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The role of wheat-rye translocation 1Bl.1Rs in wheat breeding program development of Novi Sad (Serbia)

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ABSTRACT

In the second half of 1950's, a plan to make Yugoslavia self sufficient in main crop production included all the plant breeding institutions all over the country. The Institute for Agricultural Research in Novi Sad, Serbia (today Institute for Field and Vegetable Crops Novi Sad - IFVCNS) was one of the scientific institutions included in this program. The wheat, as the main bread making crop, had a particular place in the State project. For the next 30 years the task had been not only fulfilled, but also surpassed, by far. The IFVCNS developed a very successful wheat breeding program, creating a number of high yielding, quality wheat varieties. Wheat-Rye translocation 1Bl.1Rs played a notable role in obtaining desirable genetic variability in wheat. A sample of 139 varieties of common wheat (*Triticum aestivum* L.), predominantly Serbian winter wheat varieties originated in the Institute of Field and Vegetable Crops in Novi Sad, has been examined for presence of 1Bl.1Rs wheat-rye translocation. Two large groups consisting of varieties possessing and lacking the translocation, have been compared for 20 traits and grain yield. Grain physical, chemical and technological properties, as well as, rheological results of dough, and bread baking parameters were studied. The influence of 1Bl.1Rs translocation was alsostudied in a light of wheat seed storage protein quality genetic background composition. Genotypes with and without translocation differed in observed values for the studied traits. These effects were slightly modified depending on the examined quality genetic background.

KEY WORDS: 1Bl.1Rs, translocation, wheat, rye, breeding

Introduction

The achievement of higher yield or better quality, or both has been a long time determined aim of plant breeding, and wheat breeding in particular. Wheat breeding has been progressing, step by step, by the innovation acceptance and new technologies acquiring. In past decades a scientific breakthrough has been made in molecular genetics and genomics resulting in DNA marker application in so called genomic and marker assisted (MAS) selection (Collard, and Mackill, 2008; Kiszonas, and Morris, 2017; Xu *et al*., 2020). However, there are still some issues in MAS that required to be solved, particularly concerning its application in complex quantitative traits, of the lower heritability, selection (Hospital, 2008; Xu, and Crouch, 2008; Fasoula*et al*., 2020). Hence, phenotypic screening is still a fundamental wheat breeding approach, since it reflects not only genetic background variation, but also genotype by environment interaction. Moreover, while MAS is still to be proven as widely applicable approach in plant breeding, phenotypic screening literally piggybacked the whole Green Revolution, fighting the famine and increasing the yield of cereals up to 200% comparing to 1961. The illustration of successful phenotyping approach is broadening genetic variability in Novi Sad's wheat breeding program by introducing and selecting wheat/rye translocation 1Bl.1Rs. The aim of this article is to present the role of 1Bl.1Rs translocation in yield increment and to reconcile high yield and quality in the Wheat Breeding Program of the Institute of Field and Vegetable Crops in Novi Sad, Serbia.

Material and Methods

A set of 139 wheat varieties/lines originated in a wheat-breeding program of the Institute for Field and Vegetable Crops in Novi Sad, from 1961 to early 90's, was screened for presence of the 1Bl.1Rs wheat/rye translocation using 10% SDS-PAGE following the rye gliadin secalin in the wheat genetic background and C-banding technique. HMW glutenin subunit composition was determined using 18% SDS-PAGE. Varietal trait data were obtained from the Yugoslavian Federal Committee for Varieties Releasing. The method in details is given in Dimitrijević (1997), and Dimitrijević*et al.* (2008).

Results and Discussion

Wheat/rye translocation 1Bl.1Rs, originated from German cv. Neuzucht, came into Novi Sad's Wheat Breeding Program through Lutescens 314h147 i.e. Soviet varieties Aurora and Kavkaz, as well as, Eritrospermum 315h60 i.e. Soviet variety Skorospelka 35 (Dimitrijević, 1997). Introduced at the end of 70's, the translocation was presented in about 40% of the examined wheat variation (tab. 1).

Table 1.
A comparison of 139 examined wheat varieties and lines grouped according to the presence/absence of wheat rye translocation 1Bl.1Rs, and the high molecular weight glutenin. (HMW) subunits *Glu-D1* locus allelic variation (5+10 vs. 2+12). The differences between groups were tested at the high statistical significance level of 5% and marked with an asterisk (higher values are bolded), where n is the number of compared genotypes, and $\bar{\mathbf{X}}$ – mean value.
Tabela1.
Poređenje 139 ispitivanih sort i linija pšenice, grupisanih po prisustvu/odsustvu pšenično/ražene translokacije 1Bl.1Rs i podjedinica velike molekulske mase Glu-D1 lokusa (5+10 vs. 2+12). Razlike između grupa su testirane na nivou visoke statističke značajnosti (0.05) i označavane su zvezdicom (*), više vrednosti su napisane masnim slovima, gde je n broj upoređivanih genotipova, a $\bar{\mathbf{X}}$ – srednja vrednost.

Traits	+1Rs.1Bl			-1Rs.1Bl		5+10			2+12	
	n	$\bar{X}$		n	$\bar{X}$	n	$\bar{X}$		n	$\bar{X}$
Physical										
Hectoliter mass (HLM)	39	**82.34**	*	100	80.96	89	**81.97**	*	45	80.35
Absolute mass (ABM)	39	**35.28**	*	100	33.84	89	**34.73**	*	45	33.44
Glassiness (GLS)	39	56.79		97	49.89	88	52.13		43	52.05
Chemico-technological										
Crude protein (CPN)	39	13.35		100	13.62	89	13.30	*	45	**13.97**
Sedimentation (SDM)	38	35.68	*	86	**44.57**	81	41.96		38	41.76
Flour extraction (FEX)	39	75.95		95	76.25	87	**76.46**	*	42	75.52
Wet gluten content (WGN)	39	27.15	*	100	**28.67**	89	27.39	*	45	**29.75**
Dry gluten content (DGN)	39	9.29	*	99	**9.93**	89	9.46	*	44	**10.23**
Maltose content (MAL)	38	**3.14**	*	86	2.75	81	2.90		38	2.84
Farinograph										
Water absorption (FWA)	39	61.65		99	60.63	88	60.78		45	61.19
Dough development (DDV)	39	**3.39**	*	98	2.69	88	**3.04**	*	44	2.59
Dough stability (DST)	39	2.30	*	95	**3.09**	87	**3.04**	*	42	2.37
Softening degree (SDG)	39	63.92		99	58.37	88	56.49	*	45	**67.53**
Quality number (QNO)	39	66.36		100	67.91	89	**69.24**	*	45	63.46
Extensogram										
Energy (ENE)	39	59.74	*	94	**94.84**	87	86.41		41	80.71
Resistance to extension (R)	39	258.23	*	94	**338.33**	87	**326.54**	*	41	291.95
Extensibility (E)	39	140.10	*	94	**157.78**	87	151.23		41	155.10
E/R	39	1.88	*	94	**2.23**	87	**2.22**	*	41	1.97
Baking test										
Bread yield (BY)	39	137.23	*	100	**138.68**	89	138.20		45	138.40
Bread volume yield (BVY)	39	462.13		100	456.80	89	**466.62**	*	45	440.00
Bread crumb quality number (BCQN)	38	3.89		86	4.13	81	**4.32**	*	38	3.52
Yield (3 years)										
Average grain yield (YLD)	39	**6475.72**	*	100	6011.86	89	6208.45		45	6027.22

The National Wheat Breeding Program, established at the end of 50's in S.F.R. Yugoslavia aiming to secure the independence in wheat i.e. bread production had two selection criteria – the high yield, firstly, and the good quality, secondly. Wheat breeders had tried to reconcile these two, negatively correlated, complex or "super" traits, relying on the phenotypic screening, and the quantitative and population genetics methods. Using knowledge, experience, instinct, creativity, and "naked eye" Novi Sad's wheat breeders of that time, unmistakably selected parental combinations and phenotypic variation in early generations of progenies that could provide both, through 1Bl.1Rs wheat rye translocation, and the high molecular weight (HMW) glutenin variation at the *Glu-A1*, *Glu-B1* and *Glu-D1* loci. Later on, when it was enough measurements and laboratory analyses proved them right. Hence, the favorable*Glu-D1* HMW glutenin subunit variation 5+10 appeared in about two thirds of the examined wheat varieties/lines, and about in 30% of this representative set of wheat variation combined with 1Bl.1Rs translocation (tab. 1, tab 2).

Table 2.
A comparison of 139 examined wheat varieties and lines grouped according to the presence/absence of the high molecular weight glutenin. (HMW) subunits *Glu-D1* locus allelic variation 5+10 and 2+12, with and without wheat rye translocation 1Bl.1Rs[1]. The presence/absence of the translocation was followed by the presence (Sec+), or absence (Sec-) of the rye protein secalin, the product of allelic variation of the rye gene *Sec-1*, present in the wheat genome on the long arm of 1B chromosome in case the 1Bl.1Rs wheat/rye translocation occurred. The differences between groups were tested at the high statistical significance level of 5% and marked with an asterisk (where statistically significant different averages were found, higher values are bolded). Where: n - number of compared genotypes, and $\bar{X}$ - mean value.
Tabela 2.
Poređenje 139 ispitivanih sorti i linijap šenice, grupisanih po prisustvu/odsustvu podjedinica velike molekulske mase Glu-D1 lokusa (5+10 vs. 2+12), sa i bez pšenično/ražene translokacije 1Bl.1Rs1. Prisustvo/odsustvo translokacije je praćeno na osnovu prisustva (Sec+), ili odsustva (Sec-) sekalina, protein raži, kao proizvoda alelne varijacije gena raži Sec-1, prisutnog u genomu pšenice na dužem kraku hromozoma 1B u slučaju 1Bl. 1Rs pšenično/ražene translokacije. Razlike između grupa su testirane na nivou visoke statističke značajnosti (0.05) i označavane su zvezdicom (*), više vrednosti su napisane masnim slovima, gde je n brojupoređivanih genotipova, a $\bar{X}$ – srednja vrednost.

Traits	**Glu5+10/Sec+**			**Glu5+10/Sec-**		**Glu2+12/Sec+**			**Glu2+12/Sec-**	
	n	$\bar{X}$		**n**	$\bar{X}$	**n**	$\bar{X}$		**n**	$\bar{X}$
Physical										
Hectoliter mass (HLM)	30	**82.58**	*	59	81.66	8	81.45		37	80.11
Glassiness (GLS)	30	**58.11**	*	58	49.04	8	49.93		35	52.53
Chemico-technological										
Sedimentation (SDM)	30	36.63	*	51	**45.10**	7	31.57	*	31	**44.06**
Maltose content (MAL)	30	**3.17**	*	51	2.74	7	3.00		31	2.81
Farinograph										
Dough development (DDV)	30	**3.57**	*	58	2.77	8	2.65		36	2.58
Dough stability (DST)	30	2.48	*	57	**3.34**	8	1.60	*	34	**2.55**
Softening degree (SDG)	30	62.33		58	53.47	8	70.50	*	37	66.89
Quality number (QNO)	30	68.60		59	69.57	8	57.65	*	37	**64.71**
Extensogram										
Energy (ENE)	30	61.57	*	57	**99.49**	8	55.00	*	33	**86.94**
Resistance to extension (R)	30	273.57	*	57	**354.42**	8	212.87	*	33	**311.12**
Extensibility (E)	30	138.80	*	57	**157.77**	8	143.38		33	157.94
E/R	30	2.01	*	57	**2.32**	8	1.51	*	33	**2.08**
Baking test										
Bread yield (BY)	30	137.16	*	59	**138.72**	8	137.08		37	138.68
Bread volume yield (BVY)	30	473.10		59	463.32	8	420.75	*	37	444.16
Bread crumb quality number (BCQN)	30	4.10		51	4.45	7	3.13	*	31	3.61
Yield (3 years)										
Average grain yield (YLD)	30	**6517.10**	*	59	6051.51	8	6359.75		37	5955.32

[1] The traits exhibiting statistically significant differences between mean values, at least in one pair of averages, are given in the table. All the traits where no differences were observed in all comparisons, are omitted.

The detrimental effect of 1Rs.1Bl translocation could be denoted in all the quality parameters at the significant level or as a trend. The absence of statistically significant differences may be due to an imbalance in the number of varieties in the subpopulations being compared. However, the pattern of the grain yield increment in the presence of 1Bl.1Rs translocation is conspicuous. This regularity could be observed in the different HMW glutenin subunits quality background due to allelic variation of the *Glu-A1* locus, jointly with 1Bl.1Rs translocation genotype variation. The grain yield was significantly higher in better HMW glutenin subunits genetic background 2* of *Glu-A1* locus variation (tab. 3).

Table 3.
A comparison of 139 examined wheat varieties and lines grouped according to the presence/absence of the high molecular weight glutenin. (HMW) subunits *Glu-A1* locus allelic variation 1, 2*, and N (null). The comparison of *Glu-A1* locus allelic variation with and without wheat rye translocation 1Bl.1Rs is given below[1]. The presence/absence of the translocation was followed by the presence (Sec+), or absence (Sec-) of the rye protein secalin, the product of allelic variation of the rye gene *Sec-1*, present in the wheat genome on the long arm of 1B chromosome in case the 1Bl.1Rs wheat/rye translocation occurred. The differences between groups were tested at the high statistical significance level of 5% and marked with an asterisk (where statistically significant different averages were found, higher values are bolded). Where: n - number of compared genotypes, and $\overline{X}$ - mean value.

Tabela 3.
Poređenje 139 ispitivanih sorti i linija pšenice, grupisanih po prisustvu/odsustvu podjedinica velike molekulske mase Glu-A1 lokusa (1, 2* i N-null). Poređenje varijacije Glu-A1 lokusa sa i bez pšenično/ražene translokacije je dato u nastavku 1. Prisustvo/odsustvo translokacije je praćeno na osnovu prisustva (Sec+), ili odsustva (Sec-) sekalina, protein raži, kao proizvoda alelne varijacije gena raži Sec-1, prisutnog u genomu pšenice na dužem kraku hromozoma 1B u slučaju 1Bl.1Rs pšenično/ražene translokacije. Razlike između grupa su testirane na nivou visoke statističke značajnosti (0.05) i označavane su zvezdicom (*), više vrednosti su napisane masnim slovima, gde je n broj upoređivanih genotipova, a $\overline{\mathbf{X}}$ – srednja vrednost.

Traits[2]	**1**			**2***			**N**	
	n	$\overline{X}$		**N**	$\overline{X}$		**n**	$\overline{X}$
DST	29	2.41	*	46	**3.38**	*	55	2.56
QNO	30	64.63	*	47	**70.72**		58	65.81
ENE	29	84.97		46	**90.07**	*	54	79.19
R	29	**155.86**		46	**155.67**	*	54	148.07
BCQN	28	3.70	*	41	**4.62**	*	51	3.74

Traits[2]	1/Sec+			1/Sec-		2*/Sec+			2*/Sec-		N/Sec+			N/Sec-	
	n	$\overline{X}$		n	$\overline{X}$	n	$\overline{X}$		n	$\overline{X}$	n	$\overline{X}$		n	$\overline{X}$
Physical															
HLM	23	82.06		7	80.93	16	82.41		31	81.46	16	**82.39**	*	42	80.76
GLS	23	58.20		7	53.24	16	51.76		30	53.34	16	**61.21**	*	40	46.20
Chemico-technological															
CPN	23	13.20		7	13.75	16	12.85	*	59	**13.75**	16	13.93		42	13.40
SDM	21	31.71	*	7	**44.05**	16	36.50	*	51	**46.72**	15	36.67	*	36	**43.11**
WGN	23	27.74		7	28.70	16	25.33	*	59	**29.04**	16	28.71		42	28.38
DGN	22	9.43		7	10.03	16	8.79	*	59	**10.13**	16	9.73		42	9.70
MAL	21	2.97		7	2.67	16	**3.26**	*	51	2.60	15	3.09		36	2.92
Farinograph															
DDV	22	3.21		7	2.84	16	3.38		31	2.91	16	**3.48**	*	40	2.46
DST	22	1.61	*	7	**2.66**	16	2.71	*	30	**3.74**	16	2.19		39	2.72
Extensogram															
ENE	22	54.43	*	7	**94.68**	16	61.38	*	30	**105.37**	16	60.44	*	38	**87.08**
R	22	246.43	*	7	**327.23**	16	270.94	*	30	**350.93**	16	250.69	*	38	**335.32**
E	22	141.14	*	7	**160.55**	16	139.38	*	30	**164.37**	16	140.38	*	38	**151.32**
E/R	22	1.81		7	2.12	16	1.96		30	2.21	16	1.83	*	38	**2.32**
Baking test															
BY	23	137.39		7	138.23	16	136.81	*	59	**139.56**	16	137.52		42	138.25
BCQN	21	2.67	*	7	**4.04**	16	4.58		51	4.65	15	3.74		36	3.74
Yield (3 years)															
YLD	23	6465.9		7	6122.3	16	**6571.1**	*	59	5797.3	16	6384.8		42	6122.1

[1] The traits exhibiting statistically significant differences between mean values, at least in one pair of averages, are given in the table. All the traits where no differences were observed in all comparisons, are omitted.

[2] Hectoliter mass (HLM), Absolute mass (ABM), Glassiness (GLS), Crude protein (CPN), Sedimentation (SDM), Flour extraction (FEX), Wet gluten content (WGN), Dry gluten content (DGN), Maltose content (MAL), Water absorption (FWA), Dough development (DDV), Dough stability (DST), Softening degree (SDG), Quality number (QNO), Energy (ENE), Resistance to extension (R), Extensibility (E), R/E, Bread yield (BY), Bread volume yield (BVY), Bread crumb quality number (BCQN), Average grain yield (YLD).

The moderate HMW glutenin subunits quality background was favored by selection through 7+9 subunits coming from *Glu-B1* locus. In this genetic background, 1Bl.1Rs translocation diminished most of the quality parameters, but yield appeared to be significantly higher (tab. 4).

Table 4.
A comparison of 139 examined wheat varieties and lines grouped according to the presence/absence of the high molecular weight glutenin. (HMW) subunits *Glu-B1* locus allelic variation 7, 7+9, and 7+8. The comparison of *Glu-B1* locus allelic variation with and without wheat rye translocation 1Bl.1Rs is given below[1]. The differences between groups were tested at the high statistical significance level of 5% and marked with an asterisk (where statistically significant different averages were found, higher values are bolded). Where: n - number of compared genotypes, and $\bar{X}$ - mean value.

Tabela4.
Poređenje 139 ispitivanih sorti i linija pšenice, grupisanih po prisustvu/odsustvu podjedinica velike molekulske mase Glu-B1 lokusa (7, 7+9 i 7+8). Poređenje varijacije Glu-B1 lokusa sa i bez pšenično/ražene translokacije je dato u nastavku 1. Razlike između grupa su testirane na nivou visoke statističke značajnosti (0.05) i označavane su zvezdicom (*), više vrednosti su napisane masnim slovima, gde je n brojupoređivanih genotipova, a $\bar{X}$ – srednja vrednost.

Traits[2]	7			7+9			7+8	
	n	$\bar{X}$		N	$\bar{X}$		n	$\bar{X}$
HLM	10	80.25	*	97	**81.78**	*	15	80.68
ABM	10	34.97		97	**34.34**	*	15	32.58
FEX	9	75.22		95	**76.48**	*	14	74.57
DST	9	2.68		95	**2.98**	*	14	2.07
QNO	10	63.99		97	**68.62**	*	15	61.55
BCQN	7	4.39		90	**4.21**	*	13	3.48

Traits[2]	7/Sec+			7/Sec-		7+9/Sec+			7+9/Sec-		7+8/Sec+			7+8/Sec-	
	n	$\bar{X}$		n	$\bar{X}$	n	$\bar{X}$		N	$\bar{X}$	n	$\bar{X}$		n	$\bar{X}$
Physical															
HLM	2	82.30		8	79.74	29	**82.54**	*	68	81.45	3	80.73		12	80.67
ABM	2	35.30		5	34.89	29	**35.46**	*	61	33.86	3	33.53		12	32.24
Chemico-technological															
SDM	2	35.50		5	51.80	29	36.07	*	61	**44.57**	3	33.33		10	42.30
DGN	2	10.00		8	10.25	29	9.18	*	68	**9.89**	3	9.57		11	9.35
MAL	2	3.05		5	2.78	30	**3.07**	*	61	2.79	3	**4.00**	*	10	2.63
Farinograph															
FWA	2	**62.50**	*	7	60.10	29	61.24		68	60.89	3	**64.43**	*	12	59.49
DDV	2	3.55		7	2.23	29	**3.45**	*	68	2.79	3	3.20		11	2.42
DST	2	1.85		7	2.91	29	2.45	*	66	**3.21**	3	1.70		11	2.17
Extensogram															
ENE	2	49.50		7	94.14	29	36.31	*		**95.50**	3	50.67	*	11	**96.36**
R	2	201.50		7	335.71	29	270.28	*		**339.67**	3	209.33	*	11	**338.18**
E	2	145.50		7	156.14	29	140.59	*		**158.08**	3	140.33		11	160.45
E/R	2	1.40		7	2.27	29	1.97	*		**2.23**	3	1.43		11	2.20
Baking test															
BY	2	137.9		8	137.8	29	137.00	*	68	**139.00**	3	139.47		12	137.62
Yield (3 years)															
YLD	2	6430.5		8	5709.5	29	**6496.6**	*	68	6069.6	3	6369.7		12	6035.8

[1] The traits exhibiting statistically significant differences between mean values, at least in one pair of averages, are given in the table. All the traits where no differences were observed in all comparisons, are omitted.

[2] Hectoliter mass (HLM), Absolute mass (ABM), Glassiness (GLS), Crude protein (CPN), Sedimentation (SDM), Flour extraction (FEX), Wet gluten content (WGN), Dry gluten content (DGN), Maltose content (MAL), Water absorption (FWA), Dough development (DDV), Dough stability (DST), Softening degree (SDG), Quality number (QNO), Energy (ENE), Resistance to extension (R), Extensibility (E), R/E, Bread yield (BY), Bread volume yield (BVY), Bread crumb quality number (BCQN), Average grain yield (YLD).

Finally, the behavior of 1Bl.1Rs translocation in joint allelic variation of loci *Glu-A1*, *Glu-B1*, and *Glu-D1*, reflected in Quality Score, given by Payne *et al.* (1987). Once again, the deleterious effect of the 1Bl.1Rs translocation on bread making quality parameters was noticed, as well as, the higher grain yield in the presence of translocation, which was heightened in a better quality genetic background (tab. 5).

Table 5.
A sample of 139 wheat varieties and lines are grouped according to the quality score (QS) given by Payne *et al.* (1987). QS is based on high molecular weight glutenin. (HMW) subunits allelic variation where scores 8-10 mark the best bread making quality, and 3-4 the worst. The QS variation with (WRT+) and without (WRT-) wheat rye translocation 1Bl.1Rs is given below. The differences between groups were tested at the high statistical significance level of 5% and marked with an asterisk (where statistically significant different averages were found, higher values are bolded)[1]. Where: n - number of compared genotypes, and $\bar{X}$ - mean value.

Tabela5.
Uzorak od 139 sorti i linija pšenice je grupisan na osnovu ocene kvaliteta (QS), prema Payne et al. (1987). QS je baziran na varijaciji podjedinica velike molekulske mase, gde ocena 8-10 predstavlja najbolji kvalitet hleba, a 3-4 najlošiji. Varijacija QS sa (WRT+) i bez (WRT-) pšenično/ražene translokacije 1Bl.1Rs je data u nastavku. Razlike između grupa su testirane na nivou visoke statističke značajnosti (0.05) i označavane su zvezdicom (*), više vrednosti su napisane masnim slovima, gde je n broju poređivanih genotipova, a $\bar{X}$ – srednja vrednost.

Traits^2	**Glu Score 8-10**			**Glu Score 5-7**			**Glu Score 3-4**	
	n	**$\bar{X}$**		**n**	**$\bar{X}$**		**n**	**$\bar{X}$**
ABM	66	34.06		60	34.15	**	5	**38.48**
FEX	65	76.24		57	**76.32**	*	4	74.25
WGN	66	27.29	*	60	**28.87**	*-	5	**31.70**
SDG	66	57.04		58	61.72	*-	5	**80.60**
ENE	65	**90.23**	*	56	79.59		4	69.54
R	65	**331.14**	*	56	301.77		4	283.00
BVY	66	**462.30**		60	**463.36**	*	5	373.40

Traits^2	8-10/WRT+			8-10/WRT-		5-7/WRT+			5-7/WRT-		3-4/WRT+			3-4/WRT-	
	n	$\bar{X}$		n	$\bar{X}$	n	$\bar{X}$		N	$\bar{X}$	n	$\bar{X}$		n	$\bar{X}$
Physical															
HLM	20	82.31		46	81.54	16	**82.63**	*	44	80.64	1	81.80		4	79.75
ABM	20	35.07		46	33.63	16	**35.59**	*	44	33.61	1	38.60		4	38.45
Chemico-technological															
CPN	20	12.90	*	46	**13.58**	16	13.81		44	13.47	1	12.40		4	14.90
SDM	20	35.70	*	40	**45.03**	16	35.88	*	40	**44.15**	1	32.00		1	50.00
WGN	20	25.66	*	46	**27.98**	16	28.76		44	28.91	1	26.60		4	32.98
DGN	20	8.86	*	46	**9.66**	16	9.74		44	10.03	1	8.90		4	11.13
MAL	20	3.24	*	40	**2.69**	16	3.03		40	2.80	1	2.90		1	4.40
Farinograph															
DDV	20	**3.39**	*	46	2.77	16	**3.54**	*	42	2.65	1	2.50		4	2.20
SDG	20	65.05		46	53.64	16	58.25		42	63.05	1	**114.00**	*	4	72.25
QNO	20	67.48		46	69.49	16	66.66		44	66.02	1	50.20	*	4	**63.25**
Extensogram															
ENE	20	60.90	*	45	**103.27**	16	62.69	*	40	**86.35**	1	32.00		3	82.33
R	20	271.85	*	45	**357.49**	16	256.00	*	40	**320.07**	1	161.00		3	323.67
E	20	138.00	*	45	**159.96**	16	143.88	*	40	**155.95**	1	135.00		3	145.00
E/R	20	1.99	*	45	**2.31**	16	1.84		40	2.15	1	1.20		3	2.37
Baking test															
BY	20	136.83	*	46	**138.76**	16	137.57		44	138.51	1	138.50		4	139.80
Yield (3 years)															
YLD	20	**6576.9**	*	46	6023.3	16	6414.4		44	6015.4	1	6590.0		4	5887.5

[1] The traits exhibiting statistically significant differences between mean values, at least in one pair of averages, are given in the table. All the traits where no differences were observed in all comparisons, are omitted.

[2] Hectoliter mass (HLM), Absolute mass (ABM), Glassiness (GLS), Crude protein (CPN), Sedimentation (SDM), Flour extraction (FEX), Wet gluten content (WGN), Dry gluten content (DGN), Maltose content (MAL), Water absorption (FWA), Dough development (DDV), Dough stability (DST), Softening degree (SDG), Quality number (QNO), Energy (ENE), Resistance to extension (R), Extensibility (E), R/E, Bread yield (BY), Bread volume yield (BVY), Bread crumb quality number (BCQN), Average grain yield (YLD)

*- Means statistically significant differences between the first (Glu Score 8-10) average values, and the third (Glu Score 3-4) average value, and – means no statistically significant difference between (Glu Score 5-7) average value, and the third (Glu Score 3-4) average values

** Means statistically significant differences between the first (Glu Score 8-10) average values,the third (Glu Score 3-4) average value, and statistically significant difference between (Glu Score 5-7) average value, and the third (Glu Score 3-4) average values.

As it could be seen, the effect of 1Bl.1Rs wheat/rye translocation was both, deleterious and useful. It took the toll in a breadmaking quality, particularly in dough properties, but generally increased the grain yield about 10%, on average. The results presented in this article illustrates both effects of 1Bl.1Rs translocation.All indicators obtained on the extensograph were significantly lower in genotypes with 1Bl.1Rs translocation than in those without the chromosomal aberration in question. The more quality background, the more deleterious effect on dough properties of 1Bl.1Rs is exhibited, as well as, significantly higher beneficial effect of the wheat/rye translocation in question on the grain yield increment. The farinograph, and especially extensograph results were significantly affected by the presence of 1Bl.1Rs translocation. The grain yield was higher 9-10% on average in the presence of 1Bl.1Rs wheat/rye translocation in different HMW glutenin subunits quality genetic background, which is dissonant to the novel results of Xynias*et al.* (2020). However, due to limited space, the overall averages of subpopulations divided according to *HMWGlu* loci and the presence or absence of 1Bl.1Rs wheat rye translocation, are given. This shades some individual results of genetic variation, because a number of wheat varieties within the group with the good quality genetic background of 1 or 2*(*Glu-A1*), 7+8 or 7+9 (*Glu-B1*), and 5+10 (*Glu-D1*) HMW glutenin subunits combination, appeared to be bread making quality enhancers, possessed 1Bl.1Rs translocations, like the variety Balkan, for example. According to the electrophoretic, as well as, C-banding results obtained for the individual varieties in this study there is a possibility that 1Bl.1Rs translocation suffered a genetic change, possibly deletion in the translocated region that diminished the deleterious effect of the translocation on dough properties, preserving the advantage in grain yield effect. Hence, the selection favored this aberration in the breeding process in Novi Sad's wheat breeding programe (Dimitrijević, 1997; Gustafson, *personal communication*). Further, investigations at the molecular level could shed some light in this preliminary indications.

Conclusions

The share of wheat genotypes with 1Bl.1Rs wheat/rye translocation in the extensive sample of 139 wheat varieties and lines was about 40%. Preliminary grain yield indicators, hectolitre and absolute mass (mass of 1000 grains), exhibited higher values in varieties possessing 1Bl.1Rs translocation. Among the quality parameters of flour, varieties with translocation had a lower sedimentation value, as well as gluten content, while the maltose content was increased, compared to genotypes lacking this chromosomal aberration. The property of water absorption power, which was of special importance for these study, due to the direct influence on the appearance of the sticky dough, depended on the presence of part of the 1Rs segment of rye on the 1Bl chromosome of wheat, but also on the broader genetic basis of wheat genotypes. Thus, the level of this trait in 1Bl.1Rs genotypes was identical to the results of water absorption power of 1B genotypes. In this absence of the influence of the 1Rs segment on the increase of water absorption power, could be looked for the reason for the lack of the dough stickiness in 1Bl.1Rs varieties and lines of the Novi Sad wheat breeding program. According to the other farinograph results, 1Bl.1Rs translocation generally resulted in a longer dough development time, which also depended on the broader genetic background, reduced dough stability, and increased dough softening rate. However, the adverse effect of 1Bl.1Rs translocation was most pronounced in the dough rheological properties. Observation of the effects of translocation in different quality genetic background was monitored through variation of high molecular weight gluten subunits genes (HMW Glu). The ratio of genetic variation exhibited the constant tendency of favouring the best possible quality background through selection in Novi Sad's wheat breeding program. Hence, within the allelic variation of *Glu-A1* locus better quality contributors alleles 2*, and 1, were dominated (about 65%) the null. Fairly, quality contributor allelic combinations 7+8 and 7+9 at *Glu-B1* locus were favoured by 84% comparing to the presence of other alleles of this locus. The quality superior allelic variation 5+10 on *Glu-D1* locus has been observed in 66% of the examined wheat varieties and lines. The pursuit of high grain yield combined with a good quality is also reflected in HMW Glu subunits combination where the best quality genotype 2*, 7+9, 5+10 has been denoted in almost 40% of the examined genotypes. Finally, the effects of wheat/rye translocation 1Bl.1Rs are more pronounced with a better genetic background in terms of flour, dough and bread quality. These also apply to positive effects such as an increase in wheat grain yield, but also to negative effects such as deterioration in the rheological properties of the dough. A good genetic basis in terms of quality compensates for the negative effects of 1Bl.1Rs translocation, to a greater or lesser extent depending on the trait. The smallest compensatory effect was observed with the extensogram parameters. Integrating all the results, the genetic variation favoured by phenotypically based selection in Wheat Breeding Program of the Institute of Field and Vegetable Crops, and Faculty of Agriculture in Novi Sad, Serbia in its the most fruitful years has been going toward the reconciliation of high grain yield, and good bread making quality. The genetic variation followed in this article is a consequence of this approach. Given that it is difficult to conduct direct selection for the grain yield in early generations of the offspring, before establishing preliminary experiments, testing for the presence and extent of 1Bl.1Rs wheat/rye translocation could be a good indicator of promising genotypes in terms of yield. It has also been shown that more reliable results of the effect of this translocation are obtained if it was not observed alone, but jointly with the broader genetic background, especially with the part of genetic i.e. allelic variation related to wheat quality.

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Uloga pšenično/ražene translokacije 1Bl.1Rs u razvoju oplemenjivačkog programa pšenice u NovomSadu (Srbija)

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SAŽETAK

U drugoj polovini 1950-ih, plan da Jugoslavija učini višak u proizvodnji glavnih ratarskih kultura, uklјičio je sve institucije za oplemenjivanje biljaka širom zemlje. Institut za poljoprivredna istraživanja u Novom Sadu, u Srbiji (danas Institut za ratarstvo i povrtarstvo Novi Sad - IFVCNS) bio je jedna od naučnih institucija uključenih u ovaj program. Pšenica, kao glavna kultura za proizvodnju hleba, imala je posebno mesto u državnom projektu. Tokom narednih 30 godina zadatak je bio ne samo ispunjen, već i daleko nadmašen. IFVCNS je razvio vrlo uspešan program oplemenjivanja pšenice, stvarajući brojne visoko prinosne, kvalitetne sorte pšenice. Pšenično-ražena translokacija 1Bl.1Rs imala je zapaženu ulogu u postizanju poželjne genetičke varijabilnosti pšenice. Uzorak od 139 sorti hlebne pšenice (*Triticum aestivum* L.), pretežno srpskih ozimih sorti, poreklom iz Instituta za ratarstvo i povrtarstvo u Novom Sadu, ispitan je na prisustvo pšenično-ražene translokacije 1Bl.1Rs. Upoređeno je 20 osobina i prinos zrna između dve velike grupe sorti, jedne koje poseduje i druge, koja ne poseduje ovu translokaciju. Proučavana su fizička, hemijska i tehnološka svojstva zrna, kao i reološki rezultati testova i parametri pečenja hleba.Uticaj translokacije je praćen u genetičkoj osnovi, u pogledu konstitucije gena za rezervne proteine zrna pšenice Genotipovi sa i bez translokacije razlikovali su se u rezultatima za proučavane osobine. Ovi efekti su bili u manjoj meri modifikovani u zavisnosti od varijacije gena kvaliteta.

KLJUČNE REČI: 1Bl.1Rs, translokacija, pšenica, raž, oplemenjivanje.

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