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Original scientific paper

EXPECTED GENETIC ADVANCE AND STABILITY OF PHYTIC ACID AND ANTIOXIDANTS CONTENT IN BREAD AND DURUM WHEAT

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Fifteen genotypes of bread wheat (*Triticum aestivum* L.) and fifteen genotypes of durum wheat (*Triticum durum* Desf.) were evaluated in the multi-environment trial during 2010-11. and 2011-12 vegetation seasons to investigate components of variance, heritability in a broad sense (h^2), expected genetic advance (GA), and stability of phytic acid (PA), inorganic phosphorus (P_i), phytic phosphorus (P_p)/P_i relation, yellow pigment (YP), water soluble phenolics (WSPH) and free protein sulfhydryl groups (PSH) content. The field trials were carried out at three locations in Serbia, as randomized complete block design with four replications. The genetic component of variance (σ^2_g) predominated the genotype × environment interaction (σ^2_{ge}) component for: P_i in bread wheat (3.0 times higher), P_p/P_i in bread wheat (2.1 times higher) and in durum wheat (1.2 times higher), YP content in bread wheat (2.2 times higher) and in durum wheat (1.7 times higher), and WSPH content in bread wheat (1.4 times higher). The relation σ^2_g/σ^2_{ge} for P_i content in durum wheat was equal to one. The σ^2_{ge} prevailed σ^2_g for: PA in bread wheat (1.7 times higher) and in durum wheat (5.7 times higher), PSH in durum wheat (3.7 times higher), and WSPH in durum wheat (5.2 times higher). High h^2 coupled with high expected genetic advance as percent of mean (GAM) were observed for: P_i (93.7% and 26.1%, respectively) in bread wheat, P_p/P_i relation in bread wheat (92.4% and 20.7%, respectively) and in durum wheat (87.2% and 20.8%, respectively), YP content in bread wheat (92.6% and 28.0%, respectively) and in durum wheat (90.7% and 28.1%, respectively), and WSPH content (88.9% and 25.8%, respectively) in bread

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wheat. PA content in bread and durum wheat had medium to medium high h^2 (50.5% and 77.9%, respectively), and low expected GAM (9.9% and 3.7%, respectively). GGE biplots with average-environment coordination (AEC) indicated less stability of durum wheat for PA, WSPH and PSH content.

Keywords: *Triticum aestivum, Triticum durum*, phytic acid, antioxidants, expected genetic advance, GGE (AEC) biplot

INTRODUCTION

The cereals and wheat among them represent staple foods, consequently being ideal vehicles to deliver health benefits at relatively low cost. The wheat ingredients for functional food purposes can be increased with conventional breeding, by exploiting natural variation, or by non-traditional approaches such as mutagenesis or transgenesis (SHEWRY and WARD, 2012). The flour of bread wheat (*Triticum aestivum* L.) contains large amount of protein with high-quality gluten and is being used for bread making, whereas flour of lower amount of protein is mostly used for confectionary or cakes (CABALLERO *et al*., 2007). The most important quality criteria for durum wheat (*Triticum durum* Desf.) valid today include high yield of highly refined semolina, high protein and yellow pigment content, strong gluten and good pasta cooking quality (MOHAMMED *et al*., 2012).

Phytic acid (*myo*-inositol 1,2,3,4,5,6-hexakis (dihydrogen phosphate) or InsP6) (PA) chelates micronutrients-Ca, Mg, Fe, Zn, Mn, Cu, and Co in the form of mixed salts called phytates, preventing these minerals to be available for monogastric animals, including humans. PA also interacts with proteins and vitamins, thereby restricting their bioavailability (ELKHALIL *et al*., 2001). Approximately 65 to 85% of total seed phosphorus in cereals is stored as phytic acid (GUPTA *et al*., 2015).

Significant antioxidant levels have been found in wheat, indicating its importance in a healthy diet by reducing the risk of many chronic diseases, and representing potential source of functional food ingredients (MPOFU *et al*., 2006). Yellow pigment (YP) represents the extracted carotenoids content from endosperm and is expressed as β-carotene content (mg) per 100 g of dry matter. High YP concentration, which confers intense bright yellow color for durum wheat end-use products, is highly appreciated on the market for its consumer appeal, and for the health benefits achieved through antioxidant activity and prevention of macular degeneration (ABDEL-AAL *et al*., 2007). In plants, carotenoids have several important functions related to photosynthesis and stress adaptation (DIBARI *et al*., 2012). In animals including humans, which are unable to synthesize carotenoids de novo, dietary carotenoids are essential precursors of vitamin A and retinoid compounds needed in development (FRASER and BRAMLEY, 2004). Phenolic compounds provide mechanical stability to cells, by forming polymeric constituents of support structures, such as lignin and other constituents of the cell wall. Due to their strong antioxidant activity, they protect plants from UV radiation and oxidative stress, and exhibit phytoalexin functions with antibiotic, antifungal, and antiviral properties (DELVECCHIO *et al*., 2014). Free sulfhydryl groups of proteins (PSH) exert an important function in plants as antioxidants (CHERNIKOVA *et al*., 2000), by quenching free radicals and decreasing the effects of stress (VIEIRA DOS SANTOS and REY, 2006), by reducing the trypsin inhibitors (DRAGIČEVIĆ *et al*., 2010), by taking part in the detoxification, signal transduction, apoptosis and in cell regulatory redox system (LEUSTEK *et al*., 2000).

The high heritability estimate alone is not enough to make sufficient improvement through selection, generally in advance generations, unless accompanied by substantial amount of genetic advance. The utility of heritability increases when it is used to estimate genetic advance, which indicates the degree of gain in a character achieved under a particular selection pressure (EID, 2009). If a trait of interest is controlled by non-additive gene effects, it confers high heritability but low genetic advance, while for the trait ruled by additive gene action, heritability and genetic advance both would be high (LAGHARI *et al.*, 2010), and the success of selection in the second case is anticipated.

The objectives of this research were to explore components of variance, heritability in a broad sense, expected genetic advance and stability of phytic acid and antioxidants content in bread and durum wheat, all for an assessment of breeding possibilities aiming to increase micronutrients and functional food contents.

MATERIALS AND METHODS

Plant material and field trials

The genetic material used for multi-environment testing consisted of 15 bread wheat (*Triticum aestivum* L. ssp. *aestivum*) and of 15 durum wheat (*Triticum durum* Desf.) accessions. The seeds were provided from the Institute of Field and Vegetable Crops in Novi Sad and from Maize Research Institute in Zemun Polje, both in Serbia. The names, codes, countries of origin, growth type and pedigree of used accessions are given in Supplementary table.

The field trials were carried out at the Maize Research Institute "Zemun Polje" in Zemun Polje (ZP) (44°52´N; 20°19´E), Institute of Field and Vegetable Crops in Rimski Šančevi (RS) (45°19´51´´N; 19°50´59´´E), and PKB Agroekonomik Institute in Padinska Skela (PS) (44°57´N 20°26´E), all in Serbia, during two vegetation seasons 2010-2011 (11) and 2011-2012 (12). The design of the field trials was randomized complete block with four replications. The experimental plot consisted of 5 rows of 1 m in length with the inter-row spacing of 0.2 m. The elementary plot consisted of 3 inner rows of 0.6 m^2 ($3 \times 0.2 \times 1$ m) and plants within it were used for the analyses. Sowing was done mechanically at the RS and by hand at the ZP and at the PS.

Haplicchernozem (CHha) is the soil type at RS and ZP locations and Humic Gleysol (GLhu) is at PS (IUSS WORKING GROUP WRB, 2006). The mineral fertilizers (NPK 15:15:15, MAP) were applied before seeding according to the recommendation based on the analysis of soil chemical properties and available content of P, K, and mineral N reserves. In the spring top dressing consisted of urea (46% N) (at the PS11, PS12, ZP12), CAN (27% N) (ZP11), and AN (34% N) (RS11, RS12) application. The pesticides were adequately used with their efficacy being monitored, and ultimately crop damages were avoided.

Analyses of chemical properties

Grains were ground on the Laboratory Mill 120 Perten (Perten, Sweden) and flour with particles size < 500 μm was produced. Chemical traits were determined spectrophotometrically with the Shimadzu UV-1601 spectrophotometer (Shimadzu Corporation, Japan). All analysed chemical properties were determined from four replications. The contents of PA and P_i were determined by the method given by DRAGIČEVIĆ *et al.* (2011). The phytate phosphorus (P_p) content was obtained by dividing the value of PA by a factor of 3.55 (BARAC *et al.*, 2006) and phytic phosphorus/inorganic phosphorus ($P_{p/}P_i$) relation was estimated also. Total YP was determined by the AACC (AMERICAN ASSOCIATION OF CEREAL CHEMISTS, 1995) method and expressed as µg of β-carotene equivalent (βCE) per g. The water soluble phenolics (WSPH) content was determined by the method of SIMIĆ *et al*. (2004) and expressed as µg of ferulic acid equivalent (FAE) per g. The free protein sulfhydryl groups (PSH) content was determined by the method of DE KOK *et al*. (1981) from the same extract used for phenolics determination.

Statistical analyses

The two-way fixed analysis of variance (ANOVA) was used with the effects of genotype and environment as fixed ones. Environment represented year × test location combination. ANOVA was performed by the use of the STATISTICA 9.0 (STATSOFT, 2009). Variance components, and expected genetic advance (GA) computed at 5% selection intensity (k = 2.056) for each trait were calculated as in LAMALAKSHMI *et al.* (2015). Broad sense heritability (h^2) was calculated as the ratio the genotypic variance to the phenotypic variance. Expected genetic advance as percent of mean (GAM) was calculated to compare the extent of predicted genetic advance of different traits with different measurement units. The sites regression (SREG) model (CROSSA and CORNELIUS, 1997) was used to show genotype main effects and genotype × environment interaction effects (GGE) on biplots with the average-environment coordination (AEC) view showing stability of used genotypes.

RESULTS AND DISCUSSION

The components of variance, heritability in a broad sense, coefficients of genetic and phenotypic variation, expected genetic advance and expected genetic advance as percent of mean for PA and antioxidants content in bread and durum wheat are presented in Table 1.

Table 1. Variance components, heritability in a broad sense, coefficients of genetic and phenotypic variation, expected genetic advance and expected genetic advance as percent of mean for phytic acid and antioxidants content in bread wheat and durum wheat.

Trait	Type	σ^2_g	σ^2_{ge}	σ^2_e	σ^2_p	h^2 (%)	CV$_g$ (%)	CV$_p$ (%)	GA	GAM (%)
PA	bread wheat	0.630	1.062	0.179	0.809	77.9	5.4	6.2	1.4	9.9
	durum wheat	0.138	0.789	0.135	0.273	50.5	2.6	3.6	0.5	3.7
P_i	bread wheat	0.003	0.001	0.00017	0.003	93.7	13.2	13.7	0.1	26.1
	durum wheat	0.001	0.001	0.00022	0.002	85.9	9.7	10.5	0.1	18.4
P_p/P_i	bread wheat	1.395	0.670	0.11433	1.509	92.4	10.7	11.2	2.3	20.7
	durum wheat	1.501	1.304	0.22108	1.722	87.2	11.0	11.7	2.3	20.8
YP	bread wheat	0.296	0.134	0.024	0.319	92.6	14.1	14.6	1.1	28.0
	durum wheat	0.367	0.217	0.038	0.405	90.7	14.3	15.0	1.2	28.1
WSPH	bread wheat	15182	11157	1894	17076	88.9	13.3	14.1	239.3	25.8
	durum wheat	2359	12155	2051	4411	53.5	5.4	7.3	73.3	8.1
PSH	bread wheat	-	307.00	52.93	29.82	-	-	6.7	-	-
	durum wheat	135.93	504.25	84.97	220.90	61.5	13.8	17.6	18.8	22.2

σ^2_g-genetic variance, σ^2_{ge}-variance of the genotype × environment interaction, σ^2_e- environmental variance, h^2-broad-sense heritability, CV$_g$-coefficient of genetic variation, CV$_p$-coefficient of phenotypic variation, GA-genetic advance, GAM-genetic advance as percent of mean.

Larger genetic component of variance (σ^2_g) relative to the component of variance due to the genotype × environment interaction (σ^2_{ge}) was determined for the following chemical properties: P_i in bread wheat (3.0 times higher), the ratio of P_p/P_i in bread wheat (2.1 times higher) and in durum wheat (1.2 times higher), YP content in bread wheat (2.2 times higher) and in durum wheat (1.7 times higher) similar to CLARKE *et al.* (2006), WSPH content in bread wheat (1.4 times higher) in accordance with MPOFU *et al.* (2006). The relation σ^2_g/σ^2_{ge} for P_i content in durum wheat was equal to one. The larger σ^2_{ge} when compared to σ^2_g was determined for the following chemical properties: PA content in bread wheat (1.7 times higher) and in durum wheat (5.7 times higher), PSH content in durum wheat (3.7 times higher), and WSPH content in durum wheat (5.2 times higher) similar to TADDEI *et al.* (2014). Durum wheat genotypes showed generally greater influence of genotype × environment interaction (GEI) on phytic acid and antioxidants content compared to bread wheat. The environmental component of variance (σ^2_e) was smaller than σ^2_g and σ^2_{ge} for all the measured chemical properties in bread and durum wheat.

Heritability in a broad sense was very high (> 90%) for the following chemical properties: P_i content for bread wheat, the relation P_p/P_i for bread wheat, YP content for bread and durum wheat (Table 1). High h^2 (80-90%) was obtained for the following chemical properties: P_i content for durum wheat, the relation P_p/P_i for durum wheat, WSPH content for bread wheat. Broad-sense heritability was moderately high (70-80%) for PA content in bread wheat. Medium broad-sense heritability (50-70%) was observed for the following chemical properties: PA content in durum wheat, WSPH content in durum wheat and PSH content in durum wheat. The highest value of the coefficient of genetic variation (CV_g) was 14.3% and recorded for the YP content in durum wheat. The maximum value of the coefficient of phenotypic variation (CV_p) was 17.6% and observed for PSH content in durum wheat. The minimum values of CV_g and CV_p of 2.6% and 3.6%, respectively, were shown for PA content in durum wheat.

Heritability in a broad sense for PA content was moderately high for bread wheat and medium for durum wheat, whereas CV_g and CV_p were small (CV < 10%), but twice as higher in bread wheat than in durum wheat. AHMAD *et al.* (2013) and SHITRE *et al.* (2015) observed higher h^2 of 86% for PA content in bread wheat along with higher CV_g and CV_p (> 17%) than in our study. According to SANTRA *et al.* (2005) h^2 for PA content of durum wheat was in the range from 67-93% for different breeding generations. Oppositely to GUPTA *et al.* (2015), who observed high h^2 and high GAM values of 48 F_2 bread wheat lines tested at one location of 93.4% and 32.3%, respectively, our values for these parameters were smaller 1.2 and 3.3 times, respectively.

The estimation of h^2 for P_i content and P_p/P_i relation in bread wheat was very high (> 90%), whereas in durum wheat it was high (80-90%). The lower value of h^2 for P_i content of 72% was reported by SHITRE *et al.* (2015) in bread wheat. The content of P_i and P_p/P_i relation moderately varied ($10 < CV_p < 20\%$) in bread and durum wheat, what was in accordance with SHITRE *et al.* (2015). YP is a trait controlled by additive genes with high heritability in durum wheat as reported by many authors (ELOUAFI *et al.*, 2001; CLARKE *et al.*, 2006; QUINN *et al.*, 2012). PATIL *et al.* (2008) have obtained lower h^2 for YP content in durum wheat than our observed value. The variation (CV_p) was moderate (15%) in durum wheat, whereas BAUM *et al.* (1995) and MOHAMMED *et al.* (2012) reported higher values for CV_p for 171 durum wheat landraces tested in the multi-environment trial and 16 durum wheat genotypes tested at one location, respectively. In comparison to our values for h^2 and GAM for YP content in durum wheat of 90.7% and 28.1%, respectively, MOHAMMED *et al*. (2012) reported smaller h^2 of 84.3% but higher GAM of 34.8%. h^2 for WSPH was high in bread wheat and medium in durum wheat, whereas CVg and CVp were moderate, but twice higher in bread wheat, than in durum wheat. SHEWRY *et al*. (2011) showed that among phenolic compounds alkylresorcinols showed the highest h^2 value in the range of 57-77%, whereas phenolic acids exhibit h^2 of only 6-28% range. The estimated h^2 for PSH content was medium and CV_g and CV_p were moderate in durum wheat. The genetic component of variance for PSH content was not estimated in bread wheat, because mean squares component for genotype × environment interaction-MSgl obtained from ANOVA was higher than the component of genotype MSg, therefore the negative value for σ^2_g proceeded and h^2 was not calculated. The CV_g and CV_p for PSH content in bread wheat were small.

High heritability estimate coupled with high expected GAM (assuming selection intensity of 5%) were observed for P_i content in bread wheat, P_p/P_i relation in bread and durum wheat, YP content in bread and durum wheat, and WSPH content in bread wheat (Table 1). This suggests high breeding value and more additive genetic effects, so selection can be effective for these chemical properties for the studied genetic assortment. Unfortunately, not so good perspective was observed for the possibility of PA content improvement through classical breeding techniques due to medium to medium high h^2 and low GAM in bread and durum wheat (Table 1). The other possible approach in breeding for PA is mutagenesis. The low phytic acid (lpa) mutant Js-12-LPA of *Triticum aestivum* had P_p of 48.2% of seed total P content, whereas nonmutant Js-12-WT control had P_p of 74.7% of seed total P (GUTTIERI *et al*., 2004). These lpa mutations had pleiotropic effects and adversely affected the yield in wheat by reducing it by about 25%, whereas the kernel size was decreased approximately 3 mg (GUTTIERI *et al*., 2006). Genetic engineering led to reducing PA in maize and soya bean, with no effects on agronomic performance, by using tissue-specific silencing of the expression of transporters, involved in the biosynthesis of PA (SHI *et al*., 2007).

Genotype stability estimation and GEI are specifically interrelated, and genotype is considered to be with the good stability for the trait of interest if the GEI is low (BRANKOVIĆ *et al*., 2015). The mean performance and interactions of observed bread and durum wheat genotypes for PA and antioxidants content across environments is given in Figs. 1, 2, 3, 4, 5, 6. The AEC view of the GGE biplot was used to show the mean performance and stability of PA and antioxidants content for bread wheat and durum wheat genotypes across test-environments. Length of the AEC vector was sufficient to evaluate genotypes on the basis of mean values (Figs. 1, 2, 3, 4, 5, 6). Genotype versus PA, P_i, P_p/P_i and antioxidants content of bread wheat and durum wheat by locations in 2010–2011. and 2011–2012 vegetation seasons is given in Supplementary figures (Suppl. figs 1, 2, 3, 4, 5, 6).

As shown with GGE biplot, 62.59% of the total G + GE variance for PA content of bread wheat and durum wheat genotypes were interpreted (Fig. 1). The most of the bread wheat genotypes had lower than expected PA content in the environments ZP11, ZP12, PS11 and PS12, higher than expected in RS11 and RS12, and vice versa was observed for durum wheat genotypes. P11 genotype had the lowest PA content among bread wheat genotypes and D15 among durum wheat genotypes, but their stability was not satisfactory due to crossover interactions, and we cannot report either wheat species to be more stable in terms of PA content. Interestingly the lowest PA content was observed in European varieties Apache from France, ZP AU 12 from Macedonia and ZP 87/Ip from Serbia. SINGH *et al.* (2012) reported influence of higher temperature and water-deficit conditions as the causes of maximum PA content in wheat grains. As shown by BRANKOVIĆ *et al.* (2015) models of climatic variables were useful in interpreting GEI (> 91%) and stability for PA content, and included relative humidity in June, sunshine hours in April, mean temperature in April, and winter moisture reserves for genotypes of bread wheat, as well as precipitation sum in June and April, maximum temperature in April and mean temperature in June for durum wheat.

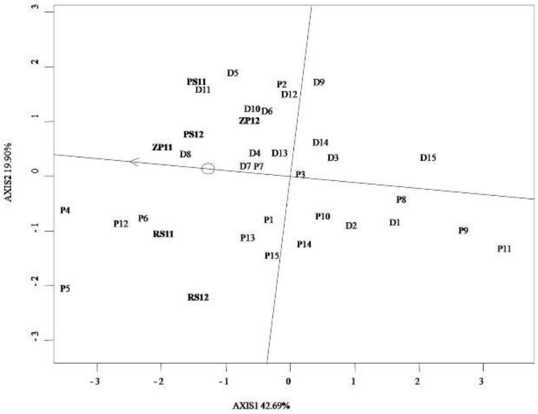

Figure 1. The average-environment coordination (AEC) view of the GGE biplot for PA content of bread wheat genotypes (P1–P15) and durum wheat genotypes (D1–D15) over tested environments.

Based on a GGE biplot, 84.77% of the total G + GE variance for P_i content of bread wheat and durum wheat genotypes was shown (Fig. 2). The majority of the bread wheat genotypes had lower than expected P_i content in the RS12 environment and higher than expected in the rest five environments, but vice versa was shown for durum wheat genotypes. P5 and D4 genotypes exerted the highest P_i content with D4 being more stable and P5 quite less stable. Varano (D4) is cultivar from Italy and other durum wheat lines 37ED. 7817 (D3), 37ED. 7820 (D12) and 37ED. 7821 (D5) with good stability and high P_i content belong to Cimmyt. Caldwell (P4), Auburn (P6) and Tecumseh (P12) are cultivars of bread wheat from USA and they showed best stability and high P_i content. WANG *et al.* (2003) reported significant and positive correlation of P_p content with initial grain filling rate, average rate of grain filling, and filling percentage, while P_i was negatively correlated with all of these indicators. BRANKOVIĆ *et al.* (2015) interpreted causes of the observed GEI (> 92%) and consequently stability for the P_i content by proposing significant models of climatic variables: precipitation in May, minimum and maximum temperatures in April, mean temperature in May for bread wheat, as well as precipitation in May, minimum temperatures in March, April and June for durum wheat.

As interpreted by GGE biplot, 81.21% of the total G + GE variance for P_p/P_i relation of bread wheat and durum wheat genotypes was shown (Fig. 3). The most of the bread wheat genotypes had lower than expected P_p/P_i relation for the ZP11, PS11 and PS12 environments, higher than expected for the ZP12, RS11 and RS12, and vice versa was reported for durum wheat, implying different GEI causes for different environments for durum wheat compared to bread wheat. P5 and D4 genotypes had the lowest P_p/P_i relation with D4 as being absolutely stable and P5 as quite unstable. The most prosperous genotypes for these traits among durum wheat were Varano (D4) from Italy, Cimmyt lines 37ED. 7817 (D3) and 37ED. 7820 (D12) and line from Serbia ZP 120/I (D15). Auburn (P6) and Frankenmuth (P7) cultivars from USA and Apache (P8) from France had below average P_p/P_i and good stability.

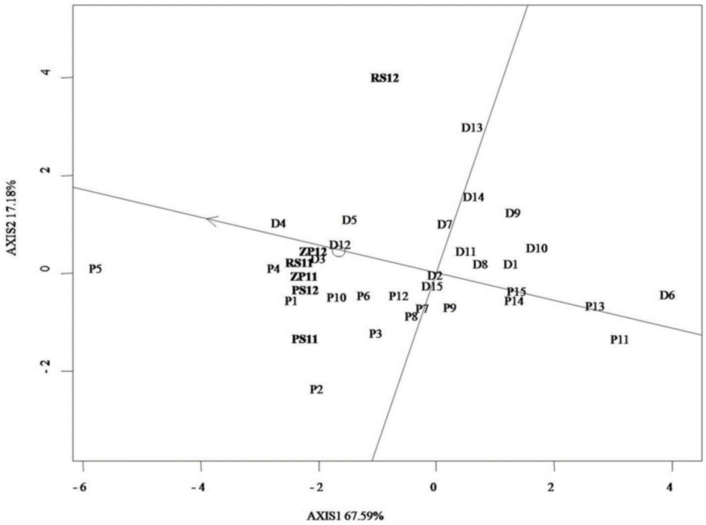

Figure 2. The average-environment coordination (AEC) view GGE biplot for P_i content of bread wheat genotypes (P1–P15) and durum wheat genotypes (D1–D15) over tested environments.

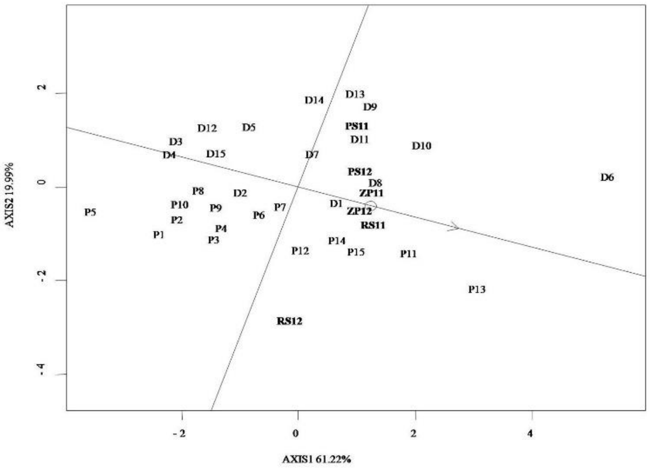

Figure 3. The average-environment coordination (AEC) view GGE biplot for P_p/P_i relation of bread wheat genotypes (P1–P15) and durum wheat genotypes (D1–D15) over tested environments.

The 81.21% of total G + GE variance for YP content was explained by GGE biplot for bread wheat and durum wheat genotypes (Fig. 4). The approximately equal number of bread wheat and durum wheat genotypes had lower than expected YP content in the ZP12, PS11 and

PS12 environments and higher than expected in the ZP11, RS11 and RS12. The genotypes P8 and D1 showed the highest YP content, with P8 being more stable than D1, which showed high instability. Highest YP content among genotypes of durum wheat was observed for 37ED. 7922 (D1), 37ED. /07 7803 (D9), 37ED. 7896 (D2) and 37ED. 7820 (D12) which are Cimmyt lines, but their stability was not high though. Among bread wheat genotypes high YP and good stability showed Apache (P8) and Marija (P10) cultivars from France and Croatia, respectively. The retention of YP into the mature wheat grains stage was lower at the locations with the longer sunshine hours, and consequently ASADA (2006) proposed that carotenoids served for the reactive oxygen species scavenging at the earlier stages of wheat development. According to BRANKOVIĆ *et al.* (2015) GEI for YP was interpreted with the 95% efficacy with the following models of climatic variables: sunshine hours in May, maximum temperature in April, and precipitation sum in May and March for bread wheat, as well as with mean temperature in March, April and May, and winter moisture reserves for durum wheat.

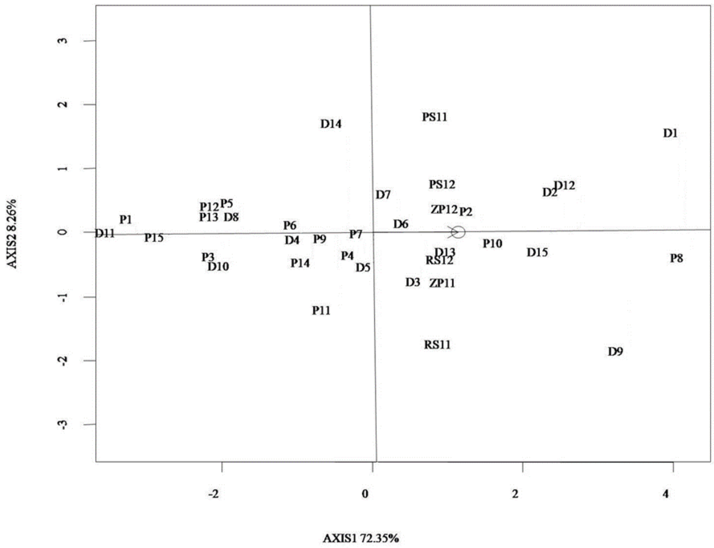

Figure 4. The average-environment coordination (AEC) view GGE biplot for YP content of bread wheat genotypes (P1–P15) and durum wheat genotypes (D1–D15) over tested environments.

As shown with GGE biplot, 73.29% of the total G + GE variance for WSPH content of bread wheat and durum wheat genotypes were interpreted (Fig. 5). All bread wheat genotypes except one had lower than expected WSPH content in the environments PS11 and RS12, higher than expected in ZP11, ZP12, RS11 and PS12, but vice versa was observed for all durum wheat genotypes. P2 and D15 had the highest WSPH content, but their stability was not satisfactory due to crossover interactions, with P2 being much more unstable than D15. As reported by BRANKOVIĆ *et al.* (2015) the GEI for WSPH was elucidated (> 94%) by the models including climatic variables: precipitation and relative humidity in March, maximum temperature in April and precipitation in May for bread wheat, as well as mean temperature in April, precipitation, relative humidity and mean temperature in May for durum wheat. The higher mean monthly temperatures and lower precipitation sums negatively influenced the total phenolic compounds in bread and durum wheat (FENG *et al*., 2007).

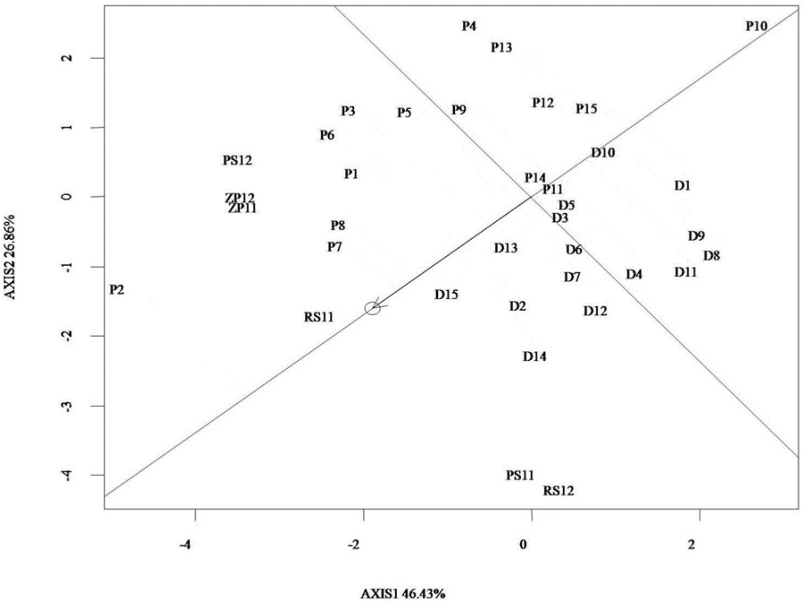

Figure 5. The average-environment coordination (AEC) view of the GGE biplot for WSPH content of bread wheat genotypes (P1–P15) and durum wheat genotypes (D1–D15) over tested environments.

Based on a GGE biplot, 60.65% of the total G + GE variance for PSH content of bread wheat and durum wheat genotypes was shown (Fig. 6). The majority of the bread wheat genotypes had lower than expected PSH content in the RS11, RS12, ZP11 and PS11 environments, higher than expected in ZP12 and PS12, but vice versa was shown for durum wheat genotypes. P4 and D15 genotypes exerted the highest PSH content but unsatisfactory stability. The genotypes with the highest observed PSH content P were Caldwell (P4), Tecumseh (P12), Abe (P5) and Frankenmuth (P7) all from USA. BRANKOVIĆ *et al.* (2015) proposed models with contributing climatic variables which interpreted GEI (> 94%) for the PSH content: maximum temperature and sunshine hours in March, mean temperature and relative humidity in April, for bread wheat, as well as maximum temperature in April, relative humidity, sunshine hours and minimum temperature in May for durum wheat. Similarly, KOCSY *et al*. (2002) reported that glutathione synthesis (GSH) is induced by low and by high temperatures.

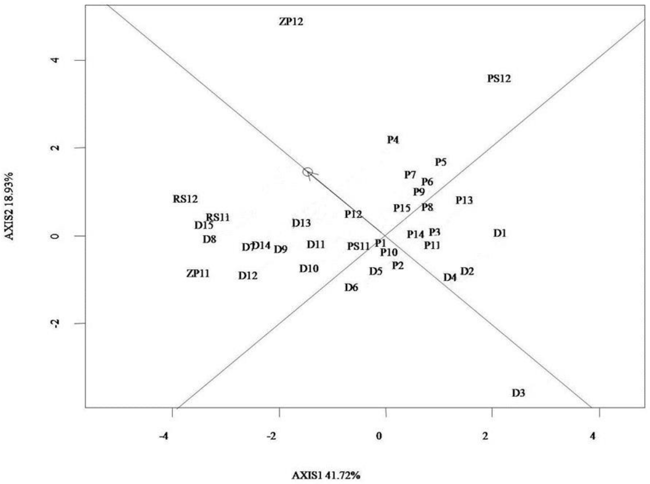

Figure 6. The average-environment coordination (AEC) view GGE biplot for PSH content of bread wheat genotypes (P1–P15) and durum wheat genotypes (D1–D15) over tested environments.

CONCLUSION

Considering high heritability in a broad sense (> 87%) coupled with high expected genetic advance as percent of mean (> 20%) for P_i content in bread wheat, P_p/P_i relation in bread and durum wheat, YP content in bread and durum wheat, and WSPH content in bread wheat, the success from classical breeding approach can be predicted for these properties. Lowering PA content through classical breeding of bread and durum wheat would not expected to be successful due to medium to medium high heritability (50.5 and 77.9%, respectively) and due to low expected genetic advance as percent of mean (9.9% and 3.7%, respectively). The ratio of the genotype × environment interaction and genetic components of variance along with GGE biplots indicated less stability in durum wheat for PA, WSPH and PSH content compared to bread wheat. The most stable genotypes of bread wheat had below-average content for PA, P_i, P_p/P_i and all antioxidants except PSH. Among most stable genotypes of durum wheat above-average values were showed for PA and P_i whereas below-average values were obtained for all antioxidants and P_p/P_i. P_p/P_i was favorably lowest and absolutely stable for durum wheat cultivar Varano. The lowest PA and highest YP content was detected among European cultivars of bread wheat, whereas USA cultivars prevailed for high content of P_i and PSH. Cimmyt lines of durum wheat proved their success contributing to high YP content.

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OČEKIVANA GENETIČKA DOBIT I STABILNOST SADRŽAJA FITINSKE KISELINE I ANTIOKSIDANASA KOD HLEBNE I DURUM PŠENICE

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Izvod

Trideset genotipova hlebne (*Triticum aestivum* L.) i durum pšenice (*Triticum durum* Desf.) je korišćeno u višelokacijskom ogledu tokom 2010-11. i 2011-12 vegetacione sezone radi određivanja komponenata varijanse, heritabilnosti u širem smislu (h^2), očekivane genetičke dobiti (GAM), i stabilnosti sadržaja fitinske kiseline (PA), neorganskog fosfora (P_i), odnosa fitinski fosfor/neorganski fosfor (P_p/P_i), žutog pigmenta (YP), fenola rastvorljivih u vodi (WSPH) i slobodnih sulfhidrilnih grupa proteina (PSH). Genetička komponenta varijanse (σ^2_g) je bila veća od komponente varijanse usled interakcije genotip × sredina (σ^2_{ge}) za sadržaj: P_i kod hlebne pšenice (3 puta); P_p/P_i kod hlebne (2,1 puta) i durum pšenice (1,2 puta); YP kod hlebne (2,2 puta) i durum pšenice (1,7 puta); WSPH kod hlebne pšenice (1,4 puta veća). Odnos σ^2_g/σ^2_{ge} za sadržaj P_i kod durum pšenice je bio jednak jedinici. σ^2_{ge} je bila veća od σ^2_g za sadržaj: PA kod hlebne (1,7 puta) i durum pšenice (5,7 puta); PSH kod durum pšenice (3,7 puta); WSPH kod durum pšenice (5,2 puta). Velika vrednost za h^2 udružena sa velikom vrednošću za GAM je dobijena za: P_i (93,7% i 26,1%) kod hlebne pšenice, P_p/P_i kod hlebne (92,4% i 20,7%) i durum pšenice (87,2% i 20,8%), YP kod hlebne (92,6% i 28%) i durum pšenice (90,7% i 28,1%), WSPH (88,9% i 25.8%) kod hlebne pšenice. Stoga se uspeh oplemenjivanja na ove karakteristike može očekivati, ali ne i na sadržaj PA kod hlebne i durum pšenice zbog srednje do srednje velike h^2 (50,5% i 77,9%) i male očekivane GAM (9,9% i 3,7%).

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