Isogenic Lines: Reaction to the Kazakhstan Population of Stem Rust (*Puccinia graminis* f. sp. *tritici*)

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**ABSTRACT**

In recent years, intensified development of stem rust of wheat has again been noted in the grain-growing regions of Kazakhstan. To determine the genetic basis of immunity in 2015 – 2019, the authors performed targeted studies in the conditions of the southeast and north of Kazakhstan on the natural and the artificially infectious backgrounds of inoculation. Their scientific novelty consisted in identifying effective Sr genes of wheat resistance to the Kazakhstan population of stem rust. The obtained results of the immunological assessment of the trap varieties show that most studied genotypes with the Sr genes were susceptible to the Kazakhstan population of stem rust. With that, the varieties carrying the Sr31 gene have been affected to varying degrees. It should be especially noted that the Sr31 gene in combination with the Sr24 gene ensured more reliable protection from the population of the stem rust pathogen. The authors have selected the obtained resistance genes by their efficiency: Sr2 complex; Sr11; Sr21; Sr31; Sr36; Sr39; Sr40, SrSatu; SrNin, as well as combinations of the Sr24 and 1RS-Am genes; Sr24.31; Sr6.31.21; Sr6,24,36,1RS-Am; Sr7a, Sr12, Sr6; and Sr31 absent. The authors recommend them as sources of resistance to the local stem rust population.

**INTRODUCTION**

Wheat rust diseases are among the most economically significant objects in the world. The yield loss caused by them often reaches 15 – 20%. In Kazakhstan, three types of rust are parasitizing on the crops of soft wheat (*Triticum aestivum* L.): stem rust (*Puccinia graminis* f. sp. *tritici*), leaf rust (*P. triticina*), and yellow rust (*Puccinia striiformis* *tritici*). In recent years, stem rust (*Puccinia graminis* f. sp. *tritici*) has become more and more harmful to spring wheat crops. It is known that it is spread to the highest degree in the northern regions of the Republic, where the continental climate with the summer temperatures regularly exceeding 25°C is favorable for the development of this pathogen (Li et al., 2019). It poses the greatest threat in the Kostanay, the Akmol, and the northern Kazakhstan regions, especially in the years when it can develop simultaneously with leaf rust or Septoria blight. The infection disrupts the water balance, resulting in delayed growth and development of the plants and crops beating down. The grain loss in this case reaches 30 – 60%. A similar phytosanitary situation had occurred in 2006 – 2007 when the prevalence of the diseases had reached 40 – 80%. Later, in 2015, the stem rust outbreak in the region affected over a million hectares of land used for wheat. A similar pattern was observed in 2016 and 2017.

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of the pathogen was detected in all the examined fields in the northern Kazakhstan region, especially in the late wheat crops, and this resulted not only in a noticeable decrease in the yield but also in the worsening of the grain quality (Koyshybaev, 2018; Rsaliyev & Rsaliyev, 2018).

The stem rust races are constantly changing and evolving, therefore the cultivated resistant varieties become susceptible to it. In this regard, there is a need for timely monitoring of their emergence and the beginning of spreading. This opportunity is largely provided by the use of trap nurseries. This set includes differential lines next to the isogenic lines and the varieties with identified genes. Most of them carry genes of resistance to pathogens in various climatic conditions and contain a wider range of the local germplasm (Natsarishvili, Sikharulidze, & Tsetskhladze, 2016).

Prior to the appearance of the new Ug99 race, stem rust had been effectively controlled worldwide for decades due to the cultivation of genetically resistant varieties. The appearance of the Ug99 race (TTKSK) or its variants is considered a serious threat to wheat production. Besides, estimates show that 80 – 90% of the world’s cultivated land used for wheat is susceptible to this disease (FAO, 2020). Currently, the pathogen is developing and expanding geographically. This is evidenced by 13 confirmed facts of the spread of new races in 13 countries: Uganda (1998, 2012, and 2014), Kenya (2001, 2006, 2007, 2008, 2009, 2013, and 2014), Ethiopia (2003, 2007, 2010, 2013, and 2018), Sudan (2006), Yemen (2006 and 2009), Iran (2007), Tanzania (2009), Eritrea (2010, 2012, and 2014), Rwanda (2014), Egypt (2014), South Africa (2000, 2007, 2009, 2010, and 2017), Zimbabwe (2009 and 2010), and Mozambique (2010 and 2013) (Berlin, 2017; Olivera Firpo et al., 2017; Olivera et al., 2015; Singh et al., 2015).

It is known that spreading northward from East Africa to the Middle East, Ug99 has the potential to affect many cultivated wheat varieties as it continues to produce new variations (FAO, 2020). Unfortunately, the Ug99 race group is not the only problem. There is also the Digalu race, which is also called TKTTF. Both these races are not genetically interconnected and consist of two different genetic types. The latter was first registered in Turkey in 2005 and is widespread in the Middle East region. Currently, the TKTTF race has also been confirmed in 11 countries: Turkey (2005), Iran (2010), Lebanon (2012), Ethiopia (2012) and Egypt (2013), Georgia, Azerbaijan, Eritrea, Yemen, Germany (2013) (Olivera Firpo et al., 2017), and Denmark (2013) (Olivera et al., 2015). To date, these races have started migrating to the countries in Central Asia. In this regard, it may also spread to the territory of Kazakhstan.

The appearance of the TTKSK race (Ug99) and its new variants threaten wheat production worldwide. The TTKSK race and its variants are virulent to most stem rust resistance genes that are currently used for wheat varieties worldwide (Zhang et al., 2010). Epidemics and local outbreaks in Ethiopia, Europe, and Central Asia show that the disease re-emerges as a threat to wheat production. It should be noted that only some stem rust resistance (Sr) genes obtained from the primary wheat gene pool ensure resistance to TTKSK; this fact is important for using them in the breeding work (Ghazvini et al., 2012). Besides, the frequent appearance of new and virulent varieties of the Puccinia graminis f. sp. tritici race groups makes studying the pathogens relevant (Olivera, Rouse, & Jin, 2018).

Monitoring the prevalence of pathogens with the use of trap nurseries provides fundamental information for the development and adoption of appropriate national and international policies, investments, and strategies in plant protection, plant breeding, seed production, and studying pathogen rust (Zhang et al., 2010).

Based on the foregoing, this study was aimed at immunologically assessing the genotypes of trap nurseries and selecting the sources of resistance to stem rust for the breeding of immune spring wheat.

**MATERIALS AND METHODS**

The field experiments were laid in 2015 – 2019 in two regions of Kazakhstan: on the artificial background of infection (43°14’17.3”N 76°41’48.0”E) – in the conditions of the Almaty region in the southeast of Kazakhstan, and on the natural background of infection (53°51’12.5”N 62°08’04.2”E) in the conditions of the Kostanay region in the north of Kazakhstan. The objects of the study were 85 wheat lines and varieties from the 9th ISRTN-15 (International Stem rust Trap Nursery). This set had been obtained from the CIMMYT. The seeds were planted manually into rows 1 m long. To amplify manifestations of the diseases, the Kazakhstanskaya-10 local variety that was susceptible to the pathogen was sown after
During the study (2015 – 2016 and 2019), the weather conditions of the vegetation period were relatively humid, which generally prevented the emergence of the pathogen, and the vegetation periods in 2017 – 2018 were relatively dry for the development of stem rust.

To create an artificial infectious background, a mixture of stem rust uredospore population from the collection material of the Institute of Plant Biology and Biotechnology (IPBB) was used as an inoculum. The uredospores had been collected from the samples taken from the production fields used for commercial wheat varieties in various geographical areas and in the areas with alternative rust hosts, as well as from wild cereals (Rsaliyev & Rsaliyev, 2018). The spores' biological purity and germination rate were 90 – 95%. Before inoculation, the uredospores had been activated. For this purpose, the spores were scattered from the ampule into Petri dishes in a thin layer, not more than 1 mm thick, and kept in a thermostat at 45°C for 30 minutes. After that, they were placed in a desiccator with high relative humidity for 6 hours. The crops were inoculated using the method of spores dusting with talcum powder in the spring wheat stem elongation phase. The infectious load of the spores was 20 mg/m² of the crops. The infestation was performed in the evening after rains, in the most favorable conditions: in calm weather with the air temperature not lower than 20 – 22°C. After inoculation, the plants were covered with plastic film for 10 – 12 hours.

The reaction of the varieties to stem rust was assessed five times in real-time during the vegetation period, from the manifestation of the first characteristic symptoms until the milky-wax ripeness of the grains in seven days’ intervals. The immunological properties of the breeding material were assessed by two indicators: the type of reaction (qualitative assessment) and the degree of the leaves and stem vulnerability (quantitative assessment). The type of reaction was determined according to the recommended CIMMYT scale (CIMMYT, 1988): 0 (immune) — no symptoms of the disease, R (resistant) — minor individual chloroses or necroses without pustulation, MR (moderately resistant) — small pustules surrounded by chlorotic or necrotic spots; M (medium) — medium-sized pustules with chlorosis or necrosis, some with chlorosis and necrosis, MS (moderately susceptible) — medium-sized pustules without necrotic spots, but with possible chlorotic spots, and S (susceptible) — large pustules without chlorosis and necrosis. The degree of the plants’ infestation was assessed in percent using the scale of R.F. Peterson modified by Cobb (Peterson, Campbell, & Hannah, 1948) with the graduation of 5, 10, 20, 40, 60 ... 100%.

The area under disease progress curve (AUDPC) was determined following the method of D. A. Johnson based on five or more accountings:

\[ S = \frac{1}{2} \sum (x_{i} + x_{i+1})(t_{i+1} - t_{i}) \]

Where S was the AUDPC, n was the number of accountings; \( x_{i} \), \( x_{i+1} \), \( x_{i} \) were the degrees of the disease development at the time of the 1st, 2nd, and the last accounting, respectively, \%, (\( t_{i+1} - t_{i} \)) was the time between the 2nd and the 1st accounting, days; (\( t_{i} - t_{i-1} \)) was the time between the last and the penultimate accounting, days.

**RESULTS AND DISCUSSION**

Statistical processing of the obtained immunological data showed that on the artificial infectious background, a high enough infestation rate of the studied set of genotypes in the trap nursery had been achieved. While in 2015, the average infestation rate of the plants had been within 40%, in the subsequent years (2016 – 2019), this value was within 14 – 18%. With that, on the natural infectious background, the susceptibility of the trap nursery was only 4% (Fig. 1 and Fig. 2).

The global climate change, evolutionary and breeding and genetic factors, the emergence of new virulent races, the loss of resistance by commercial wheat varieties, crops expansion with the cultivation of susceptible varieties, poor monitoring of new virulent types of rust, etc. may contribute to their further spread (Rsaliyev & Rsaliyev, 2018). Therefore, creating and introducing disease-resistant varieties into production is considered the most efficient, cost-effective, and environmentally friendly method of fighting pathogens. Breeding resistant varieties have a decisive role in the co-evolution of the host-pathogen system. In creating a new variety, a new resistance gene is introduced into the genotype; however, after some time, biotypes with a new virulence gene appear in the pathogen population. Besides, the wide cultivation of the varieties carrying similar resistance genes accelerates the evolution of pathogens (Rosseyeva et al., 2017).
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Fig. 1. Stem rust susceptibility of the genotypes in the trap nursery on the infectious background, Almalybak, 2015-2019

Fig. 2. The average value of stem rust susceptibility of the genotypes in the trap nursery and the local susceptible variety on the infectious background, Almalybak, 2015-2019 (ISRTN – International Stem rust Trap Nursery)
Over 70 Sr genes have been identified to date, of which approximately 31 are still effective against at least one Ug99 race (Aoun et al., 2019; Singh et al., 2015). A total of 20 lines and varieties were identified in the studies in terms of the effectiveness of the resistance genes to the local population of stem rust. Most genes studied within the set proved ineffective. Their high vulnerability was probably evidence of increasing pressure of the pathogen population on certain resistance genes. This allowed formulating a working hypothesis. Besides, in 2015, the local pathogen population probably contained more virulent pathotypes, compared to the other years of the study. For instance, in the years of the study, the infectious background of the varieties carrying stem rust resistance gene was most susceptible. However, the Seri 82 and Cham 8 varieties with the Sr31 gene showed high efficiency. This was well consistent with the data obtained by Shamanin: the Sr31 gene in the conditions of the Omsk and the Kostanay regions in 2016 showed resistance to the stem rust pathogen (Shamanin et al., 2016). Also, such varieties as Siouxland with the Sr24 + 31 genetic combination, Pavon 76 with the Sr2 complex Sisson (Sr6, 31 + 36), Fleming (Sr6, 24, 36, 1RS-Am) Satu, SrNin, Imillo, Altar, Gemmeiza 9, Arrehane, Debeira, and Guard showed good resistance.

The AUDPC is a good indicator of the adult plant resistance in the field conditions. According to the results, the AUDPC for the Gemmeiza 9 variety was only 92.5. This variety had good resistance of adult plants in the field not only to stem rust but to leaf rust as well. Resistance to leaf rust was explained by the fact that this variety contained three-leaf rust resistance genes Lr10, Lr19, and Lr35. Today, the Lr10 gene remains one of the resistance genes that are effective to the local leaf rust population.

Due to various weather conditions prevailing during the period of the studies, certain reactions of the isogenic lines were slightly different from their similar values in the previous years. This difference possibly also indicated a change in the biotypic composition of the Kazakhstan population of the stem rust pathogen, which caused susceptibility of most studied Sr genes. Meanwhile, the authors managed to isolate several effective resistance genes: Sr2 complex, Sr11, Sr21, Sr31, Sr36, Sr39, Sr40, SrSatu, and SrNin, as well as combinations of the Sr24 and 1RS-Am genes, Sr24, 31, Sr6, 31, 21, Sr6, 24, 36, 1RS-Am, Sr7a, Sr12, Sr6, and Sr31 absent. The carrier lines and varieties that provided effective protection from stem rust are shown in Table 1.

In addition to the above in Table 1, other resistance genes were also efficient in some years. For instance, in 2016 — Sr5, Sr8a, SrMcN, Sr21, Sr23, Sr26, Sr37, and combinations of the Sr1RS-Am genes; in 2017 — Sr13, SrMcN, SrTmp, Sr21, Sr27, and combinations of the Sr1RS-Am, Sr36, 6, Sr36, 6, Sr7a, Sr12, and Sr6 genes; in 2018 — SrMcN, Sr22, Sr23, Sr27, Sr33, Sr35, Sr37, and combinations of the Sr1RS-Am, Sr36, 6, Sr7a, Sr12, and Sr6 genes; in 2019 — Sr19, Sr26, Sr30, Sr31, Sr37, and combinations of the Sr1RS-Am and Sr36, 6 genes.

The Sr2 gene is one of the most important resistance genes in modern plant breeding for immunity. Although adult plant resistance (APR) to stem rust has been known for a long time, Sr2 was the only well-studied gene. Sr2 is the gene of wheat age resistance to stem rust and is effective against the Ug99 race (Vishwakarma et al., 2019). It has been used for about 60 years in the world’s breeding practice as a source of resistance. During the studies, the Sr2 gene in combination with other genes resistant to Ug99 and related isolates showed moderate resistance to local populations of stem rust.

The Sr11 gene, which ensured resistance to the TKTTF race, in 2015 – 2017 featured moderate resistance. In the subsequent years of the study, this gene lost its effectiveness by getting affected up to 50MS, while the AUDPC was 607.5. The Sr11 gene was effective in Australia, but its widespread use resulted in its susceptibility. Although the gene is susceptible to some stem rust races, it remains a valuable resistance gene for certain race groups of _P. graminis_ f. sp. _tritici_.

According to the literature data, the Sr15 gene had been previously identified as ineffective against the TTKSK race. Gao et al. (2019) made conclusions about the effectiveness of the Sr15 gene to the Ug99 race (TTKSK). The effectiveness of this gene depends on temperature. At 15 – 18°C, efficiency is observed, and at the temperature over 26°C, the Sr15 gene becomes susceptible to the pathogen. In the studies of the authors, the Sr15 gene proved moderately susceptible (MS) and susceptible (S) to the local pathogen population.
The fact is that the W2691SrTt-1 CI 17385 lines and the Cook variety are susceptible to the Sr36 gene, which is one of the important sources of resistance to the TTKSK race. This race has unusually wide combinations of virulence and induces an almost immune resistance response in many races of *Puccinia graminis f. sp. tritici*. The gene was obtained from the *Triticum timopheevii* species (Purnhauser, Bóna, & Láng, 2011). This gene, considered a valuable source of resistance, is virulent to other races of stem rust, and it is recommended to use it pyramidically linked to other resistance genes. According to the data published in the USA, this gene confers resistance to TTKSK in many adapted varieties and is widely used in the germplasm of common winter wheat varieties (Tsilo, Jin, & Anderson, 2019). Under the conditions of the studied region, the W2691SrTt-1 CI 17385 line with the Sr36 gene exhibited moderate resistance against an artificial background of infection, and the Cook variety with this gene was not affected by stem rust.

The virulence of individual races of the pathogen against the Sr24 + Sr31, Sr6 + Sr31 + Sr36 resistance genes is considered the most significant since these gene combinations also ensure resistance to other predominant races of *P. graminis f. sp. tritici*. In the studies, the above-mentioned gene combinations featured efficiency both on the natural and the artificial stem rust

### Table 1. The isogenic lines and varieties outstanding in terms of resistance to the local stem rust population, artificial background, 2015-2019

| Genes | The line reaction by the years and the regions of Kazakhstan (% type of disease) | AUDPC |
|-------|--------------------------------------------------------------------------|-------|
|       | 2015 | 2016 | 2017 | 2018 | 2019 | 2019 |
| W2691SrTt-1 CI 17385 | 20MR | 10MR | 20MR | 10MR | 5R | 92.5 |
| Trident Sr38 | 10MR | 0 | 0 | 30MR | 5R | 30.0 |
| Trident Sr38 | 5MR | 5R | 0 | 10R | 5R | 92.5 |
| Siouxiand Sr24 + Sr31 | 0 | 0 | 0 | 0 | 0 | 0.0 |
| Sisson Sr6 + Sr31 + Sr36 | 10MR | 0 | 0 | 0 | - | 32.5 |
| Fleming Sr6 + Sr24 + Sr36 + 1RS-Am | 30MR | 40MR | 0 | 5R | 5R | 92.5 |
| Pavon 76 Sr2 complex | 10R | 20MR | 5R | 20MR | 5R | 92.5 |
| Seri 82 Sr31 | 10R | 10R | 0 | 10R | 10R | 60.0 |
| Cham 8 Sr31 | 10R | 5R | 0 | 0 | 0 | 130.0 |
| Cham 10 = Kauz/Kauz/star Sr31? | 5R | 0 | 0 | 5R | 0 | 0.0 |
| Bacanora = Kauz's' Sr31 | 5R | 0 | 0 | 0 | 5R | 92.5 |
| Cook Sr36 | 40MR | 10R | 0 | 10R | 0 | 0.0 |
| Satu SrSatu | 0 | 10R | 0 | 0 | 0 | 0.0 |
| SrNin SrNin | 0 | 10R | 0 | 0 | 0 | 0.0 |
| Imillo | 5MR | 0 | 0 | 10MR | 5R | 92.5 |
| Altar | 10MR | 5R | 0 | 0 | 20R | 92.5 |
| Gemmeiza 9 | 30MR | 5R | 0 | 10R | 5R | 92.5 |
| Arrehane | 20MR | 0 | 0 | 5R | 5MR | 92.5 |
| Debeira | 0 | 10MR | 0 | 0 | 0 | 92.5 |
| Guard | 10R | 20MR | 5MR | 10MS | 5MR | 92.5 |
| Kazakhstanskaya-10 | 90S | 40S | 40MS | 30S | 30S | 612.5 |

Remarks: AUDPC: area under disease progress curve. 0: immune, R: resistant, MR: moderately resistant, MS: moderately susceptible, S: susceptible
backgrounds. This phenomenon was probably associated with the absence of virulent agents or lower diversity of the biotypic and race composition of the Kazakhstan population of the pathogen.

The Sr24 gene was obtained from *Agropyron elongatum* (Host) P. Beauv. The gene is completely linked to the Lr24 gene. The Sr24 gene is a valuable source of resistance; it is resistant to most stem rust races, including the virulent TTKSK race. However, it is not effective against the more recent variant of UG99 designated as TTKST (Lowe & Soria, 2019). In the field conditions, the susceptibility of the LcSr24Ag line with the Sr24 gene was within 20MS. At the same time, according to some authors (Shamanin et al., 2020; Shamanin et al., 2016; Sibikeev, Markelova, Baukenova, & Druzhin, 2016; Volkova, Kudinova, & Miroshnichenko, 2020), affection by the Sr31 gene was noted on the territory of the Russian Federation. According to Rsaliev (2011), the Kazakhstan stem rust population also contained the races virulent to the Sr31 gene, and the susceptibility of the Seri 82 variety with this gene was 30 – 40%. In the studies of the authors, several lines and varieties with the Sr31 gene were studied. Of these, the Sr31 (Benno)/6*LMPG-6DK42 and PBW343 = Attila with Sr31 lines had been effective in 2015 – 2016, but in the subsequent years, they lost their effectiveness, being affected by 30 – 40% with the MS type of reaction. On the contrary, in the Seri 82 and Cham 8 varieties, and the Cham 10 = Kauz/Kauz/star, Bacanora = Kauz’s’ line with the Sr31 gene, stem rust susceptibility was low, within 5 – 10% with the R reaction type. Also, in 2015 – 2016, individual lines with the Sr21 gene (T. monococcum/8*LMPG-6 DK13) and Sr31absent (Kubsa = Attila and Chamran = Attila) had been moderately resistant (MR) to the stem rust population, but in 2017, they started losing their effectiveness. More detailed studies may be required. The susceptibility of the line with Sr31 genes to the local population of stem rust depreciates its breeding value.

The use of the varieties or lines with a single gene, which is overcome by the evolution of the pathogen, is a significant drawback. Therefore, a key element in achieving long-term rust control is the use of several effective Sr genes together (Figueroa et al., 2016). For instance, in the period of the study, a high resistance reaction was achieved on the Siouxland cultivar with the Sr24 + 31 gene combination. Today, this gene combination continues to provide protection against the stem rust pathogen population in Kazakhstan. Thus, the Sr31 gene provides complete protection against the stem rust pathogen population in Kazakhstan only in combination with the Sr24 gene; when used individually, this gene becomes ineffective.

The Trident Sr38 and Trident varieties with the Sr38 resistance gene were also distinguished by resistance to the local population of stem rust. This gene, together with Lr37, Yr17 genes, located in the segment of 2NS chromosome of *Triticum ventricosum* (Tausch) and transferred to the short arm of 2AS chromosome of common wheat, conferred resistance to stem rust (*Puccinia graminis* Pers. f. sp. *tritici* Eriks. & E. Henn.), leaf rust (*Puccinia triticina* Eriks.) and yellow rust (*Puccinia striiformis* West. f. sp. *tritici* (Cristina, Turcu, & Ciucă, 2015). The area under the disease-progress curve (AUDPC) of the two varieties ranged within 30-92.5. The varieties of mature plants grown in the field had a moderate level of resistance to leaf rust and yellow rust.

In 2015 – 2018, the Sr39 and Sr40 resistance gene had ensured resistance to the Kazakhstan stem rust population. In 2019, moderately susceptible reactions within 10% were noted for these genes.

The used set of trap varieties in 2016 – 2018 had been simultaneously studied by other researchers in the conditions of the Omsk region. According to Shamanin et al. (2020), most Sr genes showed susceptibility to the stem rust population composition in the region. A similar pattern was observed for the Sr 31, Sr2 complex, Sr21, Sr36, and Sr39 genes, as well as for the Sr24 + 1RS-Am, Sr24 + Sr31, Sr6 + Sr31 + Sr36, and Sr6 + Sr24 + Sr36 + 1RS-Am gene combinations, which stood out in terms of their efficiency in the Omsk region. The similarity of the phytosanitary situation with the aero genic infection, in this case, is obvious.

In the conditions of natural infection in the Kostanay region, where spring wheat is annually sown on more than 3.5 million ha of the cultivated land, the epiphytotic development of stem rust was observed in 2007, 2015, and 2016. In addition, leaf rust is noted in the region each year, especially in humid years. With that, most of the Sr genes showed their effectiveness, which was probably evidence of the diversity of the stem rust population in the regions of Kazakhstan. Meanwhile, during the 2019 vegetation period, severely arid weather conditions occurred in the north of Kazakhstan, which resulted...
in accelerated ripening of cereals and in the suppression of the rust fungi development. The first symptoms of leaf and stem rust development were observed in early August, at the beginning of wheat ripening. With that, the susceptibility of the Morocco variety to leaf rust was within the 40S, while susceptibility to stem rust reached only 5MR. In these conditions, compared to the artificial infectious background, the Sr19, Sr26, Sr31, Sr36, Sr38, Sr1RS-Am, Sr24, 31, Sr6, 24, 36, 1RS-Am, Sr2 complex, SrSatu, and SrNin genes were affected by stem rust to a relatively lesser degree (Table 2).

In the conditions of the natural infectious background, most Sr resistance genes in the Kostanay region showed efficiency against the local stem rust population. For example, for Prelude*4/2/Marquis*6/Kenya 117A (Sr9b), Prelude*2/Norka (Sr15), Seri 82 (Sr31), PBW343 = Attila with Sr31 (Sr31), Cham 8 (Sr31), Bacanora = Kauz’s’ (Sr31), Cook (Sr36), Pavon 76 (Sr2com), Trident Sr38 (Sr38), Siouxland (Sr24,31), and McNair 701 (SrMcN) Satu (SrSatu), no symptoms of stem rust were observed. In the conditions of natural infection, the Sr31 resistance genes were not affected, except for the Sr31 (Benno)/6*LMPG-6 DK42, Kubsa = Attila, Chamran = Attila, and Cham 10 = Kauz//Kauz/star line with this gene.

The comparison of the indicators of the two infectious backgrounds showed that on the natural background, the Sr30, Sr31?, Sr37, Sr38, SrNin, and Sr1RS-Am genes were affected by stem rust to a greater degree than on the artificial infectious background. In this case, some differences were also noted in the population composition of the stem and leaf rust by the region.

Given the developing phytosanitary situation, manifestations of leaf rust were also considered. The Amigo, Coorong, Chris, Einkorn, Karim, Aguilal, and Thatcher lines featured effectiveness against leaf rust; the Trident Sr38 variety with the Lr37+Yr17+Sr38 gene, the RL 5711 Kerber with the Sr39 gene recombined with the Lr35 gene, and the Siouxland varieties with the Sr24+Sr31,Lr24,Lr26 gene combination, Fleming with Sr6+Sr24+Sr36+Sr1RS-Am, Pavon 76 with Sr2 complex, Cham 8, Cham 10 = Kauz/Kauz/star, Bacanora = Kauz’s’ with the Sr31 gene, Satu with the SrSatu gene, SrNin with the SrNin gene, as well as the Imillo, Altar, Arrehane, Debeira, Aguilal, Thatcher, and Guard (Lr10, Lr2) varieties featured complex resistance to leaf and stem rust. The above lines and varieties with effective resistance genes are valuable for further studies and breeding development for their immunological properties and are recommended in these regions as sources of resistance.
Table 2. The reaction of the Sr resistance genes to the Kazakhstan stem rust population on the natural and artificial infectious backgrounds, 2019

| Variety | Sr genes | SR (%) type | Variety | Sr genes | SR (%) type |
|---------|----------|-------------|---------|----------|-------------|
| ISr5-Ra CI 14159 | Sr5 | 5R | 40S | Sr31 (Benno)6*LMPG-6 DK42 | 5R | 5MR |
| ISr6-Ra CI 14163 | Sr6 | 5R | 40S | ER5155 S-203 (1995)Roelfs | 5R | 20MS |
| Na 101/6*Marquis | Sr7a | 10R | 5S | RL 5405 (1192) Kerber | 5R | 20MS |
| ISr7b-Ra CI 14165 | Sr7b | 5MR | 80S | RL 6099 (1997) Dyck | 10MS | 30S |
| CI 14167/9*LMPG-6 DK04 | Sr8a | 5MS | 30S | RL 6099 (1995) Dyck | 10MS | 10S |
| Barleta Benvenuto (CI 14196) | Sr8b | 5R | 40S | W2691SrTt-1 CI 17385 | 5MR | 5R |
| ISr9a-Ra CI 14169 | Sr9a | 5R | 60S | Prelude*4/Line W (W3563) | 5MS | 5R |
| Prelude*4/2/Marquis*6/Kenya 117A | Sr9b | 0 | 20MS | Trident S38 | 0 | 5R |
| ISr9d-Ra CI 14177 | Sr9d | 5MR | 30S | Tridдет S38 | 5MR | 5R |
| Vemstein PI 442914 | Sr9e | 5R | 50MS | RL 5711 Kerber | 5R | 10MS |
| Chinese Spring*7/Marquis 2B | Sr9g | 5MR | 20S | RL 6087 Dyck | 10R | 20S |
| W2691Sr10 CI 17388 | Sr10 | 10MS | 10S | TAM 107 | Sr1RS-Am | 5R | 0 |
| Lee*6*LMPG-6 DK37 | Sr11 | 5R | 50MS | Amigo | Sr24,1RS-Am | 5MR | 50S |
| Chinese Spring*5/Thatcher 3B | Sr12 | 5R | 70S | Siouxiand | Sr24,31 | 0 | 0 |
| Prelude*4/2/Marquis*6/Khapstein | Sr13 | 5R | 20S | Roughrider | Sr36,6 | 10MS | 0 |
| W2691*2/Khapstein | Sr14 | 10R | 60S | Sisson | Sr6,31,36 | 5MR | - |
| Prelude*2/Norka | Sr15 | 0 | 5S | Fleming | Sr6,24,36,1RS-Am | 5R | 5R |
| Thatcher/CS (CI 14173) | Sr16 | 5R | 10S | Chris | Sr7a, Sr12, Sr6 | 5MR | 10MS |
| Prelude/8*Marquis*2/2/Espl 518/9 | Sr17 | 5R | 30S | CsSSrTmp | Srtmp | 5MS | 10S |
| Little Club/Sr18Mq Marquis “A” | Sr18 | 5R | 20S | Bl/Wid | Swild-1 | 5MS | 5S |
| 94A 236-1 Marquis “B” | Sr19 | 5R | 5MR | Pavon 76 | Sr2 complex | 0 | 5MR |
| 94A 237-1 Marquis “C” | Sr20 | 5MS | 10MS | Einkorn | Sr21 | 5MR | 5S |
| McNair 701 | SrMcN | 0 | 80S | Seri 82 | Sr31 | 0 | 10R |
| T. monococcum*8*LMPG-6 DK13 | Sr21 | 5R | 5S | PBW343 = Attila with Sr31 | Sr31 | 0 | 10MS |
| Mq*6/Stewart*3/RL 5244 | Sr22 | 5R | 40MS | Kubsa = Attila | Sr31 absent | 5R | 5MS |
| Exchange CI 12635 | Sr23 | 5R | 90S | Chamran = Attila | Sr31 absent | 5MR | 5MS |
| LcSr24Ag | Sr24 | 5MR | 20MS | Cham 8 | Sr31 | 0 | 0 |
| Agatha (CI 14048)*9*LMPG-6 DK16 | Sr25 | 5MR | 20S | Cham 10 = Kauz/Kauz/star | Sr31? | 5R | 0 |
| Eagle Sr26 McIntosh | Sr26 | 5R | 10MR | Bacanora = Kauz’s’ | Sr31 | 0 | 5R |
Table 2. (continued)

| Variety | Sr genes | SR (%, type) | Variety | Sr genes | SR (%, type) |
|---------|----------|--------------|---------|----------|--------------|
|         |          | Kostanay     |         |          | Kostanay     |
|         |          | Almaty       |         |          | Almaty       |
| WRT 238-5 (1984) Roelfs | Sr27 | 5R | 5S | Cook | Sr36 | 0 | 0 |
| Kota RL471 | Sr28 | 5R | 30MS | Coorong (Triticale) | Sr27 | 5MR | 40S |
| Prelude/8*Marquis/2/Etiole de Choisy | Sr29 | 5MS | 20MS | Satu | SrSatu | 0 | 0 |
| Selection from Webster F3:F4 #6 | Sr30 | 10MS | 10MR | SrNin | SrNin | 5R | 0 |
| Kazakhstanskaya-10 | Sr30 | 5MS | 30S | Morocco | SrNin | 5MR | 40MS |

Remarks: 0: immune, R: resistant, MR: moderately resistant, MS: moderately susceptible, S: susceptible
CONCLUSION

Thus, from the studied 58 sources of resistance, the combination of Sr24 + Sr31 genes has provided high resistance to the Kazakhstan population of stem rust. The Sr2, Sr6 + Sr31 + Sr36, Sr6 + Sr24 + Sr36 + Sr1RS-Am, Sr31; Sr31, Sr36, Sr38, SrSatu, and SrNin genes and gene combinations, which remain resistant, have also been noted. At the same time, the reaction of the Sr31 gene susceptibility has been discovered.

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