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WINTER WHEAT RESISTANCE TO YELLOW RUST IN SOUTHEAST KAZAKHSTAN

S. DUBEKOVA[1,2*], A. SARBAEV[1,2], M. YESSIMBEKOVA[2], A. MORGOUNOV[3,4], and A. YESSERKENOV[2]

[1]Kazakh National Agrarian Research University, Almaty, Kazakhstan
[2]Kazakh Research Institute of Agriculture and Plant growing, Almaty, Kazakhstan
[3]S. Seifullin Kazakh AgroTechnical Research University, Astana, Kazakhstan
[4]Atameken-Agro JSC, Kokshetau, Kazakhstan
*Corresponding author's emails: funny.kind@mail.ru
Email addresses of co-authors: kizamans2@mail.ru, minura.esimbekova@mail.ru, alexey.morgounov@gmail.com, ajs-eserkenov@mail.ru

SUMMARY

Wheat yellow (stripe) rust (*Puccinia striiformis* f. sp. *tritici*) is a dominant type of winter wheat disease. Developing new, highly productive varieties with increased immunological indicators helps to minimize the threat of rust spread. The progressive study searched the sources of resistance to the Pst populations and determined the effectiveness of *Yr* genes in Southeast Kazakhstan. Immunological studies ensued during 2018–2022 at the Kazakh Research Institute of Agriculture and Plant growing, Almaty, Kazakhstan. Wheat's 23 isogenic lines and 193 winter wheat genotypes attained evaluation for their reactions against an artificially infectious background of infection mixed with Pst pathotypes. Determining the intensity of virulence, the effectiveness of *Yr* genes, and the resistance of genotypes to the Pst population transpired in the said region. During the vegetation period, based on weather conditions, the accumulated flow of the source, and the period of infection, wheat genotypes responded differently to the rust disease manifestation. The wheat genotypes found resistant to *P. striiformis* and promising for selection with immunity reached nomination. Their practical use centered on increasing the immunological potential of the new winter wheat cultivars for creation and further reducing the large-scale use of fungicides and the negative environmental consequences.

Keywords: Wheat (*Triticum aestivum* L.) genotypes, isogenic lines, *P. striiformis*, wheat yellow rust, wheat stripe rust, rust resistance, immunity, conventional breeding

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Key findings: The winter wheat (*Triticum aestivum* L.) genotypes resistant to *P. striiformis* and promising for selection with immunity were notable. Their practical use centered on increasing the immunological potential of new wheat cultivars for development and reducing the large-scale use of fungicides and the negative environmental consequences.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is an economically strategic and principal cereal crop, ensuring food security globally (Bome *et al*., 2022; Dutbayev *et al*., 2023). However, rust diseases cause significant crop losses in wheat and other cereals worldwide (Wellings, 2011). Wheat yellow rust (*Puccinia striiformis* f. sp. *tritici*), also known as wheat stripe rust, is one of three major wheat rust diseases, such as stem rust of wheat (*Puccinia graminis* f. sp. tritici) and leaf rust (*Puccinia triticina* f. sp. tritici). Stripe (yellow) rust, caused by *Puccinia striiformis* f. sp. tritici (Pst), is a severe disease of wheat occurring in most wheat areas with cool and moist weather conditions during the growing season. The basidiomycete fungus, an obligate biotrophic parasite, is difficult to culture on artificial media.

Wheat yellow (stripe) rust (*Puccinia striiformis* f. sp. *tritici*) is a dominant type of winter wheat rust disease (Dubekova *et al*., 2021). Pst is a macrocyclic, heteroecious fungus that requires both primary (wheat or grasses) and alternate (*Berberis* or *Mahonia* spp.) host plants to complete its life cycle. Urediniospores have the capacity for wind dispersal over long distances, which may, under high inoculum pressure, extend to thousands of kilometers from the initial infection sites. Stripe rust, considered the current chief rust disease affecting winter cereal production worldwide, has undergone intensive study for over a century.

In a favorable season of rust-disease development, a significant increase in its harmfulness emerges, causing a sharp decrease in the grain traits' productivity and quality. The population of pathogens consists of pathotypes with a diverse nature of virulence. These pathogens spread aerogenically over long distances, form new pathotypes, and overcome the wheat cultivars' resistance to the pathogen (Koishybaev, 2018). In this regard, there is a risk of virulent evolution of the infection pathogen in grain-growing regions. Pathogens can also adapt to diverse climatic conditions and spread rapidly over long distances (Hovmøller, 2001).

The frequent epiphytotics of the wheat yellow rust pathogens have been visible in Western Europe, Central and East Asia, the Middle East, North and South Africa, North and South America, and Australia (Chen, 2005; Hovmøller *et al*., 2011; Chen *et al*., 2014, 2021; Ali *et al*., 2017; Bai *et al*., 2021). As a result of the loss of stability of the *Yr9* and *Yr27* genes, high-yielding cultivars in various countries have undergone primary epiphytotics (Solh *et al*., 2012). The emergence of new aggressive Pst strains represents severe epidemics where crop losses due to pathogens can reach 70%–100% (Chen, 2005; Ali *et al*., 2014; Zhou *et al*., 2022).

In Kazakhstan, the rust species occur almost annually, excluding super dry years (Koishybaev, 2018). In the environmental conditions of Kazakhstan, various virulent rust races have been identified (Rsaliyev *et al*., 2010; Rsaliev *et al*., 2013; Rsaliyev and Rsaliyev, 2018). Creating highly productive wheat cultivars with increased immunological indicators helps minimize the threat of rust spread. Cultivating such wheat cultivars will also reduce the costs necessary to protect crops from infection.

In this regard, plant breeders and pathologists have the task of breeding high-yielding and disease-resistant wheat cultivars. The developed programs of the International Center for Agricultural Research in Dry Areas (ICARDA) and the International Maize and Wheat Improvement Center (CIMMYT) play a vital role in developing highly productive and broadly adaptive types of wheat, resistant to pathogens and abiotic stresses (Wu *et al*., 2021).

The systematic study of Kazakh breeding lines and the world collection for resistance to Pst populations becomes a prerequisite for the purposeful selection of the source material with immunity. Every year, within the framework of breeding programs, the research on immunological assessments and choices of lines and cultivars resistant to particularly harmful diseases has advanced (Esimbekova *et al*., 2019; Dubekova *et al*., 2020; Ydyrys *et al*., 2021). These promising selected populations are beneficial sources of stability, which are of fundamental and applied importance in expanding genotypic diversity. The timely study aimed to search for sources of resistance to the Pst populations and determine the effectiveness of *Yr* genes in Southeast Kazakhstan.

MATERIALS AND METHODS

The recent study on winter wheat (*Triticum aestivum* L.) ensued during 2018–2022 at the Kazakh Research Institute of Agriculture and Plant growing (N43,238193°, E76,696753°), Almaty, Kazakhstan. In the field, the adult plant resistance (APR) to the wheat yellow rust population bore appraising against an artificially infectious background. The testing of 193 winter wheat genotypes of various ecotypes proceeded for immunological parameters. The genes' effectiveness also acquired validation by the reaction of 23 isogenic Yr lines and cultivars of differentiators. In this region, analyzing significant variations of the virulence of dominant Pst pathotypes took place.

Sowing transpired using the standard method (1-m row with a 20-cm distance between rows). The pathogen-sensitive winter wheat cultivars Almaly, Steklovidnaya 24, and Bogarnaya 56, and the highly susceptible cultivar Morocco served as indicator cultivars. All these genotypes' sowing after every 20 rows helped ensure uniform and enhanced infection with the pathogen.

Inoculation and disease assessment of APR

Crop inoculation started from the tillering phase to the stem elongation of the crop. Using as an inoculum, *P. striiformis* urediniospores incurred mixing with talc in a ratio of 1:100, with a load of 20 mg of spores/m^2 (Roelfs *et al*., 1992). The yellow rust urediniospores, collected in advance, came from the collection material of the Research Institute of Biology and Biotechnology, commercial wheat cultivars production in various geographical areas where an alternative rust host grows, and from wild cereals in nature (Rsaliyev and Rsaliyev, 2018). Biological purity and germination of spores equaled 90%–95%. Immunological assessment of the APR began when the final rust severity (FRS) in susceptible controls exceeded ≥60.

Subsequent recordings progressed at intervals of 10 days before the onset of the phase of milk-wax ripeness of grain. The infection type (IT) and the degree (%) of plant damage became criteria for the resistance of winter wheat genotypes to the pathogen. The IT determination engaged the recommended CIMMYT scale (Rust scoring guide, 1986), i.e., 0 (immune) with no infection symptoms, R (resistant) with small individual necrotic zones and no pustules, MR (moderately resistant) with small pustules surrounded by chlorotic and necrotic spots, MS (moderately susceptible) with medium-sized pustules, no necrotic spots, but sometimes with chlorotic spots, and S (susceptible) with large pustules, without chlorosis and necrosis. The degree of plant damage estimation as a percentage (0%–100%) followed Peterson's scale, modified by Cobb (Peterson *et al*., 1948). Multiplying the IT constant values by FRS calculated the coefficient of infection (CI) of wheat yellow rust, using constant IT values (0 = 0.0; R = 0.2; MR = 0.4; M = 0.6; MS = 0.8; and S = 1.0) (Stubbs *et al*., 1986).

Meteorological conditions

The meteorological conditions during the study period 2022 were generally favorable (periodic precipitation, prolonged and frequent dews) for developing and exploring the rust pathogen. However, the growing seasons of 2018–2021 were dry, with high temperatures and below-normal precipitation. There was a weak crop (biomass) development and limited infectious potential of phytopathogens, resulting in the incubation period’s increase and sporulation’s decrease, which also restrained the wheat yellow rust development rate.

Data analysis

Data scrutiny employed the analysis of variance (ANOVA), with the correlation coefficient executed using R-software (https://www.r-project.org/). In comparing the genes’ effectiveness, the obtained data during the study years attained groupings by year. The study determined the variability and significance of immunological parameters and the relationship between the parameters (CI and FRS) considering the APR.

RESULTS

The study has established the immunological characteristics of the winter wheat genotypes (Figure 1). In the field, against the background of infection with a wheat yellow rust population, the genes’ effectiveness analysis used isogenic Yr lines/differentiators. Considering APR, the wheat genotypes’ resistance to the local populace of *P. striiformis* also reached evaluation.

During the study years 2018–2022, the winter wheat cultivars of local breeding standards (Almaly, Steklovidnaya 24, and Bogarnaya 56) sustained impacts up to 25 MS. The susceptibility control of the Morocco cultivar was up to 100 S, which meant a favorable infectious background acceptable for assessing and selecting resistant wheat genotypes. Phenotypic data for five seasons (2018 to 2022) indicated effective resistance of the *Yr4*, *Yr5*, *Yr10*, *Yr15*, and *YrSp* genes. However, there was a decline in the effectiveness of the *Yr8* and *Yr27* genes, with previous characterization as moderate resistance (Figure 2).

A relatively high value of the Pst CI was evident in 2022. The aggressiveness of the Pst population had manifestations from the genes *Yr6*, *Yr7*, and *Yr21*. The genes *Yr4* (Hybrid 46), *Yr5*, *Yr10*, *Yr15*, and *YrSp* emerged to be highly effective in protecting wheat at the adult stage of its growth and retaining reliability. In recent years, lines previously distinguished by MR (carriers of the *Yr8* and *Yr27* genes) began acquiring influences from the pathogen up to 10%–15% with the MS reaction type. The analysis of the obtained data provided variations of immunological indicators by year (Table 1). The mean value of the CI from 2018 to 2021 was insignificant (CI < 20). However, in 2022, a relative increase in this indicator (CI > 20) occurred. Still, the CI of wheat yellow rust varied slightly.

Phenotyping of the Pst population virulence

Understanding the Pst population distribution and its virulence to genes allows for efficient monitoring of the rising threat of yellow rust, which is crucial for developing strategies to control the pathogen. Relatedly, considering the responses of isogenic lines and cultivars of differentiators in the field, the local Pst race incurred division into virulent and avirulent types to specific genes. In Southeast Kazakhstan, it was notable that the Pst population turned out to be toxic to the genes, viz., *Yr1, Yr2, Yr3, Yr6, Yr7, Yr8, Yr9, Yr17, Yr18, Yr21, Yr25, Yr27, Yr28, Yr29, Yr31, Yr32, YrA,* and *YrND*, and avirulent to the genes, i.e., *Yr4, Yr5, Yr10, Yr15,* and *YrSp* (Table 2).

The stripe-rust resistance characteristics of the various winter wheat genotypes are an essential indicator and play a vital role in selecting new resistant cultivars. Such data also aided in developing effective protective measures to minimize crop losses from harmful pathogens. Screening a collection of 193 winter wheat genotypes also helped find the sources of resistance to yellow rust (Table 3).

Figure 1. Manifestation of wheat yellow rust on winter wheat.

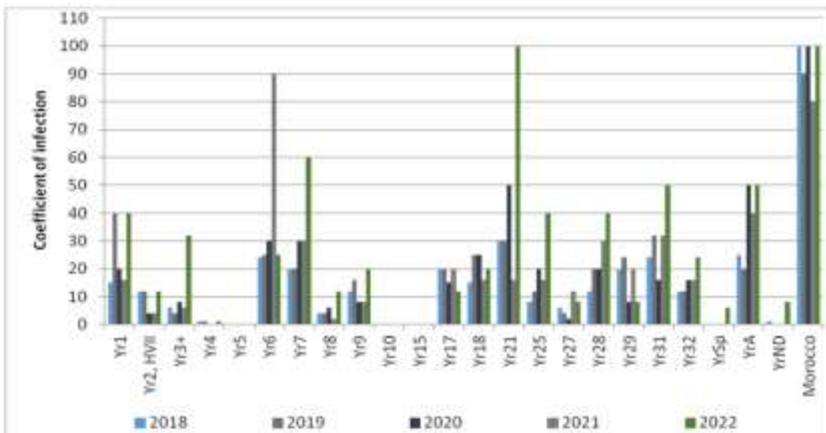

Figure 2. Changes in the efficiency of *Yr* genes, in dynamics for 2018–2022.

Table 1. The range of immunological indicators, according to the reactions of isogenic Yr lines/differentiators to the Pst population (2018–2022).

Parameters	CI_{2018}	CI_{2019}	CI_{2020}	CI_{2021}	CI_{2022}
min-max	0-100	0-90	0-100	0-90	0-100
Mean	15.29	17.12	17.83	18.92	27.83

Table 2. Virulence/avirulence formula for the Pst population in Kazakhstan.

Testing year	Pathotype/Genetic group	Virulence phenotype		Prevalence in the geographical region
2018–2022	Local race of Pst*	1,2,3,-,-,6,7,8,9,-,-,17,18,21,25,27,28,29,31,32,-,YrA,YrND		Southeast of Kazakhstan
		Avirulence formula	Virulence formula	
		Yr4, Yr5, Yr10, Yr15, and YrSp	Yr1, Yr2, Yr3, Yr6, Yr7, Yr8, Yr9, Yr17, Yr18, Yr21, Yr25, Yr27, Yr28, Yr29, Yr31, Yr32, YrA, and YrND	

*A genetic group of Pst with a high diversity of pathotypes.

Table 3. Material of winter wheat genotypes from different geographical areas for the analysis of resistance to the local Pst population.

Survey site	Genotype origin*	Number of genotypes
Southeast of Kazakhstan	Kazakhstan	86
	Uzbekistan	23
	Kyrgyzstan	32
	Tajikistan	9
	Russia	26
	Ukraine	3
	Turkey	3
	MX-TCI	2
	TR-EDR-TCI	1
	TCI	8
Grand total		193

*Origin includes the following organizations: MX – Mexico, TCI – Turkey/CIMMYT/ICARDA, TR – Turkey.

Table 4. Analysis of the significance of data on the reaction of genotypes to the Pst population.

	d.f.	Sum Square	Mean Square	F value	Pr(>F)
CI.	1	16366	16366	2579	<2e-16***
Residuals	191	1212	6		

Signifiant codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

The working collection of the winter wheat genotypes received a ranking from the resistance criteria, i.e., 0, R, MR, MS, and S, depending on their response to the dominant Pst pathotypes in Kazakhstan. Among the tested 193 winter wheat genotypes, 45 (23.3%) samples surfaced with an immune reaction and a complete absence of signs of wheat yellow rust. The 41 (21.2%) genotypes showed resistance, 33 (17.1%) genotypes showed moderate resistance, 69 (35.8%) genotypes exhibited moderate susceptibility, and only five (2.6%) genotypes occurred with complete susceptibility. Most of the winter wheat samples gained labels with the R-MR type of reaction. During the analysis, data obtained on the CI were min = 0, mean = 6.42, and max = 70.

The recognized differences in the FRS of cultivars in one geographical region were primarily due to significant differences in the genetic makeup of the host plant and the population of fungi and diverse ecotypes of the cultivars. The study of the immunological features of the wheat genotypes allowed us to identify resistant cultivars. The data obtained were combined for analysis of variance (Table 4).

Generally, positive data obtained had a high significance of the reaction (<2e-16***) of the studied wheat genotypes to the Pst population. In the assessed collection of winter wheat genotypes, the local cultivars, such as, Alatau, Zhadyra, Mayra, Konditerskaya, Manshyk, Nureke, and Krasnovodopadskaya 90, as well as exotic cultivars, i.e., Andijan 1, Bardosh, Azibrosh, Topper, Alex, Sipar, Yusufi, Vostorg, Pamyat, Petr, Moskovskaya 39, and Nacibey were distinguishable by resistance to Pst with very low CI (CI = 0-0.5) in an artificially infectious background and also significantly exceeded the standard wheat cultivars like Almaly (CI = 7.5) and Steklovidnaya 24 (CI = 11.25).

At the level of indicator, cultivars Bogarnaya 56 (MS) and Morocco (S) showed 38.4% of genotypes affected, which means their low significance for breeding with immunity to wheat yellow rust. A relatively high CI in individual genotypes, such as Aktereksky (CI = 70), Zernokormovaya 50 (CI = 30), Zhiger 2014 (CI = 30), Kazakhstanskaya 75 (CI = 22.5), Dordoy 16 (CI = 40), Zhanym (CI = 30), Kayrak (CI = 22.5), Antonina (CI = 22.5), and Gurt (CI = 30), can serve as a signal of their susceptibility

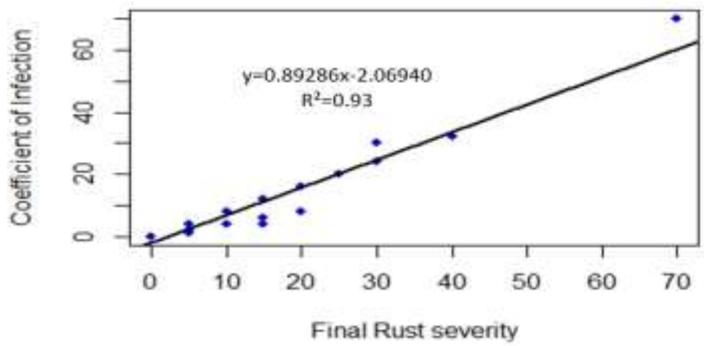

Figure 3. Regression analyses, the association between FRS and CI of *P. striiformis* f. sp. *tritici* for assessment of APR.

to the local Pst population, which during epiphytotic crop seasons can lead to significant crop losses.

Resistant winter wheat genotypes with a resistant type of response to the local Pst population obtained in 21 Kazakh breeding cultivars (Alatau, Alikhan, Akdan, Aliya, Anara, Batyr, Bayandy, Botagoz, Derbes, Zhadyra, Kokbiday, Koksy, Konditerskaya, Krasnovodopod 210, Mayra, Manshyk, Mereke 70, Nureke, Ramin, Krasnovodopadskaya 90, and Yubileynaya 75), as well as exotic cultivars of the foreign selection obtained from Uzbekistan (Andijan 1, Durdona, Jayhun, Jasmina, Jasmina, Ezoz, Yaksart, and Turkiston), Kyrgyzstan (Azibrosh, Topper, and Kasiet), Tajikistan (Alex, Ayvina, Kamol, Sipar, and Yusufi), Russia (Pamyat, Gratsia, Moskovskaya 39, Petr, Vostorg, and Kroshka), Turkey (Nacibey and Adajio), and TCI (Axe/Tosunbey, Dorade-5/3/Progr.), also indicate their significance and value in ensuring the protection of the crop from pathogens. The isolated stable winter wheat genotypes had high breeding values, which can proceed further for more improvement.

The correlation of the CI among the parameters of the FRS, rAURPC, latency period, and frequency of infection showed very high links (Sandoval-Islas *et al*., 2007; Safavi *et al.*, 2012). The relationship between the CI and FRS parameters in the studied 193 winter wheat genotypes at the adult stage of the plant was also well-defined (Figure 3). As a result of regression analysis of the dependence of the CI and the FRS, a positive correlation of the data with significant high indicators (R2 = 0.93) was evident.

DISCUSSION

The effective age-resistant genes in cultivated wheat cultivars can contribute to a slow increase in the intensity of infection due to a shorter selective pressure of pathotypes on plants (Kolmer, 1997). On immunological indicators, the relative results enunciated that yellow rust was more pronounced in winter wheat during 2022 (Figure 2, Tables 1 and 4). As a result, winter wheat cultivars with a low level of CI and other quantitative resistance parameters were most likely to have *APR* genes, and their resistance can continue for a long time, as also reported in past studies (Dehghani and Moghaddam, 2004; Singh *et al*., 2005; McIntosh *et al*., 2012; Shah *et al*., 2014).

Resistance genes found in the most widely cultivated wheat cultivars always play a decisive role in influencing the prevalence of pathogen races in a particular region. Wheat genotypes carrying effective *Yr* genes may be beneficial as a material for introducing resistance sources into commercial cultivars. There is information about the stability of genes *Yr15* and *Yr65,* some combinations of genes *Yr9* + *Yr18* and *Yr30* + *Yr46*, and the loss of effectiveness of some previously widely used genes *Yr9* and *Yr10* (Pal *et al*., 2008, 2015; Zheng *et al*., 2017).

The existing studies identified several resistant winter wheat cultivars, and there is still a further need to identify more effective resistance genes. In the past, highly effective genes were outstanding in Kazakh cultivars Dastan (*Yr5*), Karasai, Mereke 70, Naz, and Akdan (*Yr10*), Yubileynaya 60, and Dastan (*Yr15*), and a gene complex (*Yr18/Lr34*) in cultivars Ramin, Nurek, Mereke 70, Mayra, Bezostaya 1, and Almaly (Kokhmetova *et al*., 2014; Esenbekova and Kokhmetova, 2016; Ahmad *et al*., 2023). There are specific sources of resistance genes for successful wheat breeding (McIntosh *et al*., 2017). However, due to virulence variations in the pathogen population, further search for new sources of resistance and assessment of the genotypic diversity of world breeding is necessary (Park *et al*., 2011).

The presented immunological characteristics of the winter wheat genotypes of various ecotypes showed the intensity of yellow rust development in the region and confirmed a unique need to create promising cultivars combining high productivity with resistance to the pathogen *P. striiformis*. For scientific-based breeding, it is advisable to continue selecting potential lines and analyzing Pst races in the regions to strengthen further immunological research. In this regard, the next step is to study the presence of highly effective *Yr* genes in the isolated R genotypes and analyze the racial composition of Pst in the region. It requires a systematic exchange of information on the stability of wheat cultivars of various origins, monitoring the movement and virulence of rust pathogens, and strengthening international cooperation.

CONCLUSIONS

The effectiveness of known *Yr* genes against the Kazakh Pst population was well-defined. The promising winter wheat genotypes identified for yellow rust resistance represented the utmost immunological value for breeding and further improvement. These promising winter wheat genotypes, recommended for extensive use in breeding, will help develop highly productive new cultivars with improved immunological parameters. Their practical use is central to increasing the immunological potential of the winter wheat cultivars for creation and further reducing the large-scale use of fungicides and the negative environmental consequences.

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REFERENCES

Ali S, Gladieux P, Leconte M, Gautier A, Justesen AF, Hovmøller MS, Enjalbert J, de Vallavieille-Pope C (2014). Origin, migration routes and worldwide population genetic structure of the wheat yellow rust pathogen *Puccinia striiformis* f.sp. tritici. *Plos Pathog*. 10: e1003903. https://doi.org/10.1371/journal.ppat.1003903.

Ahmad J, Zulkiffal M, Anwar J, Ahsan A, Tanveer MH, Ajmal S, Sarwar M, Shair H, Javaid MM, Makhdoom M, Saleem M, Nadeem M, Shahzad R (2023). 'MH-21,' a novel high-yielding and rusts resistant bread wheat variety for irrigated areas of Punjab, Pakistan. *SABRAO J. Breed. Genet*. 55(3): 749-759. http://doi.org/10.54910/sabrao2023.55.3.13.

Ali S, Rodriguez-Algaba J, Thach T, Sørensen CK, Hansen JG, Lassen P, Nazari K, Hodson DP, Justesen AF, Hovmøller MS (2017). Yellow rust epidemics worldwide were caused by pathogen races from divergent genetic lineages. *Front. Plant Sci*. 8: 1057. https://doi.org/10.3389/fpls.2017.01057.

Bai Q, Wan A, Wang M, See DR, Chen X (2021). Molecular characterization of wheat stripe rust pathogen (*Puccinia striiformis* f. sp. *tritici*) collections from nine countries. *Int. J. Mol. Sci.* 22(17): 9457. https://doi.org/10.3390/ijms22179457.

Bome NA, Salekh S, Korolev KP, Kolokolova NN, Weisfeld LI, Tetyannikov NV (2022).

Biological potential of winter cereals in the Northern Trans-Urals, Russia. *SABRAO J. Breed. Genet*. 54(4): 789-802. http://doi.org/10.54910/sabrao2022.54.4.10.

Chen W, Wellings C, Chen X, Kang Z, Liu T (2014). Wheat stripe (yellow) rust caused by *Puccinia striiformis* f. sp. *tritici*. *Mol. Plant Pathol*. 15(5): 433-446. https://doi.org/10.1111/mpp.12116.

Chen X, Wang M, Wan A, Bai Q, Li M, López PF, Maccaferri M, Mastrangelo AM, Barnes CW, Fabricio D, Cruz C, Tenuta AU, Esmail SM, Abdelrhim AS (2021). Virulence characterization of *Puccinia striiformis* f. sp. *tritici* collections from six countries in 2013 to 2020. *Can. J. Plant Pathol*. 43(Sup2): 308-322. https://doi.org/10.1080/07060661.2021.1958259.

Chen XM (2005). Epidemiology and control of stripe rust [*Puccinia striiformis* f. sp. *tritici*] on wheat. *Can. J. Plant Pathol*. 27(3): 314-337. https://doi.org/10.1080/07060660509507230.

Dehghani H, Moghaddam M (2004). Genetic analysis of latent period of stripe rust in wheat seedlings. *J. Phytopathol.* 152(6): 325-330. https://doi.org/10.1111/j.1439-0434.2004.00848.x.

Dubekova SB, Eserkenov AK, Ydyrys AA, Kuresbek A (2020). Analiz sostoyaniya ustoichivosti ozimoi pshenitsy k zheltoi rzhavchine v usloviyakh yugo-vostoka Kazakhstana (Analysis of the state of resistance of winter wheat to wheat yellow rust in the southeast of Kazakhstan). *KazNAU, Izdenister, Nətizheler-Issledovaniya, Rezultaty* 4: 214-220.

Dubekova SB, Sarbaev AT, Ydyrys AA, Eserkenov AK, Bastaubaeva SO (2021). Immunological characteristics of winter wheat lines with resistance to rust diseases in Kazakhstan. *OnLine J. Biol. Sci.* 21(4): 356-365. https://doi.org/10.3844/ojbsci.2021.356.365.

Dutbayev Y, Kharipzhanova A, Yesserkenov A, Ten A, Garmashov S, Popova L, Konstantinova O, Sagyndykov U (2023). The harmfulness of common root rot in winter wheat varieties in Kazakhstan. *OnLine J. Biol. Sci.* 23(2): 187-192. https://doi.org/10.3844/ojbsci.2023.187.192.

Esenbekova GT, Kokhmetova AM (2016). Küzdik bïday sorttarınan sarı tat (*Puccinia striiformis* f. sp. *tritici*) awrına tözimdi gen ïelerin ïdentïfïkacïyalaw (Identification of gene holders resistant to wheat yellow rust [*Puccinia striiformis* f. sp. Tritici] from winter wheat varieties). *KazNAU, Izdenister, nətizheler-Issledovaniya, rezultaty* 1(069): 96-102.

Esimbekova MA, Mukin KB, Abugalieva AI, Abdrakhmanov K, Dubekova S, Morgunov AI (2019). Geneticheskie resursy v selektsii pshenitsy na ustoichivost k tverdoi golovne (Genetic resources in wheat breeding for resistance to stinking smut). *Agrarnaya Nauka* 1: 22-26. https://doi.org/10.32634/0869-8155-2019-326-1-22-26.

Hovmøller MS (2001). Disease severity and pathotype dynamics of *Puccinia striiformis* f.sp. *tritici* in Denmark. *Plant Pathol*. 50(2): 181-189. https://doi.org/10.1046/j.1365-3059.2001.00525.x.

Hovmøller MS, Sørensen CK, Walter S, Justesen AF (2011). Diversity of *Puccinia striiformis* on cereals and grasses. *Annu. Rev. Phytopathol*. 49: 197-217. https://doi.org/10.1146/annurev-phyto-072910-095230.

Koishybaev M (2018). Bolezni pshenitsy (Diseases of wheat). Prodovolstvennaya i selskokhozyaistvennaya organizatsiya OON (FAO) (Food and Agriculture Organization of the United Nations [FAO]), Ankara, pp. 365.

Kokhmetova AM, Sapakhova ZB, Madenova AK, Esenbekova GT (2014). Identifikatsiya nositelei genov ustoichivosti k zheltoi Yr5, Yr10, Yr15 i buroi rzhavchine Lr26, Lr34 na osnove molekulyarnogo skrininga obraztsov pshenitsy (Identification of carriers of resistance genes to wheat yellow rust *Yr5, Yr10, Yr15* and brown rust Lr26, Lr34 based on molecular screening of wheat samples). *Biotekhnologiya. Teoriya i Praktika* 1: 71-78.

Kolmer JA (1997). Virulence in *Puccinia recondite* f. sp. tritici isolates from Canada to genes for adult plant resistance to wheat leaf rust. *Plant Dis*. 81(3): 267-271. https://doi.org/10.1094/PDIS.1997.81.3.267.

McIntosh RA, Dubcovsky J, Rogers WJ, Morris C, Appels R, Xia XC (2012). Catalogue of gene symbols. KOMUGI Integrated Wheat Science Database. Available: https://shigen.nig.ac.jp/wheat/komugi/genes/symbolClassList.jsp.

McIntosh RA, Dubcovsky J, Rogers WJ, Morris C, Xia XC (2017). Catalogue of gene symbols for wheat: 2017 supplement. Available: https://shigen.nig.ac.jp/wheat/komugi/genes/macgene/supplement2017.pdf.

Pal D, Bhardwaj SC, Sharma D, S. Kumari, Patial M, Vinod, Sharma P (2015). Assessment of genetic diversity and validating rust resistance gene sources using molecular markers in wheat (*Triticum aestivum* L.). *SABRAO J. Breed. Genet.* 47(2): 89-98.

Pal D, Kumar S, Prashar M, Bhardwaj SC (2008). Gene sources and inheritance of stripe rust resistance in wheat. *SABRAO J. Breed. Genet.* 40(2): 147-152.

Park R, Fetch T, Hodson D, Jin Y, Nazari K, Prashar M, Pretoriuset Z (2011). International surveillance of wheat rust pathogens: Progress and challenges. *Euphytica* 179(1): 109-117. https://doi.org/10.1007/s10681-011-0375-4.

Peterson RF, Campbell AB, Hannah AE (1948). A diagrammatic scale for estimating rust intensity of leaves and stem of cereals. *Can. J. Res. Sect*. 26: 496-500. https://doi.org/10.1139/cjr48c-033.

Roelfs AP, Singh RP, Saari EE (1992). Rust diseases of wheat: Concepts and methods of disease management. Centro Internacional de Mejoramento de Maiz y Trigo (CIMMYT), Mexico, pp. 81.

Rsaliev ShS, Agabaeva ACh, Rsaliev AS (2013). Dinamika izmeneniya populyatsii zheltoi rzhavchiny pshenitsy (*Puccinia striiformis* f. sp. *tritici*) v Kazakhstane (Population change dynamics of wheat yellow rust in wheat [*Puccinia striiformis* f. sp. Tritici] in Kazakhstan). In: TYu Gagkaeva (editor). Problemy mikologii i fitopatologii v KhKhI veke. Materialy mezhdunarodnoi nauchnoi konferentsii (Problems of mycology and phytopathology in the 21st century. Materials of the international scientific conference). Natsionalnaya akademiya mikologii, St. Petersburg, pp. 231-234.

Rsaliyev AS, Rsaliyev ShS (2018). Principal approaches and achievements in studying race composition of wheat stem rust. *Vavilov J. Genet. Breed*. 22(8): 967-977. https://doi.org/10.18699/VJ18.439.

Rsaliyev Sh, Tileubayeva Zh, Agabayeva A, Rsaliyev A (2010). Virulence of wheat leaf, stem and yellow rust pathotypes in Kazakhstan. *Asian Aust. J. Plant Sci. Biotechnol*. 4(SI1): 71-76.

Rust Scoring Guide (1986). Centro Internacional de Mejoramento de Maiz y Trigo (CIMMYT), Mexico.

Safavi SA, Atahussaini SM, Ebrahimnejad S (2012). Effective and ineffective resistance genes and resistance reaction of promising barley lines to yellow rust in Iran. *Asian J. Plant Sci*. 11(1): 52-57. https://doi.org/10.3923/ajps.2012.52.57.

Sandoval-Islas JS, Broers LHM, Mora Aguilera G, Parlevliet JE, Osada KS, Vivar HE (2007). Quantitative resistance and its components in 16 barley cultivars to yellow rust, *Puccinia striiformis* f. sp. *hordei*. *Euphytica* 153: 295-308. https://doi.org/10.1007/s10681-006-9236-y.

Shah SJA, Hussain S, Ahmad M, Farhatullah, Ibrahim M (2014). Characterization of slow rusting resistance against *Puccinia striiformis* f. sp. tritici in candidate and released bread wheat cultivars of Pakistan. *J. Plant Pathol. Microbiol.* 5: 2. https://doi.org/10.4172/2157-7471.1000223.

Singh RP, Huerta-Espino J, William HM (2005). Genetics and breeding for durable resistance to leaf and stripe rusts in wheat. *Turk. J. Agric. For*. 29: 121-127. http://hdl.handle.net/10883/2421.

Solh M, Nazari K, Tadesse W, Wellings CR (2012). The growing threat of stripe rust worldwide. In: Borlaug Global Rust Initiative. Technical Workshop Proceedings, September 1-4, 2012, Beijing, China, pp. 1-10. Available: https://globalrust.org/sites/default/files/posters/solh_2012.pdf.

Stubbs RW, Prescott JM, Saari EE, Dubin HJ (1986). Cereal disease methodology manual. Centro Internacional de Mejoramento de Maiz y Trigo (CIMMYT), México, pp. 46.

Wellings CR (2011). Global status of stripe rust: A review of historical and current threats. *Euphytica* 179: 129-141. http://dx.doi.org/10.1007/s10681-011-0360-y.

Wu J, Yu R, Wang H, Zhou C, Huang S, Jiao H, Yu S, Nie X, Wang Q, Liu S, Weining S, Singh RP, Bhavani S, Kang Z, Han D, Zeng Q (2021). A Large-scale genomic association analysis identifies the candidate causal genes conferring stripe rust resistance under multiple field environments. *Plant Biotechnol. J*. 19(1): 177-191. https://doi.org/10.1111/pbi.13452.

Ydyrys A, Sarbaev A, Morgounov A, Dubekova S, Chudinov V (2021). Isogenic lines: Reaction to the Kazakhstan population of stem rust (*Puccinia graminis* f. sp. *tritici*). *Agrivita J. Agric. Sci.* 43(1): 221-232. https://doi.org/10.17503/agrivita.v43i1.2798.

Zheng S, Li Y, Lu L, Liu Z, Zhang C, Ao D, Li L, Zhang C, Liu R, Luo C, Wu Y, Zhang L (2017). Evaluating the contribution of Yr genes to stripe rust resistance breeding through marker-assisted detection in wheat. *Euphytica* 213: 50. https://doi.org/10.1007/s10681-016-1828-6.

Zhou X, Fang T, Li K, Huang K, Ma C, Zhang M, Li X, Yang S, Ren R, Zhang P (2022). Yield losses associated with different levels of stripe rust resistance of commercial wheat cultivars in China. *Phytopathology* 112: 1244-1254. https://doi.org/10.1094/PHYTO-07-21-0286-R.