Journal of Microbiology, Biotechnology and Food Sciences

Gregová et al. 2012 : 1 (February Special issue) 616-621

REGULAR ARTICLE

DETERMINATION OF THE WHEAT-RYE TRANSLOCATION 1BL.1RS AMONG REGISTERED BREAD WHEAT VARIETIES OF SLOVAKIA

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ABSTRACT

Genomes of wheat varieties provide an available and highly efficient polymorphic system of genetic markers. Suitable protein markers in wheat are endosperm storage proteins:gliadins and glutenins.The objective of this study was to determine the composition of high molecular weight glutenin subunits and presence or absence of economically relevant *Gli-1B3*gliadin block of 41 Slovak varieties of hexaploid wheat (*Triticumaestivum* L.) included in the List of Registered Varieties from 2010. Gliadin polymorphism was detected by electrophoresis according to the PAGE ISTA methodology. HMW-GS were assessed using the SDS-PAGE method. The allelic block *Gli-1B3*, the marker of rye translocation 1BL.1RS, also the marker of poor bread-making quality was detected in 6 genotypes (Bonita, Lívia, Malvína, Sana, Verita and Veldava). Fourteen high molecular weight (HMW) - glutenin subunits (GS) were found, three belonged to *Glu-1A*, seven to *Glu-1B* and four to *Glu-1D* locus. The most frequent (37%) HMW-GS at the *Glu-1A, Glu-1B* and *Glu-1D* complex loci were 0, 7+9, 5+10, respectively. However, low frequent alleles such as 17+18 and 20 were observed. Bread quality (class) in examined accession varied from minimum value 1 to maximum value 9. The glutenin-based quality score ranged from 4 to10.

Keywords: bread wheat, HMW-GS, 1BL.1RS translocation, *Glu-score, Rye-score*

INTRODUCTION

The proteins in wheat are encoded by gene clusters located on chromosomes of group 1 and 6, with *Gli-1* and *Gli-2* encoding for gliadins, and *Glu-1* and *Glu-3* encoding for glutenins. The most widely accepted classification puts prolamins into three functional classes: high molecular weight glutenin sub units (HMW-GS), low molecular weight glutenin sub units (LWM-GS) and gliadins. The two types of glutenins are the only prolamins that are able to for minter chain disulfidebridges, which make up the gluten back bone. Gliadins produce only weak hydrogen bonds with the other prolamins. **Andersonet al. (1989)** reported the presence of an extra cysteine residue in the central domain of sub unit 1 Dx5. This explained the positive impact of this sub unit on quality and proved that cross linking is critical for dough rheology (**Shewry*et al.*,1992**). In the basic catalogue of HMW-GS alleles **Payne and Lawrence (1983)** identified 3 HMW-GS alleles at the *Glu-1A* locus, encoding HMW-GS 1 and 2*. The third allele is the null form. They identified 14 alleles at the *Glu-1B* locus coding for a single HMW-GS or a pair of HMW-GS and 7 alleles at the *Glu-1D* locus encoding single HMW-GS or HMW-GS pairs. A correlation has also been drawn between the presence of specific HMW-GS alleles and bread-making quality and most *Glu-1* alleles have been given a score on the basis of their impact on the sodium dodecyl sulphate (SDS) sedimentation volume or gluten strength, as measured by alveograph parameter W (**Payne, 1987; Pogna *et al.*, 1989**). End-usequality differences, related to the qualitative allelic variation of glutenins and gliadins, were investigated (**Bradová and Štočková 2010; Gálová *et al.*, 2002**).

MATERIAL AND METHODS

In this study we analyzed seed storage proteins extracted from bread wheat (*Triticumaestivum* L.) grain. All samples were obtained from the collection of genetic wheat sources of the Gene Bank of the Slovak Republic in Piešťany and from the work wheat collection. Seed storage proteins were isolated from the endosperm of intact, dry and mature single seeds. Seed homogenization was carried out by grinding. Glutenins were extracted by standard referee method ISTA **(Wrigley, 1992)**. Gliadins were obtained using standard referee method ISTA in the presence of acid solution **(Draper, 1987)**. The glutenin separation was performed by discontinuous PAGE based on ISTA methodology (**Wrigley, 1992**) and using the electroseparatic unit Protean II (Biorad). The electrophoretic separation of gliadins

was followed by referee method ISTA **(Draper, 1987)** using mixture of glycine and acetic acid as electrolyte at pH 3.2. They were separated in continuous polyacrylamide gels at acid environment. Protein fractions were stained by Coomassie Brilliant Blue R-250. The separated glutenin subunits were identified by the nomenclature of **Payne and Lawrence (1983)**. According to the specific protein profile of the HMW alleles in each cultivar its quality scores (Glu-score, Rye score) were calculated by **Payne *et al.* (1987)**.

RESULTS AND DISCUSSION

Rye (*Secalecereale*L.) is a valuable source for alien chromosome translocations in wheat breeding, due to its capability to grow and sustain under inhospitable environmental conditions. Wheat germplasm with 1AL.1RS and 1BL.1RS wheat-rye chromosome translocations have been used worldwide by breeders. Determining 1AL. 1RS and 1BL. 1RS translocations in wheat is therefore important practical value for wheat improvement. Protein analyses primarily rendered data concerning the presence of high-molecular-weight glutenin subunits, and genes at *Glu-1A*, *Glu-1B*, *Glu-1D* loci encoding these HMW-GS as well as the information on presence or absence of economically relevant *Gli-1B3* gliadin block, also referred to as “rye translocation” - see Table 1. Moreover, the frequency of HMW-GS allele *Glu-1B* 7+8is increasing in Slovak wheat cultivars. This *Glu-1B* 7+8 *allele is* present in recently registered cultivars, including elite quality cultivars Axis, Alacris and Bona Dea.In addition calculated values *Glu-score* and *Rye-score* are available for each cultivar. These values correlate with wheat flour bread-making quality and can be used for prediction. The analyzed collection of wheat *Triticumaestivum* L. ssp. *aestivum* contained the following most frequently occurring alleles at individual loci: allele 0 (locus *Glu-1A*), allele 7+9 (*Glu-1B*) and allele 5+10 (*Glu-1D*). These alleles also constituted the most frequent HMW-GS genotype and phenotype – 0, 7+9, 5+10. The above-mentioned HMW-GS composition was found in 41.4% of all *Triticumaestivum* L. ssp. *aestivum* genotypes analyzed. We found altogether 10 different combinations of HMW-GS genotypes and phenotypes occurring at various frequencies. An interesting finding was that the collection of 41 genotypes with *Glu-1A* 2* had only the *Glu-1D* 5+10 allelic block present at the *Glu-1D* locus. Simultaneously, a favourable combination with *Glu-1B* – 7+9 or 7+8 was present. Therefore, such genotypes achieved the highest Glu-score values. The *Glu-1A* 1 allelic block occurring in 7 genotypes was combined with *Glu-1D* 5+10 in all cases. Most genotypes (75.6%) had the 0 subunit at the *Glu-1A* locus, which has no relevance to superior bread-making quality. The presence of

Gli-1B3 secalin allelic block (bread-making quality inhibitor) is a consequence of translocation of a rye chromosome segment into the wheat genome (*1RS/1BL*). Efficiency of the *Gli-1B3*secalin allele in marking low bread-making quality was confirmed by **ČernýandŠašek (1995)**. Even a cursory glance on the frequency of individual HMW-GS in all loci of Slovak wheat cultivars reveals a successful track record of Slovak wheat breeding and its success in creating cultivars with high bread-making quality. This can be seen particularly in allele distribution at *Glu-1B* and *Glu-1D* loci where HMW-GS have a negative impact on quality, mainly alleles at the *Glu-1B* 6+8 locus (2.4%) and *Glu-1D* 2+12 locus (17%) which occur at substantially lower rate than in West European cultivars.

Table 1 HMW glutenin composition and quality scores of wheat cultivars

Genotype	Glu-A1	Glu-B1	Glu-D1	Glu-score	Rye-score	Qualityscore
KOŠÚTKA	0	7+9	5+10	7	7	7
VIGINTA	0	7+9	5+10	7	7	7
ILONA	2*	7+9	5+10	9	9	7
LÍVIA	0	7+9	5+10	7	5	4
BLAVA	0	7+9	5+10	7	7	7
TORYSA	0	7+8	2+12	6	6	4
SANA	0	7+9	2+12	5	3	1
ASTELLA	0	7+9	5+10	7	7	6-7
MALVINA	0	7+8	2+12	6	4	x
KLEA	0	7+9	5+10	7	7	7-8
ZERDA	0	7+9	5+10	7	7	6-7
ARIDA	0	7+9	5+10	7	7	6-7
EVA	0	7+9	5+10	7	7	7
MALYSKA	0	6+8	5+10	6	6	3
VANDA	0	7+9	2+12	5	5	7
VELTA	1	7+9	5+10	9	9	5
ARMELIS	0	7+9	5+10	7	7	7
VENISTAR	0	7+9	5+10	7	7	4
PETRANA	0	7+9	5+10	7	7	7
AXIS	2*	7+8	5+10	10	10	8-7
BONITA	0	7+9	5+10	7	5	7
VIADOR	2*	7+9	5+10	9	9	7
IGNIS	0	7+9	5+10	7	7	5
STANISLAVA	0	7+9	5+10	7	7	6
VERITA	0	7+9	2+12	5	3	5-6
MARKOLA	0	7+8	5+10	8	8	5
VELDAVA	0	20	2+12	4	2	3
PAVLINA	0	7+8	5+10	8	8	4
ALACRIS	0	7+8	5+10	8	8	8
BONA DEA	0	7+8	5+10	8	8	8-9

GENOVEVA	0	7+9	2+12	5	5	6-7
IS KARPATIA	0	7+8/7+9	5+10	8,7	8,7	8-9
ŠARLOTA	1	7+9	5+10	9	9	4
IS BONNET	1	7+9	5+10	7	7	6-7
KLAUDIA	1	17+18	5+10	10	10	4
IS MEDIAN	0	7+8	5+10	8	8	7-8
IS EZOPUS	1	7+9	5+10	9	9	8-9
IS QUESTOR	1	7+9	5+10	9	9	7-8
SILVANUS	0	7+9	5+10	7	7	5-6
VÍGLANKA	0	7+9	5+10	7	7	7-8
VIOLA	1	7+8	5+10	10	10	5-6

On the other hand, HMW-GS with a positive impact on quality – alleles 7+8, 7+9 and 5+10, prevail. **Payne *et al.* (1979)** were the first to discover that HMW-GS 5+10 at the *Glu-1D* locus occurred in wheat with high bread-making quality and subunits 2+12 in wheat with low bread-making quality. This discovery was subsequently confirmed by several authors **Gálová*et al.* (1998)** and **BradováandŠašek(2005)**.Future prospects of Slovak wheat breeding as regards bread-making quality improvements can be seen in a high frequency of occurrence of the null allele at *Glu-1A* locus. For any further improvement of bread-making qualities in wheat cultivars, it will be necessary to replace the null allele with alleles 1* and 2 or with any other known alleles that have not been utilized in crop breeding so far.

Acknowledgments: This work was supported by OP Research and Development:
Development of new types of genetically modified plants with agricultural characters. No: ITMS 26220220027 from European Regional Development Fund.

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