AGRONOMIC PERFORMANCE OF WHEAT CULTIVARS AND THEIR MOLECULAR CHARACTERIZATION

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Creation of new higher yield cultivars, adaptation of existing germplasm to a global climate change, increasing resistance to diseases in new genotypes are some of the tasks that breeding have in front of it. The objectives of this research were to assess GE interaction in two different environments across two vegetation seasons and to do association analysis based on the results of the phenotypic and molecular evaluation. Grain samples were obtained from 96 winter wheat cultivars grown in 2011/12 and 2012/13 at two locations in the South Pannonia Basin region and population was profiled with 28 microsatellites. The share of genotype is high and amounts 24.84%, while the share of environments was 21.06%, when yield was evaluated. The GE interaction was also statistically significant and amounts 51.58% of the total variance. Microsatellites that exhibited a relation with yield by GLM and MLM model were: gwm357, gwm339, cfa2114, gwm631, gwm495, gwm190, barc1121 and gwm437. Markers that have demonstrated the stability of the relationship with yield in different environments can be recommended as potentially useful in wheat breeding.
Keywords: AMMI, GE interaction, microsatellites, yield, wheat.

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INTRODUCTION

Plant breeding as a science has many tasks in front of it. Creation of new higher yield cultivars, adaptation of existing germplasm to a global climate change, increasing resistance to diseases in new genotypes is only some of them. In fulfilling these goals necessity is the introduction of new techniques in conventional breeding. Yield is a super trait consisted of many individual components whose action is united where all genes in one plant, directly or indirectly, lead to the final result (MIROSAVLJEVIĆ *et al*., 2016). It presents the result of plants effort to reproduce and complex gene interaction within the genome, along with the interaction of the genome with biotic and abiotic factors (MLADENOV, 2016; KHAN *et al*., 2017). Combination among monitoring of phenotypic traits from the field with molecular characterization obtains results which represent associative analysis. In phenotyping total variance is divided into three different shares: the share of genotype, share of environment and share of genotype x environment (GE) interaction (KOSEV and GEORGIEVA, 2016; BANJAC *et al*., 2014; DIMITRIJEVIĆ *et al*., 2011). When molecular analysis is parsed, the situation is vastly different, due to the fact that some author claims that the environment share can be fully excluded (XU and CROUCH, 2007; BERTRAND and MACKILL, 2008; SCORZZARI *et al*., 2014). Associative analysis is tasked with expressing the statistical significance among investigated traits and selected microsatellites in different environments (KALIA *et al*., 2011). Nevertheless, only microsatellites that are closely related to a certain trait will achieve statistically significant relationship marker-trait, which will be recognized by associative analysis (WALL and STEVISON, 2016). Due to their accessibility microsatellites or Simple Sequence Repeat (SSR) are one of the most commonly used molecular markers in plant breeding (NIELSEN *et al*., 2014; HAO *et al*., 2011).

The objectives of this research were two folded (i) to assess GE interaction in two different environments across two vegetation seasons (ii) to perpetrate association analysis based on the results of the phenotypic and molecular evaluation.

MATERIALS AND METHODS

Field exams

Grain samples were obtained from 96 winter wheat cultivars grown in 2011/12 and 2012/13 at two locations: Novi Sad and Sremska Mitrovica (E1- Novi Sad 2012, E2 - Novi Sad 2013, E3 - Sremska Mitrovica 2012, E4 - Sremska Mitrovica 2013). The large majority of these cultivars (93) was designed in Institute of Field and Vegetable Crops, Novi Sad, Serbia (Tab. 1). When selecting genotypes focus was on maximum diversity in terms of genetic origin and creation of the representative genetic sample. The wheat cultivars were planted in a randomized complete block design with four replications. Sowing in both growing seasons was completed by the end of October, while the harvest was ended in the last ten days of June.
Table 1.

Out of 96 used genotypes, 94 were represented hexaploid bread wheat (*Triticum aestivum*), while two genotypes were representing *Triticum spelta* (Nirvana) and *Triticum compactum* (Bambi). Yield (t·ha^{-1}) was determined in the field. Tests were performed on the harvested seed of each cultivar for each replication.

Table 1. Used genotypes of winter wheat.

No.	Genotype	Y.r.	No.	Genotype	Y.r.	No.	Genotype	Y.r.
G1	Pesma	1995	G36	NS40 S	2006	G71	NS3-7289	Ком
G2	Renesansa	1994	G37	Teodora	2006	G72	NS Pudarka	2013
G3	Obrij	1983	G38	Etida	2006	G73	NS3-6767/2	Ком
G4	NS rana 5	1991	G39	Isidora	2007	G74	Sava	1970
G5	Pobeda	1990	G40	Gordana	2008	G75	Partizanka	1973
G6	Evropa 90	1990	G41	Gora	2009	G76	NS rana 2	1975
G7	Ljiljana	2000	G42	Biljana	2009	G77	Balkan	1979
G8	Sonata	2000	G43	Natalija	2009	G78	Posavka 2	1979
G9	Vila	2001	G44	NS Desetka	2010	G79	Jugoslavija	1980
G10	Kantata	2001	G45	NS Nena	2010	G80	Lasta	1987
G11	Cipovka	2002	G46	NS Dika	2010	G81	Rodna	1988
G12	Dragana	2002	G47	NS Arabeska	2010	G82	Tamiš	1988
G13	Jefimija	2003	G48	NS Artemida	2010	G83	Danica	1990
G14	Balada	2003	G49	NS Emina	2010	G84	Proteinka	1990
G15	Rapsodija	2003	G50	NS Avangarda	2010	G85	Rana niska	1990
G16	Arija	2003	G51	NS Futura	2010	G86	Milica	1992
G17	Simfonija	2003	G52	NS Ilina	2010	G87	Hejs 2	N/A
G18	Simonida	2003	G53	NS Enigma	2010	G88	Divna	1994
G19	Balerina	2003	G54	NS Tavita	2011	G89	Prima	1995
G20	Diva	2003	G55	NS 91/04	Kom	G90	Tera	1995
G21	Astra	2003	G56	NS 50/07	Kom	G91	Tiha	1995
G22	Helena	2004	G57	NS 269/08	Kom	G92	Prva	1997
G23	Oda	2004	G58	NS 48/08	Kom	G93	Zlatka	1997
G24	Milijana	2004	G59	NS3-6954	Kom	G94	Mina	1997
G25	Nirvana	2004	G60	NS3-6741	Kom	G95	Delta	1998
G26	Bambi	2004	G61	NS3-6926	Kom	G96	Sonja	1998
G27	Lana	2005	G62	NS 36/10	Kom			
G28	Zvezdana	2005	G63	NS 168/10	Kom			
G29	Janja	2005	G64	NS 55/10	Kom			
G30	Fundulea 4	1987	G65	NS 176/10	Kom			
G31	Bastijana	2005	G66	NS 128/10	Kom			
G32	Dama	2006	G67	NS 151/10	Kom			
G33	Srna	2006	G68	NS3-7106	Kom			
G34	Angelina	2006	G69	NS3-6706/2	Kom			
G35	Barbara	2006	G70	NS3-6939	Kom			

*No. number of genotype, Y.r. -year of released , Kom. -genotypes that still are in the National Commission for cultivar recognition. N/A not announced.

Molecular exams

Genomic DNA from all genotypes was isolated from fresh leaves using the CTAB protocol DOYLE and DOYLE (1990). The wheat genotype population was profiled with 28 microsatellites. The sequences of SSR markers were taken from the GrainGenes (2016) database. The additional cultivar Chinese Spring was used as a positive control and it was placed on 87 spot, instead of cultivar Heys 2. Microsatellites were positioned along almost all three genomes (Tab. 2). PCR amplifications were carried out according to the protocols given by RÖDER *et al*. (2008). The reaction in 10 μL volume contained 30 ng of DNA template, 1x buffer solution, 2 mmol L- 1 dNTPs, 1.5 mmol L- 1 MgCl2, 10 pmol of fluorescently labeled forward and unlabeled reverse primers, and 1 unit of *Taq* polymerase. PCR started with an initial denaturation at 94°C for 5 min, followed by 40 cycles of 94°C for 30 s, 52–62°C for 45 s, and 72°C for 45 s. The final extension was 10 min at 72°C. The PCR amplicons were separated by size using capillary electrophoresis on an ABI Prism 3130 genetic analyzer (Applied Biosystems). The reaction volume of 10 μL consisted of 2 μL of mixed differently labeled PCR products, 0.2 μL of GeneScan 500 LIZ size standard (Applied Biosystems), and 7.8 μL of Hi‑ Di formamide.

The dye labeled products were identified by fluorescence detection, and microsatellite analysis was performed using the GeneMapper software, version 4.0 (Applied Biosystems).

Table 2. Used molecular markers (microsatellites)

Microsatellite	Color	Chromosome	Sequence
wmc 656	ned	3D	F:AAGTAGGCGAGCGTTGT R:TTTCCCTGGCGAGATG
wmc 553	ned	6A	F:CGGAGCATGCAGCTAGTAA R:CGCCTGCAGAATTCAACAC
wmc 18	ned	2D	F:5` CTGGGGCTTGGATCACGTCATT 3` R:5` AGCCATGGACATGGTGTCCTTC 3`
wmc 457	6 fam	4D	F:5' CTT CCA TGA ATC AAA GCA GCA C 3' R:5' CAT CCA TGG CAG AAA CAA TAG C3'
barc 1047	pet	4A	F:5' GCG CAG ACC GTA CCC AAC CAG ATA G 3' R:5' CAT GCC TTG CCC TTG GTT TCA 3'
barc 1121	vic	6D	F:5' GCG AGC AAA CTG ATC CCA AAA AG 3' R:5' TAT CGG TGA GTA CGC CAA AAA CA 3'
barc 5	6 fam	2A	F:5' GCGCCTGGACCGGTTTTCTATTTT 3' R:5' GCGTTGGGAATTCCTGAACATTTT 3'
barc 65	6 fam	7B	F:5' CCCATGGCCAAGTATAATAT 3' R:5' GCGAAAAGTCCATAGTCCATAGTCTC 3'
barc 12	ned	3A	F:5` CGACAGAGTGATCACCCAAATATAA 3` R:5`CATCGGTCTAATTGTCAATGTA 3`
barc 158	pet	1A,5A	F:5' TGTGTGGGAAGAAACTGAGTCATC 3' R:5' AGGAATACCAAAAGAAGCAAACCAAC 3'
barc 110	ned	5B	F:5' CCCGAACAATGGCTTTGGTGTCGTAAT 3' R:5' CATGGTGACGGCAAGTGTGAGGT 3'
gwm 339	vic	2A	F:AATTTTCTTCCTCACTTATT R:5`AAACGAACAACCACTCAATC 3`
gwm 160	vic	4A	F:5' TTCAATTCAGTCTTGGCTTGG 3' R:5' CTGCAGGAAAAAAAGTACACCC 3'
gwm 458	6 fam	1D	F:AAT GGC AAT TGG AAG ACA TAG C R:TTC GCA ATG TTG ATT TGG C
gwm 631	pet	7A	F:GGT GAA GCA AGT TAG GCC TG R:GCG GGA GTA AGT TCT CAC GT
gwm 619	ned	2B	F:CAT CAT CGG TTC TTG GA F:AAA AGA AGC AAG AAA GAA AC
gwm 261	pet	2D	F:CTC CCT GTA CGC CTA AGG C R:CTC GCG CTA CTA GCC ATT G
gwm 636	vic	2A	F:5' CGGTAGTTTTTAGCAAAGAG 3' R:5' CCTTACAGTTCTTGGCAGAA 3'
gwm 11	6 fam	1B	F:5` GGATAGTCAGACAATTCTTGTG3` R:5` GTGAATTGTGTCTTGTATGCTTCC3`
gwm 357	vic	1A	F:TAT GGT CAA AGT TGG ACC TCG R:AGG CTG CAG CTC TTC TTC AG
gwm 495	6 fam	4B	F:5' GAGAGCCTCGCGAAATATAGG 3' R:5' TGCTTCTGGTGTTCCTTCG 3'
gwm 389	vic	3B	F:ATC ATG TCG ATC TCC TTG ACG R:TGC CAT GCA CAT TAG CAG AT
gwm 680	6 fam	6B	F:GGA AAA GAA TTC TCT TGC TT R:TTT GTG CAC CTC TCT CTC CC
gwm 437	6 fam	7D	F:GAT CAA GAC TTT TGT ATC TCT C R:GAT GTC CAA CAG TTA GCT TA
gwm 190	pet	5D	F:GTG CTT GCT GAG CTA TGA GTC R:GTG CCA CGT GGT ACC TTT G
gpw 3017	pet	4B	F:GTTTGTCGGTCGTGAAGGTT R:TGCGTTGGTTTGTCTACTGG
cfa 2114	ned	6A	F:5` ATTGGAAGGCCACGATACAC 3' R:5' CCCGTCGGGTTTTATCTAGC 3'
cfa 2155	pet	5A	F:5' TTT GTT ACA ACC CAG GGG G 3' R:5' TTG TGT GGC GAA AGA AAC AG 3'

Statistical tools

Minimum, maximum, mean values and variance were calculated as indicators of trait variability (data not shown). These statistical calculations were done using StatSoft, Inc. (2011), STATISTICA (data analysis software system), version 10 (www.statsoft.com). Genotype by environment interaction (GE) was tested using AMMI (Additive Main Effects and Multiplicative Interaction) analysis by ZOBEL *et al.* (1998). Data processing was performed in GenStat 9th Edition VSN International Ltd (www. vsn-intl.com). Results of AMMI analysis have been shown through AMMI1 and AMMI2 biplot.

The population structure based on genetic data was estimated by the Bayesian algorithm implemented in the Structure software, version 2.3.4 (PRITCHARD *et al.*, 2000). The hypothetical number of clusters was set ranging from 1 to 10, whereas the length of the burn- in and the Markov chain Monte Carlo were determined at 100.000. The real number of subpopulations was obtained by comparing log probabilities of data Pr [X|K]. Corrections were done according to EVANNO *et al.* (2005). The marker- trait associations were analyzed in the Tassel software, version 2.1. (BRADBURY *et al.*, 2007) using two models: GLM and MLM (YU *et al.*, 2006). The Q matrix for further association analysis was determined based on the average value of three iterations of log probability of data obtained by the Structure software (PRITCHARD *et al.*, 2000).

RESULTS AND DISCUSSION

Within a single genetic system, two basic genetic systems which control the yield formation can be defined: (1) the gene system responsible for adaptability (2) the gene system responsible for potential productivity (yield *per se*) (ELEKHDAR *et al.*, 2017). The genetic basis of traits which determine adaptability and yield potential is quantitative and qualitative. Although some important processes which control yield are inherited qualitatively, most of the traits are influenced by minor genes. Method of determining the genetic potential for yield per unit is consisted in studying the genetic basis of individual yield components their interaction as well as interaction with the environment (DIMITRIJEVIĆ *et al.*, 2011). By some authors yield variability depends on the environmental performance rather than the effect of genotype (DIMITRIJEVIĆ *et al.*, 2011; BANJAC *et al.*, 2014; MITROVIĆ *et al.*, 2016). On the other side the complexity of the yield as a trait is also indicated by the results of MLADENOV *et al.* (2011) and LJUBIĆIĆ *et al.* (2016) where the largest share of variability of this trait belongs to the GE interaction.

AMMI analysis of yield variance revealed that the share of the main effects in total was 44.9%. Thereof share of genotype is higher and amounts 24.84%, while the share of environments was 21.06%. The GE interaction was also statistically significant and amounts 51.58% of the total variance (Tab. 3).

Large differences among sites and vegetation seasons have caused a high sum of environmental factors in the overall variation of the experiment and led to the fact that they are the most responsible for variations in yield. In the further stream of analysis, sum of square of the GE interaction was parsed on two significant IPCA axes, which explain the majority of multivariate effect. Observing the AMMI1 biplot, large dispersion of genotype and environment points is observed. For genotypes there are larger differences in the additive effect than in multivariate part of the variance (Fig. 1a). Dispersion of environmental points indicates that there was a noticeable difference among sites and vegetation seasons and that influence of sites in the overall variance of yield was high. Only in E1 low value of interaction was achieved, while the remaining three environments (E2, E3 and E4) expressed high values of interaction.

Table 3. AMMI analysis of variance for yield for 94 genotype of wheat (Triticum vulgare L.) and by one genotype of T. spelta L. (Nirvana) and T. compactum Host (Bambi) grown in two years (2011/2012. i 2012/2013.) across two locations (Novi Sad i Sremska Mitrovica)

| Source of variation	Degrees of freedom	Sum of square	Middle of square	F value	F table		Share in variation %
					0,05	0,01	
Total	1535	4895	3.19	-	-	-	100
Treatmens	383	4772	12.46	117.03**	1,00	1,00	97.49
Genotypes	95	1216	12.8	120.18**	1,00	1,00	24.84
Environments	3	1031	343.8	2685.09**	2.6	3.78	21.06
Blocks	12	2	0.13	1.2	1.75	2.18	0.04
Interaction	285	2525	8.86	83.22**	1,00	1,00	51.58
IPCA$_1$	97	1152	11.88	111.58**	1,00	1,00	45.62
IPCA$_2$	95	781	8.22	77.16**	1,00	1,00	30.93
Residue	93	592	6.37	59.82**	1,00	1,00	-
Error	1140	121	0.11	-	-	-	-

** $p<0,01$
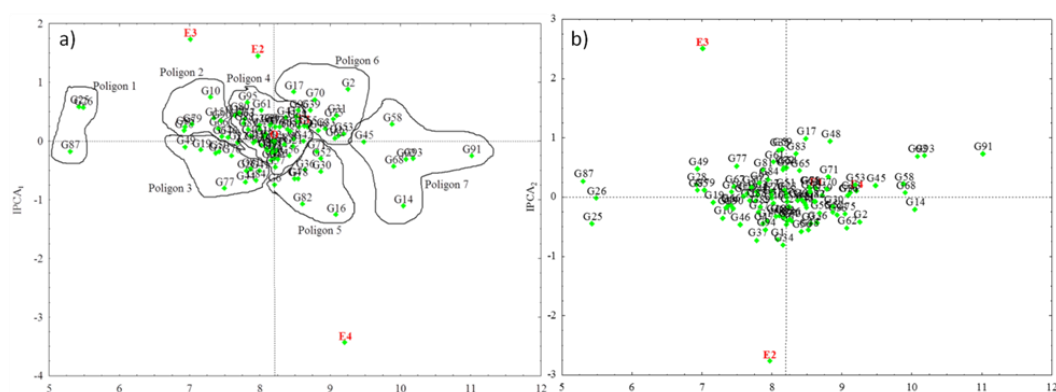
Figure 1. AMMI1 (a) and AMMI2 (b) biplot of 94 genotype of wheat (*Triticum vulgare* L.) and by one genotype of *T. spelta* L. (Nirvana) and *T. compactum* Host (Bambi) grown in two years (2011/2012. i 2012/2013.) across two locations (Novi Sad i Sremska Mitrovica)

The genotypes were divided into seven groups on AMMI1 biplot. Cultivars from first group; Nirvana, Bambi and Heys2 have achieved the lowest yield in the entire experiment. Representatives of this group have not been designed for intensive agricultural production and understandable is that they achieve less average grain yield compared to intensive wheat cultivares. Cultivars and lines that achieved the highest yield were in group seven and were led by Tiha, Zlatka, NS 706, Balada, NS 48/08 and NS Nena. In group four genotypes that achieved lowest values of interaction (under 0.1) were placed (Sonata, Cipovka, Dragana, Jefimija,

Simonida, Astra, Helena, Gordana, NS Nena, NS Tavita, NS36/10, NS 151/10 and Mina). Highest values of the interaction and most unstable reaction expressed cultivars Tamiš, Arija, Balada and Renesansa. It is cognized that AMMI1 analysis quantified genotypes as a primary source of variance, but other source of variation was left to determine and it was done by AMMI2 analysis. According to AMMI2 biplot, there was an irregularity in groups of environment points (Fig. 1b). That indicates on necessity to identify specifically for each environment that could lead to displayed distribution and realized interaction. Positive values of interaction were noted for environments E3, E1 and E4. In addition to this, genotypes achieved a higher yield than the experiment average in the environments E1 and E4. Small interaction values which indicate a stable reaction of genotypes in these conditions were obtained for environments E1 and E4. Contrary to that, highest interactions were noted in environments E3 and E2, most unfavorable environments for achieving high yield.

Large number of genotypes expressed lower yield in the first year of experiment, in which drought prevailed in South Pannonian Basin, on Sremska Mitrovica, where quality of land structure is bellow quality in Novi Sad (data not shown). What wheat breeding is tending to achieve, in addition to high yield, is the creation of a stable cultivar in different environments. The model of the cultivar that DONALD (1968) called idetype is the one that gives maximum yield in certain environments. Geneticist, breeders and physiologist seek to present yield as a *super*-trait which is the result of the action of multiple yield components. The final yield of wheat expressed in $g \cdot m^{-2}$ presents multiplication of number of spikes per m^2, number of kernels per spike and average grain weight. Number of spikes per m^2 is the result of sowing density i.e. number of plants per m^2, genetic potential of spawning and number of productive spikes (MIROSAVLJEVIĆ, 2016). The number of spikes per unit area is in negative correlation with the number of grains per spike, yield and the average mass of spike (BRDAR *et al*., 2006; RATTEY *et al*., 2011; SLAFER *et al*., 2014). This means that if the breeder increases one of the yield components some other will decrease and result in an unwanted yield fall. Traits like number of spikes per m^2 and the number of kernels per spike vary in different agroecological environments, but also from sowing density (COSSANI *et al*., 2011). However, the effects of low sowing standard and rare assembly can be compensated by increasing number of total and productive spikes per plant. The share of environments in the AMMI analysis of 21.06% is a confirmation of that assumption.

Distribution of 96 investigated genotypes in two groups was based on the polymorphism of 28 microsatellites tested (Fig. 2).

Subpopulation 1 counts more members (73) while subpopulation Q2 is composed of 23 genotypes. Division into groups was performed on the basis of the lineage. Association analysis is a unified mathematical model, which simultaneously processes datafrom phenotypic and molecular markers. The use of this model allows one to determine which molecular marker is in the relation to phenotype trait and it shows the strength of their interrelation. Two models were used, the GLM (*General Linear Model*) and MLM (*Mixed Linear Model*). Both of these models have the same purpose, but analyzes have been done to increase accuracy. In used models „*rare alleles*" were excluded (frequency below 5%). Selection of microsatellites used in this study was made on the basis of the previous data in the literature (RODER *et al*., 2002; BRBAKLIĆ *et al*., 2015; TRKULJA, 2015).
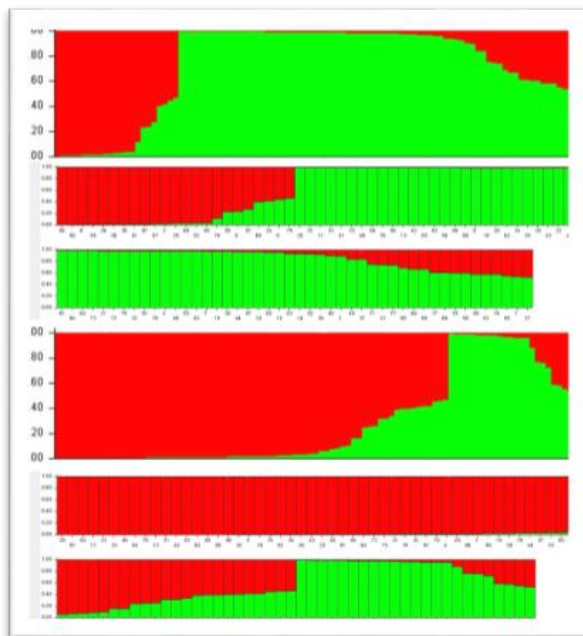
Figure 2. Members of two subpopulations (Q1 and Q2) for 94 genotype of wheat (*Triticum vulgare* L.) and by one genotype of *T. spelta* L. (Nirvana) and *T. compactum* Host (Bambi). Q1 green colour; Q2 red colour.

Table 4. Relation marker-trait among 28 microsatellites and wheat yield of 94 genotypes of winter wheat (*Triticum vulgare* L.) and by one genotype of *T. spelta* L. (Nirvana) and *T. compactum* Host (Bambi) using *GLM* (General Linear Model) and *MLM* (*Mixed Linear Model*) across four environments (E1 – Novi Sad 2011/12.; E2 – Novi Sad 2012/13.; E3 – Sremska Mitrovica 2011/12.; E4 – Sremska Mitrovica 2012/13.)

Chromosome	Microsatellite	Environment	GLM p marker	MLM p marker
1A	gwm357	E2	0.0237	0.0313
2A	gwm339	E4	0.0076	0.0092
2A	gwm339	E1	0.0434	-
2A	gwm636	E1	0.0333	-
6A	cfa2114	E1	0.006	0.0316
6A	wmc553	E1	0.0325	-
7A	gwm631	E1	0.0069	0.0456
1B	gwm11	E1	-	0.0488
2B	gwm619	E4	0.0332	-
4B	gwm495	E1	2.11E-04	0.0009
5D	gwm190	E1	2.85E-04	0.0488
6D	barc1121	E4	0.0084	0.0220
6D	barc1121	E1	0.0144	0.0439
7D	gwm437	E1	0.011	0.0154

Using GLM model 13 positive relationships among traceability and molecular markers were recorded, while using MLM model, this number was 10 (Tab. 4). Microsatellites that exibited a relation with yield in both models were: gwm357, gwm339, cfa2114, gwm631, gwm495, gwm190, barc1121 and gwm437, which is in partial accordance with ALSALEH *et al.*, (2015); ZHANG *et al.*, (2015); BRBAKLIĆ *et al.*, (2015); TRKULJA (2015); JOSHI and KNECHT (2013).

Markers assisted selection and use of new techniques in wheat breeding have largely changed access to a scientific research centers around the world. However, it is often a matter of attribution too much importance to the use of molecular technologies in breeding programs, to the limit that some authors claims that the environment share can be fully excluded, when microsatellites are used (XU and CROUCH, 2007; BERTRAND and MACKILL, 2008; SCORZZARI *et al.*, 2014). Such assertions are in the opposite to the results of this study, where markers were not exhibit links at a level of statistical significant lower than 5% in all environments, but only in some. Markers that have demonstrated the stability of the relationship with yield in different environments can be recommended as potentially useful in wheat breeding.

CONCLUSION

AMMI analysis of yield variance revealed that the share of the main effects in total was 44.9%. Thereof share of genotype is higher and amounts 24.84%, while the share of environments was 21.06%. The GE interaction was also statistically significant and amounts 51.58% of the total variance. Using GLM model 13 positive relationships among traceability and molecular markers were recorded, while using MLM model, this number was 10. Microsatellites that exibited a relation with yield in both models were: gwm357, gwm339, cfa2114, gwm631, gwm495, gwm190, barc 1121 and gwm437. The results of this and similar researches need to be expanded and directed towards most important step in future crossings, which is choice of parents.

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AGRONOMSKE OSOBINE SORTI PŠENICE I NJIHOVA MOLEKULARNA KARAKTERIZACIJA

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Izvod

Stvaranje novih prinosnijih sorti pšenice, otpornijih na bolesti i prilagođavanje istih globalnim promenama klime su samo neki od zadataka koje oplemenjivanje biljaka ima pred sobom. Ciljevi ovog rada su bili da se proceni GE interakcija u dve različite vegetacione sezone na dva lokaliteta i prikazati združenu analizu agronomskih ispitivanja kroz rezultate iz polja i molekularnih ispitivanja. U radu je korišćeno 96 genotipova pšenice, gajene tokom 2011/12 i 2012/13 na dva lokaliteta u južnom delu Panonske regije. Populacija je profilisana sa 28 molekularnih markera (mikrosatelita). Kod procene prinosa, udeo genotipa je bio visok i odneo je 24.84% ukupne fenotipske varijanse, dok je udeo agroekoloških sredina bio 21.06%. Udeo GE interakcije je takođe bio statistički značajan i izneo je 51.58% ukupne varijanse. Mikrosateliti koji su ostvarili jaku statističku vezu sa prinosom u dva modela (GLM i MLM) su bili: gwm357, gwm339, cfa2114, gwm631, gwm495, gwm190, barc1121 i gwm437. Mikrosateliti koji su iskazali jaku vezu i stabilnost sa prinosom u različitim agroekološkim uslovima mogu da se preporuče kao korisni u daljem oplemenjivačkom radu.