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PRESENT STATUS AND FUTURE PERSPECTIVES OF WHEAT (*TRITICUM AESTIVUM* L.) RESEARCH IN UZBEKISTAN

**O.S. TURAEV^{1,2,3*}, S.K. BABOEV¹, Z.M. ZIYAEV^{1,2}, J.K. NORBEKOV⁴,
 D.Sh. ERJIGITOV^{1,2}, U.Sh. BAKHADIROV^{1,2}, B.T. TURSUNMURODOVA¹,
 A.A. DOLIMOV¹, Kh.S. TURAKULOV¹, D.K. ERNAZAROVA^{1,3}, and F.N. KUSHANOV^{1,2,3}**

¹Institute of Genetics and Plant Experimental Biology, Uzbekistan

²International Innovation Center for Aral Sea Basin under the President of Republic of Uzbekistan, Uzbekistan

³Department of Biology, National University of Uzbekistan, Uzbekistan

⁴Center of Genomics and Bioinformatics, Academy of Sciences of the Republic of Uzbekistan, Uzbekistan

*Corresponding author's email: ozodturaev@gmail.com

Email addresses of co-authors: sai-baboev@yandex.com, zafaruzripi@gmail.com, jurabek42@mail.ru, dostonerjigitov68@gmail.com, umiddjan@inbox.ru, iymona0216@mail.ru, dolimovabdurauf@gmail.com, sadullaevich@yahoo.com, edilrabo64@gmail.com, fakhriddinkushanov@gmail.com

SUMMARY

Wheat (*Triticum* spp.) is one of the premier staple foods consumed by one-third of the world's population. Bread wheat (*Triticum aestivum* L.) is the only allohexaploid species with a genome formula BBAADD. Until now, from a selection point of view, a decline showed in the genetic potential of this type of wheat. However, the solution to this problem can be by developing high-yielding, disease- and pest-resistant cultivars using wheat-related species, ancient local landraces, and germplasm resources. Therefore, extensive study of the wheat gene pool using molecular tools, including identifying primary sources, is highly beneficial. For wheat improvement, breeding opportunities offer significant enhancements via genetic mapping approaches. The review focuses on the common wheat germplasm, wheat genetic approaches for genetic mapping, identification, and RWA (Russian wheat aphid) resistance, nested association mapping (NAM) population, DNA barcoding of Uzbekistan elite bread wheat cultivars, DNA marker-based screening of wheat germplasm for RWA resistance, future perspectives of wheat breeding in Uzbekistan, marker-assisted selection for abiotic stress tolerance, wheat stripe rust and its control strategies in Uzbekistan, epidemiology of the rust pathogens, pathogen characterization, and varietal resistance.

Keywords: wheat, *Triticum aestivum* L., ancient cultivars, germplasm resources, stripe rust (yellow rust), NAM population, DNA markers, DNA barcoding, marker-assisted selection (MAS)

Key findings: The review focuses on consultative information about Uzbekistan's current status and prospects for wheat research. All past findings reported herein serve as a great source and opportunity to improve future wheat research for the breeding communities in Uzbekistan.

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INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the leading cereal crops and a source of calories for humans. With the world's undeniable population growth, the demand for cereals and other food products increases annually. The population growth rate has been around 1.08% over the past 10 years (Worldbank.org, 2022), while wheat grain production was 1.8% (FAO, 2023; Statista.com, 2023). If the population growth rates remain constant and even increase at the same rate, which is about two times more than cereals, then there could be grave problems in the future in providing the next generation with cereals (Dixon *et al.*, 2009; Pardey, 2011). One vital solution to this problem is to combat biotic and abiotic stresses that adversely affect wheat productivity in diverse environments. In the present era, several fungal diseases have led to crop losses in grain fields by 50% and, in some areas, up to 80% worldwide (Buronov *et al.*, 2023). Various measures, including chemical use, are known to protect crop plants from those diseases and maintain good productivity. Given these chemicals' high cost and impacts on human health due to environmental pollution, the most effective and safe way is to develop cultivars resistant to these diseases that are also environment-friendly (Amangeldikyzy *et al.*, 2023).

In developing disease-resistant cultivars, it is crucial to identify and recognize the primary sources (donors) that fully meet these requirements. Identifying such material by using simple screening techniques is challenging. Therefore, for developing new crop cultivars, breeding processes need augmentation with advanced technologies associated with the achievements made through genetic engineering and biotechnology. The DNA marker technology used for practical selection is called marker-assisted selection (MAS). By using this method, the breeder can target the desired gene in the

genotype of interest when introduced into any cultivar and, as a result, develop a new stable cultivar, advanced line, and primary source of his choice (Gusev *et al.*, 2022; Amangeldikyzy *et al.*, 2023; Turaev *et al.*, 2023).

Therefore, it is necessary to identify the genes and quantitative trait loci (QTL) associated with economically valuable parameters and recognize the DNA markers attached to them. The use of the MAS method in selecting crops saves material and labor, reduces the size of the field sown during the experimental testing, chooses genotypes with high accuracy, and ensures the stability of QTL loci, which increases the economic value of the created diversity among lines, achieving a significant reduction. In short, DNA marker technology is one of the most resource-saving technologies in agriculture and is vital in developing new cultivars of various crops (Kushanov *et al.*, 2021).

Ancient common wheat germplasm

In Uzbekistan, the prehistoric wheat cultivars can be a tremendous source for breeding and further improvement. Hundreds of years ago, under harsh climatic conditions, the ancient wheat genotypes subsistence adapted to local environmental conditions. These wheat genotypes were prominent for drought resistance, heat, and salt tolerance, as well as being resistant to winters and having a sturdy and non-crumbling grain. The flour's good taste made it often used for making bread. In their research, the present scientists still draw on the invaluable experience of traditional breeders, studying the history of the cultivation of ancient local cultivars (Baboev *et al.*, 2015; Baboev *et al.*, 2017; Baboev *et al.*, 2021). The main aim was to search for wheat genotypes with high iron and zinc trace elements in the grain endosperm and good baking qualities. Since various wheat cultivars adapted to the region's conditions, their cultivation continued for a long time in Uzbekistan. Populations

characterized by a high content of microelements and good taste have likely survived in local cultivars.

Local ancient germplasm is grown in mountainous and foothill regions on small private farms in Uzbekistan. Sowing occurs in the fall based on the rainfall, with soil preparation comprising plowing, chiseling, and seeding manually; some farmers even use a mounted fertilizer spreader and light harrowing. Before sowing, fertilizing the soil uses phosphorus fertilizer at 100 kg/ha. During the growing season, 100 and 50 kg of nitrogen fertilizer applications are optimal with less rainfall. Using herbicides for weed control rarely transpires; fungicide application is only against rust. Crop rotation incorporates chickpea and safflower crops (Baboev *et al.*, 2015; Utebayev *et al.*, 2022).

During the expeditions in the remote regions of Uzbekistan, the collected wheat samples came from local ancient cultivars, such as, Boboki, Jaydari bugdoy, Qizil bugdoy, Qora-qiltiq, Kal bugdoy, and Tuya-tish (Baboev *et al.*, 2015; Baboev *et al.*, 2017). The morphological analysis of wheat samples by ears and grain traits showed that various landraces belong to the *Graecum*, with a white ear and white grain, and the *Erythrospermum*, with a white ear and red grain. Although there were red-ear forms belonging to the *Ferrugineum* cultivars and an admixture, there were also compact forms related to the species *T. compactum* L. In all those expeditions, using a GPS navigation device helped mark the main cultivation areas, the sowing area, and the prevalence of this ancient cultivar among the local population. These studies' findings and several surveys of the local inhabitants served as a map of the earliest cultivars' distribution in Uzbekistan (Baboev *et al.*, 2017).

Growing 10 spikes in each of these cultivars under irrigated conditions progressed at the experimental site of the institute and in rainfed conditions at an altitude of 2000 m above sea level. Three lines selected from each cultivar used the individual plant and row selection method for agronomic traits, with a sampling plot of old cultivars consisting of 114 samples (Baboev *et al.*, 2017). Growing commercial cultivars collected during the

expedition also ensued, but not in the sampling plot. Based on the number of seeds, samples collected under irrigated conditions attained sowing on three-meter parcels, and samples from rainfed environments on a one-meter area, with the seeding rate at 200 kg/ha. Since these samples adapted well to dry conditions, their watering occurred only once during seed sowing in the fall, while during the growing season, they went without water. However, heavy rains and wind persisted in May, killing several plants. Yet, when these cultivars were sown in spring to determine vernalization, their plants proved resistant to lodging and yielded well. Planting almost all these cultivars manifested better in the spring, although in Uzbekistan's surroundings, sowing these genotypes can also be done in the autumn. All the harvested cultivars were mostly early maturing; however, the fluctuation varied from three to eight days. Most of these specimens emerged tall (over 100 cm), only one cultivar was short, and two cultivars were medium in plant height (Buranov *et al.*, 2017).

Leaf rust appeared at the end of May and developed strongly in wheat fields. Almost all the cultivars had adverse effects from these pathogens, and the genotypes Kalbugdoy (awnless) and Qora qiltiq indicated resistance, including Krasnodar 99, also used as a control. According to the grain size, all the samples were coarse-grained, and the 1000-seed weight ranged from 44 to 54 g. However, only one cultivar appeared fine-grained, with a 1000-seed weight of 36 g. The lodging assessment results revealed that only three cultivars were resistant to lodging, with the rest assessed as lodging-susceptible under irrigated conditions when sown for the winter. The conducted selection had grain yield from the plots as a basis and 55 samples undergoing further study. Seeded specimens continued to assess head smut resistance, and for this, inoculation of 100 g seeds with spores of hard smut proceeded to sow on a 2-m plot with three replications. The same samples underwent seeding to evaluate other parameters on a 2-m parcel without irrigation (Buranov *et al.*, 2017).

Selecting 100 ears from each sample gained an analysis of the grain from each spike

to identify the collected samples of ancient wheat cultivars through electrophoretic analysis. The electrophoretic evaluation of untitled cultivars showed that these samples were representatives of two homogeneous cultivars, differing in electrophoretic spectra (Buranov *et al.*, 2017). A comparison of the electrophoretic scale with those of other collected cultivars revealed that these genotypes were the separate varieties developed by traditional selection a long time ago. Among the collected samples, several samples appeared under the cultivar names, viz., Qizil bugdoy and Oq bugdoy. These cultivars were distinguishable by their grain color; therefore, the local population defined them accordingly. Interestingly, all the cultivars named Qizil bugdoy collected from different regions have primary cultivation at more than 1500 m above sea level altitude, revealing the same electrophoretic spectrum (Buranov *et al.*, 2017).

Also, collecting a sample called Boboki from this region was high-yielding, with large grains and a sturdy stem, morphologically similar to the cultivar Qizil bugdoy. Although, electrophoretic analysis showed that these cultivars belong to different genotypes. Another cultivar called Oq bugdoy with a white ear and white grain belongs to the Graecum cultivars by morphological basis, in the Kashkadarya region called Oq bugdoy and in the Jizzakh region, as Grekum. The electrophoretic spectra of all samples of the Oq bugdoy cultivar collected in the Kashkadarya region were identical, but also differed through electrophoretic ranges from the Grekum cultivar collected from the Jizzakh region. It illustrates that these two cultivars, although respective of the same cultivar, were genotypically different cultivars (Baboev *et al.*, 2017).

The commercial cultivar Surkhak, zoned in the 1950s of the last century and included in the list of ancient cultivars, has been cultivated in Uzbekistan for 70 years and occupies the main areas of rainfed zones. Electrophoretic and morphological analysis of different samples of this cultivar revealed numerous impurities in other cultivars. Since these impurities occurred mainly in single ears

and small quantities, their rejection followed, isolating only two Surkhak cultivars from two different regions, which also differed through the electrophoretic spectra of gliadin. Therefore, the identification of ancient local cultivars of Uzbekistan by the electrophoretic spectra of gliadin illustrated that all samples called Qizil bugdoy with white spike and red grain, belonging to the cultivar Erythrosperrum, originated from the same cultivar and remained in a homogeneous state. Specimens of the cultivars Oq bugdoy and Grekum belonging to the same cultivar Graecum came out as different cultivars. Samples of untitled cultivars belonged to cultivars of Erythrosperrum, according to varied spectra among themselves, and the cultivar Qizil bugdoy indicated that these genotypes originated from different cultivars (Baboev *et al.*, 2017).

The cultivar Surxak, sown over a large area, belongs to two genotypes. Clarifying their origin and relationship requires additional research. The results revealed the restoration of the cultivar Qayraqtash, through individual selection by spike, multiplying, and transferring later to the GSE. After testing on cultivar plots under rainfed conditions, its inclusion in the register as a promising cultivar has existed since 2020. The cultivar, with continuing selection in institute fields, also has its multiplication in the regions of Jizzakh and Kashkadarya on a 10-ha area in each plot and on several small private farms (Baboev *et al.*, 2017).

Wheat genetic approaches for mapping, identification, and RWA resistance

Nested association mapping (NAM) population in wheat

With advances in genetic mapping approaches, identifying DNA markers associated with economically important traits accelerates breeding processes significantly (Kushanov *et al.*, 2021; Yoon *et al.*, 2015). Developing distinct, efficient approaches helped identify genomic regions and genes that control and manage economically important traits in crop plants (Kushanov *et al.*, 2017, 2022). In

particular, employing linkage mapping, linkage disequilibrium (LD)-based association mapping (AM), and nested association mapping (NAM) methods has benefited the mapping of quantitative trait loci (QTL) in different crop plants (Xu *et al.*, 2017). Traditional QTL mapping approaches also identified numerous DNA markers that impact economically valuable traits in plant crops. Some of these markers were specific to local genotypes and not genetically associated with economically vital features of the genotypes developed in other geographical locations (Turaev *et al.*, 2017). The LD-based AM approach's first successful implementation evaluated genetic diversity in germplasm resources and identified valuable genes in wheat (Bresseghele and Sorrells, 2006).

The main limitations of an AM approach were relative to the crop germplasm's structure, size, and age (Mackay and Powell, 2007). The purpose of designing the NAM was to eliminate limitations and accumulate the advantages of the earlier-mentioned approaches. Yu *et al.* (2008) introduced the

NAM design, with McMullen *et al.* (2009) implementing it. They have developed a maize NAM population, including 4,699 recombinant inbred lines (RILs) using B73 as the common parent line while crossing 25 diverse parental genotypes, to dissect the genetic architecture of maize flowering time. Bajgain *et al.* (2016) developed the first wheat NAM population by studying the molecular basis of the stem rust resistance. Norbekov *et al.* (2019) established the first wheat NAM populations in Uzbekistan to study the molecular basis of wheat complex traits. Subsequently, the enhancement of wheat genomic studies via genome-wide association studies (GWAS) of economically crucial qualities used molecular markers, such as, simple sequence repeats (SSRs) and single nucleotide polymorphisms (SNPs). The wheat NAM population development used a common parental cultivar, Morocco, that is susceptible to yellow rust and 17 diverse wheat donor lines at the Center of Genomics and Bioinformatics, Academy of Sciences, Republic of Uzbekistan (Figure 1) (Norbekov *et al.*, 2019).

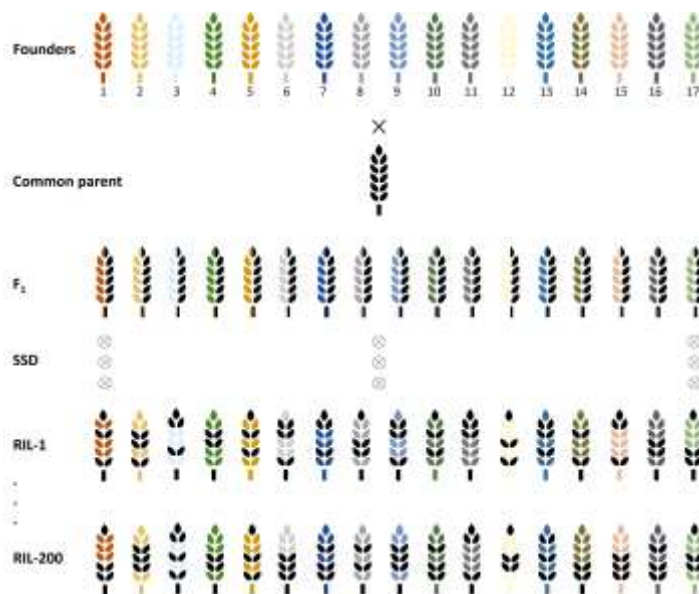


Figure 1. The wheat nested association mapping (NAM) population scheme. Founders: 1 - Yr 5/6 Avocet S; 2 - Yr 6/6 Avocet S; 3 - Federation; 4 - Yr 15/6 Avocet S; 5 - Yr32/6*Avocet S; 6 - Carstens V (W; Yr32); 7 - Yr SP/6* Avocet S; 8 - Avopcet R; 9 - Inia 66; 10 - Avocet "S"; 11 - Jupateco "R" (S); 12 - Jupateco "S"; 13 - Anza; 14 - Cook (S); 15 - ATTILA CM85836-50Y; 16 - PASTOR; 17 - Cham 4; Common parent: Morocco (recipient); F₁: First generation hybrids; SSD: Single seed descent; RIL-1 – RIL-200: 1-200 Recombinant inbred lines.

Designating the resistance of 18 parental lines and 3,400 F₂ populations of 17 NAM families under field conditions ran through spreading uredinospores of *Puccinia graminis*. Field experimentations determined the level of yellow rust disease infection rates and the estimation of plant resistance in the later stages of development using the "International Trap Nurseries" method (Natsarishvili *et al.*, 2016). In addition, other phenotypic evaluations also took place, such as, spike length (cm), grain weight, and grain number per spikelet (g) on infected F₃ populations of the NAM population and their parental genotypes (Norbekov *et al.*, 2019). Besides, genotyping the parental genotypes of the NAM population used 144 SSR markers associated with economically valuable traits, including yellow rust resistance, drought tolerance, and salt tolerance. As a result, the generation of 188 alleles occurred, and the polymorphic loci were two, 24, and 25 for the BARC, WMC, and WMS primers, respectively. The NAM populations with immense genetic and phenotypic segregation will be beneficial in mapping valuable genes through molecular approaches, such as GWAS, to introduce marker-assisted selection in wheat breeding in Uzbekistan (Norbekov *et al.*, 2019).

DNA barcoding of Uzbekistan elite bread wheat cultivars

Differences among the wheat accessions depend on phenotypic characteristics' descriptions, such as, plant height, spike length, grain size and form, early maturity, and disease resistance. However, these characteristics vary depending on environmental conditions, resulting in phenotypic variations not inherited by generations. Therefore, identifying individuals based solely on phenotypic characteristics is considerably unreliable. However, the genetic diversity of wheat cultivars is much lower than their wild forms due to the historical domestication of this crop under permanent breeding pressure for early maturity and insect and disease resistance; consequently, it became more challenging to identify new cultivars accurately. The development of

molecular marker technology allowed quick and accurate identification of crop cultivars at the DNA level, which is also not sensitive to environmental factors. Given the reliability of DNA markers, the International Union for the Protection of New Cultivars of Plants (UPOV) has permitted the use of molecular markers in examining the DUS (Distinctness, Uniformity, and Stability) test in crop cultivars (UPOV, 2013).

Researchers have also recently developed DNA fingerprints for 32 wheat cultivars at the Center of Genomics and Bioinformatics, Academy of Sciences of the Republic of Uzbekistan (Adylova *et al.*, 2018). This study used 36 out of 144 SSR markers associated with resistance to yellow rust and other economically important traits in constructing DNA barcodes. Results can allow breeders international affirmation of their new cultivars and intellectual property protection.

DNA marker-based screening of wheat germplasm for RWA resistance

The Russian wheat aphid (RWA, *Diuraphis noxia*) is one of cereal crops' most economically critical and invasive insect pests, including wheat. The aphids cause a significant decrease in wheat yield by sucking plant sap and infecting it with diverse infections, including viruses and fungi. Solving this problem requires great attention to studying the biology, ecology, distribution, and reproduction of aphids. The most effective way to control RWA is by identifying and developing resistant cultivars (Tolmay *et al.*, 2020). Therefore, it is imperative to determine the molecular mechanism of aphid resistance in wheat. Recently, Turaev *et al.* (2023) studied the RWA resistance in 80 bread wheat accessions under field conditions and conducted PCR screening with eight DNA markers, Xgwm44 (Liu *et al.*, 2002), Xgwm111 (Liu *et al.*, 2002), Xgwm635 (Ma *et al.*, 1998), Xbarc76 (Ward *et al.*, 2003), Xbarc172 (Ward *et al.*, 2003; Fazel-Najafabadi *et al.*, 2014), Xbarc214 (Valdez *et al.*, 2012), Xksud14 (Anderson *et al.*, 2003), and Wmc473 (Valdez *et al.*, 2012), associated with RWA-resistant *Dn* genes. According to the results, seven *Dn*

genes, such as, *Dn1*, *Dn2*, *Dn4*, *Dn5*, *Dn6*, *Dn8*, and *DnCl2401*, determined in bread wheat accessions, belonged to the Uzbekistan wheat breeding. The confirmed findings can be a powerful tool in implementing marker-assisted selection for RWA resistance in Uzbekistan wheat (Turaev *et al.*, 2023).

Future perspectives of wheat breeding in Uzbekistan

In Uzbekistan, wheat crops often experience drought, salt, and heat stresses. It is necessary to study wheat abiotic stress tolerance at the molecular level, including identifying resistance QTLs and genes and their introduction in molecular breeding approaches.

Marker-assisted selection for abiotic stress tolerance

In the halophytic agricultural system in the Aral Sea regions, wheat genotypes were chiefly intensive cultivars due to the varied effects of water scarcity, heat, and salinity conditions. Limited wheat productivity and grain quality are insufficient to meet today's requirements because most bread wheat cultivars are highly susceptible to the mentioned stress factors. Therefore, discovering and introducing new high-yielding wheat cultivars with resistance to abiotic stresses is one of the much-needed research areas in Uzbekistan today. Insufficient use of the world's bread wheat diversity is also a crucial shortcoming in breeding this crop. The involvement of new loci/genes of donor genotypes in the breeding process sets the stage for developing new primary sources with new gene immune systems tolerant to heat, salinity, and drought-stress conditions (Sapakhova *et al.*, 2022). The creation of new wheat cultivars that adapt well to the Aral Sea halophyte-mixed farming system and their introduction will play an essential role in mitigating the impact of these problems (Turaev *et al.*, 2023).

The applied project 'AL-5721122059' recently began with the support and funds from the Innovative Development Agency under the Ministry of Higher Education, Science, and Innovation. The project aimed to

develop new bread wheat cultivars tolerant to drought, heat, and salinity stresses using marker-assisted selection (MAS). Obtaining initial results developed new bread wheat cultivars with improved agronomic traits, combining QTL loci associated with abiotic stress tolerance. Employing MAS in creating new wheat cultivars increases breeding efficiency and significantly reduces the time required to develop a cultivar, saving labor costs. The most important thing was selecting the trait under study in the newly developed cultivar proceeded with great precision (Turaev *et al.*, 2023).

Study of dehydrins encoding genes response in wheat drought tolerance

Dehydrins are a multifamily of proteins that play a vital protective role in drought and cold tolerance in cereal crops. Despite massive research on dehydrins, the foremost wheat dehydrins for developing drought-tolerant genotypes still need reliable identification. The scientific publications also provide limited information about the significance, functioning, and influence of genes encoding dehydrins in stress responses to drought. Future studies need to learn the role of individual genes encoding bread wheat dehydrins in drought tolerance. Such studies will further allow the development of molecular breeding as marker-assisted selection for wheat tolerance to water scarcity (Turaev *et al.*, 2023).

Wheat stripe rust and its control in Uzbekistan

Stripe rust, caused by *Puccinia striiformis* f. sp. *tritici* (Pst), is notably the most influential wheat disease, causing a reduction in wheat grain yield yearly in Uzbekistan. Although stripe rust's discovery has been known for a long time, it has become a pressing constraint on wheat production in the past 20 years. It has been reflected in four epidemic occurrences of stripe rust since 1999, with the most recent in 2016. Wheat cultivars grown in the main areas were susceptible to stripe rust, revealing poor resistance. Limited information is also accessible about the stripe rust

pathogen, including prevalent races and epidemiology. Likewise, Uzbekistan has a lean understanding of effective stripe rust-resistant genes, with little known data on the resistance genes found in wheat's advanced breeding lines and commercial cultivars. Therefore, assessing annual losses caused by stripe rust on wheat production in Uzbekistan is challenging since this disease has fungicides controlling it. However, past experimental findings showed yield losses of up to 90% in susceptible wheat cultivars (Beksultanov, 2003).

During the past Soviet Union period, stripe rust epidemics were uncommon across the country. One of the reasons for the irregular and less severe epidemic could be that the wheat-grown area was smaller in Uzbekistan before 1994 (Ziyaev *et al.*, 2011). Later, however, the country increased its wheat production due to a concern for food security, diverting about one million hectares of irrigated cotton land to wheat in the mid-1990s in Uzbekistan (Khalikulov *et al.*, 2009). Despite a general lack of historical documentation of stripe rust epidemics in the region, there were several reports on varietal screening and resistance to stripe rust in Uzbekistan. The last 10 years have seen the publication of several reports on wheat stripe rust. The stripe rust conferences for CWANA organized in 2001–2009 primarily made this documentation easy (Sharma *et al.*, 2009). However, the Central Asia Phytopathology Institute mainly conducted comprehensive rust research until Independence Day in 1991. Yellow rust race identification in Central Asia started in 1963, and a new system began on the world and Europe differential set in 1977 (Ziyaev *et al.*, 2011). These differential sets had 45 yellow rust races identified in 1978–1989. After independence, the continued conduct of these research activities started with international organizations, such as, ICARDA, FAO, CIMMYT, and BGRI, with annual surveillance on monitoring wheat rust pathogens and collecting stripe rust samples from infected fields, then shared with rust labs in Denmark and the USA for race identification and learning on effective resistance genes (Ziyaev *et al.*, 2011).

Epidemiology

In Uzbekistan, little systematic information is available on the epidemiology of Pst. Considering regional coverage, winter wheat growing occurs in all neighboring countries. Cultivating the winter wheat crop transpires in October–November, with harvesting in June–July of the following year. In addition, planting facultative cultivars during the autumn and early spring continues in areas with mild winters. Thus, wheat is visible in the fields almost year-round, and stripe rust pathogen survives on wheat and wild grasses. Stripe rust inoculum persists in commercially grown wheat and wild grasses. Overwintering of the pathogen on an autumn-infected wheat crop or alternate hosts and any ensuing epidemics depend on weather conditions in the autumn (rainfall) and winter (temperature) months (Koishibayev and Kurmanov, 2006).

Urediniospores, formed in the spring from overwintered rust pustules on living plants, are the prime source of renewed infection in wheat. In the country, cultivating susceptible wheat cultivars over larger areas and favorable spring weather conditions play a critical role in the proliferation of stripe rust epidemics (Sharma *et al.*, 2009). During a 1999 stripe rust epidemic in Uzbekistan, the susceptible wheat cultivar 'Yuna' was planted in 70% of the irrigated wheat area. When analyzing weather data for Kazakhstan and Uzbekistan, Koishibayev and Kurmanov (2006) reported that higher relative humidity (65%–75%) and rainfall (80–150 mm) persisted in the epidemic years of 2000 and 2001 compared with lower humidity (50%–60%) and precipitation (40–50 mm) in the non-epidemic years of 2001, 2004, and 2005. Sharma *et al.* (2009) gave similar trends in weather conditions for the stripe rust epidemic year of 2009 in Uzbekistan. Three times, stripe epidemics occurred in 2010, 2013, and 2016, respectively.

Pathogen characterization

Different countries in the CAC have disclosed several Pst pathotypes. Yahyaoui (2000) reported pathogenicity differences among the

stripe rust populations in Central Asia. Absattarova *et al.* (2002) also listed the dominant pathotypes, i.e., 6E20, 6E148, 7E140, 7E148, 7E150, 7E156, 15E150, and 39E158, in Kazakhstan, Kyrgyzstan, Tajikistan and Uzbekistan. A worldwide study of stripe rust isolates showed that PstS5 and PstS9 dominated the Central Asian population (more than 90%) (Ali *et al.*, 2017). Recently, Hovmøller *et al.* (2019) revealed that PstS9 is, by far, the most prevalent group (most common virulence phenotype: 1, 2, 3, 4,-, 6,-, -,9,-,-,17,-, 25, 27, 32,-, AvS, and Amb), with the same being observed in 2016–2017 in Uzbekistan. Based on studying virulence combinations, *Yr5*, *Yr7*, *Yr8*, *Yr10*, *Yr15*, and *Yr24* are holding resistance to prevalent races; however, reports on virulence pathogens have come out for genes *Yr7*, *Yr8*, and *Yr10* (Hovmøller *et al.*, 2019).

Varietal resistance

The development of resistant and high-yielding wheat cultivars has been the most salient objective of the winter wheat improvement programs in Uzbekistan since the 1998 stripe rust epidemic. Testing of local and foreign wheat cultivars also surfaced in Uzbekistan (Absattarova *et al.*, 2002; Amanov and Nurbekov, 2002; Baboev, 2003; Nurbekov, 2003; Tulyaganov and Shakirov, 2003; Khalikulov *et al.*, 2009; Ziyaev *et al.*, 2015). Besides testing material within the region, the national program has received improved winter wheat germplasm and advanced breeding lines from the International Winter Wheat Improvement Program (IWWIP) for several years. These international collaborations have undoubtedly enriched the national wheat programs with high-yielding, stripe rust-resistant germplasm (Morgounov *et al.*, 2005; 2019; Sharma, 2009).

Despite the inflow of resistant germplasm, several commercial cultivars of winter wheat occupied substantial areas in the region and were also susceptible to stripe rust. The leading commercial cultivars showing susceptibility to stripe rust were Grom and Krasnodar 99 in Uzbekistan (Sharma *et al.*, 2009). In 2009, 13 of 22 commercial cultivars

were highly susceptible, which showed 60% or even higher severity to stripe rust in farmers' fields in Uzbekistan. However, in the same year, several advanced wheat breeding lines exhibited resistance (severity 20%) to stripe rust in Uzbekistan. Some of these wheat lines displayed higher grain yield and desirable agronomic traits, such as, early maturity, plant height, and 1000-kernel weight, and a few were also found resistant to powdery mildew. Wheat lines that indicated significantly lower severities to the stripe rust compared with the Kvz/T171/3/Maya//Bb/Inia/4/Kardj2/5/Anza/6/Oref, Jup/4/Clf/3/II14.53/Odin//CI13431/5/IL-75-2534, and Agri/Nac//Mlt/5/Gov/Fz//Mus/3/Dodo/4/Bow/6/Vorona/TR810200, have significantly higher grain yields than the cultivars Zamin-1, Turkistan, and Tanya (Sharma *et al.*, 2009).

Four stripe rust-resistant lines also demonstrated resistance (severity 20%) to leaf rust. These results showed that stripe rust-resistant lines introduced in Uzbekistan through regional and international cooperation were also superior in grain yield and agronomic characteristics (Khalikulov *et al.*, 2009). Their results further revealed that 25% of 272 wheat genotypes, including advanced breeding lines from IWWIP, commercial cultivars, and landraces, provided the highest level of stripe rust resistance in Uzbekistan. Ziyaev *et al.* (2015) studied 448 winter wheat lines in response to the prevailing Pst populations under controlled conditions, and 80 were immune, while 73 lines showed moderate to high resistance levels under field conditions. After agronomic assessments, 55 lines leveled up to advanced multi-site yield trials, and numerous selected wheat lines' distribution to other research institutions proceeded. Several winter and facultative stripe rust-resistant bread wheat cultivars developed in recent years have attained release, such as, Bardosh, Gozgon, Bunyodkor, and Shams (Yigezu *et al.*, 2022).

Wheat stripe rust control strategies in Uzbekistan

The factors prescribe the future course of stripe rust research and the development of

resistant cultivars include the availability of suitable germplasm, strengthening facilities for field screening, greenhouse and laboratory analyses, intake and training of young researchers for rust research, exchange of germplasm and information at regional and international levels, and funding support. Available data on improved wheat germplasm through international transfer suggests an increase in the introduction of stripe rust-resistant germplasm to the country. New launches may be suitable for direct release following national testing, while others could serve as parental genotypes in conventional hybridization programs. Using known resistance genes, viz., *Yr5*, *Yr10*, and *Yr15*, will improve further deployment of wheat cultivars. In addition, implementing molecular markers and double haploid technologies will accelerate the breeding process, resulting in resistant cultivars delivered to the hot spot areas in the early stages (Ren et al., 2017; Madenova et al., 2021).

A need exists to strengthen field screening and testing facilities for stripe rust in Uzbekistan. International cooperation in the region through ICARDA, CIMMYT, BGRI, FAO, and the special laboratories in Australia, Denmark, and the Regional Cereal Rust Research Center in Izmir, Turkey, is helping national wheat programs understand disease epidemiology and pathogen diversity and improve capacity development (Ziyaev et al., 2010; Hovmøller et al., 2017).

CONCLUSIONS

This review has reported Uzbekistan's current status and future perspectives on bread wheat (*Triticum aestivum* L.) research. Recently collected ancient common wheat cultivars from mountainous and foothill regions of Uzbekistan, as well as, DNA barcoding, the molecular screening of wheat germplasm for biotic and abiotic stresses, and newly developed and well-characterized wheat-NAM populations, would be marvelous sources for dissecting complex traits by genetic mapping and breeding approaches. Besides, the ancient wheat germplasm resources and the obtained

data from all the experiments mentioned earlier will serve as a noble opportunity for further wheat improvement using modern approaches, such as, CRISPR/Cas and GWAS, for the breeding communities in Uzbekistan.

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