

DOI: 10.12731/2658-6649-2023-15-4-158-179

UDC 633.11:632.9



Original article

POSTULATION OF YR RESISTANCE GENES TO STRIPE RUST IN 12 COMMERCIAL WHEAT CULTIVARS OF RUSSIAN BREEDING

I.P. Matveeva, G.V. Volkova, Yu.S. Kim, Ya.V. Yakhnik

Stripe rust (Puccinia striiformis f. sp. tritici) is a common wheat disease of economic importance in all world wheat production regions. In most of the regions stripe rust causes yield losses of 10-70 %, depending on the time infection occur, host susceptibility, disease development, and the duration of the epidemics. In South Russia even in unfavourable conditions for the pathogen, stripe rust occurred in the region every year, and in some areas there are foci of the disease with of up to 50% severity.

Phytopathological testing is one of the least expensive and most effective methods for the rapid identification of juvenile resistance genes in varieties against pathogens. It allows to obtain detailed information about the genetics of the host and pathogen in a short time. In the research Yr resistant genes and its combinations were postulated in winter wheat varieties of Russian breeding to North-Caucasus population of stripe rust by this method.

Purpose of this study was identification of known stripe rust resistance genes in 12 commercial winter wheat cultivars by phytopathological testing.

Material and methods: The postulation of known resistance genes was carried out in a greenhouse complex (seedling stage) and at the research station (adult plant stage) of the Laboratory of Plant Immunity to Diseases of the Federal Scientific Center for Biological Plant Protection (Krasnodar).

For postulation, we chose the method by Dubin et al. (1989), based on the comparison of response types of differential cultivars and studied varieties to Pst isolates.

Results. In 10 out of 12 winter wheat varieties of Russian breeding, 13 stripe rust resistance genes and their combinations were postulated.: Yr3, Yr3a, Yr6, Yr32, Yr2+6, Yr2+9, Yr39+Alp, Yr4+12, Yr4b, Yr3a+4a+H46, YrA, YrSp, YrSU. The following resistance genes have not been identified: Yr2, Yr5, Yr10, Yr10+Mor, Yr24, Yr27, Yr25+32, since no isolates virulent to carriers of these genes were isolated from the North Caucasian population of *P. striiformis*; and they are high-

ly effective against this population. Highly effective (Yr3, Yr2+9, Yr3a, Yr4+12, Yr3a+4a+H46) resistance genes were identified in the Kurs, Morozko, and Step' varieties. We note a combination of effective Yr2+6 genes in the Gurt variety.

In field conditions, high resistance (degree of damage up to 10%) to the North Caucasian population of the stripe rust pathogen was shown by lines and differential cultivars containing the following resistance genes: Yr2, Yr3, Yr8, Yr10, Yr24, Yr25, Yr27, Yr10+Mor, Yr3a, Yr25+32, Yr3a+4a+H46, Yr3c+Min, Yr4+12, Yr7+25, Yr8+19, 8+6+25, YrSp. Due to the low degree of damage, these genes and their combinations are classified as highly effective and can be involved in the breeding process to create new resistant varieties. Varieties containing these genes can also be recommended for breeders and used in production for effective disease control.

Keywords: gene postulation; genetic resistance; pathotype; *Puccinia striiformis*; resistance; stripe rust; wheat

For citation. Matveeva I.P., Volkova G.V., Kim Yu.S., Yakhnik Ya.V. Postulation of Yr Resistance Genes to Stripe Rust in 12 Commercial Wheat Cultivars of Russian Breeding. *Siberian Journal of Life Sciences and Agriculture*, 2023, vol. 15, no. 4, pp. 158-179. DOI: 10.12731/2658-6649-2023-15-4-158-179

Научная статья

ПОСТУЛИРОВАНИЕ YR-ГЕНОВ УСТОЙЧИВОСТИ К ЖЕЛТОЙ РЖАВЧИНЕ ПШЕНИЦЫ В 12 КОММЕРЧЕСКИХ СОРТАХ РОССИЙСКОЙ СЕЛЕКЦИИ

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Желтая ржавчина (*Puccinia striiformis* f. sp. *tritici*) является распространенным заболеванием пшеницы, имеющим экономическое значение во всех регионах мира, возделывающих данную культуру. В большинстве регионов желтая ржавчина вызывает потери урожая от 10 до 70 % в зависимости от времени заражения, восприимчивости растения-хозяина, степени развития болезни и продолжительности эпифитотий. На юге России даже в годы с неблагоприятными условиями желтая ржавчина встречается ежегодно, а в отдельных районах встречались очаги с распространением до 50 %.

Фитопатологическое тестирование является одним из наименее дорогих и наиболее эффективных методов быстрой идентификации ювенильных

генов устойчивости сортов к патогенам. Он позволяет в короткие сроки получить подробную информацию о генетике хозяина и возбудителя. В исследованиях этим методом постулированы гены устойчивости Yr и их комбинации у сортов озимой пшеницы российской селекции к северокавказской популяции желтой ржавчины.

Целью исследований стала идентификация известных генов устойчивости к желтой ржавчине в 12 коммерческих сортах озимой пшеницы методом фитопатологического тестирования.

Материалы и методы. Постулирование известных генов устойчивости проводили в тепличном комплексе (ювенильная стадия) и на полево-м станции (стадия взрослых растений) лаборатории иммунитета растений к болезням Федерального научного центра биологической защиты растений (г. Краснодар). Для постулирования был использован метод Дубина с соавторами (1989), основанный на сравнении типов реакции сортов-дифференциаторов и изучаемых сортов на изоляты возбудителя желтой ржавчины пшеницы.

Результаты. В 10 из 12 сортов озимой пшеницы российской селекции были постулированы 13 генов устойчивости к желтой ржавчине и их комбинаций: Yr3, Yr3a, Yr6, Yr32, Yr2+6, Yr2+9, Yr39+Alp, Yr4+12, Yr4b, Yr3a+4a+H46, YrA, YrSp, YrSU. Не выявлены гены устойчивости Yr2, Yr5, Yr10, Yr10+Mor, Yr24, Yr27, Yr25+32, так как из северокавказской популяции *P. striiformis* не было выделено изолятов, вирулентных к носителям этих генов, и они являются высокоэффективными по отношению к данной популяции. В сортах Курс, Морозко и Степь были выявлены высокоэффективные (Yr3, Yr2+9, Yr3a, Yr4+12, Yr3a+4a+H46) гены устойчивости. В сорте Гурт – сочетание эффективных генов Yr2+6.

В условиях поля высокую устойчивость (степень поражения до 10 %) к северокавказской популяции возбудителя желтой ржавчины проявили линии и сорта-дифференциаторы, содержащие гены устойчивости Yr2, Yr3, Yr8, Yr10, Yr24, Yr25, Yr27, Yr10+Mor, Yr3a, Yr25+32, Yr3a+4a+H46, Yr3c+Min, Yr4+12, Yr7+25, Yr8+19, 8+6+25, YrSp. Из-за низкой степени поражения данные гены и их сочетания относятся к категории высокоэффективных и эффективных и могут быть вовлечены в селекционный процесс для создания новых устойчивых сортов. Сорта, содержащие данные гены, также могут быть рекомендованы практической селекции и использованы в производстве для эффективного контроля заболевания.

Ключевые слова: постулирование генов; генетическая устойчивость; патотипы; *Puccinia striiformis*; устойчивость; желтая ржавчина; пшеница

Для цитирования. Матвеева И.П., Волкова Г.В., Ким Ю.С., Яхник Я.В. Постулирование Yr-генов устойчивости к желтой ржавчине пшеницы в 12 коммерческих сортах российской селекции // *Siberian Journal of Life Sciences and Agriculture*. 2023. Т. 15, №4. С. 158-179. DOI: 10.12731/2658-6649-2023-15-4-158-179

Introduction

Cereal rusts are one of the biggest threats to food security and the most economically important group of wheat diseases worldwide [19]. The fungal pathogen *Puccinia striiformis* f.sp. *tritici* West, causing stripe (yellow) rust, is among the most damaging diseases in cereal crops. It's common in all major grain-producing regions of the world. Stripe rust develops best in foothill zones with moderate temperatures and high humidity. Yield losses due to stripe rust epidemics range from 10-70% up to 100% [9]. Recent research shows that the pathogen has become even more aggressive [26].

Stripe rust was rare in Russia, primarily in the North Caucasus, until the end of the 60s. However, episodic manifestations of the pathogen have still been registered [5]. Since 1990, in the North Caucasus, including Krasnodar Krai, there has been a tendency to expand the range of the pathogen [7, 8, 25]. Since 2005–2007, stripe rust was recorded in Leningrad (Gulyaeva et al., 2007), Pskov and Novgorod regions [2].

In recent years, the incidence of the disease in the North Caucasus continues to grow. This is due to the cultivation of susceptible varieties, the formation of aggressive races, climate change in the region, and the introduction of infection from adjacent territories [8, 24].

Variety resistance plays an important role among the known methods for effective disease control. It prevents the occurrence of epidemics and reduces the number of chemical treatments. Rusts are predisposed to the intensive formation of new, more aggressive physiological races, which negatively affects the resistance of varieties [9]. In this regard, a regular search for resistance genes is required for breeding new varieties and understanding the genetic potential of the existing ones.

Phytopathological testing (postulation) is one of the least expensive and most effective methods for the rapid identification of juvenile resistance (R) genes against pathogens. This approach allows obtaining detailed information about the genetics of the host and pathogen in a short time [17]. The postulation of the R genes in wheat cultivars has been actively used since the discovery of Flor's gene-for-gene theory [14]. The method is based on the complementary interaction of host plant R genes and virulence genes of pathogen isolates [10].

The DNA marker method is also widely used to identify rust resistance genes in wheat and related plants. Tyryshkin et al., noted significant differences in the postulation of effective *Lr9* and *Lr41* resistance genes in *Aegilops* accessions using a phytopathological test and DNA markers. They concluded that the results of the latter method cannot be considered as reliable evidence for the presence/absence of specific resistance gene alleles in wheat related plants [6].

In turn, the accuracy of phytopathological testing depends on the genetic diversity of differential cultivars and isolates used. Most often, close isogenic lines are the best option as differential cultivars. However, they do not accurately identify R genes if polygenic resistance is present in the tested varieties. Differential cultivars with combinations of genes are more suitable for the task.

The best results are obtained when isolates with the maximum difference in the set of virulence genes are used in the experiment [17]. A phytopathological test is only possible if there are genotypes of pathogens marked by virulence to effective R genes. It is considered to be a reliable method for identifying specific resistance genes [6, 22, 23]. Although recent papers by Russian researchers indicate that this method is insufficiently informative for characterizing the genetic determination of resistance without the use of molecular approaches [15, 21].

The postulation method is widely used both in the world [12, 17, 19, 26] and in Russia [6, 8, 24] and is often combined with molecular genetic analysis. Sharma et al. identified *Yr2*, *Yr6*, *Yr8*, *Yr9*, *Yr10*, *Yr15*, *YrA*, *YrSU* stripe rust resistance genes in 52 lines of emmer wheat by postulation method [20]. In 2012, Dawit et al. postulated *Yr2*, *Yr3a*, *Yr4a*, *Yr6*, *Yr7*, *Yr8*, *Yr9*, *Yr27*, *Yr32*, and *YrSU* in 22 Ethiopian wheat varieties [10]. In 2016, Australian scientists postulated *Yr1* and *Yr27* resistance genes in 4 out of 51 spring wheat varieties [19].

Since the R genes postulation is carried out at the seedling stage, differential cultivars with juvenile R genes are involved in the experiment. Differential cultivars with genes for race-specific (*Yr: 11, 12, 13, 14, 16*) and non-specific (*Yr: 18, 29*) APR are excluded, as these genes work at later stages of host plant development [12, 17].

In this paper we aim to identify the known R genes (*Yr*) to the wheat stripe rust pathogen in 12 widely distributed varieties of Russian breeding by phytopathological testing.

Materials and Methods

Seed material. We selected 12 widely released varieties of Russian breeding included in the State Register of the Russian Federation in 2015-2021: 7 varieties of winter wheat bred by the National Grain Center named after. P.P. Lukyanenko (Krasnodar), 3 varieties – by Federal Rostov Agrarian Scientific

Center (Rostov region), 1 variety -by the North Caucasian Federal Scientific Agrarian Center (Stavropol Krai), and 1 variety -by the Prikum Experimental Breeding Station (Stavropol Krai). See Table 1.

Table 1.

List of soft wheat fibers included in the phytopathological survey, 2021

№	Variety	Accession	Year of inclusion in the state register	Pedigree
P. P. Lukyanenko National Grain Center				
1	**Kavalerka	lutescens	2019	(Lutescens 9274h222 / Lutescens 9394h13) / (Lutescens 7643hG12-12 / Krasnodarskaja 99)
2	**Karavan	lutescens	2018	L.918yav2 / Zorjana nosovskaja
3	** Step'	lutescens	2018	L.369-93k14 x Back Palenque
4	**Markiz	lutescens	2019	Irishka x Yunona
5	**Gurt	lutescens	2016	Tanja x Frontana
6	**Kurs	lutescens	2015	(Rosinka tarasovskaja / Krasnodarskaja 99) / (Lutescens 9269 h 7-19 / Batko)
7	**Morozko	lutescens	2015	(Lutescens 7278 h 111 / Lutescens 8989 h 177) / (KS 91 WGRS 21 / Krasnodarskaja 99)
Prikum Experimental Breeding Station				
8	**Korona	erythropermum	2019	(Don 95 / Lutescens r-126768) / (Lutescens r-140356 / Ukrainka odesskaja)
North Caucasian Federal Scientific Agrarian Center				
9	**Karolina 5	erythropermum	2017	Krasnodarskaja 99 x Seljanka odesskaja
Federal Rostov Agricultural Research Center				
10	**Akapella	erythropermum	2020	1334/07 x Gubernator Dona
11	**Bogema	lutescens	2021	Spalah/Donskaja Lira
12	** Palmira 18	-	on trial	911/16 Delta /782/00
*according to http://wheatpedigree.net/ (last updated 1.09.2017, accessed 06.10.2021)				
** according to https://glavagronom.ru/ (accessed 06.10.2021)				

We used 38 differential cultivars (global, European, Australian and additional sets) with *Yr* R genes and their combinations for phytopathological testing (Table 2).

Table 2.

List of differential cultivars used to postulate *Yr R* genes in winter wheat varieties, 2021

Variety/ line	<i>Yr</i> -gene	Variety/ line	<i>Yr</i> -gene
Chinese 166	1	Heines VII	2+ <i>HVII</i>
Kalyansona	2	Carstens V	25+32
Felix	3	Alpowa	39+ <i>Alp</i>
NIL Avocet S*	5	Bon Fermier	3a
NIL Avocet S*	6	Hybrid 46	3b+4a+ <i>H46</i>
NIL Avocet S*	8	Nord Despres	3a+4a+ <i>ND</i>
NIL Avocet S*	9	Vilmorin 23	3a+ <i>V23</i>
NIL Avocet S*	10	Minister	3c+ <i>Min</i>
NIL Avocet S*	15	Mega	4+12
NIL Avocet S*	17	Vuka	4b
Lemhi	21	Lee	7+22+23
NIL Avocet S*	24	Reichesberg 42	7+25
Carina	25	Compare	8+19
NIL Avocet S*	26	Heines Peko	8+6+25
NIL Avocet S*	27	NIL Avocet R*	<i>A</i>
NIL Avocet S*	32	Daws	<i>Da1+Da2</i>
Moro	10+ <i>Mor</i>	Strubes Dockkopf	<i>SD</i>
Heines Kolben	2+6	Spalding Prolific	<i>Sp</i>
Clement	2+9	Suwon 92 x Omar	<i>SU</i>

Since the experiment was carried out at the seedling stage, race-specific *Yr11*, *Yr12*, *Yr13*, *Yr14*, *Yr16* and race-non-specific *Yr18* and *Yr29* APR genes were excluded.

Pathogenic material. To postulate the known *Yr R* genes, 17 races of the North Caucasian population of *Puccinia striiformis* with a different set of virulence genes were taken from the “State Collection of Entomocariphages and Microorganisms” (Table 3): 0E0, 0E4, 1E8, 6E0, 12E8, 15E0, 32E0, 32E59, 33E0, 37E129, 38E194, 39E2, 46E0, 97E226, 129E0, 173E28, 239E218.

Classification of isolates by racial composition was carried out according to *Johnson et al.* using a standard set of differential cultivars. Reproduction and accumulation of spore biomaterial was performed in the greenhouse complex on the control variety KAW [16]

Inoculation. The seed material of differential cultivars and test varieties was germinated in a humid chamber at +23°C. Then, three-day-old seedlings were sown with tweezers in flowerpots with sand 25 ml, five grains each. The flowerpots were placed in a tray with Knop’s nutrient solution and into a climatic chamber (Binder KBF 720), at +20°C [8].

Table 3.

Race virulence formulas of the North Caucasian population *P. striiformis*

Race	Virulence to <i>Yr</i> genes
0E0*	<i>4b, 4+12, 17, 21, 25, 6, 39+Alp</i>
0E4	<i>4b, 6, 8, 9, 15, 17, 25, 26, 39+Alp, 8+6+25</i>
1E8	<i>4b, 1, 25, 3a+4a+ND+12</i>
6E0	<i>4b, 17, 21, 2+6, 7+22+23</i>
12E8	<i>9, 21, 25, 2+6, 39+Alp, 3a+4a+ND+12, 3a+V23</i>
15E0	<i>4b, 1, 2+6, 39+Alp, 3a+V23, 7+22+23</i>
32E0	<i>4b, 8, 9, 21, 25, 39+Alp, 3a, SD</i>
32E59	<i>4b, 6, 21, 26, 25+32, 39+Alp, 3a, 3a+4a+H46, 3a+4a+ND+12, 3c+Min, 7+25, 8+19, A, Da1+Da2, SD</i>
33E0	<i>4b, 1, 32, 39+Alp, SD</i>
37E129	<i>4b, 1, 3, 6, 9, 17, 21, 25, 32, 2+6, 2+VII, 39+Alp, 3a, 3a+4a+H46, 4+12, A, SD</i>
38E194	<i>4b, 6, 15, 21, 25, 26, 32, 2+6, 2+VII, 3a, 4+12, 7+22+23, 7+25, A, SD, Sp</i>
39E2	<i>4b, 1, 8, 9, 25, 2+6, 39+Alp, 3a+4a+H46, 7+22+23, SD</i>
46E0	<i>4b, 15, 21, 25, 2+6, 39+Alp, 3a+V23, 7+22+23, SD</i>
97E226	<i>4b, 1, 6, 9, 21, 25, 26, 32, 2+VII, 25+32, 39+Alp, 3a, 4+12, 7+25, SD, Sp, SU</i>
129E0	<i>4b, 1, 21, 2+9, 3a</i>
173E28	<i>4b, 1, 3, 6, 9, 25, 26, 32, 2+6, 2+9, 39+Alp, 3a, 3a+4a+ND+12, 3a+V23, 3c+Min, 4+12, 8+19, 8+6+25, SD</i>
239E218	<i>4b, 1, 3, 6, 9, 15, 17, 21, 25, 26, 32, 2+6, 2+9, 2+VII, 39+Alp, 3a, 3a+4a+ND+12, 3a+V23, 4+12, 7+22+23, 7+25, 8+19, A, Da1+Da2, SD, Sp, SU</i>
* - virulence genes of four isolates belonging to this race PST	

Plants in the 1-2 leaf phase were inoculated with a water-spore suspension at the rate of 5 mg of spores per 10 ml of water. Infected plants were incubated for 24 hours at +9...+12 °C and relative humidity 100%, then they were again transferred to a climatic chamber with a day/night cycle of 14/10 h, +17...+12 °C, humidity 80% [19].

Plant record. Records were made 14-16 days after inoculation using a modified 4-point scale adapted from McNeal *et al.* [18]: 0 - highly resistant type of reaction, no signs of the disease; 1 - necrosis with rare and small pustules; 2 - chlorosis and necrosis with an average number of pustules; 3 - copious amounts of pustules and chlorosis; 4 - extensive confluent pustules, chlorosis is minimal or absent. Thus, reaction types 0–2 were considered avirulent, 3–4 were considered virulent [12, 19].

According to Flor's gene-on-gene theory [13], the gene postulation was conducted using the method proposed by Dubin *et al* [11]. Here, the presence

of *Yr*-genes was determined by the comparison of response types of the studied variety and the differential cultivar (the presence of a specific gene in which is precisely known). If the response type on one of the leaves differed from the others, then the response type of the majority of plants was recorded.

Field experiment. A field experiment was conducted in 2020-2021 at a research station with an artificial infectious background of wheat stripe rust (FRCBPP, Krasnodar), (Figure 1).

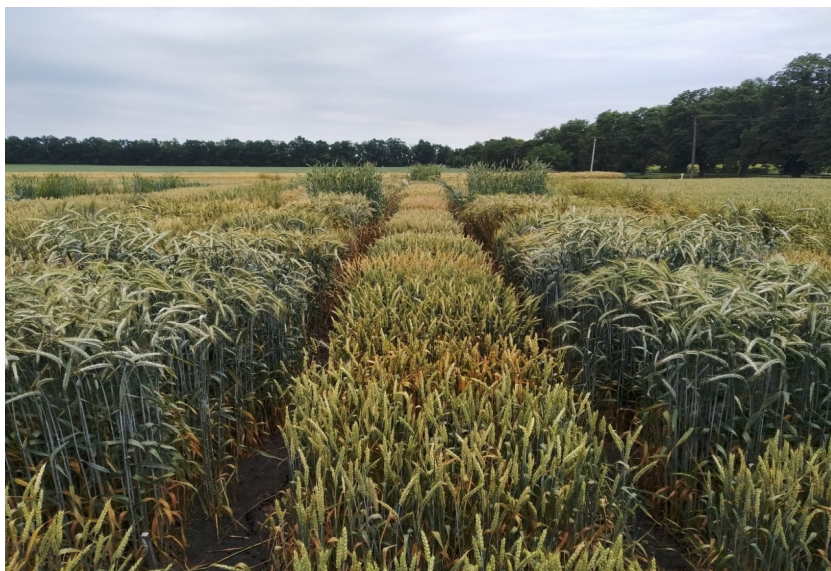


Figure 1. Research station with an artificial infection background *P. striiformis* (FRCBPP, Krasnodar), 2021

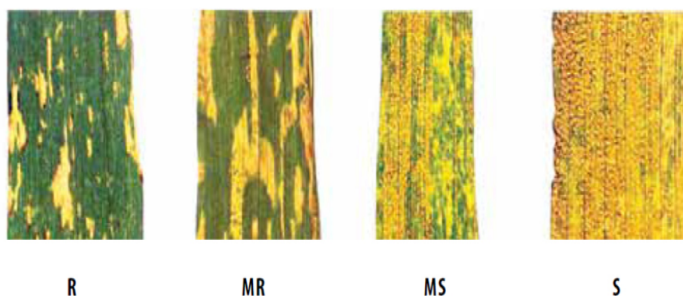


Figure 2. CIMMYT scale to account for *P. striiformis* damage to grain crops [30].

3	Felix	3	0	3	0	0	0	0	0	0	0	0	2	3	0	1	2	1	1	2	2	0	R
5	NIL Avocet S*	1	0	1	0	0	0	0	0	0	0	2	0	0	0	0	0	1	0	1	0	0	R
6	NIL Avocet S*	3	0	3	0	0	0	3	0	0	0	2	0	3	1	3	2	3	3	3	3	15	MR
8	NIL Avocet S*	0	3	0	0	1	0	0	2	0	2	0	3	0	0	0	0	3	0	0	0	0	R
9	NIL Avocet S*	3	3	3	0	2	0	0	1	3	2	2	3	3	0	2	0	3	2	3	0	50	S
10	NIL Avocet S*	0	0	1	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	R
15	NIL Avocet S*	1	2	2	0	2	0	0	0	0	0	3	0	0	3	0	3	0	3	0	2	25	MR
17	NIL Avocet S*	2	0	3	1	1	3	0	0	0	2	0	2	3	3	1	1	3	0	2	2	25	MR
21	Lemhi	2	0	3	3	0	3	0	0	3	3	0	3	3	0	3	3	2	3	3	2	40	MS
24	NIL Avocet S*	0	0	0	1	1	0	0	0	0	0	0	2	0	0	0	0	2	0	0	0	10	R
25	Carina	3	3	3	3	3	2	0	0	3	3	0	3	3	0	3	0	3	2	3	3	5	R
26	NIL Avocet S*	3	0	1	0	0	0	0	0	0	0	0	3	0	3	2	3	3	3	0	40	MS	
27	NIL Avocet S*	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	R
32	NIL Avocet S*	3	2	3	1	1	0	0	1	0	0	3	0	3	0	3	1	2	2	3	2	40	MS
10+Mor	Moro	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	R
2+6	Heines Kolben	3	3	3	0	1	3	0	3	3	3	0	2	3	0	3	0	2	2	1	15	MR	
2+9	Clement	3	0	2	0	0	0	0	0	0	0	2	0	3	0	2	3	0	2	2	0	15	MR
2+VII	Heines VII	1	0	3	0	0	0	0	0	0	0	0	3	0	3	0	0	2	3	0	20	MR	
25+32	Carstens V	0	0	2	0	0	0	0	0	2	0	0	1	2	0	2	0	0	3	3	0	5	R
39+Alp	Alpowa	3	3	3	0	0	0	3	3	3	3	3	4	0	0	0	3	4	3	3	60	S	
3a	Bon Fermier	3	0	3	0	0	0	0	0	0	0	3	4	0	3	3	2	3	3	0	10	R	
3b+4b+H46	Hybrid 46	1	3	3	0	0	0	0	2	0	2	0	2	0	2	0	0	3	2	0	0	R	
3a+4a+ND+12	Nord Despres	3	0	2	0	3	0	0	0	3	2	0	2	3	0	2	0	0	3	0	2	10	R
3a+V23	Vilmorin 23	3	0	2	1	1	2	0	3	3	3	2	2	3	0	2	0	2	2	2	10	R	
3c+Min	Minister	3	0	2	0	0	0	0	0	0	0	0	1	2	0	0	0	0	3	2	2	0	R
4+12	Mega	3	0	3	0	0	0	0	0	0	0	0	3	0	3	2	2	0	3	3	5	R	
7+22+23	Lee	2	3	0	0	2	3	1	3	1	3	0	2	3	0	3	0	1	0	2	2	30	MR
7+25	Reichesberg 42	2	0	2	0	0	0	0	0	0	0	0	1	4	0	3	0	0	3	3	0	5	R
8+19	Compare	3	0	2	0	0	0	0	0	0	0	2	0	3	0	2	0	2	3	2	0	10	R
8+6+25	Heines Peko	3	1	1	0	0	0	0	0	0	0	1	0	2	0	2	0	3	0	2	0	5	R
A	NIL Avocet R*	2	0	3	0	0	1	0	0	0	0	1	0	3	0	3	0	0	3	0	0	20	MR
Da1+Da2	Daws	1	0	2	0	0	0	0	1	0	0	2	0	3	0	2	0	0	3	2	0	0	R
SD	Strubes Dickkopf	3	3	3	0	0	0	0	0	0	3	3	3	3	2	3	1	0	3	3	2	35	MS
Sp	Spalding Prolific	1	0	2	0	0	0	0	0	0	0	2	2	3	0	3	0	0	2	3	2	1	R
SU	Suwon x Omar	1	0	1	0	0	0	0	0	0	0	2	0	3	0	2	0	0	3	0	35	MS	

As a result of plant infection with pathogen races, we did not reveal isolates virulent/avirulent to all differential wheat cultivars. The *Yr2*, *Yr5*, *Yr10*, *Yr10+Mor*, *Yr24*, *Yr27*, *Yr25+32* genes were highly effective, since they showed a stable response type on all races of wheat stripe rust included in the experiment.

Table 5.

Response of seedlings of 12 winter wheat varieties inoculated with 20 virulent isolates of *P. striiformis* (FRCBPP greenhouse complex, 2021)

Variety	173E28	39E2	37E129	0E0	1E8	6E0	0E0	15E0	12E8	46E0	33E0	32E0	239E218	0E0	38E194	129E0	0E4	32E59	97E226	0E0	Field evaluation	
Akapella	3	0	2	3	3	3	2	3	3	3	3	3	4	0	0	2	2	3	0	0	40 MS	
Bogema	3	3	3	0	2	3	3	3	3	2	3	3	0	3	0	0	2	0	0	0	35 MS	
Gurt	3	0	1	0	0	0	0	0	0	0	2	0	3	0	2	3	0	3	2	3	40 MS	
Kavalerka	1	0	0	0	3	0	0	2	2	2	0	1	3	0	0	0	0	1	3	0	10 R	
Karavan	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	1R	
Karolina	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	2	3	0	0	30 MR	
Korona	1	0	2	0	0	2	0	0	0	0	0	0	3	0	3	0	0	2	3	0	35 MS	
Kurs	3	0	3	0	0	0	0	0	0	0	3	0	4	0	2	0	0	3	0	1	5 R	
Markiz	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2	1	0 R
Morozko	3	0	3	1	1	0	0	0	0	0	0	0	3	0	0	0	2	1	3	1	5 R	
Palmira 18	3	0	0	0	2	3	0	3	3	2	0	1	2	0	1	0	0	2	0	2	40 MS	
Step'	3	0	3	0	0	0	0	0	0	0	1	0	4	0	0	0	0	0	0	0	40 MS	

The following R genes *Yr1*, *Yr9*, *Yr 25*, *Yr26*, *YrSD*, *Yr3a+V23*, *Yr3a+4a+ND*, *Yr 8+19*, *Yr3c+Min*, *Yr17*, *Yr21*, *Yr7+22+23*, *Yr15*, *Yr2+VII*, *Yr8*, *Yr25+32* were not postulated in any of the studied varieties.

Virulent and avirulent response types on test isolates in Akapella coincide with *differential* wheat cultivars Vuke and Alpowa. This suggests the occurrence of two R genes, *Yr4b* and *Yr39+Alp*.

Varieties Kurs, Morozko and Step' give a high response type on the races 173E28, 37E129, 239E218, that are virulent to *Yr3*, *Yr3a*, *Yr32* and a low response type on the races that are avirulent to the above genes. This suggests that these cultivars contain the *Yr3*, *Yr3a*, and *Yr32* genes alone or in combination with other *Yr* R genes. The combination of *Yr4+12* genes was also postulated in Morozko and Step' varieties. The *Yr12* gene is a race-specific APR gene. Therefore, most likely, *Yr4* plays a key role in the seedling phase.

A high similarity of response types on Pst isolates with *differential* wheat cultivar Heines Peko (*Yr 2+6*) was noted in Bogema and Palmira 18. There was also noted an average similarity of response types with the close-isogenic line NIL Avocet S* (*Yr6*). Hence, we assume a combination of two genes occurring in these varieties.

Korona response types coincide by 80% with the avirulent and virulent response types of *differential* wheat cultivar Spalding Prolific. Thus, we can positively postulate the *YrSp* gene in this variety.

Kavalerka variety shows a low response type on 18 stripe rust isolates avirulent to *YrSU* and a high response type on two isolates (races 239E218, 97E226) virulent to the above gene. It is likely that the aforementioned variety contains this R gene.

Karolina 5 shows a low response type on 16 isolates avirulent to Hybrid 46 and a high response type on one isolate (race 32E59) virulent to this differential cultivar. This variety is likely to contain a combination of *Yr3b+4b+H46* R genes.

Gurt demonstrates a high response type on 3 isolates (races 173E28, 239E128, 129E0) virulent to *Yr2+9* and a low response type to 15 isolates avirulent to the same combination of genes. Therefore, the variety contains this R gene.

We were unable to postulate *Yr* R genes in Karavan and Markiz varieties due to their high resistance and the lack of differential isolates.

Field evaluation of varieties and differential cultivars.

On an artificial infectious background in field conditions, among the studied winter wheat varieties of Russian breeding, Karavan had a resistant response type, as well as differential wheat cultivars with highly effective R genes: *Yr3*, *Yr5*, *Yr8*, *Yr10*, *Yr27*, *Yr10+Mor*, *Yr3c+Min*, *YrDal+Da2*, *Yr3b+4b+H46*.

Four out of twelve cultivars were highly resistant to stripe rust. (1R-10R): Markiz, Kurs, Morozko, Kavalerka. No R genes have been postulated for Markiz. The high degree of Kurs resistance is explained by the *Yr3a* gene, since the response type and the degree of damage coincides with the differential cultivar Bon Fermier (10R). The response type and severity of damage in Morozko matched the carrier of the *Yr4+12* (Mega) R gene combination previously postulated in the seedling phase. The *YrSU* gene was postulated in the seedling phase in Kavalerka. Under field conditions, the variety exhibits high resistance, in contrast to differential cultivar. This fact suggests that resistance is provided by some other genes or their combination.

Korona had a moderate susceptibility to the North Caucasian population of stripe rust (35 MS). Since Spalding Prolific, containing *YrSp*, postulated at the seedling stage, showed a highly resistant response type (1R) in the field, its resistance is probably provided by other, unidentified genes.

The degree of damage to Step' did not exceed 5R. This does not coincide with the *Yr3*, *Yr3a*, and *Yr32* genes postulated at the seedling stage (0, 10R, and 40MS, respectively), but coincides with the Mega response type (*Yr4+12*). Therefore, we assume the presence of this combination of R genes in the variety.

Akapella, Bogema, Palmira 18 and Gurt were moderately susceptible varieties (35MS-40MS). In Bogema (35MS) and Palmira 18 (40MS) response

type and degree of damage do not match those of differential cultivar Heines Kolben (15MR, *Yr2+6*). Also the response types differed from NIL Avocet S* Yr6 (15MR). Most likely, these varieties contain other, less effective R genes.

In Gurt, the *Yr2+9* genes combination was postulated at the seedling stage. Under field conditions, response type and degree of damage (40MS) do not match those of differential cultivar Clement (15MR). Separately, Kalyansona (*Yr2*) and Avocet S* (*Yr9*) display different response types: 1R and 50S, respectively. We believe that it is the combination of highly effective and ineffective R genes that provides a moderately resistant response type to the Gurt variety.

Conclusion

Wheat stripe rust represents an economically significant fungal disease worldwide. Its distribution area and pathogenicity is constantly [26]. Range expansion of the pathogen is observed in Southern Russia as well [4, 8, 25]. The most effective and eco-friendly method of disease control remains the use of resistant varieties [9]. The resistance of varieties, in turn, is determined by the effectiveness of the known R genes (*Yr*) to the pathogen. Phytotest postulation is one of the fastest and most liable methods for identifying juvenile pathogen R genes in a host plant at the seedling stage [12].

The PCR method is often used in the identification of R genes. However, using only the analysis of the presence/absence of amplification products with specific primers cannot reliably determine the presence or absence of effective R genes in wheat accessions. More reliable results are obtained with a phytopathological test. Such results, in turn, should, if possible, be supported by hybridological analysis [6].

In 10 out of 12 winter wheat varieties of Russian breeding, we postulated 13 R genes to stripe rust (*Puccinia striiformis*) and their combinations by phytopathological testing: *Yr3*, *Yr3a*, *Yr32* (Kurs, Morozko, Step'), *Yr2+6* (Bogema, Palmira 18), *Yr2+9* (Gurt), *Yr4b*, *Yr39+Alp* (Akapella), *Yr4+12* (Morozko, Step'), *Yr3a+4a+H46* (Karolina 5), *YrA*, *YrSp* (Korona), *YrSU* (Kavalerka). The studied varieties are new, recently included in the State Commission of the Russian Federation for Selection Achievements Test and Protection

We were unable to identify the following R genes *Yr2*, *Yr5*, *Yr10*, *Yr10+Mor*, *Yr24*, *Yr27*, and *Yr25+32* in the studied varieties, since no isolates virulent to carriers of these genes were isolated from the North Caucasian population of *P. striiformis*. They are highly efficient against it.

Highly effective (*Yr3*, *Yr2+9*, *Yr3a*, *Yr4+12*, *Yr3a+4a+H46*) R genes were identified among the postulated *Yr* genes in Kurs, Morozko, and Step' at the seedling stage. We assume a combination of effective *Yr2+6* genes in the Gurt variety.

Under field conditions, similar response types and the degree of damage were observed in adult plants for the following varieties and differential cultivars: Kurs and Bon Fermier (*Yr3a*); Morozko, Step' and Mega (*Yr4+12*). This corresponds to the data of the phytotest on seedlings and suggests the presence of the *Yr3a* and *Yr4+12* genes in the listed varieties. Most of the postulated R genes in relation to the North Caucasian population of stripe rust are classified as weakly effective or ineffective. The *Yr3a* and *Yr4+12* genes, on the other hand, are highly effective in adult plants stage.

Funding

The study in greenhouse was financially supported by the Russian Foundation for Basic Research and Krasnodar Krai within the scientific project No. 19-44-0008.

Field-based studies of the resistance of varieties and differential cultivars to stripe rust pathogen were carried out in accordance with the State assignment of the Ministry of Science and Higher Education of the Russian Federation as part of the research on topic No. FGRN-2022-0004

Acknowledgments

The postulation of *Yr* resistance genes by phytopathological testing was performed using isolates of the bioresource collection of the Federal Research Center of Biological Plant Protection "State Collection of Entomocariphages and Microorganisms" and a unique scientific facility «Phytotron for isolation, identification, study and maintenance of races, strains, phenotypes of pathogens» (<https://ckp-rf.ru/catalog/usu/671925/>).

The authors are grateful to the breeding centers for the kindly provided variety samples and to the staff of the Laboratory of Plant Immunity to Diseases for their help in conducting the research.

References

1. Gul'tyaeva E.I., Levitin M.M., Semenyakina N.F., Nikiforova N.V., Savel'eva N.I. Bolezni zernovykh kul'tur v Severo-Zapadnom regione Rossii [Diseases of grain crops in the North-West region of Russia]. *Zashchita i karantin rastenij* [Plant Protection and Quarantine], 2007, no. 6, pp. 15-16.

2. Gul'tyaeva E.I., Levitin M.M., Semenyakina N.F., Nikiforova N.V., Kazakevich E.V. Fitosanitarnaya situaciya na posevah zernovykh kul'tur Severo-Zapadnom regione [Phytosanitary situation on grain crops in the North-West region]. *Zashchita i karantin rastenij* [Plant Protection and Quarantine], 2008, no. 5, pp. 50-51. <https://cyberleninka.ru/article/n/fitosanitarnaya-situatsiya-na-posevah-zernovykh-kultur-v-severo3zapadnom-regione>
3. Kojshybaev M., SHamanin V.P., Morgunov A.I. *Skrining pshenicy na ustojchivost' k osnovnym boleznyam: metodicheskie ukazaniya* [Screening of wheat for resistance to major diseases: guidelines]. Ankara: FAO-SEC, 2014, 64 p. <https://www.fao.org/3/i5550r/i5550r.pdf>
4. Matveeva I.P., Volkova G.V. ZHeltaya rzhavchina pshenicy. Rasprostranenie, vredonosnost', mery bor'by (obzor) [Wheat stripe rust. Distribution, damage, control measures (review)]. *Vestnik Ul'yanovskoj gosudarstvennoj sel'skohozyajstvennoj akademii* [Bulletin of the Ulyanovsk State Agricultural Academy], 2019, no. 2 (46), pp. 102-116. <https://doi.org/10.18286/1816-4501-2019-2-102-116>
5. Morozova A.A. Vidovoj sostav rzhavchiny ozimoi pshenicy i ih rasprostranenie v Krasnodarskom krae [Species composition of winter wheat rust and their distribution in Krasnodar Krai]. *Trudy Kubanskogo SKHI* [Proceedings of the Kuban Agricultural Institute], 1974, vol. 79, no. 107, pp. 49-55.
6. Tyryshkin L.G., Kolesova M.A. Ispol'zovanie molekulyarno-geneticheskogo i fitopatologicheskogo metodov dlya identifikacii genov ef-fektivnoj ustojchivosti k listovoj rzhavchine u obrazcov egilopsov [Using molecular genetics and phytopathological methods to identify genes for effective resistance to leaf rust in *Aegilops speciemens*]. *Trudy po prikladnoj botanike, genetike i selekcii* [Works on Applied Botany, Genetics and Breeding], 2020, vol. 181 (2), pp. 87-95. <https://doi.org/10.30901/2227-8834-2020-2-87-95>
7. CHuprina V.P., Sokolov M.S., Anpilogova L.K., Goncharov V.T., Pi-kusheva E.A., Kireenkova A.E., SHamina V.Z. Fitosanitarnoe sostoyanie posevov ozimoi pshenicy na yuge Rossii [Phytosanitary condition of winter wheat crops in Southern Russia]. *Zashchita i karantin rastenij* [Plant Protection and Quarantine], 1998, no. 4, pp. 22-24.
8. Shumilov Yu.V. *Agrobiologicheskoe obosnovanie priemov snizheniya infektzionnogo potentsiala vozbuditelya zheltoy rzhavchiny pshenitsy na Severnom Kavkaze* [Agrobiological substantiation of methods for reducing the infectious potential of the wheat yellow rust pathogen in the North Caucasus]: PhD thesis: 06.01.07; Saratov State Agrarian University named after N.I. Vavilov, Saratov, 2013, 277 p.

9. Chen X M. Epidemiology and control of stripe rust (*Puccinia striiformis* f. sp. *tritici*) on wheat. *Canadian Journal Plant Pathology*, 2005, vol. 27, pp. 314-337. <https://www.tandfonline.com/doi/abs/10.1080/07060660509507230>
10. Dawit W., Flath K., Webber W.E., Schumann E., Röder M.S., Chen X. Postulation and mapping of seedling stripe rust resistance genes in Ethiopian bread wheat cultivars *Journal of Plant Pathology*, 2012, vol. 94(2), pp. 403-409. <https://www.sipav.org/main/jpp/index.php/jpp/article/view/2568/1244>
11. Dubin H J, Johnson R, Stubbs RW. Postulated genes for resistance to stripe rust in selected CIMMYT and related wheats *Plant Disease*, 1989, no. 73, pp. 472-475. https://www.apsnet.org/publications/plantdisease/backissues/Documents/1989Articles/PlantDisease73n06_472.PDF
12. Feng J., Zhang Zh., Lin R., Xu Sh. Postulation of seedling resistance genes in 20 wheat cultivars to yellow rust (*Puccinia striiformis* f. sp. *tritici*). *Agricultural Sciences in China*, 2009, vol. 8(12), pp. 1429-1439. <https://www.sciencedirect.com/science/article/abs/pii/S1671292708603569>
13. Flor H. H. Current status of the gene-for-gene concept. *Annual Review Phytopathology*, 1971, vol. 9, pp. 275-296. <https://www.annualreviews.org/doi/abs/10.1146/annurev.py.09.090171.001423>
14. Flor H.H. The complementary genic systems in flax and flax rust. *Adv Genet*, 1956, vol. 8, pp. 29-54. <https://www.sciencedirect.com/science/article/abs/pii/S0065266008604988?via%3Dihub>
15. Gulyaeva E.I., Shaidayuk E.L., Rsaliyev A.S. Identification of leaf rust resistance genes in spring soft wheat samples developed in Russia and Kazakhstan. *Plant Protection News*, 2019, vol. 3(101), pp. 41-49. <https://plantprotect.ru/index.php/vizr/article/view/4805>
16. Johnson R., Stlibbs K.W., Euchs E., Chamberlain N H. Nomenclature for physiologic races of *Puccinia striiformis* infecting wheats. *Transactions of the British Mycological Society*, 1972, vol. 58, pp. 475-480. <https://www.sciencedirect.com/science/article/abs/pii/S0007153672800962>
17. Li M. Feng J., Cao Sh., Lin R., Cheng G., Yu Ya., Chen W. and Xu Sh. Postulation of Seedlings Resistance Genes to Yellow Rust in Commercial Wheat Cultivars from Yunnan Province in China. *Agricultural Sciences in China*, 2011, vol. 10(11), pp. 1723-1731. https://www.agriculturejournals.cz/public-Files/137_2015-PPS.pdf
18. McNeal F H, Konzak C F, Smith E P, Tate W S, Russel T S. A uniform system for recording and processing cereal research data. *Agricultural Research Service*, 1971, vol. 42, pp. 34-121. <https://naldc.nal.usda.gov/download/CAT40003231/pdf>

19. Randhawa M., Bansal U., Lillemo M., Miah H., Bariana H. Postulation of rust resistance genes in Nordic spring wheat genotypes and identification of widely effective sources of resistance against the Australian rust flora. *J Appl Genetics*, 2016, vol. 57, pp. 453–465. <https://doi.org/10.1007/s13353-016-0345-6>
20. Sharma S., Louwers J.M., Karki C.B., Snijders C.H.A. Postulation of resistance genes to yellow rust in wild emmer wheat derivatives and advanced wheat lines from Nepal. *Euphytica*, 1995, vol. 81, pp. 271-277. <https://link.springer.com/article/10.1007/BF00025617>
21. Shishkin N.V., Derova T.G., Gulyaeva E.I., Shaydayuk E.L. Identification of the genes resistant to brown rust in winter soft wheat varieties with the use of conventional and modern research methods. *Grain Economy of Russia*, 2018, vol. 5(59), pp. 63-67. <https://doi.org/10.31367/2079-8725-2018-59-5-63-67>
22. Tyryshkin L.G. About DNA-markers as sole criteria for postulation of Lr-genes of the *Triticum aestivum* L. resistance to *Puccinia triticina* Erikss.: critical essay. *Agricultural Biology*, 2010, vol. 45(3), pp. 76-81. <http://www.agrobiolgy.ru/3-2010tirishkin-eng.html>
23. Tyryshkin L.G. Genetic control of effective juvenile resistance to leaf rust in collection samples of *Triticum aestivum* L. *Russian Journal of Genetics*, 2006, vol. 42(3), pp. 377-384. <https://link.springer.com/article/10.1134/S1022795406030094>
24. Volkova G.V., Kudinova O.A., Vaganova O.F. Postulation of leaf rust resistance genes of 20 wheat cultivars in southern Russia. *Journal of Plant Protection Research*, 2020, vol. 60(3), pp. 225-232. <http://www.plantprotection.pl/pdf-120656-54566?filename=Postulation%20of%20leaf%20rust.pdf>
25. Volkova G.V., Matveeva I.P., Kudinova O.A. Virulence of the Wheat Stripe Rust Pathogene Population in the North-Caucasus Region of Russia. *Mycology and Phytopathology*, 2020, vol. 54 (1), pp. 33–41 <https://doi.org/10.31857/S0026364820010110>
26. Wamalwa M.N., Owuochi J., Ogenjo J., Wanyera R. Multi-Pathotype Testing of Selected Kenyan Wheat Germplasm and Watkin Landraces for Resistance to Wheat Stripe Rust (*Puccinia striiformis* f. sp. *tritici*) Races. *Agronomy*, 2019, vol. 9, 770. <https://www.mdpi.com/2073-4395/9/11/770>

Список литературы

1. Гультяева Е.И., Левитин М.М., Семенякина Н.Ф., Никифорова Н.В., Савельева Н.И. Болезни зерновых культур в Северо-Западном регионе России // Защита и карантин растений. 2007. №6. С. 15-16.

2. Гультяева Е.И., Левитин М.М., Семенякина Н.Ф., Никифорова Н.В., Казакевич Е.В. Фитосанитарная ситуация на посевах зерновых культур Северо-Западном регионе // Защита и карантин растений. 2008. №5. С. 50-51. <https://cyberleninka.ru/article/n/fitosanitarnaya-situatsiya-na-posevah-zernovyh-kultur-v-severo3zapadnom-regione>
3. Койшыбаев М., Шаманин В.П., Моргунов А.И. Скрининг пшеницы на устойчивость к основным болезням: методические указания. // Анкара: ФАО-СЕК, 2014. С. 64. <https://www.fao.org/3/i5550r/i5550r.pdf>
4. Матвеева И.П., Волкова Г.В. Желтая ржавчина пшеницы. Распространение, вредоносность, меры борьбы (обзор). // Вестник Ульяновской государственной сельскохозяйственной академии. 2019. № 2 (46). С. 102-116. <https://doi.org/10.18286/1816-4501-2019-2-102-116>
5. Морозова А.А. Видовой состав ржавчины озимой пшеницы и их распространение в Краснодарском крае // Тр. Кубанского СХИ, 1974. Вып. 79, № 107. С. 49-55.
6. Тырышкин Л.Г., Колесова М.А. Использование молекулярно-генетического и фитопатологического методов для идентификации генов эффективной устойчивости к листовой ржавчине у образцов эгилопсов // Труды по прикладной ботанике, генетике и селекции. 181 (2), 2020. С. 87-95. <https://doi.org/10.30901/2227-8834-2020-2-87-95>
7. Чуприна В.П., Соколов М.С., Анпилогова Л.К., Гончаров В.Т., Пикушева Э.А., Киреевкова А.Е., Шамина В.З. Фитосанитарное состояние посевов озимой пшеницы на юге России // Защита и карантин растений. 1998. № 4. С. 22-24.
8. Шумилов, Ю.В. Агробиологическое обоснование приемов снижения инфекционного потенциала возбудителя желтой ржавчины пшеницы на Северном Кавказе: дисс. ... канд. с.-х. наук: 06.01.07/ Шумилов Юрий Валерьевич; ФГБОУ ВПО «Саратовский государственный аграрный университет имени Н.И.Вавилова», Саратов, 2013. С. 277.
9. Chen X M. 2005. Epidemiology and control of stripe rust (*Puccinia striiformis* f. sp. *tritici*) on wheat // Canadian Journal Plant Pathology. Vol. 27. P. 314-337. <https://www.tandfonline.com/doi/abs/10.1080/07060660509507230>
10. Dawit W., Flath K., Webber W.E., Schumann E., Röder M.S., Chen X. Postulation and mapping of seedling stripe rust resistance genes in Ethiopian bread wheat cultivars // Journal of Plant Pathology. 2012. Vol. 94(2). P. 403-409. <https://www.sipav.org/main/jpp/index.php/jpp/article/view/2568/1244>
11. Dubin H J, Johnson R, Stubbs RW. Postulated genes for resistance to stripe rust in selected CIMMYT and related wheats // Plant Disease, 1989. № 73.

- P. 472-475. https://www.apsnet.org/publications/plantdisease/backissues/Documents/1989Articles/PlantDisease73n06_472.PDF
12. Feng J., Zhang Zh., Lin R., Xu Sh. Postulation of seedling resistance genes in 20 wheat cultivars to yellow rust (*Puccinia striiformis* f. sp. *tritici*) // Agricultural Sciences in China. 2009. Vol. 8(12). P. 1429-1439 <https://www.sciencedirect.com/science/article/abs/pii/S1671292708603569>
 13. Flor H. H. Current status of the gene-for-gene concept // Annual Review Phytopathology, 1971. Vol. 9. P. 275-296. <https://www.annualreviews.org/doi/abs/10.1146/annurev.py.09.090171.001423>
 14. Flor H.H. The complementary genic systems in flax and flax rust. // Adv Genet. 1956. Vol. 8, P. 29-54. <https://www.sciencedirect.com/science/article/abs/pii/S0065266008604988?via%3Dihub>
 15. Gulyaeva E.I., Shaidayuk E.L., Rsaliyev A.S. Identification of leaf rust resistance genes in spring soft wheat samples developed in Russia and Kazakhstan // Plant Protection News. 2019. Vol. 3(101). P. 41-49. <https://plantprotect.ru/index.php/vizr/article/view/4805>
 16. Johnson R., Stilbbs K.W., Euchs E., Chamberlain N H. Nomenclature for physiologic races of *Puccinia striiformis* infecting wheats // Transactions of the British Mycological Society, 1972. Vol. 58. P. 475-480. <https://www.sciencedirect.com/science/article/abs/pii/S0007153672800962>
 17. Li M. Feng J., Cao Sh., Lin R., Cheng G., Yu Ya., Chen W. and Xu Sh. Postulation of Seedlings Resistance Genes to Yellow Rust in Commercial Wheat Cultivars from Yunnan Province in China // Agricultural Sciences in China, 2011. Vol. 10(11). P. 1723-1731. https://www.agriculturejournals.cz/publicFiles/137_2015-PPS.pdf
 18. McNeal F H, Konzak C F, Smith E P, Tate W S, Russel T S. A uniform system for recording and processing cereal research data // Agricultural Research Service, 1971. Vol. 42. P. 34-121. <https://naldc.nal.usda.gov/download/CAT40003231/pdf>
 19. Randhawa M., Bansal U., Lillemo M., Miah H., Bariana H. Postulation of rust resistance genes in Nordic spring wheat genotypes and identification of widely effective sources of resistance against the Australian rust flora // J Appl Genetics. 2016. Vol. 57. P. 453-465. <https://doi.org/10.1007/s13353-016-0345-6>
 20. Sharma S., Louwers J.M., Karki C.B., Snijders C.H.A. Postulation of resistance genes to yellow rust in wild emmer wheat derivatives and advanced wheat lines from Nepal // Euphytica. 1995. Vol. 81. P. 271-277. <https://link.springer.com/article/10.1007/BF00025617>
 21. Shishkin N.V., Derova T.G., Gulyaeva E.I., Shaydayuk E.L. Identification of the genes resistant to brown rust in winter soft wheat varieties with the use of conventional and modern research methods // Grain Economy of Russia. 2018. Vol. 5(59). P. 63-67. <https://doi.org/10.31367/2079-8725-2018-59-5-63-67>

22. Tyryshkin L.G. About DNA-markers as sole criteria for postulation of Lr-genes of the *Triticum aestivum* L. resistance to *Puccinia triticina* Erikss.: critical essay // *Agricultural Biology*. 2010. Vol. 45(3). P. 76-81. <http://www.agrobiology.ru/3-2010tirishkin-eng.html>
23. Tyryshkin L.G. Genetic control of effective juvenile resistance to leaf rust in collection samples of *Triticum aestivum* L. // *Russian Journal of Genetics*. 2006. Vol. 42(3). P. 377-384. <https://link.springer.com/article/10.1134/S1022795406030094>
24. Volkova G.V., Kudina O.A., Vaganova O.F. Postulation of leaf rust resistance genes of 20 wheat cultivars in southern Russia // *Journal of Plant Protection Research*. 2020. Vol. 60. № 3. P. 225-232. <http://www.plantprotection.pl/pdf-120656-54566?filename=Postulation%20of%20leaf%20rust.pdf>
25. Volkova G.V., Matveeva I.P., Kudina O.A. Virulence of the Wheat Stripe Rust Pathogene Population in the North-Caucasus Region of Russia // *Mycology and Phytopathology*, 2020. Vol. 54 (1). P. 33–41. <https://doi.org/10.31857/S0026364820010110>
26. Wamalwa M.N., Owuochi J., Ogendo J., Wanyera R. Multi-Pathotype Testing of Selected Kenyan Wheat Germplasm and Watkin Landraces for Resistance to Wheat Stripe Rust (*Puccinia striiformis* f. sp. *tritici*) Races // *Agronomy*. 2019. Vol. 9, 770. <https://www.mdpi.com/2073-4395/9/11/770>

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Поступила 08.12.2022

После рецензирования 30.12.2022

Принята 31.01.2023

Received 08.12.2022

Revised 30.12.2022

Accepted 31.01.2023