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Genetic parameters of *Triticum aestivum* and *Triticum durum* for technological quality properties in Serbia

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Abstract

Proteins are important in determining the nutritional value of wheat, and among them gluten determines the baking quality of bread wheat and pasta-making technological properties of wheat. By assessing genetic parameters of wheat quality traits, it is possible to elucidate potential for improvement. The plant material consisted of 30 genotypes of bread and durum wheat of worldwide origin. The trials were sown at three locations in Serbia during two vegetation seasons 2010–2011 and 2011–2012. Protein content, wet gluten content, Zeleny sedimentation volume and deformation energy were determined by near infrared spectrometry. The objectives of this investigation were to assess: i) variability, components of variance, heritability in a broad sense (h_b^2), expected genetic advance for protein content, wet gluten content, Zeleny sedimentation volume and deformation energy; ii) associations between agronomic characteristics and protein content, wet gluten content, Zeleny sedimentation volume and deformation energy in order to determine indirect selection feasibility. In durum wheat, the highest coefficients of genetic and phenotypic variation (CV_g and CV_{ph}) were recorded for deformation energy in bread wheat (18% and 18.4%, respectively), whereas the lowest values of 4.1% and 4.6% were shown for protein content. The relation genetic component of variance (σ_g^2) / component of variance due to genotype \times environment interaction (σ_{ge}^2) > 1 was observed for protein content (3.2), wet gluten content (2.9) and deformation energy (3.9), and equal to one for Zeleny sedimentation volume, in bread wheat. In durum wheat, $\sigma_{ge}^2 / \sigma_g^2 > 1$ was detected for protein content (1.4), wet gluten content (1.5), Zeleny sedimentation volume (2.1) and deformation energy (1.4). Considering very high and high h_b^2 observed for deformation energy and Zeleny sedimentation volume (95.8% and 86.2%, respectively) in bread wheat, coupled with high genetic advance (36.3% and 28.1%, respectively), success from classical breeding can be anticipated. Grain thickness was strongly associated with Zeleny sedimentation volume, and to a lesser extent with protein content, wet gluten content and deformation energy in bread and durum wheat, and along with grain vitreousness in durum wheat, can serve for indirect selection.

Key words: common wheat and durum wheat, expected genetic advance, gluten strength, proteins, wet gluten, Zeleny sedimentation volume.

Introduction

The major wheat species covering 95% of world wheat production is a hexaploid *Triticum aestivum* L., known as “common” or “bread” wheat, being adapted to a wide range of moisture conditions from xerophytic to littoral (Monneveux et al., 2012). At the second place regarding total wheat world production of 35–40 millions of tonnes is tetraploid species *Triticum durum* Desf.,

being adapted to the hot, dry conditions surrounding the Mediterranean Sea, and similar climates in other regions (Shewry, Hey, 2015). The flour from common wheat is used for making bread, cookies and pastries, whereas semolina and flour from durum wheat is used for pasta, couscous, leavened and unleavened bread, bulgur and freekeh.

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Protein content represents an important factor for price determination in wheat trading, commanding higher prices of higher protein hard wheat, and of lower protein soft wheat (Carver, 2009). Improving quality is one of the most important goals of durum wheat breeding programs in the European Union (EU), with premiums to boost the cultivation of high-quality cultivars (Royo, Briceño-Félix, 2011). The EU durum wheat quality index increased by 6.25% by decreasing protein content by ~10%, but by increasing protein per ha at a rate of 0.35% year⁻¹, and also by increasing gluten strength by 27.9–32.1% year⁻¹ (Subira et al., 2014). Protein content of 12,600 genotypes in the USDA World Wheat Collection ranged from 7% to 22% of the dry weight, but the majority of the genotypes had 10–15% of the dry weight (Shewry, Hey, 2015). Protein content is a typical quantitative trait controlled by complex genetic arrangements under high influence of environmental factors.

Gluten has a key role in determining the unique baking quality of wheat by conferring water absorption capacity, cohesiveness, viscosity and elasticity on dough (Wieser, 2007). The gluten proteins consist of glutenins and gliadins as the most important wheat storage proteins, representing 75–85% of the total grain proteins, exhibiting richness in asparagine, glutamine, arginine, proline, and scarcity of lysine, tryptophan and methionine (Žilić et al., 2011). Genetic effects are generally considered to be the most significant for qualitative characteristics of gluten. Wet gluten is correlated with protein content and represents common flour specification required by end-users in the food industry. The Zeleny sedimentation volume test is based on the ability of the endosperm storage proteins to swell and flocculate in a lactic acid solution, showing positive correlations with gluten strength and bread-making quality, but also with the cooking quality of pasta and with bread-loaf volume (Deng et al., 2013). Both higher gluten content and a better gluten quality give rise to slower sedimentation, and ultimately higher Zeleny test values.

The wheat dough rheological properties are essential in bread-making technology, by controlling dough mechanical handling, proofing and baking, influencing the quality of the bakery products (Gaines et al., 2006). One of the most relevant dough rheological properties is the deformation energy or dough strength, predicting flour processing behaviour and sufficient firmness of well-cooked semolina products (Vizitiu et al., 2012).

The objectives of this research were to explore the variability and estimate components of variance, heritability in a broad sense, and expected genetic advance for protein, wet gluten, Zeleny sedimentation volume and deformation energy in bread and durum wheat genotypes from the multi-environment trial in Serbia. The genotype by trait analysis was used for determination of the associations of agronomic traits with these four technological quality properties in order to perceive the notion of the indirect selection.

Materials and methods

Plant material, experimental design and field trials. The genetic material grown in a multi-environment trial comprised 15 bread wheat (*Triticum aestivum* L. ssp. *aestivum*) and 15 durum wheat (*Triticum durum* Desf.)

genotypes from the GeneBank of the Institute of Field and Vegetable Crops in Novi Sad and from the GeneBank of the Maize Research Institute “Zemun Polje” in Belgrade, both in Serbia. The names, codes and countries of origin of bread wheat genotypes are: ‘Žitarka’ (P1), Croatia, ‘Stephens’ (P2), USA, ‘Renan’ (P3), France, ‘Caldwell’ (P4), USA, ‘Abe’ (P5), USA, ‘Auburn’ (P6), USA, ‘Frankenmuth’ (P7), USA, ‘Apache’ (P8), France, ZP AU 12 (P9), Macedonia, ‘Marija’ (P10), Croatia, 87/Ip (P11), Serbia, ‘Tecumseh’ (P12), USA, ‘Pobeda’ (P13), Serbia, ‘Zemunska rosa’ (P14), Serbia and ‘Ludwig’ (P15), Austria. The names, codes and countries of origin of durum wheat genotypes are: 37EDUYT No. 7922 (D1), Mexico, 37EDUYT No. 7896 (D2), Mexico, 37EDUYT No. 7817 (D3), Mexico, ‘Varano’ (D4), Italy, 37EDUYT No. 7821 (D5), Mexico, 37EDUYT No. 7880 (D6), Mexico, 10/I (D7), Serbia, SOD 55 (D8), Slovakia, 37EDUYT /07 No. 7803 (D9), Mexico, DSP-MD-01 No. 66 (D10), Syria, 34/I (D11), Serbia, 37EDUYT No. 7820 (D12), Mexico, 37EDUYT /07 No. 7857 (D13), Mexico, 37EDUYT /07 No. 7849 (D14), Mexico and 120/I (D15), Serbia. The durum wheat genotypes from Mexico belong to CIMMYT-International Maize and Wheat Improvement Centre from 37EDUYT-37th Elite Durum Unreplicated Yield Trial, and a durum wheat genotype from Syria belong to ICARDA-International Centre for Agricultural Research in the Dry Areas from DSP-MD-01-Durum Segregating Populations-Mediterranean Dryland (season 2000–2001).

The locations of field trials were: 1) Rimski Šančevi (RS) (45°19'51" N, 19°50'59" E) within the Institute of Field and Vegetable Crops, 2) Zemun Polje (ZP) (44°52' N, 20°19' E) within Maize Research Institute “Zemun Polje” and 3) Padinska Skela (PS) (44°57' N, 20°26' E) within PKB-Agricultural Corporation Belgrade, Agroekonomik Institute; all three in Serbia. The investigation was conducted during two vegetation seasons 2010–2011 (1st year) and 2011–2012 (2nd year). Field experiments were laid out in a randomized complete block design with four replications. The experimental plot consisted of 5 rows of 1 m in length with the inter-row spacing of 20 cm. The elementary plot consisted of three inner rows of 0.6 m² (3 × 0.2 × 1 m), and seeds from elementary plot were used for the analyses. According to WRB (2014), *Haplic Chernozem (CHha)* soil is at the RS and ZP locations, whereas *Humic Gleysol (GLhu)* is at the PS. The rates of fertilizers were determined based on the soil chemical characteristics and available amounts of phosphorus (P), potassium (K) and nitrogen (N) in the soil. A total of 45 kg ha⁻¹ N, 45 kg ha⁻¹ P and 45 kg ha⁻¹ K were applied in PS1 and PS2 environments, while 18 kg ha⁻¹ N and 78 kg ha⁻¹ P were applied prior to sowing in the ZP1, ZP2, RS1 and RS2 environments. Sowing in both seasons was done by hand at RS location in mid-October, and by hand at PS and ZP locations, in late October, and early November, respectively. The top dressing was employed in March and April with the application of 46 kg ha⁻¹ N in PS1 and PS2 environments, 92 kg ha⁻¹ N in ZP2 environment, 54 kg ha⁻¹ N in ZP1 environment, and 51 kg ha⁻¹ N in RS1, ZP1 and RS2 environments. Integral protection against pests and weeds at all field locations was successfully accomplished by a proper use of adequate pesticides.

Analysis of technological quality traits. Protein content, wet gluten content, Zeleny sedimentation

volume and deformation energy were determined by near infrared spectrometry (NIRS) with the analyser Infraneo (Chopin Technologies, France). The standard methods for calibration used in this study were as follows: protein content (EN ISO 16634-1:2006), wet gluten content (EN ISO 21415-2:2006), Zeleny sedimentation volume (EN ISO 5529:2006) and deformation energy (EN ISO 27971:2006). Quality tests for wet gluten content, Zeleny sedimentation volume and deformation energy were performed on intact grains of each genotype for each environment at 14% moisture level, whereas protein content was expressed on dry weight basis. Seeds were harvested at full maturity, the average moisture content after harvesting ranged from 12.2% to 12.8% in bread wheat and from 11.4% to 12.1% in durum wheat, consistently across genotypes of bread and durum wheat, respectively. NIRS represents rapid analysis for quality control and is widely used in the wheat processing industry for measuring moisture and protein contents, but also for detection of Zeleny sedimentation volume, mixograph dough parameters, extensigraph dough characteristics and alveograph dough properties (Surma et al., 2012).

Analysis of agronomic traits. Plots were hand-harvested at maturity, and grain yield (YLD) was determined per elementary plot and expressed as kg ha⁻¹. Plant height (PH), number of grains per spike (GNS) and spike length (SL) were measured on 20 representative plants per elementary plot per replication. Thousand grain weight (TGW) was assessed from the harvested grain as three samples of 1000 grains per elementary plot per replication. The grain length (GL), grain width (GW) and grain thickness (GT) were measured by a digital electronic micrometre from the samples of twenty grains per elementary plot per replication. According to Tukey (HSD) test, the number of different homogenic sub-groups for grain thickness was 8 and 7 in bread and durum wheat, respectively. The productive tillering coefficient (PTC) was determined as a ratio of the number of spikes in the stage of maturation and the number of overwintered plants determined in the spring at the elementary plot per each replication. Grain vitreousness (GV) was determined by the method given in Kaluderski and Filipović (1998) with a farinator, allowing 50 wheat grains to be held firmly while a blade cuts them transversely. The percentage of vitreous grains was calculated by examining the cross-section of the grains and by obtaining the mean value of the 50 grains \times 2 following the formula:

$$\text{Grain vitreousness (\%)} = A + \frac{3}{4}B + \frac{1}{2}C + \frac{1}{4}D,$$

where A is number of fully vitreous grains, B – number of vitreous grains with more than 75% of grain cross-section being vitreous, C – number of vitreous grains with 50% to 75% grain cross-section being vitreous, D – number of vitreous grains with 25% to 50% grain cross-section being vitreous.

Statistical analysis. The two-way analysis of variance (ANOVA) based on random complete block design, with the fixed effects of genotype and environment, served for the quantification of the mean squares of the sources of variation, which were used for the calculation of the components of variance according to Falconer and Mackay (1996). Environment represented vegetation season \times location combination. Multivariate analysis of variance (MANOVA) was performed as tests of between-subjects effects. Testing the statistical significance of the

difference in trait means between bread wheat and durum wheat was carried out using *t*-test, whereas Tukey (HSD) test designated statistical significance of the difference in trait means between genotypes of bread wheat for each trait and independently, between genotypes of durum wheat for each trait. Broad sense heritability (h_b^2) was calculated as the ratio the genotypic variance to the phenotypic variance, and expected genetic advance as part of the mean for each trait at 5% selection intensity ($k = 2.056$) was evaluated as in Falconer and Mackay (1996). In order to compare the extent of predicted genetic advance of different traits with different measurement units, expected genetic advance as percent of mean (%) was computed. The genotype-by-trait ($G \times T$) biplot was used to visualise associations of agronomic traits, technological quality properties, and also profiles of genotypes by traits. The ANOVA, Tukey (HSD) test, MANOVA and $G \times T$ analysis were done within the computing environment R (R Development Core Team, 2013).

Results and discussion

Variability of the examined technological quality traits and descriptive statistical parameters are given in Table 1.

The protein content varied from 12.4% to 15.4% in bread wheat, and from 14.3% to 17.1% in durum wheat (Table 1). According to our results, a similar range for protein content of 10.5–16.3% was reported by Yang et al. (2014) for 330 Chinese bread wheat cultivars, whereas larger variation of 8.3–17.6% for 162 bread wheat cultivars from European Wheat Catalogue was shown by Branlard et al. (2001). Mean value for protein content of bread wheat (13.8%) was higher than in Polish and German (12.5%) and American (12.7%) cultivars of winter wheat (Table 1) (Fufa et al., 2005; Rozbicki et al., 2015), but similar to 14.5% of the bread wheat from the worldwide collection (Bordes et al., 2008). Lower values than ours for protein content mean value of durum wheat were from 12–13.9% as shown by other authors (Bilgin et al., 2010; Žilić et al., 2010). The homogenic groups of 10 and 11 were observed for protein content, according to Tukey (HSD) test, in bread and durum wheat, respectively. The wet gluten content ranged from 22.8% to 30.3% for bread wheat genotypes, and from 28.9% to 36.3% for durum wheat genotypes (Table 1), which is smaller range of variation compared to variation of 24–40.5% and 14–48% for wet gluten content reported in bread wheat and in durum wheat by Bilgin et al. (2010) and Yang et al. (2014), respectively. Žilić et al. (2010) documented 1.6-fold higher wet gluten content in durum wheat than in bread wheat, which is slightly higher than analogous value from our study of 1.3. The Tukey (HSD) test determined 9 and 7 homogenic sub-groups for wet gluten content in bread and durum wheat, respectively. The gliadins are responsible for the viscous properties of dough during mixing, whereas glutenins as polymeric proteins reduce dough extensibility and increase dough strength (Różyło, Laskowski, 2011). The Zeleny sedimentation volume was from 39.4 to 67.1 mL in bread wheat genotypes and from 37.4 to 48.3 mL in durum wheat genotypes (Table 1), which is a higher and wider range in comparison to results of Kaya and Akçura (2014) for bread wheat, and of Szumiło et al. (2010)

Table 1. Protein content, wet gluten content, Zeleny sedimentation volume and deformation energy of bread and durum wheat genotypes represented as mean values across six environments

Genotype	Code	Protein content %	Wet gluten content %	Zeleny sedimentation volume mL	Deformation energy 10 ⁻⁴ J
<i>Triticum aestivum</i> L. ssp. <i>aestivum</i> (bread wheat)					
Žitarka	P1	15.1 i	30.3 i	64.2 j	333.8 j
Stephens	P2	13.5 de	26.2 ef	43.0 b	205.0 b
Renan	P3	15.1 i	29.2 ghi	67.1 k	313.2 i
Caldwell	P4	12.5 a	23.1 ab	46.1 d	219.2 c
Abe	P5	14.3 gh	28.9 g	48.3 e	242.6 e
Auburn	P6	14.1 fg	26.4 ef	44.5 c	259.4 f
Frankenmuth	P7	13.0 b	25.8 def	39.4 a	179.3 a
Apache	P8	13.3 cd	24.9 cd	55.6 h	246.1 e
ZPAU 12	P9	13.1 bc	23.4 ab	55.6 h	231.5 d
Marija	P10	14.0 f	26.8 f	52.1 g	279.8 g
ZP 87/Ip	P11	12.4 a	22.8 a	59.4 i	241.4 e
Tecumseh	P12	15.4 j	30.1 hi	60.5 i	357.8 k
Pobeda	P13	14.5 h	29.0 gh	64.9 j	294.6 h
Zemunska rosa	P14	13.0 b	24.3 bc	50.5 f	247.7 e
Ludwig	P15	13.7 e	25.5 de	52.6 g	267.6 f
Mean		13.8 A	26.5 A	53.6 A	261.2 A
CV (%)		6.9	9.6	15.8	18.4
Min		12.4	22.8	39.4	179.3
Max		15.4	30.3	67.1	357.8
<i>Triticum durum</i> Desf. (durum wheat)					
37ED.7922	D1	16.7 j	34.7 ef	43.5 cd	321.7 f
37ED.7896	D2	15.1 c	31.1 b	37.9 a	295.7 bcd
37ED.7817	D3	16.0 g	33.6 cd	43.4 cd	296.5 bcd
Varano	D4	16.8 j	35.2 ef	42.9 c	306.9 e
37ED.7821	D5	16.5 i	35.4 fg	48.3 h	338.8 g
37ED.7880	D6	16.3 h	34.6 ef	41.4 b	316.9 f
ZP 10/I	D7	15.5 de	31.1 b	41.6 b	303.0 de
SOD 55	D8	14.9 b	31.0 b	47.9 gh	289.8 b
37ED./07 7803	D9	15.5 d	32.7 c	44.8 e	291.3 bc
DSP 66	D10	16.6 ij	35.0 ef	43.1 c	354.6 h
ZP 34/I	D11	15.6 e	33.1 c	42.4 bc	302.0 de
37ED.7820	D12	15.9 f	32.9 c	44.5 de	298.8 cde
37ED./07 7857	D13	17.1 k	36.3 g	46.2 f	357.1 h
37ED./07 7849	D14	16.0 fg	34.4 de	46.8 fg	318.0 f
ZP 120/I	D15	14.3 a	28.9 a	37.4 a	267.1 a
Mean		15.9 B	33.3 B	43.5 B	310.6 B
CV (%)		4.9	6.2	7.3	7.9
Min		14.3	28.9	37.4	267.1
Max		17.1	36.3	48.3	357.1

Note. Mean values in each column labelled with the same lowercase letter are not significantly different ($p < 0.05$) based on the Tukey (HSD) test; means in each column labelled with the same uppercase letter are not significantly different between wheat species according to the t -test ($p < 0.05$); CV – coefficient of variation.

for durum wheat. Sedimentation values evaluated as <15 mL represent weak, 16–24 mL medium, 25–36 mL strong and over 36 very strong gluten (Başıftçi, Kınacı, 2015), inferring strong gluten quality in all durum wheat genotypes and 10 bread wheat genotypes in our study. The mean value for Zeleny sedimentation volume (53.6 mL) in bread wheat in our study was higher than the mean value of 30.7 mL of hard red winter wheat from Nebraska (Fufa et al., 2005), of 30.3 mL of Chinese bread wheat cultivars (Yang et al., 2014) and of 28.6 mL of 162 bread wheat cultivars from European Wheat Catalogue (Branlard et al., 2001), but similar to the value of 52.8 mL reported by Zanetti et al. (2001). According to Tukey (HSD) test, the number of homogenic sub-groups for Zeleny sedimentation volume was different in bread and durum wheat – 11 and 8, respectively. The

deformation energy ranged from 179.3 to 357.8 10⁻⁴ J for bread wheat genotypes, and from 267.1 to 357.1 10⁻⁴ J for durum wheat genotypes (Table 1), whereas the wider range of variation for bread wheat of 208–573 10⁻⁴ J was obtained by Maghirang et al. (2006), and smaller ranges of 209.2–287.6 10⁻⁴ J and of 64.3–187.6 10⁻⁴ J were reported in bread wheat by Surma et al. (2012) and in durum wheat by Abinasa et al. (2012), respectively. The number of homogenic sub-groups for deformation energy was 11 and 8, in bread and durum wheat, respectively, based on Tukey (HSD) test. It is interesting to notice that the same top three genotypes of bread wheat with the highest values for protein content, wet gluten content and deformation energy were ‘Tecumseh’ from USA, ‘Žitarka’ from Croatia and ‘Renan’ from France, corroborating the correlations between these quality traits. In regard to

Zeleny sedimentation volume, the promising genotypes of bread wheat with the highest mean values were 'Žitarka' and 'Pobeda' from Croatia and Serbia, respectively, representing genetic material bred in Balkan's agro-ecological region. Durum wheat lines from CIMMYT 37th Elite Durum Unreplicated Yield Trial (37ED./07 7857, 37ED.7922 and 37ED.7821) and Italian cultivar 'Varano' proved to be superior genotypes regarding the highest values observed for protein content and wet gluten content, whereas the same CIMMYT 37EDUYT lines (37ED./07 7857 and 37ED.7821) as previously, another two lines (37ED./07 7849 and Slovakian cultivar SOD 55) were the best for Zeleny sedimentation volume. The same two CIMMYT 37EDUYT lines (37ED.7857 and 37ED./07 7821) as previously and the line DSP-

MD-01 No. 66 from ICARDA DSP-MD-01-Durum Segregating Populations-Mediterranean Dryland (season 2000–2001) were the most promising for quality regarding high deformation energy. According to the *t*-test, significant differences were observed between means of all examined technological quality traits, with the values of protein content, wet gluten content and deformation energy being higher in durum wheat, and with the values of Zeleny sedimentation volume being higher in bread wheat (Table 1).

MANOVA was presented as multiple tests of between-subjects effects for bread and durum wheat, separately, showing statistical significance ($p < 0.001$) of all sources of variation (Table 2).

Table 2. Multivariate analysis of variance (*MANOVA*) for technological quality traits of bread and durum wheat

Source of variation	Dependent variable	bread wheat			durum wheat		
		<i>F</i>	<i>p</i>	Partial η^2	<i>F</i>	<i>p</i>	Partial η^2
Location (L)	PC	3313.5	0.000	0.961	935.6	0.000	0.874
	WG	1104.2	0.000	0.891	232.1	0.000	0.632
	ZS	4311.4	0.000	0.970	790.8	0.000	0.854
	W	1559.0	0.000	0.920	401.4	0.000	0.748
Season (S)	PC	7506.3	0.000	0.965	29940.9	0.000	0.991
	WG	2218.7	0.000	0.892	7305.7	0.000	0.964
	ZS	756.2	0.000	0.737	8375.7	0.000	0.969
	W	3762.7	0.000	0.933	12120.6	0.000	0.978
Genotype (G)	PC	476.9	0.000	0.961	573.0	0.000	0.967
	WG	106.5	0.000	0.847	103.8	0.000	0.843
	ZS	984.8	0.000	0.981	186.1	0.000	0.906
	W	589.3	0.000	0.968	197.4	0.000	0.911
L × S	PC	1107.0	0.000	0.891	5351.3	0.000	0.975
	WG	311.5	0.000	0.698	1613.6	0.000	0.923
	ZS	219.4	0.000	0.619	105.2	0.000	0.438
	W	531.6	0.000	0.797	4007.3	0.000	0.967
G × L	PC	20.1	0.000	0.676	145.1	0.000	0.938
	WG	3.8	0.000	0.283	33.9	0.000	0.778
	ZS	170.8	0.000	0.947	58.2	0.000	0.858
	W	18.2	0.000	0.654	63.3	0.000	0.868
G × S	PC	40.6	0.000	0.678	121.4	0.000	0.863
	WG	15.0	0.000	0.437	19.4	0.000	0.501
	ZS	126.7	0.000	0.868	59.7	0.000	0.756
	W	32.2	0.000	0.625	26.4	0.000	0.578
L × S × G	PC	20.3	0.000	0.678	70.7	0.000	0.880
	WG	5.6	0.000	0.368	9.2	0.000	0.487
	ZS	105.8	0.000	0.916	32.8	0.000	0.773
	W	28.1	0.000	0.745	18.0	0.000	0.652

PC – protein content, WG – wet gluten content, ZS – Zeleny sedimentation volume, W – deformation energy

The hierarchy of importance of sources of variation for the examined quality traits according to partial η^2 from *MANOVA* were: $S > L = G > L \times S > G \times S = L \times S \times G > G \times L$ (PC-bread wheat) and $S > L \times S > G > G \times L > L \times S \times G > L > G \times S$ (PC-durum wheat); $S > L > G > L \times S > G \times S > L \times S \times G > G \times L$ (WG-bread wheat) and $S > L \times S > G > G \times L > L > G \times S > L \times S \times G$ (WG-durum wheat); $G > L > G \times L > L \times S \times G > G \times S > S > L \times S$ (ZS-bread wheat) and $S > G > G \times L > L > L \times S \times G > G \times S > L \times S$ (ZS-durum wheat); $G > S > L > L \times S > L \times S \times G > G \times L > G \times S$ (W-bread wheat) and $S > L \times S > G > G \times L > L > L \times S \times G > G \times S$ (W-durum wheat) (Table 2).

The greater significance of environmental variation for Zeleny sedimentation volume and deformation energy in durum wheat, and for protein content and wet gluten content in bread and durum wheat, in this study, is compliant with the results of Drezner et al. (2007) and Bilgin et al. (2010), stating strong environmental impact on bread and durum wheat quality traits-protein content, wet gluten content and deformation energy. Rozbicki et al. (2015) pointed out that the genotype as source of variation was more important than ecological factors on gluten quality coupled to Zeleny sedimentation for bread wheat, similarly as shown in this study. Hristov and Mladenov (2005) also showed for 20 cultivars of bread

wheat statistical significance ($p < 0.01$) of all interaction effects ($G \times L$, $G \times S$, $L \times S$ and $L \times S \times G$) on wet gluten content and Zeleny sedimentation volume variation, across five locations in Serbia.

Genetic parameters of wheat technological quality were under scrutiny of other authors (Bilgin et al., 2010; Tsegaye et al., 2012). The gluten quality and content are controlled by major genes, whereas protein

content is determined by major genes and quantitative trait loci (QTLs) also. Larger genetic component of variance (σ_g^2) relative to the component of variance due to the genotype \times environment interaction (σ_{ge}^2) in this study was observed for the following technological quality traits in bread wheat: protein content (3.2 times higher), wet gluten content (2.9 times higher) and deformation energy (3.9 times higher) (Table 3).

Table 3. Variance components and genetic parameters of protein content, wet gluten content, Zeleny sedimentation volume and deformation energy in bread and durum wheat

Trait	Type	σ_g^2	σ_{ge}^2	σ_e^2	σ_p^2	h_b^2 %	CV_g %	CV_{ph} %	GA	GAM %
PC	bread wheat	0.861	0.265	0.046	0.907	94.9	6.28	6.44	1.86	12.60
	durum wheat	0.486	0.691	0.116	0.602	80.7	4.12	4.58	1.29	7.62
WG	bread wheat	5.98	2.075	0.406	6.388	93.6	9.25	9.56	4.88	18.43
	durum wheat	3.41	4.967	0.869	4.279	79.7	5.54	6.21	3.40	10.19
ZS	bread wheat	61.96	59.124	9.93	71.88	86.2	14.69	15.82	15.05	28.09
	durum wheat	7.53	15.532	2.64	10.18	74.0	6.32	7.34	4.87	11.19
W	bread wheat	2213.92	564.494	98.01	2311.93	95.8	18.01	18.41	94.85	36.31
	durum wheat	490.92	679.848	116.38	607.30	80.8	7.13	7.94	41.04	13.21

σ_g^2 – genetic variance, σ_{ge}^2 – variance of the genotype \times environment interaction, σ_e^2 – environmental variance, σ_p^2 – phenotypic variance, h_b^2 – broad sense heritability, CV_g – coefficient of genetic variation, CV_{ph} – coefficient of phenotypic variation, GA – genetic advance, GAM – genetic advance as percent of mean; PC – protein content, WG – wet gluten content, ZS – Zeleny sedimentation volume, W – deformation energy

The relation $\frac{\sigma_g^2}{\sigma_{ge}^2}$ for Zeleny sedimentation volume content in bread wheat was equal to one. The larger σ_{ge}^2 when compared to σ_g^2 was determined for all technological quality traits in durum wheat: protein content (1.4 times higher), wet gluten content (1.5 times higher), Zeleny sedimentation volume (2.1 times higher) and deformation energy (1.4 times higher) (Table 3), which is in accordance with the findings of Bilgin et al.

(2010) regarding $\frac{\sigma_{ge}^2}{\sigma_g^2}$ relation of 2 and 2.4 for protein content and wet gluten content, respectively. Durum wheat genotypes exhibited generally larger influence of genotype \times environment interaction on technological quality traits compared to bread wheat. The existence of large genotype \times environment interaction indicates the necessity of carrying out the selection in a range of environments and breeding different genotypes adaptable for specific environments (Falconer, Mackay, 1996). The environmental component of variance (σ_e^2) was smaller than σ_g^2 and σ_{ge}^2 for all the traits, both in bread and durum wheat.

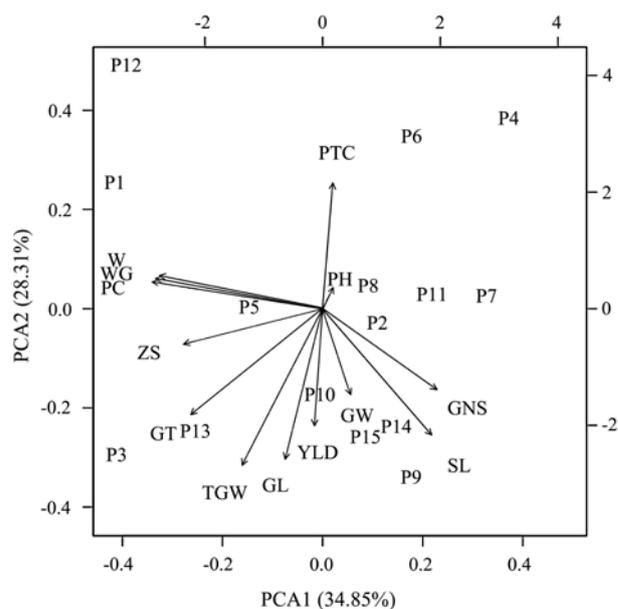
Heritability in a broad sense (h_b^2) was very high (>90%) for protein content, wet gluten content and deformation energy in bread wheat (Table 3). Higher h_b^2 values (>95%) than ours for protein content in *Triticum aestivum* recombinant inbred lines (RILs) and improved lines, were reported by Zanetti et al. (2001) and Başçiftçi and Kinacı (2015). The probable explanation for such high h_b^2 values is the genetic control of the phenotypic expression for protein content with several genes with major and/or minor effects. Šarčević et al. (2014) obtained very high (>94%) values for h_b^2 for protein content, wet gluten content and Zeleny sedimentation volume for 19 winter wheat cultivars under both high

and low N fertilization level, whereas Aydin et al. (2010) showed h_b^2 for protein content and Zeleny sedimentation volume to be 87.4% and 89.1% for 25 genotypes of bread wheat, respectively. Conversely, Kaya and Akcura (2014) reported small to medium values for h_b^2 for protein content, wet gluten content and Zeleny sedimentation volume of 45%, 41% and 52%, respectively, for 20 genotypes of bread wheat. High h_b^2 (80–90%) was showed for protein content and deformation energy in durum wheat and for Zeleny sedimentation volume in bread wheat (Table 3), differently from small to medium values h_b^2 for Zeleny sedimentation volume of 67%, obtained for 162 cultivars of bread wheat according to Branlard et al. (2001), and to 45% for protein content in most widely grown Turkish durum wheat cultivars, according to Kaya and Akcura (2014). Broad sense heritability was moderately high (70–80%) for wet gluten content and Zeleny sedimentation volume in durum wheat (Table 3), whereas Kaya and Akcura (2014) reported lower value for Zeleny sedimentation volume.

The highest values of the coefficient of genetic variation (CV_g) and coefficient of phenotypic variation (CV_{ph}) were recorded for deformation energy (18.01% and 18.41%, respectively) in bread wheat (Table 3). The minimum values of CV_g and CV_{ph} of 4.12% and 4.58%, respectively, were shown for protein content in durum wheat, quite smaller than CV_{ph} of 18.37% reported by Bilgin et al. (2010). CV_g and CV_{ph} were small (<10%) for all examined traits except for Zeleny sedimentation volume and deformation energy in bread wheat, which showed medium variation ($10\% < CV_{ph} < 20\%$), in accordance with the findings of other authors (Fufa et al., 2005; Žilić et al., 2010; Yang et al., 2014).

Heritability estimate is insufficient to make significant improvement through selection unless accompanied by favourable amount of genetic advance (Bilgin et al., 2010). Non-additive gene effects relate to high heritability but low genetic advance of a trait of interest, whereas additive gene action stipulates high, both, heritability and genetic advance, leading to the success of selection (Laghari et al., 2010). Very high and high h_b^2 estimate of 95.8% and 86.2% coupled with high expected genetic advance (>20%) were shown for deformation energy and Zeleny sedimentation volume in bread wheat, respectively, whereas very high h_b^2 estimate (>93%) and moderate expected genetic advance of 12.6% and 18.4% were observed for protein content and wet gluten content in bread wheat, respectively (Table 3). Başçıftçi and Kınacı (2015) obtained higher genetic advance for Zeleny sedimentation volume in bread wheat lines of 30.1%. The smallest genetic advance value (7.6%) was determined for protein content in durum wheat. Contrary to our results, Bilgin et al. (2010) showed both small h_b^2 (<40%) and genetic advance (<9%) values for protein content and wet gluten content in 25 genotypes of durum wheat, similarly to 51% and 4.9%, respectively, for protein content in 23 durum wheat genotypes reported by Tsegaye et al. (2012).

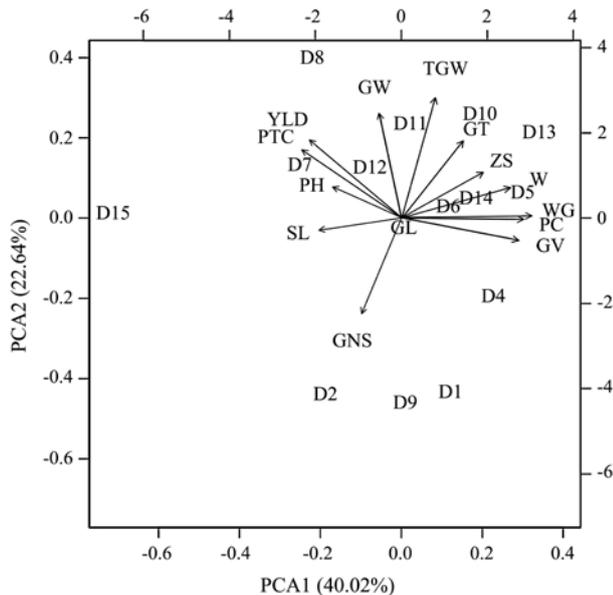
Genotype-by-trait analyses of interrelationship between agronomic characteristics and technological quality properties calculated from multi-environment trial data for bread and durum wheat are shown (Figs 1–2). Across the 15 tested bread wheat genotypes grain yield was positively associated with Zeleny sedimentation volume, but negatively with the other three technological quality properties – protein content, wet gluten content and deformation energy (Fig. 1). These relations suggest that it is difficult to combine higher grain yield, protein content, wet gluten content and deformation energy in a single genotype. Similarly, Kaya and Akcura (2014) showed negative correlation between grain yield and protein content, and grain yield and wet gluten content in twenty genotypes of bread wheat. The positive associations were found for grain thickness and Zeleny sedimentation volume and to lesser extent between grain thickness and protein content, grain thickness and wet gluten content, grain thickness and deformation energy, making grain thickness suitable agronomic trait that can be indirect selection criterion. Varga et al. (2003) found positive correlation between grain thickness and wet gluten content for winter wheat genotypes, whereas Drikvand et al. (2013) showed positive correlation between grain width and protein content for 92 bread wheat cultivars and breeding lines. All four investigated parameters of technological quality were negatively associated with grain number per spike and spike length. Bread wheat genotypes ‘Žitarka’ and ‘Renan’ had the highest values for protein content, wet gluten content, Zeleny sedimentation volume and deformation energy, with ‘Renan’ being superior in regard to grain yield and thousand grain weight. If it is desirable to further improve grain yield of ‘Žitarka’, cross ZP AU 12 × ‘Žitarka’ may be useful.



YLD – grain yield, TGW – thousand grain weight, PH – plant height, SL – spike length, GNS – grain number per spike, GL – grain length, GW – grain width, GT – grain thickness, PTC – productive tillering coefficient; PC – protein content, WG – wet gluten content, ZS – Zeleny sedimentation volume, W – deformation energy

Figure 1. Genotype by trait ($G \times T$) biplot of 15 bread wheat genotypes (P1–P15) by nine agronomic and four technological quality characteristics measured across six environments

Across the 15 tested durum wheat genotypes grain yield was negatively correlated with protein content, wet gluten content, Zeleny sedimentation volume and deformation energy, suggesting impediment for combining higher grain yield, and four examined technological quality properties in a single genotype (Fig. 2). According to Bilgin et al. (2010), the negative correlation observed between protein content and grain yield resulted mainly from protein dilution by non-nitrogen compounds in the grain during grain filling. Grain thickness proved to be highly positively associated with Zeleny sedimentation volume and to a lesser extent to deformation energy, protein content and wet gluten content, respectively. Grain vitreousness was positively associated with protein content, and to lesser extent to wet gluten content, deformation energy and Zeleny sedimentation volume, which was also showed by El-Khayat et al. (2006) and Bilgin et al. (2010), as positive correlation of grain vitreousness and protein content and wet gluten content. Grain thickness and grain vitreousness can be indirect selection criteria for improving Zeleny sedimentation volume, protein content, deformation energy and wet gluten content in durum wheat. All four examined technological quality properties were negatively associated with the following agronomic characteristics: grain number per spike, spike length, plant height and productive tillering coefficient. The durum wheat genotypes 37ED/07 7857 and 37ED.7880 had the highest protein content, wet gluten content, Zeleny sedimentation volume and deformation



YLD – grain yield, TGW – thousand grain weight, PH – plant height, SL – spike length, GNS – grain number per spike, GL – grain length, GW – grain width, GT – grain thickness, GV – grain vitreousness, PTC – productive tillering coefficient; PC – protein content, WG – wet gluten content, ZS – Zeleny sedimentation volume, W – deformation energy

Figure 2. Genotype by trait ($G \times T$) biplot of 15 durum wheat genotypes (D1–D15) by ten agronomic and four technological quality characteristics measured across six environments

energy, with the first one being more superior in regard to the most of the investigated agronomic traits. If it is desirable to further improve grain yield level of 37ED./07 7857 and 37ED.7880, the cross with ZP 10/1 can be recommended.

Conclusions

1. Very high (95.8%) and high (86.2%) heritability in a broad sense (h_b^2) for deformation energy and Zeleny sedimentation volume, respectively, in the studied genotypes of bread wheat, coupled with high expected genetic advance as percent of mean of 36.3% and 28.1%, respectively, and predominant genetic variance (σ_g^2), the success from classical breeding approach can be anticipated for these two traits.

2. The moderately high heritability in a broad sense (74–80.8%) was determined for grain protein content, wet gluten content, Zeleny sedimentation volume and deformation energy, accompanied by small genetic advance (7.6%) for protein content and moderate genetic advance (10–13.2%) for wet gluten content, Zeleny sedimentation volume and deformation energy, along with genotype \times environment variance (σ_{ge}^2) larger for about 1.4–2.1 to σ_g^2 , scored less success in breeding for protein content, wet gluten content, Zeleny sedimentation volume and deformation energy improvement in the studied genotypes of durum wheat.

3. The ratio of σ_g^2 and ($\sigma_g^2 / \sigma_{ge}^2$) indicated greater stability for protein content, wet gluten content

and deformation energy in the studied genotypes of bread wheat, and instability for all examined traits of technological quality in the studied genotypes of durum wheat.

4. Grain yield was positively correlated with Zeleny sedimentation volume, but negatively with protein content, wet gluten content and deformation energy, in the studied genotypes of bread wheat, whereas in the studied genotypes of durum wheat it showed negative correlations with all four technological quality properties. Taking into account strong positive association between grain thickness and Zeleny sedimentation volume, and to a lesser extent between grain thickness and protein content, grain thickness and wet gluten content, grain thickness and deformation energy, grain thickness can be a suitable agronomic trait that can serve as indirect selection criterion in the studied genotypes of bread wheat and durum wheat improvement of examined technological quality properties. Grain vitreousness was positively correlated with protein content and to a lesser extent to wet gluten content, deformation energy and Zeleny sedimentation volume and can be also considered as the attribute of indirect selection for these technological quality traits in the studied genotypes of durum wheat.

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***Triticum aestivum* ir *T. durum* genetiniai parametrai kokybės technologinėms savybėms Serbijoje**

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Santrauka

Baltymai yra svarbus kviečių maistinės vertės rodiklis; vienas jų – glitimas – lemia duoninių kviečių kepimo kokybę ir makaronų gamybai skirtų kviečių technologines savybes. Vertinant kviečių kokybės savybių genetinius parametrus galima nustatyti jų gerinimo galimybes. Augalinę medžiagą sudarė 30 pasaulyje paplitę duoninių ir kietųjų kviečių genotipai. Bandymai buvo atlikti trijose Serbijos vietovėse du vegetacinius sezonus 2010–2011 ir 2011–2012 m. Baltymų kiekis, šlapio glitimo kiekis, sedimentacijos (Zeleny) tūris ir deformacijos energija buvo nustatyti naudojant artimosios srities infraraudonųjų spindulių spektrometriją.

Siekiant nustatyti netiesioginės atrankos galimybę, tyrimo metu siekta įvertinti: 1) kintamumą, variantiškumo komponentus, paveldimumą plačiąja prasme (h_b^2), tikėtiną genetinę pažangą baltymų kiekiui, šlapio glitimo kiekiui, Zeleny sedimentacijos tūriui ir deformacijos energijai; 2) ryšius tarp agronominių savybių ir baltymų kiekio, šlapio glitimo kiekio, Zeleny sedimentacijos verčių ir deformacijos energijos. Kietųjų kviečių didžiausi genetinės ir fenotipinės variacijos koeficientai (CV_g ir CV_{ph}) buvo nustatyti deformacijos energijos duoniniuose kviečiuose, atitinkamai 18 ir 18,4 %; mažiausios 4,1 ir 4,6 % vertės buvo nustatytos baltymų kiekiui. Genetinio variantiškumo komponento (σ_g^2) / variantiškumo komponento ryšys dėl genotipo \times aplinkos sąveikos (σ_{ge}^2) > 1 buvo nustatytas baltymų kiekio (3,2), šlapio glitimo kiekio (2,9) bei deformacijos energijos (3,9) ir buvo lygus vienetai sedimentacijos vertėms duoniniuose kviečiuose. Kietuosiuose kviečiuose $\sigma_{ge}^2 / \sigma_g^2 > 1$ buvo nustatytas baltymų kiekio (1,4), šlapio glitimo kiekio (1,5), Zeleny sedimentacijos tūrio (2,1) ir deformacijos energijos (1,4). Atsižvelgiant į nustatytą labai aukštą ir aukštą deformacijos energijos ir Zeleny sedimentacijos tūrio h_b^2 , atitinkamai 95,8 ir 86,2 % duoniniuose kviečiuose kartu su didele genetinė pažanga, atitinkamai 36,3 ir 28,1 %, galima tikėtis klasikinės selekcijos sėkmės. Grūdų storis buvo labiau susijęs su sedimentacijos tūriu ir mažiau – su baltymų kiekiu, šlapio glitimo kiekiu ir deformacijos energija duoniniuose bei kietuosiuose kviečiuose ir kartu su stikliškumu kietuosiuose kviečiuose gali būti naudojami netiesioginei selekcinei atrankai.

Reikšminiai žodžiai: baltymai, glitimo stiprumas, paprastieji ir kietieji kviečiai, šlapias glitimas, tikėtina genetinė pažanga, sedimentacija.