Stem rust in Western Siberia – race composition and effective resistance genes

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Abstract. Stem rust in recent years has acquired an epiphytotic character, causing significant economic damage for wheat production in some parts of Western Siberia. On the basis of a race composition study of the stem rust populations collected in 2016–2017 in Omsk region and Altai Krai, 13 pathotypes in Omsk population and 10 in Altai population were identified. The race differentiation of stem rust using a tester set of 20 North American Sr genes differentiator lines was carried out. The genes of stem rust pathotypes of the Omsk population are avirulent only to the resistance gene Sr31, Altai isolates are avirulent not only to Sr31, but also to Sr24, and Sr30. A low frequency of virulence (10–25 %) of the Omsk population pathotypes was found for Sr11, Sr24, Sr30, and for Altai population – Sr7b, Sr9b, Sr11, SrTmrp, which are ineffective in Omsk region. Field evaluations of resistance to stem rust were made in 2016–2018 in Omsk region in the varieties and spring wheat lines from three different sources. The first set included 38 lines and spring bread wheat varieties with identified Sr genes – the so-called trap nursery (ISRTN – International Stem Rust Trap Nursery). The second set included spring wheat lines from the Arsenal collection, that were previously selected according to a complex of economically valuable traits, with genes for resistance to stem rust, including genes introgressed into the common wheat genome from wild cereal species. The third set included spring bread wheat varieties created in the Omsk State Agrarian University within the framework of a shuttle breeding program, with a synthetic wheat with the Ae. tauschii genome in their pedigrees. It was established that the resistance genes Sr31, Sr40, Sr2 complex are effective against stem rust in the conditions of Western Siberia. The following sources with effective Sr genes were selected: (Benno)/6*LMPG-6 DK42, Seri 82, Cham 10, Bacanora (Sr31), RL 6087 Dyck (Sr40), Amigo (Sr24, 1RS-Am), Siouxland (Sr24, Sr31), Roughrider (Sr6, Sr36), Sisson (Sr6, Sr31, Sr36), and Fleming (Sr6, Sr24, Sr36, 1RS-Am), Pavon 76 (Sr2 complex) from the ISRTN nursery; No. 1 BC$_2$F$_2$ (96 × 113) × 145 × 113 (Sr2, Sr36, Sr44), No. 14a F$_3$ (96 × 113) × 145 (Sr36, Sr44), No. 19 BC$_2$F$_3$ (96 × 113) × 113 (Sr2, Sr36, Sr44), and No. 20 F$_3$ (96 × 113) × 145 (Sr2, Sr36, Sr40, Sr44) from the Arsenal collection; and the Omsk State Agrarian University varieties Element 22 (Sr31, Sr35), Lutescens 27-12, Lutescens 87-12 (Sr23, Sr36), Lutescens 70-13, and Lutescens 87-13 (Sr23, Sr31, Sr36). These sources are recommended for inclusion in the breeding process for developing stem rust resistant varieties in the region.

Key words: bread wheat; stem rust; pathotype; effective resistance genes; breeding.

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Стеблевая ржавчина в Западной Сибири – расовый состав и эффективные гены устойчивости

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Аннотация. Стеблевая ржавчина пшеницы в последние годы приобрела эпифитотийный характер, нанося значительный экономический ущерб производству зерна пшеницы в отдельных областях Западной Сибири. По результатам изучения расового состава популяций стеблевой ржавчины, собранных в 2016–2017 гг.
Introduction

Stem rust of wheat caused by *Puccinia graminis* f. sp. *tritici* Eriks. for a long time had a weak manifestation in the territory of Western Siberia and only in the recent years acquired an epiphytotic nature, causing significant economic damage for wheat production in the region. First of all, this is due to the deterioration of the phytosanitary situation in the region, the general trend of climate warming and cultivation of susceptible wheat varieties on large area (Shamanin et al., 2015, 2016a). The threat of stem rust race *Ug99* appearance and the emergence of new pathotypes of this race, affecting varieties with genes *Sr24* and *Sr36* present a serious threat for wheat production in West Siberian region. Genetic diversity of cultivated wheat varieties for resistance to *Ug99* and stem rust in general is very limited (Shamanin et al., 2016b).

Enhancement of genetic resistance to pathogens can be solved germplasm exchange, and also cultivation of varieties with different level of resistance to diseases and to different races. Crop protection is necessary to restrain the evolution of pathogens and the emergence of new virulent races. Such programs are widely used in Europe and America. The duration of the variety cultivation in advanced countries is 3–4 years, while in Russia – 7–10 years (Sanin, 2016). In this regard, the breeding of spring wheat varieties, which have a diverse genetic basis of resistance to stem rust, is very relevant.

Since the 1950s, many resistance genes introduced into bread wheat have lost their effectiveness (Singh et al., 2008). The most significant genes for breeding practice are *Sr2*, *Sr23*, *Sr24*, *Sr25*, *Sr31*, *Sr33*, *Sr36*, *Sr38*, *Sr45*, *Sr50*, *SrTmp*, and *Sr1RS* 

Introgresion of resistance genes of wild and cultivated wheat relatives allows to expand the genetic diversity of varieties and contributes to their long-term protection (Leo

ova et al., 2014). To date, about 86 *Sr* genes have been identified, of which 26 stem rust resistance genes have been transferred into bread wheat from other cereal species (McIntosh et al., 2013). For example, *T. turgidum* was the source of the stem rust resistance genes *Sr2*, *Sr9d*, *Sr9e*, *Sr9g*, *Sr11*, *Sr12*, *Sr13*, *Sr14*, and *Sr17*, of which the *Sr2*, *Sr13*, and *Sr14* genes are effective against *Ug99* race; *T. monococcum* was the source of *Sr21*, *Sr22*, and *Sr35* genes (Singh et al., 2011).

Genes that caused the resistance to stem rust have been introduced into wheat gene pool from the genome of various *Aegilops* L. species: *Ae. speltoides* – *Sr32*, *Sr39*, *Sr47*; *Ae. comosa* – *Sr34*; *Ae. ventricosa* – *Sr38* (Schneider et al., 2008). *Ae. tauschii* contributed genes *Sr33*, *Sr45*, *Sr46* (Kerber, Dyck, 1979). Direct hybridization of *T. aestivum* with *Ae. tauschii* and following backcrosses allowed introduction of new resistance genes *SrTA1662*, *SrTA1017*, and *SrTA10187* effective against *Ug99* race (Olson et al., 2013). The search of new resistance genes in wild wheat relatives continues, for example, G. Yu et al. (2017) identified two new *Sr* genes in *Ae. sharonensis*.

One of the objectives of Kazakh-Siberian Spring Wheat Improvement Network (KASIB) is expanding of the genetic polymorphism of new varieties, including resistance to harmful diseases (Gomez-Beccera et al., 2006). This is based on shuttle breeding with CIMMYT (Mexico). Varieties and breeding lines developed through shuttle breeding with participation of *Ae. tauschii* and *T. dicoccum*, as well as lines of the “Arsenal” collection, which have wild species in their pedigree are of interest for breeding for resistance to stem rust in the region.

The aim of the research was analysis of the racial composition of the Western-Siberian stem rust population, resistance assessment of spring bread wheat lines and varieties with
identified resistance genes and identification of the sources with effective Sr genes for breeding under Western Siberian conditions.

**Material and methods**

The racial composition of *Puccinia graminis f. sp. tritici* populations collected in 2016–2017 in Omsk region (15 entries of the nursery KASIB-16, Omsk State Agrarian University (SAU)) and Altai region (12 breeding samples, Altay Breeding Center) were analyzed in the Global Rust Reference Center (GRRC, Denmark; http://agro.au.dk/forskning/internationale-platforme/wheatrust).

Selection of single pustule isolates according to requirements of GRRC protocols (www.wheatrust.org) was carried out. Monopustule isolates were reproduced to identify race Ug99 with usage of the test PCR-Stage 1. A total of 19 single pustule isolates were selected from Omsk population and 20 – from Altai population (Table 1).

Differentialiation of stem rust races was performed with use of the set of 20 North American differentiator lines containing Sr genes: *Sr*5 (ISr5-Ra), *Sr*21 (CnSr Triticum monoc. Deriv.), *Sr*9e (Verstein), *Sr*7b (ISr7b-Ra), *Sr*11 (ISr11-Ra), *Sr*6 (ISr6a-Ra), *Sr*8a (ISr8a-Ra), *Sr*9g (CnSr9g), *Sr*36 (W2691SrTt-1), *Sr*9b (W2691Sr9b), *Sr*30 (BtSr30Wst), *Sr*17+13 (Combination VII), *Sr*9a (ISr9a-Ra), *Sr*9d (ISr9d-Ra), *Sr*10 (W2691Sr10), *Sr*Temp (CnsSrTmp), *Sr*24 (LeSr-r24Ag), *Sr*7f (Benno Sr31/6*LMPG), *Sr*38 (VPM-1), *Sr*McN (McNair 701). Infected plants were evaluated in 14–16 days after inoculation according to modified E.C. Stakman scale (Roelfs, Martens, 1988). Virulence phenotypes were classified according to North American system (Jin et al., 2008).

The varieties and lines of bread wheat from three germplasm sets were evaluated in Omsk at least 4–5 times for reaction to stem rust on scales recommended by Koyshibaev et al. (2014). The type of reaction on E.B. Mains and H.S. Jackson scale (1926) and severity – on modified Peterson scale (Peterson et al., 1948) were considered: 0 – immunity, uredopusules not formed; R (Resistance – high resistance), 1 score, severity 5–10 %; M (Moderately resistant – average resistance), 2 score, severity 10–25 %; M (heterogeneous type), pustules of different sizes, surrounded by chlorotic and necrotic spots or without them; MS (Moderately susceptible – average susceptibility), 3 score, severity 40–50 %; S (Susceptible – susceptibility), 4 score, severity more than 60 %.

In 2016–2018, International Stem Rust Trap Nursery with 58 genotypes with identified Sr genes was evaluated to Omsk stem rust population (Table 2). Varieties and lines of nursery-trap were sown manually in 100 cm-long rows with stem rust resistant (Element 22) and susceptible checks (Chernyava 13) alternating every entries.

In 2015, 9 spring wheat lines originating from wide crosses “Arsenal” collection were kindly provided by I.F. Luchok for evaluation in Omsk. These lines carry a pyramid of stem rust resistance genes (Luchokhina et al., 2017) – No. 1 [BC2F3 (96 × 113) × 113]; No. 13, 14a [F3 (96 × 113) × 145]; No. 16, 17, 17a [BC2F3 (96 × 113) × 113]; No. 19 [BC2F3 (96 × 113) × 113]; No. 20, 22a [F3 (96 × 113) × 145]. The lines were studied in 2016–2018 in un-replicated trial with the plot size of 2 m².

Nine spring wheat varieties and breeding lines from advanced yield trial at Omsk SAU developed through utilization of synthetic wheat with the *Ae. tauschii* genome (Lutescens 24-12 (Kasibovskaya), Lutescens 27-12, Lutescens 87-12, Lutescens 70-13, Lutescens 87-13, Lutescens 88-13 (Silantiy), Lutescens 124-13, Lutescens 53-15, Lutescens 128-15) were evaluated for stem rust resistance and other traits in 2016–2018. The plot size was 25 m² with four replications. The checks were Pamyati Aziieva (early maturing), Duet (medium maturing), and Element 22 (late maturing).

Sr genes of Omsk SAU varieties were identified using molecular markers: Xsts638 – Sr13, Xcfa2123 – Sr22, Xgwm210 – Sr23, Xscs73 – Sr24, Xwmc221 – Sr25, BE518379 – Sr26, Xscm09 – Sr31, SC51, Xcfa2170 – Sr35, Xstms773-2 – Sr36, Venturiap-LN2 – Sr38, Lr34plus – Sr57, according to established protocol (http://maswheat.ucdavis.edu/protocols/StemRust/index.htm). The

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**Table 1. Phenotypic composition and virulence of pathotypes of *Puccinia graminis f. sp. tritici* in Omsk and Altai regions (2016–2017)**

| Parameter | Experimental field of Omsk SAU, 2016 | Experimental field of Altai Breeding Center, 2017 |
|-----------|--------------------------------------|-----------------------------------------------|
| No. of samples | 15 | 12 |
| No. of single pustule isolates | 19 | 20 |
| No. of pathotypes | 13 | 10 |
| The indexes of pathotypes | RRGTF, TKRPF, RKRSP, RFRSF, THRTP, RHRTP, TKRTP, QHHSF, RCTRT, SHHHSF, RCTRT, QFRSF, RFRTF | SFRSF, NFMSE, QKCSF, MPMT, LHCATS, LFRSF, LKCSF, LKTSF, LTMSE, QHMSE |
| High frequency of virulence ≥25 % | S5, S6, S7b, S8a, S9a, S9b, S9d, S9e, S9g, S10, S17, S21, S36, S38, SrMcN, SrTmp | S5, S8a, S9a, S9d, S9e, S9g, S10, S17, S21, S36, S38, SrMcN |
| Low frequency of virulence 10–25 % | Sr11, Sr24, S30 | Sr7b, S9b, Sr11, SrTmp |
| Avirulence | Sr31 | Sr24, S30, Sr31 |
**Table 2.** Results of evaluation of lines and varieties with identified Sr genes on resistance/susceptibility to stem rust, experimental field of Omsk SAU, 2016–2018

| No. | Variety, line | Genes | Infection response, %/type |
|-----|--------------|-------|-----------------------------|
| 1   | Element 22   | 22    | R 5MR 5MR                    |
| 2   | Chernyaya 13 | Susceptible checks | 80S 60S 80S |
| 3   | Morocco      | 14159 | 70S 50S 40S |
| 4   | In 13 Ra Cl 14159 | Sr5 | – 50S 40S |
| 5   | Na 101/6 Marquis | Sr7a | 25% 40MS 30S |
| 6   | In 167 Ra Cl 14165 | Sr7b | 10MS 65S 40S |
| 7   | Cl 14167/9 LMPG-6 DK04 | Sr8a | 30MS 5M 25MS |
| 8   | Barleta Benvenuto (Cl 14196) | Sr8b | – 50S 30S |
| 9   | In 9a Ra Cl 14169 | Sr9a | 10MS 65S 40S |
| 10  | Prelude*4/2 Marquis*6/ Kenya 117A | Sr9b | 30M 10M 20M |
| 11  | Vernstein Pi 442914 | Sr9e | 20S 10M 10M |
| 12  | Chinese Spring*7/Marquis 2B | Sr9g | 20S 10M 40S |
| 13  | W2691 Sr10 CI 17388 | Sr10 | 5MR 40MS 60S |
| 14  | Lee*6/LMPG-6 DK37 | Sr11 | 10M 5M 20M |
| 15  | Chinese Spring*5/Thatcher 3B | Sr12 | 10M 5M 40S |
| 16  | Preude*4/2 Marquis*6/ Khapstein | Sr13 | 5M 5M 10M |
| 17  | W2691*2 Khapstein | Sr14 | 5M 5M 30M |
| 18  | Preude*2 Norka | Sr15 | 30MS 10M 30M |
| 19  | Thatcher/CS (Cl14173) | Sr16 | 20S 5M 30S |
| 20  | Prelude*8/ Marquis*2/2/ Exp518/9 | Sr17 | 20S 5M 50S |
| 21  | Little Club/Sr18 Marquis “A” | Sr18 | 20S 70S 40S |
| 22  | 94A 236-1 Marquis “B” | Sr19 | 5MR 20MS 10M |
| 23  | 94A 237-1 Marquis “C” | Sr20 | 40S 30S 5MS |
| 24  | T. monococcum*8/LMPG-6 DK13 | Sr21 | 10M 10M 20M |
| 25  | Einkorn | Sr22 | 10MR 3MR 10M |
| 26  | Mg*6/Stewart*3/ RL 5244 | Sr23 | 20M 40M 50S |
| 27  | Exchange Cl 12635 | Sr24 | 10MR 5MR 10MR |
| 28  | Lee/Sr24 Ag + Btsr24 Ag | Sr25 | 10MR 10MR 10MR |
| 29  | Agatha (CI 14048)*9/LMPG-6 DK16 | Sr26 | 25MR 15M 10M |
| 30  | Eagle Sr26 McIntosh | Sr27 | 15MR 3MR 10M |
| 31  | WRT 238-5 (1984) Roeufs | Sr28 | – 20MS 10M |
| 32  | Kota RL 471 | Sr29 | 10MR 10MR 10MR |
| 33  | Prelude/8 Marquis2/Etioloe de Choisy | Sr30 | 25M 10M 15S |
| 34  | Selection from Webster F3*4#6 | Sr31 | 60S 5MR 10MR |
| 35  | Sr31 (Benno)/6/LMPG-6 DK42 | Sr32 | 5MR 10MR 10MR |
| 36  | Seri 82 | Sr33 | R R R |
| 37  | PBW343 = Attila with Sr31 | Sr34 | 5MR 5MR 10MR |
| 38  | Cham 10 = Kauz/Kauz/star | Sr35 | R R R |
| 39  | Bacanora = Kauz’ | Sr36 | R R R |
| 40  | ERS155 5-203 (1995) Roeufs | Sr37 | – 10MR 10M |
| 41  | RL 5405 (1192) Kerber | Sr38 | 15MR 10MR 30S |
| 42  | RL 6098 (1997) Dyck | Sr39 | – 40MS 50S |
| 43  | RL 6099 (1995) Dyck | Sr40 | 20M 40MS 30S |
| 44  | W2691 SrTt-1 Cl 17385 | Sr41 | – 10MR 10M |
| 45  | Prelude*4/Line W (W3583) | Sr42 | 10M 5M R |
| 46  | Trident Sr38 | Sr43 | 5MR R R |
| 47  | Trident | Sr44 | 5MR R R |
| 48  | RL 5711 Kerber | Sr45 | 10MR 5MR 10M |
| 49  | RL 6087 Dyck | Sr46 | 5MR 10MR 10M |
| 50  | Amigo | Sr24 + 1RS-Arm | R R |
| 51  | Siouxland | Sr24 + Sr31 | R R |
| 52  | Roughrider | Sr6 + Sr36 | R 5MR R |
| 53  | Sisson | Sr6 + Sr31 + Sr36 | R R R |
| 54  | Bt Wild | SrWild1 | 15MR 20M 10M |
| 55  | Fleming | Sr6 + Sr24 + Sr36 + 1RS-Arm | 10MR 5MR 10MR |
| 56  | Chris | Sr7a + Sr12 + Sr6 | – 10MR 30S |
| 57  | CsSsrTmp | SrTmp | – 40MS 30S |
| 58  | Pavon 76 | Sr2 complex | R R 5M |
resistance genes of spring bread wheat lines and varieties from nursery-trap and from collection “Arsenal” were identified earlier (McIntosh et al., 2013, 2017; Lapochkina et al., 2017).

In 2016, weather conditions in Omsk region were relatively dry, which contributed to moderate development of stem rust. In 2017, there was an intensive development of the disease, the degree of severity of susceptible accessions varied within 20S–80S. In 2018 high severity of stem rust was observed as the growing season was characterized by cool weather and more precipitation. The degree of severity of susceptible accessions was 30S–80S.

Results
The race composition analysis of stem rust populations identified a significant number of pathotypes: in the Omsk population – 13 and in Altai population – 10 (see Table 1). Unlike many regions of the world where stem rust is a harmful disease for decades, for example in Krasnodar region of Russia (Ablova et al., 2016), for Western Siberia this is surprising result considering a short period of time since its appearance. Most of the identified pathotypes of stem rust population in Omsk and Altai regions were not identical in virulence to the pathotypes, which were found in recent years in Asia and Africa (http://wheatrust.org/fileadmin/www/pathotypes). In all studied Western-Siberian populations of *P. graminis Ug99* and Sicilian races were not identified. Genes of stem rust pathotypes of Omsk population were avirulent only to *Sr31* gene, while Altai pathotypes were avirulent to *Sr31, Sr24*, and *Sr30*.

Low frequency of virulence (10–25 %) of Omsk population pathotypes was established for *Sr11, Sr24, Sr30* genes, for Altai population – for *Sr7b, Sr9b, Sr11, SrTmp* genes, which were ineffective in Omsk region. The results of laboratory evaluation of virulence of *P. graminis* pathotypes collected in Omsk region were confirmed by field of trap nursery with identified *Sr* genes (see Table 2).

Genotypes with *Sr31*: *Sr31*(Benno)/6*LMPG-6* DK42, Seri 82, PBW343=Attila with *Sr31*, Cham 10=Kauz/Kauz star, Bacanora=Kauz’s showed high level of resistance to Omsk stem rust population in all years of study (2016–2018). Line 28 LeSr24Ag + BTSr24Ag with *Sr24* gene was characterized by moderate resistance. For some *Sr* genes, resistant type of reaction under epiphytotic conditions was observed on the stage of adult plants, and susceptible type – on the seedling stage in the laboratory conditions.

For example, variety Trident (entries 46 and 47) with *Sr38* gene had high resistance (R–5MR) in the field; variety Einkorn (entry 25) with *Sr21* gene, and line W2691SrTt-1 CI 17385 (entry 44) with *Sr36* gene had moderate resistance (10M) in the field conditions. In the laboratory conditions the seedlings plants with above mentioned genes were classified as susceptible. Genotypes of ISRTN nursery with a gene pyramid had high resistance to stem rust in all years of research: entry 50 Amigo (*Sr24+1RS-Am*), entry 51 Siouxland (*Sr24+Sr31*), entry 52 Roughrider (*Sr6+Sr36*), entry 53 Sisson (*Sr6+Sr31+Sr36*), entry 55 Fleming (*Sr6+Sr24+Sr36+1RS-Am*). The results of stem rust resistance evaluation of “Arsenal” collection and Omsk SAU germplasm are presented in Table 3.

Lines from “Arsenal” collection are of great interest as sources of resistance to pathogen since they possess the gene pyramid: *Sr2 (T. turgidum), Sr36, Sr40 (T. timopheevii), Sr44 (Th. intermediate)*. The pedigree of selected lines contains spring wheat line 13/00/i-4 with 7 resistance genes:

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### Table 3. Results of the assessment for resistance to stem rust of lines and the best varieties of spring bread wheat of Competitive Variety Trial, experimental field of Omsk SAU, 2016–2018

| Variety, line | %/type | 2016 | 2017 | 2018 | Resistance genes |
|--------------|--------|------|------|------|------------------|
| Pamyati Azieva, susceptible standard | 80S | 40S | 70S | – |
| Element 22, resistant standard | R | 5MR | 5MR | *Sr31, Sr35* |
| Lines from “Arsenal” collection | | | | |
| No. 1 BC₂F₂ (96×113)×145×113 | R | R | 10MR | *Sr2, Sr36, Sr44* |
| No. 14a F₂ (96×113)×145 | R | R | R | *Sr36, Sr44* |
| No. 19 BC₂F₂ (96×113)×113 | R | R | – | *Sr2, Sr36, Sr44* |
| No. 20 F₂ (96×113)×145 | R | R | 5MR | *Sr2, Sr36, Sr40, Sr44* |
| Omsk SAU germplasm | | | | |
| Lutescens 27-12 | R | R | 25MR | *Sr23, Sr36* |
| Lutescens 87-12 | R | R | 40M | *Sr23, Sr36* |
| Lutescens 70-13 | 5MR | R | 5MR | *Sr23, Sr31, Sr36* |
| Lutescens 87-13 | 5M | 5MR | 10MR | *Sr23, Sr31, Sr36* |
| Lutescens 88-13 | 5MR | R | 25MR | *Sr23* |
In Omsk SAU varieties 3 resistance genes were identified: Sr23, Sr31, Sr36. Variety Element 22, which has winter wheat Aurora in its pedigree also possesses wheat-rye translocation 1BL.1RS with Sr31 gene (Shamanin et al., 2016b). The combination of effective resistance genes Sr31 and Sr35 in this variety results a high level of resistance to stem rust. Element 22 is one of the few varieties with combined resistance to stem and leaf rust. It was included into State register of breeding achievements in Western Siberian region. This variety is the check of the late maturity group at the State Variety Trials in Omsk region.

Stem rust resistant breeding lines Lutescens 27-12, Lutescens 70-13, Lutescens 87-13, Lutescens 88-13 were selected from a cross Lutescens 30-94*2/3/T. dicoccon PI 94625/Ae. squarrosa (372)/3*Pastor involving Kazakhstan spring wheat line Lutescens 30-94 and CIMMYT line developed by hybridization of synthetic wheat with variety Pastor. The line Lutescens 87-12 originated from a cross Kazakhstan-

In modern conditions, stem rust is the most dangerous disease for grain production in Western Siberia. In the epiphytotic years the grain losses of wheat in the region were about 2 million tons. Unfortunately, stem rust resistant varieties included into the State register occupy about 10–15 % of the total wheat sowing area in the region. In 2015–2016, evaluation of spring wheat varieties at Moskalenskiy State Variety Trial of Omsk region (southern forest-steppe zone) demonstrated that out of 57 varieties tested only Element 22 (Sr31+Sr35), Omskaya 37, Simga, Uralosibirskaya (Sr31), and Sigma 2 (Sr31+Sr25) were resistant to stem rust (5–15MR). The other varieties were affected by pathogen in medium and high degree requiring the use of chemical protection (Lapochkina et al., 2017). Previously, Shamanin et al. (2016b) identified the stem rust resistance genes in the germplasm developed by breeding institutions of Western Siberia. High frequency of genes Sr25, Sr31, and their combination was observed. High variability of the race composition of the pathogen population, as shown in our studies, and the uniformity of resistance genes to stem rust in cultivated varieties, threaten grain production stability in Western Siberia.

The breeding strategy should focus on limiting disease development in the region. The study of the populations of *P. graminis*, formed on wheat in the different regions, is very essential to guide the breeding efforts. There were no clones avirulent to Sr24 gene in Omsk population of *P. graminis* while in Altai region there were no clones virulent to Sr24, which remains its effectiveness in Novosibirsk region (Skolotneva et al., 2018). The results of the population composition comparison suggest that Omsk and Altai subpopulations have relatively independent sources of genetic diversity and the contact zone. Western Siberian population of *P. graminis* has quite complex structure. Two subpopulations are assumed to exist: Omsk and Altai – with independent sources of genetic diversity, and zone of genotypic exchange on wheat crop in Novosibirsk region (Skolotneva et al., 2020).

Omsk stem rust population analysis showed that the spectrum of effective resistance genes has narrowed due to losses of some genes to the local population of *P. graminis*.

Highly resistant varieties and lines of ISRTN nursery were identified: Sr31 (Benno)/6*LMPG-6 DK42, Seri 82, Cham 10, Babanora (Sr31), RL 6087 Dyck (Sr40), Amigo (Sr24, IRS-Am), Siouxland (Sr24, Sr31), Roughrider (Sr6, Sr36), Sisson (Sr6, Sr31, Sr36), Fleming (Sr6, Sr24, Sr36, IRS-Am), Pavon 76 (Sr2 complex). Selected varieties and lines are recommended for using as sources of resistance in breeding programs to create resistant wheat varieties to stem rust. Effective resistance genes Sr31, Sr40, Sr2 complex, and their combinations with ineffective genes are recommended for use in breeding, taking into account the constant rotation, combination of genes of nonspecific resistance, as well as the possibility of infection threat from neighboring territory.

The resistance gene Sr2, widely used in breeding for resistance to virulent stem rust races, is common in commercial varieties in a number of countries around the world, particularly in the United States, Australia, India, and Mexico. This gene is practically absent in the commercial varieties of Russian Federation, however, for effective protection against stem rust, its pyramiding with other resistance genes is recommended (Barnova et al., 2015).

For the development of varieties with long-term resistance, the strategy of combining genes responsible for different types of resistance in one genotype is used. Pyramiding of specific resistance genes (Sr11, Sr24, Sr30, and Sr31) with APR gene Sr2, which causes the slow development of the disease (slow rusting), will provide longer protection of wheat crops from stem rust in Western Siberia in the present phytosanitary situation.

In this regard, the lines from “Arsenal” collection – No. 1 BC_F2 (96×113)×145×113 (Sr2, Sr36, Sr44); No. 14a F3 (96×113)×145 (Sr36, Sr44); No. 19 BC_F3 (96×113)×113 (Sr2, Sr36, Sr44); No. 20 F3 (96×113)×145 (Sr2, Sr36, Sr40, Sr44) represent a promising starting material for breeding and creation of varieties with long-term resistance.

It is justified to include resistance sources to stem rust with minimum number of negative traits that reduce their breeding value. In this regard, stem rust resistant germplasm from Omsk SAU with identified effective genes Element 22 (Sr31, Sr35), Lutescens 27-12, Lutescens 87-12 (Sr23, Sr36), Lutescens 70-13, Lutescens 87-13 (Sr23, Sr31, Sr36), Lutescens 88-13 (Sr23) are valuable starting material for breeding in the region.

**Conclusion**

Thus, the genetic similarity of spring wheat varieties on stem rust resistance genes cultivated over large areas in Western Siberia, and the predominance of varieties with race specific
resistance genes contribute to spreading and high variability of the pathogen. The lines from collection “Arsenal” – No. 1 BC, F$_1$ (96 × 113) × 145 × 113 (Sr2, Sr36, Sr44), No. 14a F$_3$ (96 × 113) × 145 (Sr36, Sr44), No. 19 BC, F$_2$ (96 × 113) × 113 (Sr2, Sr36, Sr44), No. 20 F$_3$ (96 × 113) × 145 (Sr2, Sr36, Sr40, Sr44), varieties of Omsk Agrarian University – Element 22 (Sr31, Sr35), Lutescens 27-12, Lutescens 87-12 (Sr23, Sr36), Lutescens 70-13, Lutescens 87-13 (Sr23, Sr31, Sr36) are recommended for inclusion into breeding process of the creation of resistant to stem rust varieties in the region. Further monitoring of the virulence of stem rust pathogen and coordination strategy of breeding programs in Western Siberia, and neighboring regions of the Kazakhstan Republic is recommended. Incorporation of effective resistance genes, in particular Sr2 and Sr40, will improve the phytosanitary situation and expand the segment of resistant varieties in the region.

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