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## STUDY OF BREAD WHEAT LINES WITH GENETIC MATERIAL OF *Triticum* SPECIES FOR RESISTANCE TO FUNGAL DISEASES

O.A. ORLOVSKAYA ✉, S.I. VAKULA, L.V. KHOTYLEVA

*Institute of Genetic and Cytology of National Academy of Science of Belarus*, 27, ul. Akademicheskaya, Minsk, 220072  
Republic of Belarus, e-mail O.Orlovskata@igc.by (✉ corresponding author), svettera@yandex.ru, L.Khotyleva@igc.by

ORCID:

Orlovskaya O.A. [orcid.org/0000-0002-1187-1317](https://orcid.org/0000-0002-1187-1317)

Khotyleva L.V. [orcid.org/0000-0003-0295-5022](https://orcid.org/0000-0003-0295-5022)

Vakula S.I. [orcid.org/0000-0002-2242-7107](https://orcid.org/0000-0002-2242-7107)

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### Abstract

*Triticum aestivum* L. yield losses caused by phytopathogens can reach 40-80 % in epiphytotic years. Wild and cultivated relatives of common wheat are promising sources of broadening the genetic diversity of resistance loci for modern varieties. For the first time differences in the degree of infection by fungal pathogens of wheat lines obtained from crossing with *Triticum dicoccoides*, *T. dicoccum*, *T. durum*, *T. kiharae* were shown on the basis of long-term monitoring under conditions of the natural infectious background of Belarus. In our work, we studied the resistance of bread wheat lines with *Triticum* species introgressions to powdery mildew (*Blumeria graminis*), septoria (*Zymoseptoria tritici*), and leaf rust (*Puccinia triticina*) in a natural infectious background. We studied 30 introgression lines obtained in the Institute of genetics and cytology NAS of Belarus from crossing of six varieties of common wheat (Rassvet, Saratovskaya 29, Festivalnaya, Chinese Spring, Belorusskaya 80, Pitic S62) with accessions of tetraploid species *T. dicoccoides*, *T. dicoccum*, *T. durum* (AABB,  $2n = 28$ ) and with hexaploid synthetic variety *T. kiharae* (A'A'GGDD,  $2n = 42$ ). Twelve of the studied wheat lines were obtained with *T. durum* contribution, 7 — with *T. dicoccoides*, 6 — with *T. kiharae*, 5 — with *T. dicoccum*. The evaluation of resistance to the diseases was performed in a naturally occurring infectious background on the experimental fields of the Institute of Genetics and Cytology of the NAS of Belarus during 2012, 2014-2016, 2018, 2019 field seasons using Geshele's scale. We used the extent of flag leaf damage in the milky-wax ripeness phase as an indicator of resistance: 0-5 % — highly resistant plants, 5-10 % — resistant, 10-15 % — medium resistant, 15-25 % — medium susceptible, 25-40 % — susceptible. Statistica 10.0 software package was used for statistics (Kruskal-Wallis test, box-and-whiskers diagram, two-way ANOVA). The extent of flag leaf damage for the susceptible spring bread wheat variety Thatcher accounted 40-60 % by *B. graminis* and 15-25 % by *Z. tritici* during studied period. *P. triticina*, which causes wheat leaf rust, was detected only in 2012 and 2014 in a naturally occurring infectious background of Belarus (the degree of damage of susceptible control was 50 %). ANOVA confirmed the differences in the average degree of damage to wheat plants by fungal pathogens under weather conditions of six field seasons ( $p < 0,01$ ). The highest sensitivity of wheat lines to powdery mildew and leaf rust was noted in 2014, to septoria blight — in 2012. The weather conditions of these years contributed to the intensive development of diseases (high precipitation, relatively low average daily air temperatures, Selyaninov's hydrothermal coefficient above 1.5). The least favorable conditions for the development of fungal pathogens were recorded in dry 2015 year (hydrothermal coefficient = 0.7). The species of genus *Triticum* were superior to common wheat varieties in resistance to fungal diseases. It was found that 60.0 % of introgression lines showed a high level of resistance to leaf rust, 56.7 % to septoria, and 36.7 % to powdery mildew. The highest number of highly resistant to powdery mildew and septoria genotypes were noted among the lines created on the base of *T. dicoccoides* (71.4 % and 85.7 %, respectively). Resistance to leaf rust (80 %) was common among lines with *T. dicoccum* genetic material. A significant statistical difference in the degree of damage by powdery mildew and septoria was shown between the groups of lines created using the species *T. dicoccoides*, *T. dicoccum*, *T. durum*, *T. kiharae*, and under different weather conditions. A total of 26.7 % of introgression lines demonstrated resistant to two diseases (lines 11-1, 13-3, 15-7-2, 16-5, 34-1, 34-2, 183/2-2, 184/1-6), 23.3 % — to three infections (lines 29, 8, 15-7-1, 1-3, 2-7, 19, 25-2). These lines are of interest in breeding for fungal disease resistance.

Keywords: genus *Triticum*, introgression lines, powdery mildew, septoria, leaf rust

Powdery mildew (pathogen *Blumeria graminis* (DC.) Speer f. sp. *tritici* March.), septoria (pathogen *Zymoseptoria tritici* (Desm.) Quaedvl. & Crous), and brown (leaf) rust (pathogen *Puccinia triticina* Erikss.) are the most common diseases of the aboveground organs of common wheat (*Triticum aestivum* L.). Their harmfulness is manifested mainly in a decrease in the leaf surface area (and, as a consequence, in the productivity of photosynthesis) and in a violation of the water balance, which causes premature death of the leaf apparatus, a decrease in grain yield, and a deterioration in its quality. Not only leaves are affected but also leafy sheaths, stems, and even an spike in years favorable for the development of powdery mildew [1].

Infection of plants with fungal pathogens is possible in a wide temperature range. For example, urediniospores of *P. triticina* and conidia of the fungus *B. graminis* germinate at 2.5-31 °C in the presence of drip moisture. Conidia of septoria pathogens spread mainly with raindrops and begin to germinate at temperatures from 5 to 35 °C [1]. Crop losses due to infection with these pathogens are usually 15-35%, but with severe epiphytotics, they can reach 40-80% [2-4].

The most effective method to control fungal wheat diseases has become the creation of varieties with long-term resistance to pathogens. Currently, genes are known that control resistance to powdery mildew (more than 90 *Pm* genes), leaf rust (more than 75 *Lr* genes), and septoria blight (more than 15 *Stb* genes) [5]. It should be borne in mind that the effectiveness of known resistance genes decreases over time, and new virulent biotypes of pathogens appear that can cause significant damage to crops of cultivated cereals [6, 7]. In this regard, the search for new genes for resistance to leaf-stem infections is an urgent task in wheat breeding.

It is known that wild and cultivated relatives of *Triticum aestivum* are a promising source of enlargement of the genetic diversity of modern cultivars by resistance loci [8-10]. In order to enrich and improve the common wheat gene pool, species of the *Triticum* genus (*T. dicoccoides*, *T. dicoccum*, *T. durum*, *T. kiharae*) were involved in crosses with *T. aestivum* varieties. Previously, the authors analyzed the nature of foreign introgression in the obtained lines using SSR markers [11] and assessed their cytological stability in comparison with the parental forms [12].

In this paper, on the basis of long-term monitoring under conditions of the natural infectious background of the Republic of Belarus, for the first time, differences in the degree of infection by fungal pathogens of wheat lines created using the species *Triticum dicoccoides*, *T. dicoccum*, *T. durum*, *T. kiharae* were shown.

The research goal was to study the resistance to powdery mildew, septoria blight, and leaf rust of common wheat lines with introgression of the genetic material of the genus *Triticum* against a natural infectious background.

*Materials and methods.* The study included 30 introgressive lines obtained at the Institute of Genetics and Cytology of the National Academy of Sciences of Belarus from crossing the varieties of common wheat Rassvet, Saratovskaya 29, Festivalnaya, Chinese Spring (CS), Belorusskaya 80, Pitic S62 with samples of tetraploid species *T. dicoccoides*, *T. dicoccum*, *T. durum* (AABB,  $2n = 28$ ) and a hexaploid artificially synthesized species *T. kiharae* (A<sup>1</sup>A<sup>1</sup>GGDD,  $2n = 42$ ). Samples of foreign donors were obtained from the All-Union Research Institute of Plant Breeding collection (VIR) (St. Petersburg, Russia), information on the genealogy of individual samples has not been preserved (the VIR catalog numbers are not indicated). Of the 30 lines studied, 12 were created with the participation of the *T. durum* sample (CS × *T. durum* – lines 183/2-2, 184/1-6; *T.*

*durum* × CS – 190/4-1, 190/5-3, 190/6-1, 191/6-3, 195-3, 196-1, 202-2, 200-3; *T. durum* × Belorusskaya 80 – 221-1 and 226-7), 7 lines – with the participation of *T. dicoccoides* (Rassvet × *T. dicoccoides* k-5199 – line 29; Saratovskaya 29 × *T. dicoccoides* – line 8; *T. dicoccoides* × Festivalnaya – lines 11-1, 13-3, 15-7-1, 15-7-2, 16-5), 6 lines – with *T. kiharae* (*T. kiharae* × Saratovskaya 29 – lines 19, 20-1, 25-2; *T. kiharae* × Festivalnaya – 28, 34-1, 34-2) and 5 lines – with *T. dicoccum* (*T. dicoccum* k-45926 × Festivalnaya – lines 1-3, 2-7; Pitic S62 × *T. dicoccum* k-45926 – 206-2, 208-3, 213-1).

The resistance of hybrid wheat lines, their parental forms, and the susceptible variety of spring bread wheat Thatcher to powdery mildew, septoria blight, and leaf rust was assessed in a natural infectious background on the experimental fields of the Institute of Genetics and Cytology of the National Academy of Sciences of Belarus in 2012, 2014-2016, 2018, 2019 according to the scale of Geshele. To describe the weather conditions, the authors used the values of meteorological parameters for April-August, provided by the website "Reliable Prognosis" (<http://rp5.by>). The authors used the extent of flag leaf damage in the milky-wax ripeness phase as an indicator of resistance: 0-5% – highly resistant plants, 5-10% – resistant, 10-15% – medium resistant, 15-25% – medium susceptible, 25-40% – susceptible, more than 40% are highly susceptible [13].

The Statistica 10.0 software package (StatSoft, Inc., USA) was used for statistical data processing. Significant differences between the means were tested using the Kruskal-Wallis test (non-parametric statistics module). To assess the degree of resistance, box-and-whiskers diagrams were used, categorized according to the year of experiment and the pathogen being investigated. Differences in resistance to fungal pathogens between groups of lines under conditions of a natural infectious background of 6 field seasons were determined using two-way analysis of variance. Histograms were built using Microsoft Excel.

**Results.** During the observation period, the infection of the susceptible cultivar Thatcher by the pathogen *B. graminis* was 40-60%, and that of *Z. tritici* was 15-25%. *P. triticina*, which causes leaf rust, was identified only in 2012 and 2014 (50% degree of damage of the susceptible controls). The maximum degree of damage by powdery mildew of the Thatcher variety was noted in 2012 – 60%, in other years it was 40%. The greatest septoria infection (25%) was also observed in 2012.

In 2012 and 2014, the most favorable weather conditions developed for the development of fungal diseases. The growing season of spring bread wheat was characterized by increased air temperatures, except for June, when the indicator was lower than the average long-term values. In both years, heavy rainfall was observed in June and August. The highest values of the hydrothermal coefficient (HTC) for 6 years were noted for the growing seasons of 2012 and 2014 – 2.2 and 1.6, respectively. The least favorable conditions for the development of fungal pathogens were formed in 2015: the highest temperature regime was recorded in June-August; the HTC was 0.8, which characterizes the growing season as arid. Especially low HTC values were noted in June (0.2) and August (0.1). In 2016 and 2018, the average monthly temperatures throughout the growing season were higher than the average annual values. In May, June, and August, the amount of precipitation was slightly lower, and in July – much higher than the average annual. The HTC was 1.5 in 2016 and 1.3 in 2018. In June 2019, an excess of air temperature and a lack of precipitation were observed in comparison with the norm. In July-August, the average monthly temperature was below optimal values and heavy rainfall fell, the HTC was 1.2.

Analysis of variance showed significant differences in the manifestation of fungal diseases in the studied wheat genotypes over 6 seasons ( $p < 0.01$ ).

When assessing the resistance to leaf rust, only the degree of damage to the leaf blade in 2012 and 2014, when the pathogen was detected in the field, was analyzed. On average, for all genotypes, the highest sensitivity to *B. graminis* and *P. triticina* was noted in 2014, to *Z. tritici* – in 2012, when weather conditions contributed to the intensive development of diseases (Fig. 1).

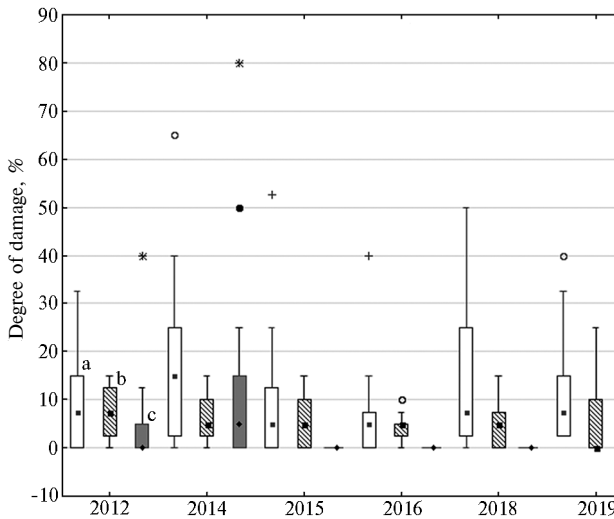


Fig. 1. The degree of damage by powdery mildew (*Blumeria graminis*) (a), septoria (*Zymoseptoria tritici*) (b), and brown rust (*Puccinia triticina*) (c) to lines of spring bread wheat with introgression of genetic material of *Triticum dicoccoides*, *T. dicoccum*, *T. durum*, and *T. kiharae* during six field seasons: O, ● – spikes, +, ✖ – extremes.

For powdery mildew, KW-H(5;234) = 17.93,  $p = 0.003$ ; for septoria, KW-H(5;234) = 101.94,  $p = 0.000$ ; for brown rust, KW-H(5;234) = 26.37,  $p = 0.000$ , where KW-H is the Kruskal-Wallis test,  $p$  is the significance level (the experimental field of the Institute of Genetics and Cytology NASB).

In 2014, in some samples, the incidence of powdery mildew exceeded 60% (lines 206-2, 213-1, 190/5-3), of brown rust 80% (line 206-2), which was significantly higher than in other years of field experiments. The smallest number of genotypes with high resistance to powdery mildew (27.8%) and leaf rust (44.4%) was also noted. Throughout the entire observation period, the number of genotypes highly resistant to septoria was 39.4-60.5%, their minimum number was detected in 2012.

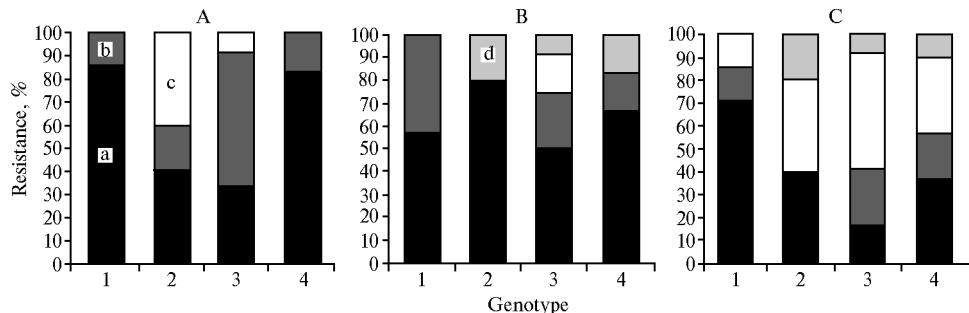
**1. Degree of damage (%) to parental forms of spring bread wheat introgressive lines caused by powdery mildew (*Blumeria graminis*), septoria (*Zymoseptoria tritici*), and brown rust (*Puccinia triticina*) (the experimental field of the Institute of Genetics and Cytology NASB, 2012, 2014-2016, 2018, 2019)**

Genotype	Average/maximum value		
	powdery mildew	septoria	brown rust
<i>Triticum aestivum</i> varieties			
Rassvet	0/5	5/10	15
Saratovskaya 29	15/40	10	15
Festivalnaya	15/25	15	0/5
Chinese spring	25/40	15	15
Belarusskaya 80	15/25	15/25	15
Pitic S62	25	15	10
Samples of genus <i>Triticum</i>			
<i>T. dicoccum</i> k-45926	0	0	0
<i>T. dicoccoides</i>	0	0-5/5	0
<i>T. dicoccoides</i> k-5199	0	0-5	0
<i>T. kiharae</i>	5/10	0	0

The damage to parental *T. aestivum* cultivars with brown rust did not exceed 15% (Table 1). The greatest sensitivity to septoria blight was shown by the cultivar Belarusskaya 80, the degree of damage of which reached 25% in the years most favorable for the development of the pathogen. The parental wheat varieties were susceptible to powdery mildew: in some years, the flag leaf infestation was 25-40%. The only exception was the Rassvet variety, which demonstrated high resistance to *B. graminis* (see Table 1). The species of the genus *Triticum* were characterized by immunity to fungal diseases throughout the entire

observation period (see Table 1). It can be noted that synthetic wheat *T. kiharae* was slightly affected by powdery mildew.

On average, for all the years of research, resistance to septoria was noted for lines with foreign genetic material: 56.7% of genotypes were highly resistant, 33.3% were resistant, and 10% were medium resistant. Among the lines with the genetic material of *T. dicoccoides*, highly resistant genotypes were the most numerous — 85.7% (lines 29, 8, 13-3, 15-7-1, 15-7-2, 16-5) (Fig. 2, A). No susceptible lines were identified (see Fig. 3, A).

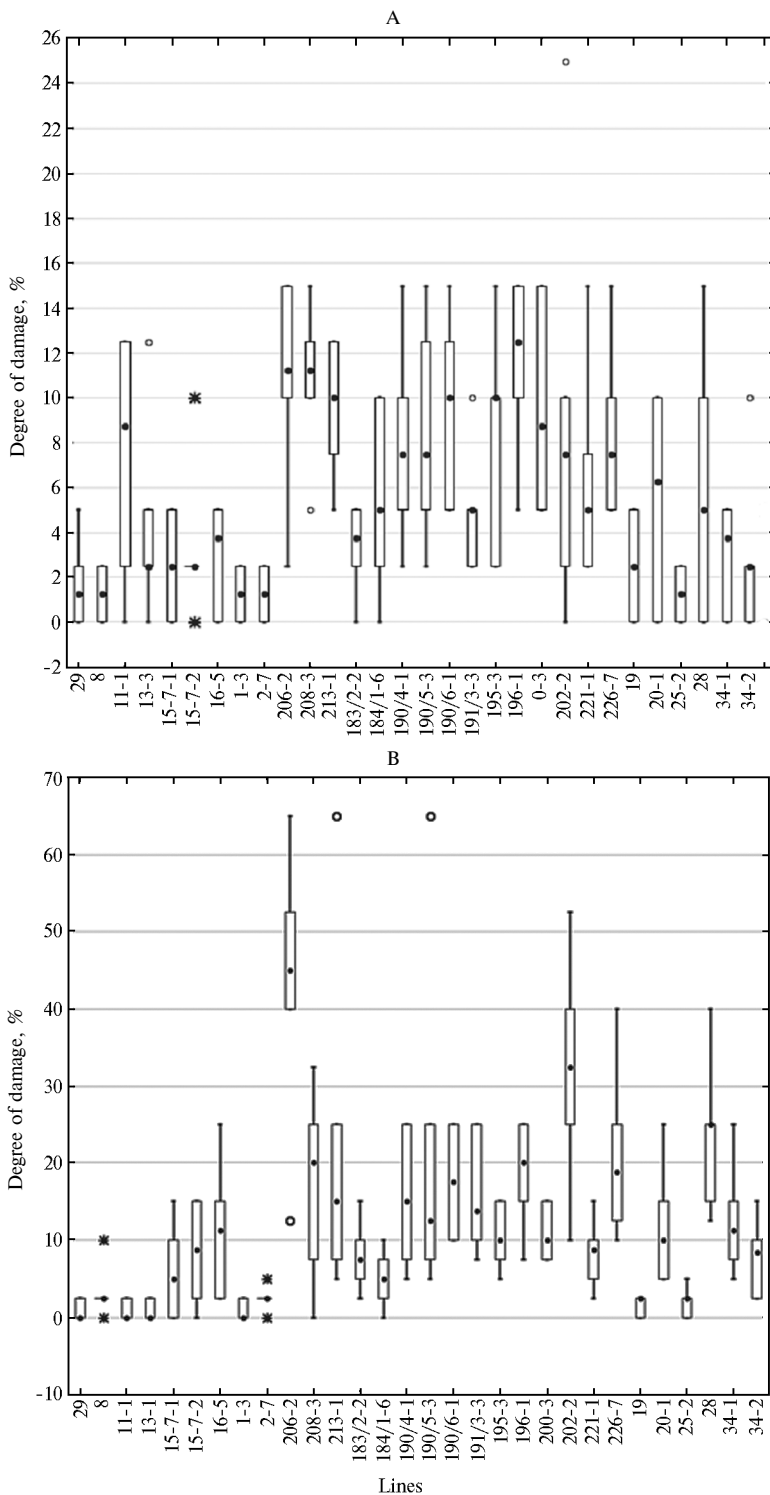


**Fig. 2.** Distribution of spring bread wheat lines with introgression of genetic material of *Triticum dicoccoides* (1), *T. dicoccum* (2), *T. durum* (3), and *T. kiharae* (4) by resistance to septoria (*Zymoseptoria tritici*) (A), brown rust (*Puccinia triticina*) (B), and powdery mildew (*Blumeria graminis*) (C): a — highly resistant, b — resistant, c — medium resistant, d — susceptible (the experimental field of the Institute of Genetics and Cytology NASB, 2012, 2014–2016, 2018, 2019).

All the studied lines exceeded the parental wheat varieties in resistance to the Belarusian population of Septoria blight, which suggests the presence of genes that determine resistance to Septoria blight in foreign genetic material transferred into the common wheat genome. This fact is of great interest, since in recent years, there has been an expansion of the area of Septoria blight of spring wheat and an increase in the disease, and the resistance reserve of cultivated varieties is almost exhausted [14]. Currently, genes for resistance to this pathogen are predominantly mapped in the genome of soft and durum wheat [15]. Wild species as donors of genes for resistance to Septoria blight are not sufficiently involved in wheat breeding.

Introgressive lines showed a certain degree of resistance to leaf rust in 2012 and 2014: 60.0% were highly resistant, 23.3% were resistant, 6.7% were moderately resistant, and 10.0% were susceptible. Of the 30 studied hybrid genotypes, only 3 were susceptible, i.e., lines 226-7 (*T. durum* × Belorusskaya 80), 206-2 (Pitic S62 × *T. dicoccum*) and 20-1 (*T. kiharae* × Saratovskaya 29). In these genotypes, the sensitivity to the leaf rust pathogen was even higher than in both parental forms. Possibly, genes for resistance to leaf rust, which are effective in the genome of tetraploid wheat, lose their protective properties upon introgression into the genome of a hexaploid species [16].

Among the lines created with the participation of *T. dicoccum*, the largest number of highly resistant ones (80%) was found. The lines *T. kiharae*/*T. aestivum* were also characterized by a high value for this indicator and were distributed in terms of resistance to leaf rust as follows: 66.6% were highly resistant, 16.7% were resistant, and 16.7% were susceptible (see Fig. 2, B). Only highly resistant and resistant lines were isolated in cross combinations based on *T. dicoccoides* (see Fig. 2, B). It should be noted that lines 29 (Rassvet × *T. dicoccoides* k-5199) and 8 (Saratovskaya 29 × *T. dicoccoides*) showed high resistance to *P. triticina*, despite the fact that the disease incidence of parental wheat varieties was 15%.



**Fig. 3. Degree of damage (%) by septoria (*Zyzoseptoria tritici*) (A) and powdery mildew (*Blumeria graminis*) (B) infection in lines of spring bread wheat with introgression of genetic material from *Triticum dicoccoides*, *T. dicoccum*, *T. durum*, and *T. kiharae*: ● — median, □ — 25-75%, I — maximum/minimum values, ○ — spikes, \* — extremes. For septoria, KW-H(29;180) = 86.57,  $p = 0.00$ ; for powdery mildew, KW-H(29;180) = 120.75,  $p = 0.0000$ , where KW-H is the Kruskal-Wallis test,  $p$  is the significance level (the experimental field of the Institute of Genetics and Cytology NASB, 2012, 2014-2016, 2018, 2019).**

Species of the genera *Triticum* and *Aegilops* are often used as sources of new genes for resistance to leaf rust [17-19], since most of the *Lr* genes identified to date are alien [5]. For example, among the introgressive lines of spring wheat with high genetic diversity in resistance to this disease studied by Russian scientists, there were carriers of *Lr* genes transmitted from *T. durum*, *T. persicum*, *T. timopheevi*, *Aegilops tauschii*, *T. kiharae* [20].

Introgressive wheat lines were found to be the most susceptible to powdery mildew. In three samples out of 30 (10.0%), the damage to the leaf blade exceeded 25%. The line 206-2 (Pitic S62 × *T. dicoccum*) had the highest sensitivity: on average, over the entire study period, the disease incidence was more than 40%, and in some years, it reached 65% (see Fig. 3, B). Susceptibility to powdery mildew was also shown by lines 202-2 (*T. durum* × CS) and 28 (*T. kiharae* × Festivalnaya). The maximum disease incidence for these genotypes was 40-50% and, as a rule, only in 2014. In the remaining years of observation, the indicator was 10-25% (see Fig. 3, B).

Unequal resistance to powdery mildew was shown by 27 lines: highly resistant genotypes accounted for 36.7%, 20.0% were resistant, 33.3% were medium resistant. The resistant genotypes could be attributed to the lines with the genetic material of *T. dicoccoides*. i.e., 71.4% of the lines showed a highly resistant type (see Fig. 2, C). All lines created with the participation of this genus species exceeded the parental wheat varieties in resistance to powdery mildew. Lines 29, 11-1, and 13-3 should be particularly highlighted, which, as a rule, were not affected by the pathogen throughout the entire study period. According to the literature, the wild emmer *T. dicoccoides* is one of the most immune to leaf-stem infections among the common wheat related species. It serves as a source of valuable genes for resistance to powdery mildew, which are expressed both at the seedling stage (*Pm26*, *Pm42*, and *Pm49*) and in adult plants (*Pm16*, *Pm30*, *Pm31*, *Pm36*, *Pm41*, *Pm42*, *Pm49*, and *Pm50*) [21, 22]. More than 90% of *T. dicoccoides* samples from the VIR world collection have field resistance to powdery mildew [23].

## 2. Two-way analysis of variance for resistance to leaf-stem infections in lines of spring common wheat with introgression of genetic material from *Triticum dicoccoides*, *T. dicoccum*, *T. durum*, and *T. kiharae* (the experimental field of the Institute of Genetics and Cytology NASB, 2012, 2014-2016, 2018, 2019)

Trait	Factor	df	SS	MS	F
Resistance to powdery mildew ( <i>Blumeria graminis</i> )	Genotype of the species of the genus <i>Triticum</i>	3	4175.65	1391.88**	9.90
	Weather conditions	5	2539.03	507.81**	3.61
	Genotype of the species of the genus <i>Triticum</i> × weather conditions	15	1405.61	93.71	0.67
	Error	156	21937.08	140.62	
Resistance to septoria ( <i>Zymoseptoria tritici</i> )	Genotype of the species of the genus <i>Triticum</i>	3	737.33	245.78**	12.68
	Weather conditions	5	278.63	55.73*	2.88
	Genotype of the species of the genus <i>Triticum</i> × weather conditions	15	313.60	20.91	1.08
	Error	156	3022.62	19.38	
Resistance to brown rust ( <i>Puccinia triticina</i> )	Genotype of the species of the genus <i>Triticum</i>	3	96.32	32.11	0.36
	Weather conditions	5	3707.39	741.48**	8.30
	Genotype of the species of the genus <i>Triticum</i> × weather conditions	15	457.16	30.48	0.34
	Error	156	13939.23	89.35	

Note. df — number of degrees of freedom, SS — sum of squares, MS — mean square, F — Fisher's test.

\* and \*\* Statistically significant at  $p < 0.05$  and  $p < 0.001$ , respectively.

The *T. kiharae*/*T. aestivum* lines were characterized by varying degrees of resistance to powdery mildew, i.e., 36.7% lines were highly resistant, 20.0% resistant, 33.3% moderately resistant. The lowest degree of resistance to powdery mildew was found for lines from combinations of crosses with the participation of *T. durum* (see Fig. 2, C): highly resistant genotypes accounted for only 16.7%

(lines 183/2-2 and 184/1-6). Introgressed resistance genes are increasingly being used to protect wheat varieties from powdery mildew. At present, it is known that 26 resistance genes from various species of the genus *Triticum*, 11 from *Aegilops* ssp., 5 from *Secale cereale* L., 6 from *Dasyphyrum villosum* (L.) Borbas, *Thinopyrum ponticum* (Popd.) Z.-W. Lin & R.-C. Wang, *Thinopyrum intermedium* (Host) Barkworth & DR Dewey, and *Agropyron cristatum* (L.) Gaertn. are introduced into the wheat genome [24].

A significant statistical difference in the degree of damage by powdery mildew and septoria was shown between the groups of lines created using the species *T. dicoccoides*, *T. dicoccum*, *T. durum*, *T. kiharae*, and under different weather conditions (Table 2).

When creating donors of genes for immunity to fungal diseases, samples with complex resistance to several pathogens are of particular value. Close relatives of wheat are often resistant to many fungal diseases. For example, at the Research Institute of Agriculture of the South-East (Saratov, Russia), more than 250 constant lines were created from the crossing of the wheat varieties Saratovskaya 29, Saratovskaya 55, and Saratovskaya 58 with *T. monococcum*, *T. dicoccum*, *T. timopheevii*, *T. persicum*, *T. militinae*. Of these, 178 lines with group resistance to diseases were selected against the background of strong natural epiphytotics and with artificial infection in a greenhouse [25]. Work on the creation of new varieties of wheat with complex resistance to stress factors of the environment by attracting wild relatives and other cultivated cereals is also carried out at the Lukyanenko Krasnodar Research Institute of Agriculture [9] and at the Siberian Research Institute of Agriculture [26].

In this study, 26.7% of introgressive lines (lines 11-1, 13-3, 15-7-2, 16-5, 34-1, 34-2, 183/2-2, 184/1-6) showed resistance to two diseases simultaneously, 23.3% (lines 29, 8, 15-7-1, 1-3, 2-7, 19, 25-2) to three diseases. The lines created with the participation of *T. dicoccoides* were characterized by group resistance. High resistance to three pathogens was found for lines 29, 8 and 15-7-1, to two – for lines 11-1, 13-3, 15-7-2, 16-5. The wild emmer *T. dicoccoides* is considered one of the ancestors of common wheat and is the source of genes for resistance to many diseases. Some genes for resistance to powdery mildew (*Pm16*, *Pm26*, *Pm30*, *Pm36*, *Pm41*), brown and yellow rust (*Lr53*, *Yr15*, *Yr35*, *Yr36*) have been mapped in *T. dicoccoides* using molecular markers [21, 27]. Currently, only a small part of these genes is introgressed into the genome of cultivated wheat. Also, group resistance to three pathogens was exhibited by two lines with *T. kiharae* genetic material (19 and 25-2) and two lines with *T. dicoccum* genetic material (1-3 and 2-7). It is known that *T. kiharae* isolated at VIR from the amphidiploid of *T. timopheevii* × *Ae. taushii* combines a complex of traits of both parental species, including resistance to most diseases and pests [28]. *T. dicoccum* (cultivated emmer) has been cultivated by humans since ancient times, and at present, its popularity is growing due to its unpretentiousness to growing conditions and valuable nutritional properties of grain [29]. The cultivated emmer is also of interest as a donor of genes for resistance to biotic and abiotic stresses. Thus, as a result of crossing with *T. dicoccum*, Russian scientists obtained 43 lines of spring bread wheat resistant to leaf rust and powdery mildew. With the participation of *T. dicoccum* and *T. persicum* species, 30 *T. aestivum* lines with complex resistance were obtained [30].

For lines with introgression of *T. durum* genetic material, high resistance was noted to only two pathogens, they are lines 183/2-2 and 184/1-6 (CS × *T. durum*), 221-1 (*T. durum* × Belorusskaya 80). In general, the lines created with the participation of this tetraploid species were characterized by the highest susceptibility to leaf-stem infections. A particularly high degree of damage was noted for



lines 202-2 (*T. durum* × CS) and 226-7 (*T. durum* × Belorusskaya 80). However, the influence of the variety should not be excluded either, since CS and Belorusskaya 80 were characterized by the highest susceptibility to fungal pathogens among the parent varieties of common wheat (see Table 1). The role of the recipient cultivar in the manifestation of resistance was also traced among the lines created with the participation of *T. dicoccoides*, *T. dicoccum*, and *T. kiharae*. Thus, for genotypes with genetic material *T. dicoccoides* and *T. kiharae* obtained on the basis of cultivars Rassvet and Saratovskaya 29, a higher resistance to powdery mildew and septoria was revealed than when using the Festivalnaya cultivar.

In addition to the fact that wheat varieties are characterized by unequal resistance to leaf-stem infections, they can affect the creation of distant hybrids: according to the literature, the fertility of hybrids, cytological stabilization, and the nature of recombination events in the hybrid genome depend on the parental wheat variety [31, 32]. All these processes lead to the creation of lines with different numbers, lengths, and localizations of fragments of foreign genetic material and, as a consequence, with different characters. In the works of a number of researchers, it was shown that the spectrum of substitutions and translocations was significantly different in introgressive lines resistant and susceptible to leaf rust and powdery mildew [33, 34]. It is obvious that the differences in resistance to fungal diseases revealed in the lines analyzed by the authors are also due to recombination events with the participation of chromosomes of wheat related species that occurred during the stabilization of hybrid genomes. The results of the authors' earlier assessment of the genetic diversity of the collection of introgression wheat lines using C-banding and SSR analysis methods indicate that most of the lines differ in both the number and localization of foreign fragments. It was found that introgression of foreign genetic material into the *T. aestivum* genome occurred both in the form of small regions and in the form of whole chromosomes (intergenomic substitutions) and their fragments (centric and terminal translocations). The highest frequency of introgression is shown for chromosomes 1A, 1B, 2A, 5B [11, 35]. In order to localize genetic factors that have a positive effect on resistance to fungal pathogens, a detailed analysis will be carried out in the future.

Thus, the lines of spring bread wheat containing the genetic material of *Triticum dicoccum*, *T. dicoccoides*, *T. durum*, and *T. kiharae* showed high resistance to brown rust (60.0% of lines), septoria (56.7% of lines), and powdery dew (36.7% of lines) against a natural infectious background in the Republic of Belarus. All studied lines, regardless of weather conditions, exceeded the parental varieties in resistance to the Belarusian population of the septoria pathogen, which suggests the presence of genes that determine resistance to septoria blight in the alien genetic material of the hybrid wheat genome. A significant statistical difference in the degree of damage by powdery mildew and septoria was shown between the groups of lines created using the species *T. dicoccoides*, *T. dicoccum*, *T. durum*, *T. kiharae*, and under different weather conditions. The largest number of genotypes highly resistant to powdery mildew and Septoria blight (71.4 and 85.7%, respectively) was found among the lines created with the participation of *T. dicoccoides*. Combined resistance to two diseases occurred in 26.7% of the studied introgression lines, to three diseases in 23.3%. These lines are of interest for breeding for resistance to fungal diseases.

## REFERENCES

1. Figueroa M., Hammond-Kosack K.E., Solomon P.S. A review of wheat diseases — a field perspective. *Molecular Plant Pathology*, 2018, 19(6): 1523-1536 (doi: 10.1111/mpp.12618).

2. Luck J., Spackman M., Freeman A., Trebicki P., Griffiths W., Finlay K., Chakraborty S. Climate change and diseases of food crops. *Plant Pathology*, 2011, 60(1): 113-121 (doi: 10.1111/j.1365-3059.2010.02414.x).
3. Röhl G., Batchelor W.D., Castro A.C., Simón M.R., Graeff-Hönninger S. Development and evaluation of a leaf disease damage extension in Cropsim-CERES wheat. *Agronomy*, 2019, 9(3): 120 (doi: 10.3390/agronomy9030120).
4. Duveiller E., Singh R.P., Nicol J.M. The challenges of maintaining wheat productivity: pests, diseases, and potential epidemics. *Euphytica*, 2007, 157(3): 417-430 (doi: 10.1007/s10681-007-9380-z).
5. McIntosh R.A., Dubcovsky J., Rogers J., Morris C., Xia X.C. *Catalogue of gene symbols for wheat: 2017 supplement*. Available: <http://www.shigen.nig.ac.jp/wheat/komugi/genes/symbolClassList.jsp>. Accessed: 20.05.2020.
6. Pakholkova E.V., Sal'nikova N.N., Kurkova N.A. Genetic structure of regional populations of *Mycosphaerella graminicola* (*Septoria tritici*), the septoria leaf blotch agent of wheat (*Triticum aestivum* L.). *Sel'skokhozyaistvennaya biologiya*, 2016, 51(5): 722-730 (doi: 10.15389/agrobiology.2016.5.722eng).
7. Stadlmeier M., Jørgensen L.N., Corsi B., Cockram J., Hartl L., Mohler V. Genetic dissection of resistance to the three fungal plant pathogens *Blumeria graminis*, *Zymoseptoria tritici*, and *Pyrrenophora tritici-repentis* using a multiparental winter wheat population. *G3 (Bethesda)*, 2019, 9(5): 1745-1757 (doi: 10.1534/g3.119.400068).
8. *Disease resistance in wheat*. I. Sharma (ed.). CABI, Wallingford, 2012.
9. Davoyan E.R., Davoyan R.O., Bebyakina I.V., Davoyan O.R., Zubanova YU.S., Zinchenko A.N., Kravchenko A.M. *Vavilovskii zhurnal genetiki i seleksii*, 2012, 16(1): 116-122 (in Russ.).
10. Pietrusinska A., Żurek M., Piechota U., Stowacki P., Smolinska K. Searching for diseases resistance sources in old cultivars, landraces and wild relatives of cereals. A review. *Annales UMCS sectio E Agricultura*, 2019, LXXIII(4): 45-60 (doi: 10.24326/asx.2018.4.5).
11. Leonova I.N., Badaeva E.D., Orlovskaya O.A., Roder M.S., Khotyleva L.V., Salina E.A., Shumnyi V.K. *Genetika*, 2013, 49(11): 1276-1283 (doi: 10.7868/S00116675813110131) (in Russ.).
12. Orlovskaya O.A., Solovei L.A., Dubovets N.I., Khotyleva L.V. *Molekulyarnaya i prikladnaya genetika*, 2019, 27: 52-61 (in Russ.).
13. Geshele E.E. *Osnovy fitopatologicheskoi otsenki v seleksii rastenii* [Fundamentals of phytopathological assessment in plant breeding]. Moscow, 1978 (in Russ.).
14. Arraiano L., Brown J. Sources of resistance and susceptibility to *Septoria tritici* blotch of wheat: resistance and susceptibility to Septoria of wheat. *Molecular Plant Pathology*, 2016, 18(2): 276-292 (doi: 10.1111/mpp.12482).
15. Ferjaoui S., M'Barek S.B., Bahri B., Slimane R.B., Hamza S. Identification of resistance sources to *Septoria tritici* blotch in old Tunisian durum wheat germplasm applied for the analysis of the *Zymoseptoria tritici*-durum wheat interaction. *Journal of Plant Pathology*, 2015, 97(3): 471-481 (doi: 10.4454/JPP.V97I3.028).
16. Herrera-Foessel S.A., Singh R.P., Huerta-Espino J., William H.M., Garcia V., Djurle A., Yuen J. Identification and molecular characterization of leaf rust resistance gene *Lr14a* in durum wheat. *Plant Disease*, 2008, 92(3): 469-473 (doi: 10.1094/PDIS-92-3-0469).
17. Gill B.S., Huang L., Kuraparthi V., Raupp W.J., Wilson D.L., Friebe B. Alien genetic resources for wheat leaf rust resistance, cytogenetic transfer, and molecular analysis. *Australian Journal of Agricultural Research*, 2008, 59(3): 197-208 (doi: 10.1071/AR07315).
18. Narang D., Kaur S., Steuernagel B., Ghosh S., Bansal U., Li J., Zhang P., Bhardwaj S., Uauy C., Wulff B.B.H., Chhuneja P. Discovery and characterisation of a new leaf rust resistance gene introgressed in wheat from wild wheat *Aegilops peregrina*. *Sci. Rep.*, 2020, 10(1): 7573 (doi: 10.1038/s41598-020-64166-2).
19. Aktar-Uz-Zaman M., Tuhina-Khatun M., Hanafi M.M., Sahebi M. Genetic analysis of rust resistance genes in global wheat cultivars: an overview. *Biotechnology & Biotechnological Equipment*, 2017, 31(3): 431-445 (doi: 10.1080/13102818.2017.1304180).
20. Gul'tyaeva E.I., Sibikeev S.N., Druzhin A.E., Shaidayuk E.L. Enlargement of genetic diversity of spring bread wheat resistance to leaf rust (*Puccinia triticina* Eriks.) in Lower Volga region. *Sel'skokhozyaistvennaya biologiya [Agricultural Biology]*, 2020, 55(1): 27-44 (doi: 10.15389/agrobiology.2020.1.27eng).
21. Peng J.H., Sun D.F., Peng Y.L., Nevo E. Gene discovery in *Triticum dicoccoides*, the direct progenitor of cultivated wheats. *Cereal Research Communications*, 2013, 41(1): 1-22 (doi: 10.1556/CRC.2012.0030).
22. Hua W., Liu Z., Zhu J., Xie C., Yang T., Zhou Y., Duan X., Sun Q., Liu Z. Identification and genetic mapping of *pm42*, a new recessive wheat powdery mildew resistance gene derived from wild emmer (*Triticum turgidum* var. *dicoccoides*). *Theor. Appl. Genet.*, 2009, 119: 223-230 (doi: 10.1007/s00122-009-1031-4).
23. Akhmedov M.A. *Genetika*, 1998, 34(10): 1376-1382 (in Russ.).
24. Kang Y., Zhou M., Merry A.M., Barry K.M. Mechanisms of powdery mildew resistance of wheat — a review of molecular breeding. *Plant Pathology*, 2020, 69(4): 611-617 (doi: 10.1111/ppa.13166).
25. Markelova T.S., Ivanova O.V., Baukenova E.A., Naryshkina E.A., Salmova M.F. *Agrarnyi vest-*

- nik Yugo-Vostoka*, 2014, 1-2: 25-27 (in Russ.).
26. Belan I.A. *Rossiiskaya sel'skokhozyaistvennaya nauka*, 2016, 1: 5-8 (in Russ.).
  27. Ben-David R., Xie W., Peleg Z., Saranga Y., Dinooor A., Fahima T. Identification and mapping of *PmG16*, a powdery mildew resistance gene derived from wild emmer wheat. *Theor. Appl. Genet.*, 2010, 121(3): 499-510 (doi: 10.1007/s00122-010-1326-5).
  28. Liu X., Zhang M., Liu X., Li H., Hao M., Ning Sh., Yuan Zh., Liu D., Wu B., Chen X., Chen W., Zhang L. Molecular cytogenetic identification of newly synthetic *Triticum kiharae* with high resistance to stripe rust. *Genetic Resources and Crop Evolution*, 2018, 65: 1725-1732 (doi: 10.1007/s10722-018-0649-y).
  29. Smekalova T.N., Kobylanskii V.D. *Trudy po prikladnoi botanike, genetike i selektsii*, 2019, 180(4): 148-151 (in Russ.).
  30. Markelova T.S., Vedeneeva M.L., Kirillova T.V. *Vestnik zashchity rastenii*, 2003, 3: 25-30 (in Russ.).
  31. Bashir T., Mishra R.C., Hasan M.M., Mohanta T.K., Bae H. Effect of hybridization on somatic mutations and genomic rearrangements in plants. *International Journal of Molecular Science*, 2018, 19(12): 3758 (doi: 10.3390/ijms19123758).
  32. Whitford R., Fleury D., Reif J.C., Garcia M., Okada T., Korzun V., Langridge P. Hybrid breeding in wheat: technologies to improve hybrid wheat seed production. *Journal of Experimental Botany*, 2013, 64(18): 5411-5428 (doi: 10.1093/jxb/ert333).
  33. Badaeva E.D., Budashkina E.B., Bilinskaya E.N., Pukhalskiy V.A. Intergenomic chromosome substitutions in wheat interspecific hybrids and their use in the development of a genetic nomenclature of *Triticum timopheevii* chromosomes. *Russian Journal of Genetics*, 2010, 46(7): 769-785.
  34. Petrash N., Leonova I., Adonina I., Salina E. Effect of translocations from *Aegilops speltoides* Tausch on resistance to fungal diseases and productivity in common wheat. *Russian Journal of Genetics*, 2016, 52(12): 1253-1262 (doi: 10.1134/S1022795416120097).
  35. Orlovskaya O.A., Dubovets N.I., Solovey L.A., Bondarevich E.B., Leonova I.N. Molecular cytogenetic analysis of alien introgressions in common wheat lines with *T. kiharae* genetic material. *Proc. of the Fifth International scientific conference «Current challenges in plant genetics, genomics, bioinformatics, and biotechnology»*. A. Kochetov, E. Salina (eds.). Novosibirsk, 2019: 235-237.