

VARIABILITY, AMMI AND CLUSTER ANALYSIS FOR QUALITY COMPONENTS OF DIFFERENT WHEAT GENOTYPES

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ABSTRACT

The present study was carried out to investigate the variability and heritability of wheat quality components and to evaluate the stability of ten wheat genotypes in different environmental conditions. The experiment was conducted in the Center for Small Grains in Kragujevac, Serbia during two growing seasons (2010 and 2011). Thousand grain weight had the highest value of GCV and PCV (7.13 and 7.7%), while test weight had the lowest PCV (3.24%) and protein content had the lowest GCV (1.82%). The highest heritability was observed for thousand grain weight ($H^2=85.37\%$), while the lowest one was found for protein content ($H^2=19.56\%$). The AMMI analysis showed significant effect of the $G \times E$ interaction, where first main component was significant for all components. Genotypes KG-56, Arsenal and Osječanka are close to the average values for all components and expressed the highest stability. Genotypes with the highest or lowest average values for analyzed traits, such as Norin 10, Mironovskaya 808, Gruža and Spartanka, showed moderate to high instability. Cluster analysis categorized the genotypes into four groups. The genotype Norin 10 showed the highest distance from other genotypes, whereas the stable genotypes grouped together.

Key words: *Heritability, AMMI analysis, stability, cluster.*

INTRODUCTION

Wheat (*Triticum aestivum* L.) is the most commonly planted and used crop in the world. Therefore, development of high yielding varieties with good end-use quality is a challenging objective for many wheat breeding programs (Abdipour *et al.*, 2016). Wheat grain yield and protein content are the dominant determinants in the economic value of the harvest product (Shewry, 2007). Test weight, thousand grain weight and protein content are the important traits for wheat breeding programs (Aydin *et al.*, 2010). Grain protein content and thousand grain weight are the most important indirect quality traits and can be used for the purpose of quality

predictions at the early generations of breeding programs (Mut *et al.*, 2010). Heritability is a parameter which is widely used in establishment of breeding programs and formation of selection indexes (Falconer, 1985). Heritability is low for the traits with agronomical importance because these traits are influenced by a large number of genes. Many authors observed low heritability for protein content (Zečević *et al.*, 2007 and Taghouti *et al.*, 2010) and moderate to high heritability for thousand grain weight and test weight (Aydin *et al.*, 2010). The G×E interaction complicates breeding of superior genotypes (Hintsä and Fetien, 2013). Therefore, assessing any genotype without including its interaction with environment is incomplete (Crossa, 1990). The additive main effect and multiplicative interaction (AMMI) analysis, using principal component axis (PCA), can be used to determine stability of genotypes across environments and, therefore, it has been efficient tool in determining stable and high yielding genotypes (Zobel and Gauch, 1988). The goal of this study was to determine variability and heritability of wheat quality components and to evaluate the stability of different wheat genotypes in various environments.

MATERIAL AND METHODS

Ten wheat genotypes (Arsenal, KG-56, Gruza, Mironovskaya 808, Norin 10, Rana Niska, Spartanka, Sterna, Osjecanka, and Szegedi 765) were tested in two different vegetation seasons (2010 and 2011) at the Center for Small Grains in Kragujevac, Serbia. Growing season 2010 was determined by higher total sum of precipitation in April, May and June (293.2 mm) in relation to 2011 growing season (119.1 mm) in region of Kragujevac (Republic Hydro-meteorological Service of Serbia). The trial was conducted in randomized complete block design with three replications. It is performed rare sowing where seeds were sown in 1 m long rows, with 20 cm space between the rows and 10 cm distance between each seed in a row. Rare sowing was applied to allow that genotypes express their maximal genetic potential for tillering and other spike characteristics. Three quality components are analyzed: thousand grain weight, test weight and protein content. Analysis of variance and cluster analysis based on squared Euclidean distance and Linkages between groups method were calculated using the IBM SPSS Statistics Trial Version 22.0 (<https://www.ibm.com/>). The generated components of the variance were used to estimate the genotypic and phenotypic variance and broad-sense heritability. Genotype × environment (G×E) interaction was calculated through AMMI and biplot analysis using GenStat Trial Version 18.1.0.17005 (<https://www.vsni.co.uk/>).

RESULTS AND DISCUSSION

For all analyzed traits, the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV), which indicates that environment has significant effect on present variation. This is in agreement to results obtained by Tyagi *et al.* (2016). Thousand grain weight had the highest values of GCV and PCV (7.13 and 7.70%, respectively), while the test weight had the lowest PCV (3.24%) and grain protein content had the lowest PCV (1.82%). Similar results for GCV and PCV of thousand grain weight were reported by

Başçıftçı *et al.* (2013). Heritability estimates in broad sense were high for thousand grain weight (85.37%), while moderate for test weight (61.67%), which indicated a high response to selection in these traits. The low heritability (19.56%) was observed for grain protein content, which indicated low inheritance of this trait and high effect of environment. This is in accordance with results obtained by Zecevic *et al.* (2007) (Table 1).

Table 1. The mean value, variance and heritability of analyzed yield components

Traits ¹	Mean values	Estimates of variance components ²				CV (%)	GCV (%)	PCV (%)	H ² (%)
		σ^2_g	σ^2_{ph}	$\sigma^2_{g \times y}$	σ^2_E				
PC	16.47	0.09	0.46	1.01	0.36	5.03	1.82	4.11	19.56
TGW	37.02	6.97	8.13	2.68	1.16	6.39	7.13	7.70	85.37
TW	76.80	3.83	6.21	6.93	2.37	2.27	2.54	3.24	61.67

¹PC – protein content, TGW – thousand grain weight, TW – test weight; ² σ^2_g , σ^2_{ph} , $\sigma^2_{g \times y}$ and σ^2_E indicate the genetic, phenotypic, genotype and phenotype interaction and environment variance, respectively

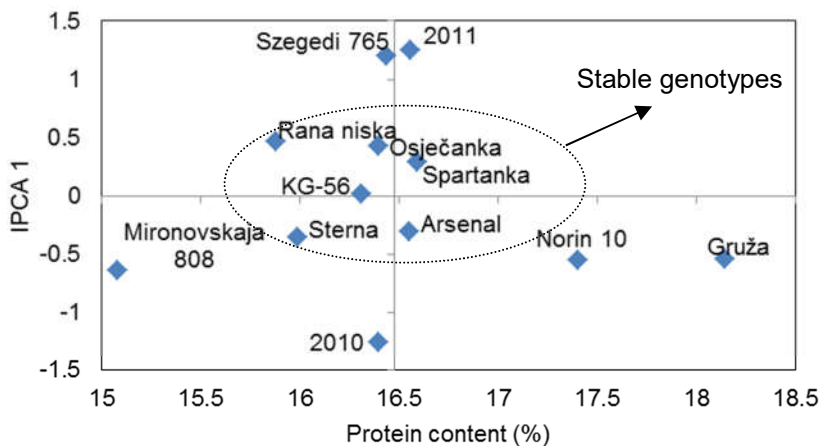
AMMI analysis shows highly significant influence of genotype and G×E interaction for all analyzed traits. The significance of G×E interaction effects demonstrated that genotypes responded differently to various environmental conditions. Main effects had the highest share in total variation for all traits, where the largest share belonged to genotype effect. In relation to protein content, Taghouti *et al.* (2010) observed larger variances associated with genetic effects than the variances associated with G×E interaction. Higher genotype effects than environment effect is found by Altinabas *et al.* (2004) for thousand grain weight. The total contribution in G×E interaction gave the first principal component (IPCA1), which confirmed that the additive effects were more important than multivariate effects in all of analyzed traits (Table 2). Mladenov *et al.* (2012) also reported that protein content, thousand grain weight and test weight are important to IPCA1.

Table 2. AMMI ANOVA for protein content, thousand grain weight and test weight of ten wheat genotypes in two growing seasons

Source of variation	df	Protein content			Thousand grain weight			Test weight		
		SS	MS	F-value	SS	MS	F	SS	MS	F-value
Total	59	77.09	-	-	966.8	-	-	720.7	-	-
Genotypes	9	37.29	4.14	17.05**	658.9	73.2	30.3**	503.0	55.9	99.1**
Environments	1	0.40	0.40	1.65	117.1	117.1	48.4**	2.8	2.77	4.92
Interactions	9	29.69	3.29	13.57**	94.2	10.4	4.33**	192.4	21.4	37.9**
IPCA1	9	29.69	3.29	13.57**	94.2	10.4	4.33**	192.4	21.4	37.9**
IPCA2	7	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Error	40	9.72	0.24	-	96.7	2.42	-	22.6	0.56	-

** p<0.01; *p<0.05

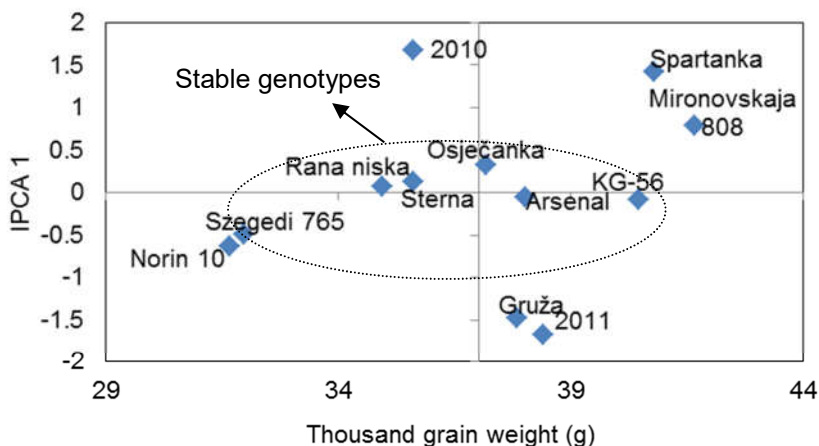
AMMI 1 biplot (Graph 1) shows that genotypes KG-56, Spartanka, Osječanka, Arsenal, Rana Niska and Sterna are found near to origin and considered to be stable.



Graph 1. AMMI 1 biplot for the protein content of 10 wheat genotypes in two growing seasons

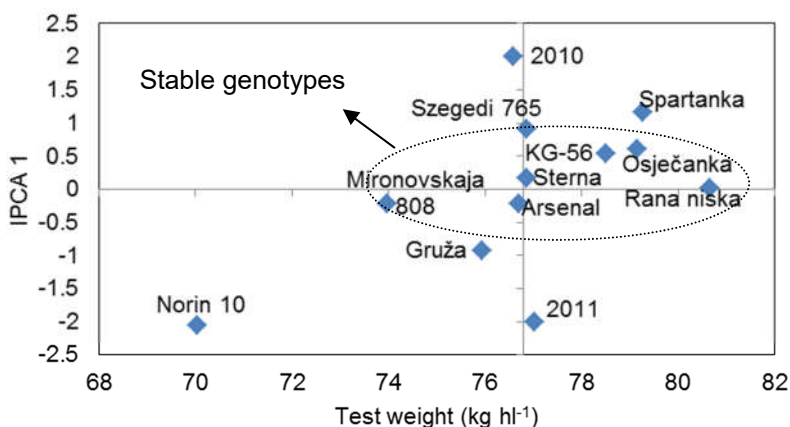
Genotypes Norin 10 and Gruža, with protein content higher than grand mean (17.4 and 18.14%, respectively), were middle stable genotypes. This indicates that it is harder to achieve stability in genotypes with high value of certain trait. Genotype Mironovskaya 808 with the lowest protein content (15.08%) had low adaptability, also. Genotype Szegedi 765 achieved the strongest interaction with the agroecological conditions of the second growing season, which is distinguished by lower amount of precipitation (Graph 1). Mut *et al.* (2010) also observed that grain protein content was higher in low rainfall environments.

Genotypes Rana niska, Sterna, Arsenal, KG-56, Osječanka and Szegedi 765 lie near the origin of biplot and hence shows high stability in thousand grain weight. Genotypes Mironovskaya 808 and Spartanka, as non stable genotypes, had the highest value of thousand grain weight (41.66 g and 40.81 g, respectively). The lowest value of this trait is recorded in genotype Norin 10 (31.66 g), which is characterized by middle stability. Genotype Gruža showed high instability and strong interaction with environmental condition of second year which was characterized by optimal amount of precipitation. Analyzed genotypes achieved higher thousand grain weight in 2011 year than in 2010 year which was distinguished by higher amount of precipitation that led to the appearance of wheat diseases (Graph 2).



Graph 2. AMMI 1 biplot for the thousand grain weight of 10 wheat genotypes in two growing seasons

Genotypes Mironovskaya 808, Arsenal, Sterna, KG-56, Osječanka and Rana niska had high stability and the lowest values of IPCA1 for test weight (Graph 3).

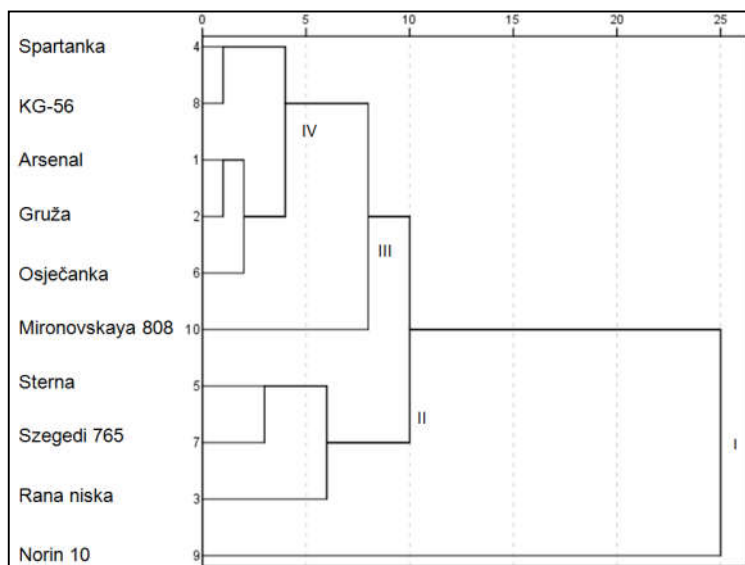


Graph 3. AMMI 1 biplot for the test weight of 10 wheat genotypes in two growing seasons

Genotype Rana niska, with the highest value of test weight (80.67 kg hl^{-1}) showed the highest stability. The lowest test weight was observed in genotype Norin 10 (70.04 kg hl^{-1}), which had the strongest $G \times E$ interaction. Genotypes Szegedi 765 and Gruža were characterized by middle stability and test weight around the grand mean, while genotype Spartanka had middle stability and test weight above the grand mean. In both growing seasons genotypes achieved test weight near the grand mean (Graph 3).

Cluster analysis based on squared Euclidean distance divided analyzed genotypes into four major groups. Cluster 1 including only genotype Norin 10 which showed the highest distance from others genotypes, and it is observed in AMMI 1 biplot,

also. This genotype had the lowest values of test weight and thousand grain weight and it is characterized by middle to low stability. Cluster II including genotypes Sterna, Szegedi and Rana niska, which showed the high stability in thousand grain weight. Also, Mutwaly *et al.* (2016) reported that stable and well-associated genotypes with all end-use quality attributes grouped together in same cluster. Genotype Mironovskaya 808 is allocated in Cluster III and it is distinguished by highest value of thousand grain weight and lowest value of protein content. Genotypes which are grouped in Cluster 4, Spartanka, KG-56, Arsenal, Gruža and Osječanka, had the highest average stability in all analyzed genotypes (Graph 4). Grouping of genotypes by the cluster analysis highly corresponds with grouping genotypes in the AMMI 1 biplot.



Graph 4. Dendrogram of cluster analysis for ten wheat genotypes in two years for analyzed quality components

CONCLUSION

In relation to our results, it can be concluded that environment has significant effect on present variation in all quality traits. The significance of $G \times E$ interaction effect indicated that genotypes responded differently to various environment conditions. Thus, testing genotypes under different environment conditions, and using analysis such as AMMI, is important for evaluating stability of genotypes. Genotypes Norin 10, Mironovskaya 808, Gruža and Spartanka, showed moderate to high instability, where genotype Norin 10 had the lowest average values of analyzed traits. Genotypes Arsenal, Osječanka and KG-56 have the highest stability and average values of analyzed traits near or above grand mean. Therefore, these genotypes can be used as a good breeding material for future breeding programs in terms of quality components.

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