ORIGINAL ARTICLE

Molecular genetic tagging of wheat varieties genes resistant to *Septoria tritici* in northern Kazakhstan

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Abstract

Aim: The aim of the research was to isolate sources of wheat resistance to *Septoria tritici* and identify genes that provide resistance to this disease based on the methodology common for phytopathological and molecular genetic studies**. Materials and Methods:** During the study, 303 spring wheat varietiesof different ecological and geographical origin were screened. At this, 36 samples resistant to *S. tritici* were isolated at the artificial infectious background. **Results:** In consequence of molecular genetic tagging of resistance genes in 36 varieties of wheat, it was determined that the majority of the analyzed samples carried in their genotype resistance genes ineffective to *S. tritici*. Just resistance gene *Stb2* was characterized by the moderate efficiency. Among the studied varieties with this gene, eight samples were identified: Strain 36/12-1, Laban, GN06600, MN 94382, SD 80-89, Roblin, Yesaul, and Nota. Field resistance against the disease can be provided by varieties with a large number of resistance genes, such as Laban and Krabat. Varieties of gene *Stb8* with efficient resistance to the *S. tritici* pathogen are of the greatest interest for selection for immunity to *S. tritici*. **Conclusion:** In consequence of the conducted research, two varieties of Laban and A.C. crystal with an effective resistance gene *Stb8* were identified. These varieties should be used in breeding process as resistance donors to *S. tritici*.

Key words: Molecular markers, *Septoria tritici*, spring wheat, *Stb* genes

INTRODUCTION

Over the past 25 years, the attention to the *Septoria* diseases of wheat has significantly increased. Two pathogens, namely, *Septoria tritici* and *Septoria nodorum* of the *Septoria* genus, are of great importance in world wheat production. Yield losses of grain crops due to these two diseases in the world amount to 9 million tons.[1]

Mycosphaerella graminicola ((Fukel) Schroet. in Cohn) (or anamorph of *S. tritici* Rob. et Desm.) is economically dangerous pathogen in some European countries and North America. The pathogen can cause yield losses up to 30-40%. Thus, in the UK, in 1998 yield losses from *S. tritici* were estimated at £35.5 million.[2]

Spring wheat is the main export crop in Kazakhstan. Over recent years its acreage increased from 10.8 to 12.6 million ha. The record yield for the years of independence was harvested in 2016 and amounted to 17.9 million tons of grain. Export potential of Kazakhstan is estimated at 8-10 million tons.[3]

According to Koishybayev, in Kazakhstan during the years of leaf rust epiphytotic and *S. tritici* at the dominance of one or the other disease, the harvest of spring wheat have been reduced by 15-25% and more.[4] Epidemics in the North of Kazakhstan occur 5 times per every 10 years. According to the monitoring of the *S. tritici* pathogenic mechanism in Akmola region, there is a trend to increased development and severity of the disease,

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at that, in recent years, the morbidity rate has reached a critical level. The disease manifested itself even during the years of hard drought (2003-2010). Strong development of *S. tritici* was observed in 2013, 2014, and 2016.[5]

The main method to control this disease is the use of crop-protection agents, creation of resistant varieties, and the observance of cultivation methods. One of the most efficient and environmentally friendly ways of dealing with *Septoria* disease is cultivation of resistant and weakly susceptible wheat varieties, though currently, the Republic of Kazakhstan lacks such cultivars.

Genetic mapping of *Stb* resistance genes has been rapidly developed after 1995, and currently 17 genes are identified, which are mapped with one or several associated molecular markers.[6] Research conducted by Pakholkova *et al.*[7] showed that 6 of the 8 of known resistance genes (*Stb1-Stb5, Stb7*) had only partial functionality in natural populations of *M. graminicola* in Russia, the *Stb6* gene was highly effective against five populations of *M. graminicola*. The *Stb8* gene was efficient in absolute sense against all tested isolates.

To breed varieties resistant to *S. tritici* in the conditions of Northern Kazakhstan, it is necessary to study the genetic resources of spring wheat and identify sources with known resistance to this disease.

In this regard, the aim of the present research was to isolate the sources of resistance to *Septoria* spot of wheat and identify genes that provide resistance to this disease.

MATERIALS AND METHODS

A screening of 303 varieties of spring wheat represented by different ecological-geographical groups was carried out in 2015-2016 to isolate sources of resistance to *S. tritici*. The study was performed in the infectious nursery situated in the Scientific Production Center of Grain Farming named after A.I. Barayev (Shortandy township, Kazakhstan) in accordance with the methodology of All-Russian Research Institute of Phytopathology (VNIIF Moscow, Russia).[8] Both resistant (affected up to 15%) and weakly susceptible (16-25%) wheat samples were selected for further study.

Identification of *Stb* genes resistant to *S. tritici* pathogen was carried out at the VNIIF using molecular genetic tagging in selected spring wheat varieties. The 36 samples of soft spring wheat were selected for the analysis. The isogenic strains with known resistance genes: Bulgaria88, *Stb1*, Veranopolis, *Stb2*, Tadinia, *Stb4*, CS (Synthetic 7D), *Stb5*, Estanzuela Federal, *Stb7*, and Synthetic W7984, *Stb8* were used as control samples.

To analyze *Stb* genes of resistance, microsatellite markers linked to the resistance genes were selected based on literature data [Table 1].[9-14]

The DNA was extracted from the cutoff wheat seedlings grown in Petri dishes on filter paper, pretreated with 0.05% of $KMnO_4$ solution. The DNA extraction was carried out using a kit of reagents SAMPLE-CTAB (DNA-technology).

The polymerase chain reaction (PCR) was conducted at the annealing temperature: 1 cycle: 94°C - 5 min; 30 cycles: 94°C, 30 s, 55°C, 30 s, 72°C, 50 s; 1 cycle: 72°C, 5 min in accordance with the Schuelke[15] method. The first PCR round consisted in the synthesis of the PCR product using the direct (0.04 pmol/µl) and reverse primers (0.16 pmol/µl). The second round of PCR consisted in tagging of the obtained PCR product at annealing temperature of 53°C. The obtained product was analyzed by the fragment analysis method using the sequenator ABI 3130xl Genetic Analyzer (Applied Biosystems).

RESEARCH RESULTS

In consequence of the evaluation of 303 collection and selected varieties of spring wheat we identified the ambiguous nature of the morbid affection with *S. tritici*. Most varieties were susceptible and highly susceptible to *S. tritici*. Among the studied varieties, 36 resistant samples and samples weakly susceptible to desease were selected.

The conformity of PCR-amplification spectra of microsatellite markers shown by electrophoregrams in seven monogenic strains with the known *Stb* resistance genes was seen as a positive signal indicating presence of the gene. To clarify the lengths of the resulting PCR-product we conducted fragment analysis of the studied samples in comparison with the control variety with the use of all molecular markers. As examples, Table 2 shows the results of the fragment analysis with molecular markers *Xgwm335, Xgwm111,* and *Xgwm44* linked to the resistance genes *Stb1, Stb4,* and *Stb5*, respectively.

The results show that the selected markers and amplification conditions have contributed to a preliminary identification of *Stb* genes resistant to *S. tritici*. Definitions of possible *Stb* genes in 36 tested varieties are given in Table 3.

Identification of the *Stb1* gene was carried out using microsatellite marker *Xgwm335*. As a result of the amplification of microsatellite molecular marker *Xgwm335* on the wheat varieties, it was revealed that the amplification type identical to the monogenic strains with the resistance gene *Stb1*was found in 22 samples highlighted in Table 3 by colored cell. However, a full coincidence of the amplified fragments by length, 236 base pairs, was detected only in the control sample Oazis and the analyzed varieties of Krabat and Strain 277/12.

We can assume the existence of a resistance gene *Stb1* also in the following variety samples: Krabat, Guadalupe, A.C. Crystal, Gus, Bezenchukskaya 202, Shortandinskaya 2007,

Table 1: Genes resistant to *Septoria tritici* and microsatellite markers linked to them

Gene	Location	Marker associated with the gene	Donor
Stb1	5BL	*Xgwm335*	Bulgaria 88
Stb2	3BS	*Xgwm389, Xgwm533.1* (both distally) and *Xgwm493* (proximal)	Veranopolis
Stb4	6D	*Xgwm111* (0.7 cM)	Tadinia
Stb5	7DS	*Xgwm44* (proximal 7.2 cM)	CS (Synthetic 7D)
Stb7	4AL	*Xwmc313* (0.5 cM)	Estanzuela Federal
Stb8	7BL	*Xgwm146* и *Xgwm577*, flanking	Synthetic W7984

Table 2: Results of fragment analysis with markers *Xgwm335, Xgwm111*, and *Xgwm44*

Sample marking	Name of the variety	The length of the distinguished fragment, base pairs		
		Xgwm335	***Xgwm111***	***Xgwm44***
S1	Strain 277/12	236	229	190
S2	Strain 36/12-1	219	243	190
S3	Strain 36/12-2	208	241	190
S4	Velutinum-15	223	229	194
S5	Apasovka	219	241	190
S6	Lutestsens 360/96-6	221	203	196
S7	Lutestsens 363/96-4	230	245	196
S8	Laban	221	202	196
S9	GN06600	232	221	198
S10	Krabat	236	223	196
S11	Bulgaria 88 (*STB1*)	258	-	-
S12	Oazis (*STB1*)	236	-	-
S15	Tadinia (*STB4*)	-	223	-
S16	CS (Synthetic 7D) (*STB5*)	-	-	196

Roblin, TselinnayaYubileynaya, Krasnodarskaya, Delta, Rufa, Yasaul, Moskvich, and Note, as well as in strains SD 8089, SD 8080, and hybrids - strain 167/11-2, strain 167/11-3, strain 277/12, 167/11-3 F4, strain 4303, and strain 25/95-564.

According to the literature, resistance gene *Stb2* is concatenated with three SSR (microsatellite) markers: *Xgwm389, Xgwm533.1,* and *Xgwm493*. The length of molecular marker *Xgwm 389* in samples strain 36/12-1, Laban, GN06600, MN 94382, SD 8089, Roblin, Yesaul, and Nota corresponded to a fragment of Veranopolis cultivar, carrying the *Stb2* gene, and obtained from DNA matrix.

The marker *Xgwm533* from Veranopolis cultivar was amplificated as a fragment detected in 21 tested samples: Strain36/12-1, Laban, GN06600, Guadalupe, A.C. Crystal, MN 94382, Gus, SD 8089, SD 0027, SD 3391, 3290 SD, Bezenchukskaya 202, Roblin, TselinnayaYubileynaya,Strain 167/11-2; Strain 167/11-3; Shortadinskaya 2007, Strain 4303; Strain 25/95-564; Krasnodarskaya, Delta, Yesaul, Moskvich, and Note.

The amplification products of the *Xgwm493* marker in 17 tested samples coincided in length with a fragment identified in Veranopolis cultivar. These included: Strain 36/12-1, Laban, GN06600, Guadalupe, A.C. Crystal, MN 94382, Gus, SD 8089, SD 3290, Bezenchukskaya 202, Roblin, Tselinnaya Yubileynaya, Strain 167/11-1; Strain 167/11-3; Shortadinskaya 2007, Strain 4303; Strain 25/95-564; Delta, Yesaul, and Nota.

Using three molecular markers we were able to form relatively small number of samples, whose genome, as we might assume with great probability, included *Stb2* gene resistant to *S. tritici*. These included following samples: Strain 36/12-1, Laban, GN06600, MN 94382, SD 8089, and wheat varieties Roblin, Yesaul, and Nota. These samples are highlighted in Table 3 by colored cells. Figure 1 shows the results of amplification of markers linked with the *Stb2* resistance gene in some samples of wheat [Note 1].

The amplification profiles of microsatellite marker *Xgwm111* to the gene *Stb4* coincided with that for control sample Tadinia and the following samples: Krabat, A.C. Crystal, Gus, SD 8089, Strain 167/11-2; Strain 167/11-3; Shortadinskaya 2007; Strain 4303; and Strain 25/95-564. In consequence of the refining procedure of the length of

Table 3: Molecular genetic analysis results of genes resistant to the *Septoria tritici* pathogen in isogenic strains and varieties of soft spring wheat

Variety, strain	Gene								
	Stb1	*Stb2*			*Stb4*	*Stb5*	*Stb7*	*Stb8*	
	Xgwm335	*Xgwm389*	*Xgwm493*	*Xgwm533*	*Xgwm111*	*Xgwm44*	*Xwmc313*	*Xgwm146*	*Xgwm577*
Bulgarea 88 (*STB1*)	+								
Oazis (STB1)	+								
Veranopolis (STB2)		+	+	+					
Israel (STB3)									
Tadinia (*STB4*)					+				
CS (Synthetic 7D) (*STB5*)						+			
Estanzuela Federal (*STB7*)							+		
Synthetic W-7984 (*STB8*)								+	+
Strain 277/12	+	-	-	-	-	-	-	-	-
Strain 36/12-1	-	+	+	+	-	-	-	-	-
Strain 36/12-2	-	-	-	-	-	-	+	-	-
Velutinum-15	-	-	-	-	-	-	+	-	-
Apasovka	-	-	-	-	-	-	-	-	-
Lutestsens 360/96-6	-	-	-	-	-	+	+	-	-
Lutestsens 363/96-4	-	-	-	--	-	+	+	-	-
Laban	-	+	+	+	-	+	-	+	+
GN06600	-	+	+	+	-	-	-	-	-
Krabat	+	-	-		+	+	+	-	-
Guadalupe	+	-	+	+	-	-	+	-	-
A.C. Crystal	+	-	+	+	+	+	+	+	+
MN 94382	-	+	+	+	-	-	+	-	-
Gus	+	-	+	+	+	-	-	-	-
SD 8089	+	+	+	+	+	+	-	-	+
SD 0027	-	-	-	+	-	-	+	+	-
SD 3391	-	-	-	+	-	-	+	-	-
SD 8080	+	-	-	-	-	-	+	-	-
SD 3290	-	-	+	+	-	+	+	-	+
Bezenchukskaya 202	+	-	+	+	-	-	+	-	-
Roblin	+	+	+	+	-	-	-	+	-
TselinnayaYubileynaya	+	-	+	+	-	-	+	-	-
Strain167/11-1	-	-	+	-	-	-	+	-	-
Strain167/11-2	+	-	-	+	+	-	+	-	+
Strain167/11-3	+	-	+	+	+	-	-	-	-
Shortandinskaya 2007	+	-	+	+	+	-	+	-	-
Strain4303	+	-	+	+	+	+	+	-	+
Strain25/95-564	+	-	+	+	+	-	+	-	-
Istok	+	-	-	-	-	-	+	-	-
Krasnodarskaya	+	-	-	+	-	-	+	-	-
Lira	-	-	-	-	-	+	+	+	-
Delta	+	-	+	+	-	-	+	-	-
Rufa	+	-	-	-	-	-	+	+	-

(Contd...)

Table 3: *(Continued)*

Variety, strain	Gene								
	Stb1		***Stb2***		***Stb4***	***Stb5***	***Stb7***	***Stb8***	
	Xgwm335	***Xgwm389***	***Xgwm493***	***Xgwm533***	***Xgwm111***	***Xgwm44***	***Xwmc313***	***Xgwm146***	***Xgwm577***
Yesaul	+	+	+	+	-	-	+	-	-
Moskvich	+	-	-	+	-	-	+	-	-
Nota	+	+	+	+	-	-	+	+	-

Note 1: Control samples are marked in red	
S1	Strain 277/12
S2	Strain 36/12-1
S3	Strain 36/12-2
S4	Velutinum-15
S5	Apasovka
S6	Lutestsens 360/96-6
S7	Lutestsens 363/96-4
S8	Laban
S9	GN06600
S10	Krabat
S13	Veranopolis (STB2)

Note 2: Control samples are marked in red	
S1	Strain 277/12
S2	Strain 36/12-1
S3	Strain 36/12-2
S4	Velutinum-15
S5	Apasovka
S6	Lutestsens 360/96-6
S7	Lutestsens 363/96-4
S8	Laban
S9	GN06600
S10	Krabat
S18	Synthetic W-7984(STB8)

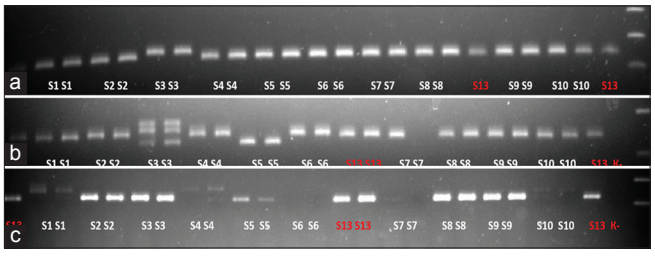

Figure 1: Electrophoregram of amplification products of microsatellite markers linked to the *Stb2* resistance gene. (a) Microsatellite marker *Xgwm493,* (b) microsatellite marker *Xgwm389*, (c) microsatellite marker *Xgwm533*

the diagnostic fragment we revealed the coincidence of the lengths, 223 base pairs, in a sample of Krabat and monogenic Strain Tadinia (*Stb4*).

As a result of the PCR analysis, it was revealed that the marker in the sample CS (Synthetic 7D) was close in length to the fragments amplificated on samples of Lutescens 360/96-6, Lutescens 363/96-4, Laban, and Krabat.

Length of amplificated marker *Xgwm44 (*196 base pairs) in varieties of Laban, Krabat, and samples of Lutescens 360/96-6 and Lutescens 363/96-4 coincided with the marker fragment of the control sample CS (Synthetic 7D) carrying the resistance gene *Stb5*.

At amplification of the marker *Xgwm313* in the studied matrices we revealed coincidence of PCR lengths of product in 22 wheat samples with the control sample of Estanzuela Federal (*STB7*) carrying resistance gene *Stb7*. According to the literature, resistance gene *Stb8* is linked with two SSR (microsatellite) markers: *Xgwm577* and *Xgwm147*. The analysis of the amplification spectra of the molecular marker *Xgwm147* in samples A.C. Crystal, Laban, SD 0027, Roblin, Lira, Rufa, and Nota revealed fragments identical to the monogenic strain of Synthetic W7984 with the resistance gene *Stb8*. The PCR analysis for molecular marker Xgwm533 showed genotypic similarity of the Synthetic W7984 strain in 5 samples: A.C. Crystal, Laban, SD 8089, SD 3290, Strain 167/11-2, and Strain 4303. The use of two molecular markers allowed selecting only two varieties of wheat, namely, A.C. Crystal and Laban, whose genome with high probability contained the *Stb8* gene for resistance to *S. tritici*.

The results of amplification of microsatellite markers linked to the resistance gene *Stb8* are shown in Figure 2 [Note 2].

DISCUSSION

The generalization of the results of molecular marking of genes for resistance to *S. tritici* pathogen in wheat varieties allowed identifying the polygenic nature of inheritance of resistance to *S. tritici*. We have identified from 1 to 5 resistance genes [Table 4].

The conducted study showed that the fragment with the length of 236 base pairs amplificated at DNA of Strain 277/12 variety was identical to diagnostic fragment of monogenic strain of Oazis that indicated the presence of the *Stb1* resistance gene.

Table 4: Preliminary identification of genes for resistance to *Septoria tritici* pathogen in spring wheat cultivars

Resistance genes	Number of samples	Varieties
Stb1	1	Strain 277/12
Stb2	2	Strain36/12-1, GN06600
Stb7	5	SD 0027; SD 3391; Strain167/11-1; Strain36/12-2, Velutinum-15
Stb1, Stb2	1	Roblin
Stb1, Stb4	2	Gus; Strain167/11-3
Stb1, Stb7	9	Guadalupe, SD 8080, Bezenchukskaya 202, Tselinnaya Yubileynaya, Istok, Delta, Krasnodars kaya, Rufa, Moskvich
Stb2, Stb7	1	MN 94382
Stb5, Stb7	4	SD 3290, Lira, Lutestsens 360/96-6, Lutestsens 363/96-4
Stb1, Stb2, Stb7	2	Yesaul, Nota
Stb1, Stb4, Stb7	3	Strain 167/11-2, Strain 25/95-564, Shortadinskaya 2007
Stb2, Stb5, Stb8	1	Laban
Stb1, Stb2, Stb4, Stb5	1	SD 80-89
Stb1, Stb4, Stb5, Stb7	2	Krabat, Strain 4303
Stb1, Stb4, Stb5, Stb7, Stb8	1	A.C. Crystal

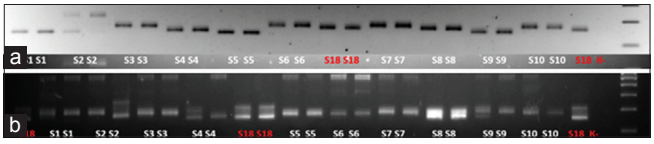

Figure 2: Electrophoregram of amplification products of microsatellite markers linked to the *Stb8* resistance gene. (a) Microsatellite marker *Xgwm577*, (b) microsatellite marker *Xgwm147*

Amplification profiles in samples of Strain 36/12-1 and GN06600 coincided in three microsatellite markers *Xgwm389*, *Xgwm533*, and *Xgwm493* with a control sample carrying the *Stb2* resistance gene. We could assume the presence of the *Stb2* gene in these samples.

The possible presence of the *Stb7* resistance gene was determined in the following cultivars: SD 0027; SD 3391; Strain 167/11-1, Strain36/12-2, and Velutinum-15 due to the identical diagnostic fragments, which were identified in these samples and the monogenic strain of Estanzuela Federal carrying the *Stb7* resistance gene.

In 17 analyzed wheat samples, we can assume the presence of two resistance genes in various combinations. The Roblin cultivar possibly contains resistance genes *Stb1* and *Stb2* that is revealed by the similarity of their respective markers: *Xgwm 335* marker in Roblin, Bulgaria 888, and Oasis varieties carrying the *Stb1*, and *Xgwm 389, Xgwm 493, Xgwm 533*markers in Roblin and Veranopolis cultivar carrying *Stb2*. Guscultivar, the Strain 167/11-3 supposedly carry in their genotype *Stb1* and *Stb4*resistance genes. We have obtained similar amplification profiles of relevant markers with monogenic strains of Bulgaria 888, Oazis and Tadinia. At this, eight varieties, namely, Guadalupe, Bezenchukskaya 202, Tselinnaya Yubileynaya, Istok, Krasnodarskaya, Delta, Rufa, Moskvich, and SD 8080 sample may have in their genotype *Stb1* and *Stb7* genes ineffective against the *S. tritici* pathogen. Variety of MN 94382 may have the *Stb7* gene identical to the monogenic strain of Estanzuela Federal and the *Stb2* resistance gene with identical amplification fragments of the Veranopolis cultivar. We can assume the presence of *Stb5* and *Stb7* resistance genes in the Lira cultivar and three samples of wheat - SD 3290, Lutestsens 360/96-6, and Lutescens 363/96-4 - judging by the identical results in marking of these samples and monogenic strains CS (Synthetic 7D) with the *Stb5* resistance gene and Estanzuela Federal with the *Stb7* gene for resistance to *S. tritici*.

Four studied varieties and two hybrid strains presumably carry in their genotype three resistance genes, two of which are ineffective for *S. tritici* blotch (*Stb1* and *Stb7*). The Yesaul and Nota cultivars, besides these genes, may contain the *Stb2* resistance gene: All three markers for this gene (*Xgwm 389, Xgwm 493,* and *Xgwm 533*) coincided in length with the diagnostic fragments amplificated in Veranopolis monogenic strain. Two hybrid strains - Strain 167/11-2; Strain 25/95-564 –and Shortadinskaya 2007 cultivar, except of two ineffective resistance genes *Stb1* and *Stb7,* may contain the *Stb4* resistance gene, as they have manifested marker fragments identical to the monogenic strain with the *Stb4* resistance gene. Presumably, Laban cultivar carries in its genotype resistance genes *Stb2*, *Stb5,* and *Stb8*, one of which is ineffective for *S. tritici* blotch (*Stb5*). The *Stb2* resistance gene is moderately effective. The *Stb8* gene for resistance to *S. tritici*, capable of protecting wheat from disease, is of great interest. The presence of this gene in the variety is determined through comparative analysis with the results of the amplification of *Xgwm146* and *Xgwm577* markers in

Synthetic W7984 monogenic strain with the *Stb8* resistance gene and Laban cultivar.

We can assume the presence of four resistance genes in three wheat cultivars. Among them, three genes *Stb1, Stb4,* and *Stb5* are common. However, the SD 8089 variety, in addition to these genes, possibly contains *Stb2* gene, because all three marker systems for gene showed identity with the corresponding diagnostic fragments of Veranopolis cultivar. Hybrid Strain 4303 and Krabat cultivar differ from SD 8089 by presence of an ineffective resistance gene *Stb7* in the genotype. However, the complementary interaction of these resistance genes can provide partial resistance of cultivar (syn. field, horizontal, slow rusting, slow disease progression, etc.) that can lead to a significant reduction in the intensity of disease progression and ultimately to the preservation of the crop.

The A.C. Crystal cultivar supposedly has in its genotype five genes resistant to *S. tritici*: *Stb1, Stb4, Stb5, Stb7,* and *Stb8*. Among the identified genes, the great interest is paid to effective gene for resistance to the *S. tritici* pathogen, namely, Stb8, capable of protecting wheat from disease. The presence of this gene in the cultivar is determined based on a positive comparison of the *Xgwm146* and *Xgwm577* markers amplification relative to Synthetic W7984 monogenic strain with the *Stb8* resistance gene.

CONCLUSION

In consequence of molecular genetic tagging of resistance genes in 36 wheat varieties, it was determined that the majority of the analyzed samples carried in their genotype genes ineffective for resistance to *S. tritici*. The moderate efficiency is peculiar to the *Stb2* resistance gene. Eight samples with this gene were identified among the studied varieties. These include: Strain 36/12-1, Laban, GN06600, MN 94382, SD 8089, Roblin, Yesaul, and Nota. Field resistance to the disease can be provided by varieties with a large number of resistance genes, such as Laban and Krabat. The varieties with the *Stb8* gene, efficient for resistance to the *S. tritici* pathogen, are of great interest in selection for immunity to *S. tritici* blotch. The conducted research allowed identifying 2 varieties of Laban and A.C. Crystal with an effective resistance gene *Stb8*. These varieties should be used in selection process as resistance donors to *S. tritici*.

Conducted studies have shown that the use of a large number of molecular markers allows more reliably identifying genes for resistance to disease and exclude possible errors.

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