the winter oat breeding lines demonstrated the need for the extensive testing in multiple environments to identify high-yielding and stable lines.

The AMMI analysis extracted six significant interaction principal component axes (IPCAs). The first interaction principal component axis (IPCA1) accounted for 50.69% of the total variation in the GE interaction. The second and third in-

Table 1. Additive main effect and multiplicative interactions (AMMI) analysis of variance for grain yield

Source	df	SS	MS	Variation explained, %
Total	639	1292409130	2022549	
Genotypes	19	123194089	6483899***	9.63
Environments	7	859701394	122814485***	67.23
Interactions	133	295832272	2224303***	23.13
IPCA1	25	149960608	5998424***	50.69
IPCA2	23	67516607	2935505***	22.82
IPCA3	21	33468475	1593737***	11.31
IPCA4	19	22330861	1175308***	7.55
IPCA5	17	12703861	747286***	4.29
IPCA6	15	5526860	368457***	1.87
Residuals	13	4324999	332692^{ns}	1.46

*** significant at the 0.01 probability level; ns – not significant

Table 2. Grain yield (kg/ha) of 20 winter oat genotypes in 8 growing seasons (2003-04 – 2010-11) and the first two Principal Components derived from AMMI analysis

Genotype	2003-04	2004-05	2005-06	2006-07	2007-08	2008-09	2009-10	2010-11	Total	IPC1	IPC2
G1	5101	5610	3694	2630	6312	3868	2318	5373	4363	-13.30	5.06
G2	4825	5766	3465	2102	6238	3659	2101	5307	4183	-19.97	4.91
G3	5518	8394	4761	4531	8047	4251	2386	5575	5433	-21.97	-34.00
G4	4177	5446	2963	2060	5802	2951	1312	4439	3644	-17.28	-5.83
G5	4674	3217	2865	1964	4865	3332	1949	4651	3440	3.55	24.26
G6	4833	4196	3284	2894	5500	3442	1926	4612	3836	3.04	7.28
G7	4671	4005	3112	2698	5320	3283	1773	4461	3665	3.00	7.98
G8	5077	3935	3450	3259	5496	3633	2143	4694	3961	9.14	9.78
G9	4773	4009	3275	3377	5415	3297	1738	4266	3769	9.57	1.06
G10	4445	3832	2898	2485	5123	3059	1544	4240	3453	2.61	7.37
G11	4832	3916	3412	4214	5455	3237	1615	3922	3825	18.61	-8.09
G12	5615	3816	4100	5510	5826	3883	2277	4275	4413	32.22	-7.77
G13	4874	5228	3837	5301	6223	3226	1411	3729	4229	16.39	-32.37
G14	5018	4880	3752	4447	6042	3473	1790	4248	4206	11.48	-15.04
G15	5074	5556	3614	2251	6245	3889	2374	5509	4314	-16.46	9.99
G16	5132	6181	3798	2450	6603	3968	2399	5618	4519	-20.62	3.51
G17	4366	5379	3033	1739	5822	3191	1620	4817	3746	-19.74	3.05
G18	4634	5944	3454	2712	6295	3383	1722	4811	4119	-15.78	-8.78
G19	5484	2515	3666	4778	5054	3751	2289	4188	3966	37.79	9.78
G20	5252	4465	3579	2613	5791	3948	2510	5334	4187	-2.29	17.84
Total	4919	4815	3501	3201	5874	3536	1960	4703	4063	-13.30	5.06

teraction principal component axis (IPCA2 and IPCA3) explained a further 22.82% and 11.31% of the sum of squares of GE interaction. The first six interaction principal component axes (IPCA 1-6) accounted for 98.54% of total GE interaction, leaving 1.46% of the variation in the GE interaction in the residual.

The grain yields (kg/ha) of studied genotypes of winter oat grown in 8 years and IPCA 1 and 2 are presented in Table 2. The yields of oat genotypes ranged from 1312 kg/ha for G4 (2004-05) to 8394 kg/ha for G3 (2009-10). The highest yield were recorded in 2007-08 growing season (5874 kg/ha) followed by 2003-04 and 2004-05 growing seasons with mean yields of 4919 and 4815 kg/ha, respectively. The highest mean yield (5433 kg/ha) showed G3. Two breeding lines G12 (4413 kg/ha) and G16 (4519 kg/ha) had a higher mean grain yield than the standard varieties Dunav 1 (4363 kg/ha) and Resor 1 (4183 kg/ha).

In addition, the AMMI analysis selected best genotypes in each environment (Table 3). In four growing season breeding line G3 was selected as best genotype by AMMI. The breeding lines G16 and G20 were ranked first in one growing season and G12 in two growing seasons.

In the AMMI model 1, X axis represents the genotypes and environment main effect and *Y* axis represents the effects of interaction (Figure 1). In the biplot, the broken vertical line passing through the center of the biplot was the

Table 3. AMMI selections of genotypes per environment

Environment	Mean, kg/ha	Score	First four AMMI selections			
			1	2	3	4
E1	4919	14.03	G12	G3	G19	G20
E2	4814	-49.76	G3	G16	G18	G2
E3	3501	7.37	G3	G12	G13	G16
E4	3201	52.87	G12	G13	G19	G3
E5	5874	-15.59	G3	G16	G1	G18
E6	3536	3.96	G3	G16	G20	G15
E7	1960	4.94	G20	G16	G3	G15
E8	4704	-17.82	G16	G3	G15	G1

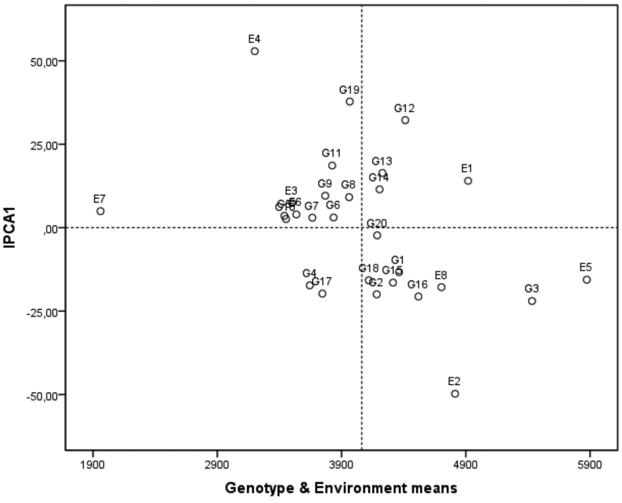

Fig. 1. AMMI1 biplot for grain yield (kg/ha) of 20 winter oat genotypes and 8 enviroments

grand mean of the experiment. Ten oat genotypes (G1, G2, G3, G12, G13, G14, G15, G16, G18, and G20) and four environments (E1, E2, E5 and E8) located at the right side of the grand mean were considered as high yielding genotypes and environments. The genotypes (G4, G5, G6, G7, G8, G9, G10, G11, G17, and G19) and environments (E3, E4, E6, and E7) positioned at the left side of the grand mean had the lower yield.The genotypes with PC1 scores close to zero expressed general adaptation whereas the larger scores depicted more specific adaptation to environments. Oat genotypes G5, G6, G7 and G20 had IPCA score value closer to zero, and were classified as stable whereas the IPCA scores of breeding lines G12 and G19 were comparatively large, and those genotypes could be classified as highly unstable. AMMI1 biplots identified G3 as the highest yielding genotype showing intermediate stability. Genotypes G16 and G12 presented higher grain yield compared to the check varieties (G1 and G2) but G12 had high IPCA value, indicating specific adaptability while G16 shown intermediate stability.

The partitioning of genotype and genotype by environment interaction through GGE biplot analysis showed that PCA 1 and PCA 2 accounted for 43.86% and 29.68% of GGE sum of squares for oat grain yield, explaining a total of 73.54% variation as shown in Figure 2. The hypothetical ideal genotype is defined as genotype which having the greatest PC1 score (highest mean performance) and with zero GEI (absolutely stable), as presented by the small circle on the axis of average genotype yield with the pointed arrow. The genotypes that are located closer to the ideal genotype are more desirable than other genotypes which are located far away from the ideal genotype (Yan and Tinker, 2005). The genotype-focused comparison of genotypes in this study, revealed that G3 fell closest to the ideal genotype and therefore identified as the best genotype (Figure 2). The genotypes are more desirable if they are located closer to the ideal genotype. Therefore, G16 and G13 can be considered as genotypes with high breeding value.The check variety Resor 1 (G2) is also among the high yielding and relatively stable genotypes.

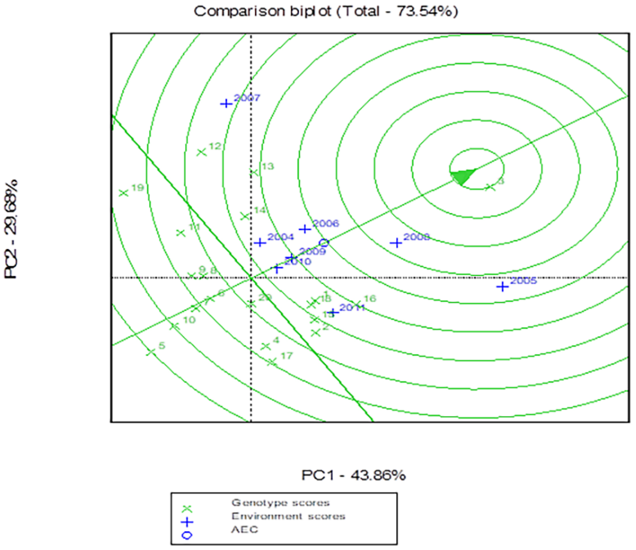

Fig. 2. GGE-bioplot based on genotype-focused scaling for comparison the genotypes with the ideal genotype

Stability analysis is often used in multi-location trials, but it can also be applied to measure the response of genotypes in the same location to changes occurring in different years (Genchev, 2010; Pržulj et al., 2015; Stoyanov et al., 2017; Kurt Polat et al., 2018). Climate changes may result in strong impacts on crop growth and yield. Grain yield is largely determined by climate conditions during the growing season and even minor deviations from optimal conditions can seriously threaten yield. The simultaneous selection for grain yield and yield stability is of the extreme importance in rainfed conditions, where the environment is changeable and unpredictable (Vaezi et al., 2017). Although the annual rainfall in Southeast Bulgaria is more 500 mm, it‘s very irregularly distributed during oat vegetation. The large variation due to environments in our study also confirmed the high diversity of climatic conditions during growing seasons.

A genotype is considered stable if its performance is constant across environments. Becker & Leon (1988) established a biological or static concept of stability under which a stable genotype shows a minimal variance across different environments. However, this concept is of less importance to breeders, who prefer genotypes with high yields and the potential to respond positively to agronomic inputs and favorable environmental conditions (Becker, 1981). Dynamic stability or agronomical concept of stability implies that a stable genotype has a constant high yield response to changes in the environment and as small as possible G x E interaction.Usually, the most stable genotypes would not necessarily give the best yield performance as it was the case in our study

In the current investigation, GGE biplots and AMMI were used to compare the performance of different genotypes in different environments. Despite the possibility of their complementing each other due to their equivalent features, there has been discussion among authors about the effectiveness of AMMI and GGE in depicting the adaptive responses of genotypes over environments (Yan & Tinker, 2005; Gauch, 2006; Yan & Tinker, 2006; Yan et al., 2007; Gauch et al., 2008). According to some of those studies, GGE biplot is more effective and informative than AMMI in mega-environment analysis and GEI evaluation (Yan et al., 2007; Amira et al., 2013). The methodology of GGE biplot was considered to be superior because the concept of the analysis considers both and only genotype plus genotype by environment interaction and not all of the phenotypic variation which may be misleading. Oliveira et al. (2010) concluded that 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 scale, the performance of the AMMI method tends to be better.

In our research both models prove to be very useful in assessing the performance of genotypes and showed no differences in selection of best genotypes. Similarly, Miranda et al. (2009)**,** Mitrovic et al. (2012), Hagos & Abay (2013), Rad et al. (2013) and Jeberson et al. (2017) suggested that both GGE and AMMI biplots were important for evaluating stable and adaptable genotypes.

Conclusions

The magnitude of genotype-by-environment interaction (GEI) for grain yield of 20 oat genotypes tested during 8 growing seasons in the region of Southeast Bulgaria was larger than that of genotype main effect, but smaller than that of environment main effect. AMMI and GGE biplots were powerful enough for visualizing the response patterns of genotypes. The line G3 ranked first in in grain yield and showed relative stability and can be selected for further evaluation for variety release. The line G13 and G16 are suggested for further inclusion in the breeding program of winter oat due to its high grain yield and intermediate stability.

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