Phenotypic evaluation of seedling and adult-plant stripe, leaf, and stem rust resistance in the A-genome diploid relatives of wheat

by

Buket Sahin

B.S., Namık Kemal Üniversitesi, Turkey, 2016
M.S., Namık Kemal Üniversitesi, Turkey, 2019

A THESIS

submitted in partial fulfillment of the requirements for the degree

MASTER OF SCIENCE

Interdepartmental Genetics
College of Agriculture

KANSAS STATE UNIVERSITY
Manhattan, Kansas

2021

Approved by:

Major Professor
Bernd Friebe

Copyright

© Buket Sahin 2021.

Abstract

Wheat (*Triticum aestivum* L.) is one of the most significant cereal crops in the world, ranking third following rice and maize. The various rust diseases that attack this crop – leaf rust (*Puccinia triticina*), stripe rust (*Puccinia striiformis* f. sp. *tritici*) and stem rust (*Puccinia graminis* f. sp. *tritici*) are important limitations for increasing wheat production in the world. In order to stay ahead of constantly evolving rust pathogens, it is necessary to increase genetic diversity by identifying genetic resistance from sources besides common wheat. Wild relatives of wheat are tractable sources of wheat rust resistance genes. The mini core collection of diploid A-genome species covering about 90 percent of the genetic variation of these species, including 59 accessions of *T. monococcum* subsp. *aegilopoides*, 24 accessions of *T. monococcum* subsp. *monococcum*, and 25 accessions of *T. urartu*, spanning their whole area of geographic distribution has been established by using genotype-by-sequencing (GBS). These accessions were evaluated for their seedling resistance to leaf rust, stripe rust, and stem rust under greenhouse conditions and were screened for adult plant resistance under both greenhouse and field conditions. Among the evaluated accessions in this study, *T. monococcum* subsp. *monococcum* showed a higher number of resistant accessions, followed by *T. monococcum* subsp. *aegilopoides* and *T. urartu*. Consequently, these species may have a high potential as donors of resistance to stripe rust, leaf rust, and stem rust.

Table of Contents

List of Figures vi
List of Tables vii
Acknowledgements viii
Introduction 1
Literature Review 5
The Evolution and Domestication of Wheat 5
Origin of the A Genome 7
Wheat Rust Diseases 8
Stripe Rust 10
Leaf Rust 13
Stem Rust 16
Resistance Genes of Wheat Rusts 20
Materials and Methods 24
Plant Materials 24
Pathogen Isolates 24
Disease Evaluation: Seedling Stage 25
Stripe Rust 25
Leaf Rust 26
Disease Evaluation: Adult Plant Stage 27
Greenhouse Experiments 27
Field Experiments 29
Data Analysis 30
Results 31
Seedling Stage 31
Stripe Rust 31
Leaf Rust 32
Data Analysis 33
Adult Plant Stage 33
Greenhouse Evaluations 33

Stripe Rust 33
Leaf Rust 33
Stem Rust 34
Data Analysis 35
Field Evaluations 35
Stripe Rust 35
Leaf Rust 36
Stem Rust 36
Data Analysis 37
Discussion 38
Conclusion 47
References 48
Appendix A - Supplementary Material 120

List of Figures

Figure 1. Pictures show the A-genome diploid relatives of wheat at different adult plant stages in greenhouse conditions. 109
Figure 2. Examples pictures of stripe rust (A), leaf rust (B), and stem rust (C) nurseries in Rocky Ford (leaf rust and stem rust) and Rossville Experiment Stations (stripe rust), 2021. 110
Figure 3. Distribution of infection types of 108 accessions evaluated for seedling resistance stripe rust and leaf rust under greenhouse conditions. 111
Figure 4. Distribution of infection types of 80 accessions evaluated for stripe rust at the adult plant stage under greenhouse conditions. 112
Figure 5. Frequency distribution of 80 accessions evaluated for leaf rust and stem rust at the adult plant stage under greenhouse conditions. 113
Figure 6. Frequency distribution of 108 accessions evaluated for stripe rust, leaf rust, and stem rust at the adult plant stage under field conditions..... 114
Figure 7. Illustration of the Stakman 0-4 infection-type scale using stripe rust on accessions of A genome diploid wheat at the seedling stage. 115
Figure 8. Illustration of the Stakman 0-4 infection type scale using leaf rust on accessions of A genome diploid wheat at the seedling stage. 116
Figure 9. Illustration of the Cobb scale using stripe rust on accessions of A genome diploid wheat at the adult plant stage from field experiments. 117
Figure 10. Illustration of the Cobb scale using leaf rust on accessions of A genome diploid wheat at the adult plant stage from field experiments. 118
Figure 11. Illustration of the Cobb scale using stem rust on accessions of A genome diploid wheat at the adult plant stage from field experiments. 119

List of Tables

Table 1. List of 108 A-genome diploid wheats collected from different countries and evaluated for wheat rusts in this study. 65

Table 2. Disease reactions recorded here are the average infection types for two experiments with two replicates of each disease. 69

Table 3. ANOVA for stripe rust and leaf rust scores of 108 accessions evaluated at the seedling stage. 79

Table 4.Disease reactions recorded here are the median infection types for greenhouse experiments with three replicates of each disease at the adult plant stage. 80

Table 5. ANOVA for stripe rust, leaf rust and stem rust scores of 80 accessions evaluated at the adult plant stage in the greenhouse conditions. 90

Table 6.Disease reactions recorded here are the median infection types for field experiments with three replicates of each disease at the adult plant stage. 92

Table 7. ANOVA for stripe rust, leaf rust, and stem rust scores of 108 accessions evaluated at the adult plant stage in the field conditions during 2020 and 2021. 106

Acknowledgements

I would like to thank my advisor, Dr. Bernd Friebe, for guiding me throughout my thesis work and sharing his knowledge, valuable opinions, and experiences with me. I am particularly thankful to the members of my graduate committee, Dr. Robert Bowden, and Dr. Jesse Poland, for providing me with timely and honest comments on my study.

I am grateful to the students and faculty of the plant pathology department at KSU for providing me with a welcoming atmosphere to do my research. Thank you to the members of the KSU Wheat Genetics Resource Center, Duane Wilson, John Raupp, Dal Hoe Koo, Yoonha Ju and Laxman Adhikari, for always being encouraging and giving constructive suggestions. Thank you for all your unwavering support.

In addition, I thank my sponsor the Turkish Ministry of National Education for their support during my stay in Manhattan.

Finally, and most importantly, huge thank you to my family for their constant encouragement throughout my study period.

Introduction

Wheat (*Triticum aestivum* L.) is one of the most important cereal crops cultivated on nearly 240 million ha with 750 million tons production worldwide and is also an important source of plant-derived protein. By 2050, it is estimated that the world population may exceed 9 billion, which will require an increase in wheat production of 1 billion tons. Challenges impeding higher crop yields and quality, together with sustainability of the agroecosystem, include the reduction of agricultural land, lack of adequate irrigation water, degradable soil health, and abiotic and biotic stresses. Global issues, such as climate change and deterioration of the growing environment at local levels, have increased the chance of evolving new races of pathogens, such as Ug99, a devastating race of wheat stem rust. Pathogenic fungi already significantly limit wheat production, as they account for annual yield losses of 15-20% (Gupta et al., 2008). Therefore, genetic, and genomic dissecting of disease resistance and identifying new sources of resistance is critical to minimize crop loss.

The three rust diseases, stripe, leaf, and stem are among the most serious biotic threats to wheat production in the world (Murray and Brennan, 2009). Rust diseases cause significant losses in yield and quality. Losses due to stem rust were estimated at 6.20 million ton per year, 5.76 million tons per year for leaf rust, and 5.47 million tons for stripe rust (Beddow et al., 2015). Although partial to complete chemical control of these diseases is possible, it negatively affects the environment and human health, and it is very expensive to growers. Therefore, the most effective strategy to control rust diseases is the development of the resistant cultivars.

Utilizing and integrating genetic resistance to wheat rusts requires characterizing genetic resources with potentially novel genes for resistance. Wild relatives and landraces are an important resource for identifying new resistance genes (Bux et al., 2012a). Resistance genes

from wild wheat relatives have been transferred to cultivated wheat (McFadden, 1930; Kilian et al., 2011; Zaharieva and Monneveux, 2014). Diploid wild wheats are also a great genetic resource for improving cultivated wheat. This study is aimed at identifying seedling and adult-plant resistance in a set of A-genome wheat species. Einkorn wheat, which was domesticated approximately 10,000 years ago, was gradually replaced by durum and bread wheat (Tanno and Willcox, 2012). Einkorn cultivation is still quite limited and only takes place in a few select locations across the world. The excellent nutritional content, great digestibility, and better acceptance by those with gluten sensitivity have recently led to the rediscovery of einkorn wheat as a health food (Özkan et al., 2007). Einkorn is also a good grain for organic farming because of its resistance to pests and diseases, minimal input requirements, and overall performance in poor soils (Konvalina et al., 2010). Consumer's interest in its nutritious value and production requirements made it more ecologically friendly. As a result, some areas saw an increase in einkorn production (Zaharieva et al., 2010). Breeding efforts in numerous countries have given more productive cultivars to organic farmers. As with emmer wheat, increasing demand for einkorn products may necessitate a greater understanding of its nutritional content, traceable production chain and the health benefits of derived products (Zaharieva et al., 2010).

Along with its nutritious value, einkorn wheat has long been seen as a possible source of important genetic diversity for wheat breeding. The difficulty in producing interspecific hybrids with appropriate fertility slowed its successful application. Using bridge crosses of tetraploid/einkorn amphiploids, this challenge has been partially solved (Kerber and Dyck, 1973). Einkorn is already widely used in breeding programs, for example, at ICARDA (International Center for Agricultural Research in Dry Areas), to improve rust resistance in tetraploid wheat, and at the Agricultural Research Institute of the Hungarian Academy of

Sciences to introduce biotic stress resistance to hexaploid wheat (Kovács et al., 2012). Furthermore, einkorn wheat is projected to play a growing role in wheat genetic research, particularly in QTL mapping and gene identification. However, so far only limited information is available about the genetic diversity of A-genome diploids. As a result, efforts are necessary to construct in situ conservation programs, generate well-documented collections, evaluate global genetic diversity, and develop core-collections that facilitate the discovery of valuable agronomical and nutritional characteristics.

Van Slageren (1994) identified two subspecies of the A-genome diploid *Triticum monococcum* L. (2n = 2x = 14); subsp. *monococcum* and subsp. *aegilopoides*). The other A-genome diploid species, *T. urartu* Tumanian ex Gandilyan, is considered the A-genome donor of cultivated wheat. However, *T. monococcum* subsp. *aegilopoides* is thought to be the A-genome donor for cultivated einkorn (Dvorak, 1988). For wheat breeding, diploid A-genome wheat has been used as a valuable genetic resource. For instance, *T. monococcum* was used as the source of genes for resistance to stripe, leaf and stem rust, and powdery mildew (He et al., 2007; McIntosh et al., 1984; Yao et al., 2007). From *T. monococcum* subsp. *aegilopoides*, two genes for resistance to leaf rust and one to stem rust (*Sr*22) were transferred into common wheat (Hussien et al., 1998; Paull et al., 1994).

Because few transfers of wheat rust resistance genes from A-genome diploid relatives of wheat are successful, evaluating their genetic diversity is crucial. By direct hybridization in WGRC (Wheat Genetics Resource Center) germplasm lines WGRC23, WGRC32, and WGRC34, new genes for leaf rust resistance were introgressed from diploid wheat (Gill et al., 2006). Different diploid wheats cross with common wheat in different ways. Female fertile F1 hybrids between hexaploid wheat and *T. monococcum* subsp. *aegilopoides* were generated from

these crossings, obtaining WGRC32 and WGRC34. Except for plants with accession PI355520, the majority of wheat/*T. monococcum* subsp. *monococcum* hybrids were female sterile. The WGRC23 was created by crossing PI266844, a leaf rust resistant donor accession, with PI355520, and then crossing the F1 hybrid to a recipient wheat cultivar. On the other hand, *Triticum urartu* produces limited pollen, making direct hybrids with hexaploid or common wheat difficult.

The A-genome minicore set of the WGRC was selected using different selection parameters, such as genetic diversity, geographical distribution, phenotypic variation, and population structure (Adhikari et al., 2021). Because the A-genome core collection represents the majority of the genetic diversity in this species, screening this collection is a very effective approach in identifying potential new sources of rust resistance that can be employed in wheat improvement.

Literature Review

The Evolution and Domestication of Wheat

As the first plant known to be grown by humans, wheat was cultivated in Southwest Asia ~10,000 years ago. The development of wheat and civilization progressed in parallel. The development and distribution of wheat was entirely dependent on human beings, and a large amount of variation has led to plant improvements and the production of about 17,000 different wheat cultivars (Kimber and Feldman, 1987).

De Candolle (1886) made the first studies on the origin of wheat, which is among the first cultivated plants in the history of the world and used as a basic food source for many years. De Candolle reported that wheat first appeared in Asia, whereas spelt wheat was first in Europe and Anatolia. Wheat belongs to the *Triticinae* subtribe of the genus *Triticum*, family *Poaceae*, tribe *Triticeae* from the *Poaidea* subfamily (Yürür, 1998).

The first wheat cultivation began in the Neolithic period, 10-12 thousand years ago, in the region of Mesopotamia within the Fertile Crescent region, enabling human communities to transition from hunter-gatherers to permanent settlements. The first cultivated wheat forms were reported to be diploid (2n=2x=14, AA genomes) (*Triticum monococcum*) and tetraploid (2n=4x=28, AABB) (*Triticum turgidum*) (Shewry, 2009; Peng et al., 2011). Einkorn and emmer wheat are reported to be beneficial in the development and spread of wheat agriculture throughout the world and have been an important source of nutrition for human over millennia (Shewry, 2009). The genetic relationship of einkorn and wild emmer wheat were examined, and their center of diversity was determined to be the Karacadag Region, Diyarbakir, Turkey (Heun et al., 1997; Dubcovsky and Dvorak, 2007; Shewry, 2009; Özkan et al., 2011). These wheat species grow naturally in the Fertile Crescent (Özkan et al., 2011; Peng et al., 2011).

Cultivated emmer wheat (*T. turgidum* L. (2n=4x=28, AABB) was domesticated as a result of natural/artificial selections from *T. turgidum* subsp. *dicocoides* (Körn. Ex Asch. & Graebn.) Thell. This wheat subspecies is known today as wild emmer wheat. Emmer wheat cultivation spread from the Fertile Crescent region eastward, into the natural habitat of *Aegilops tauschii* Coss (2n=2x=14, DD) species, known as goat grass, along the southern and western edges of the Caspian Sea (Nesbitt, 1996; Salamini et al., 2002). Wild emmer wheat naturally hybridized with *Ae. tauschii* and formed hexaploid wheat *T. aestivum* (2n=6x=42, AABBDD), as a result of chromosome doubling, emerged ~7,000-9,000 BCE.

Heun et al., (1997) reported six species within the genus *Triticum*, with 17 subspecies, three of which were wild and 14 cultivated. The diploid *T. urartu* (A^uA^u) is found only as a wild form, whereas *T. aestivum* L. (2n=6x=42, AABBDD) and *T. zhukovskyi* Menabde & Ericz. (2n=6x=42, $A^mA^mA^uA^uGG$) only exist as cultivated forms. Additionally, both wild and cultivated types of other species are present today. The A-genome diploid (2n=2x=14 chromosomes) wild wheat species *T. urartu* and *T. monococcum* subsp. *aegilopoides* (Link) Thell. (A^bA^b) cannot be hybridized and have completely different plant morphology, and they diverged from each other about 0.5-1 million years ago (Matsuoka, 2011).

The cultivated form of diploid wheat, *T. monococcum* subsp. *monococcum* (A^mA^m), known as einkorn wheat, appeared for the first time in the Fertile Crescent region as a result of the domestication of *T.m. aegilopoides* (Heun et al.,1997). Einkorn is a local word from Germany meaning ‘single kernel’ (Zaharieva and Monneveux, 2014). The other wild diploid wheat species, *T. urartu*, also originated in the Fertile Crescent region and, although never domesticated, is the source of the AA genome in cultivated tetraploid and hexaploid wheats (Dvorak et al., 1988; Peng et al., 2011; Matsuoka, 2011).

The two wild subspecies of tetraploid wheat are *T. turgidum* subsp. *dicoccoides* (2n=4x=28, A^uA^uBB) and *T. timopheevii* (Zhuk.) Zhuk. subsp. *armeniacum* (Jakubz.) van Slageren (2n=4x=28, A^uA^uGG) (Zohary and Hopf, 2000; Matsuoka, 2011). Even though morphologically similar, their genome structures are quite different. *T.t. dicoccoides* can be easily hybridized with cultivated tetraploid wheat (*T. timopheevi)*, whereas *T. araraticum,* a wild tetraploid wheat, does not easily hybridize with *T.t. dicoccoides*. The cultivated species *T. timopheevii* (A^uA^uGG) is found in Caucasus region of western Georgia along with the hexaploid wheat species *T. zhukovskyi* (Matsuoka, 2011).

The wild tetraploid wheat subspecies *T.t. dicoccoides* played an important role in the emergence of durum and bread wheat, which are widely cultivated throughout the world. Bread and durum wheat received the B genome from *T.t. dicoccoides*. Wild and cultivated tetraploid and hexaploid wheat receive their A genomes from *Triticum urartu*. *T. urartu*, unlike its sister species *Triticum monococcum*, was never domesticated and is still widely spread in the Fertile Crescent, where it contributed to breed the first wild forms that were later domesticated. In short, this species has held a key place in the domestication of wheat (Peng et al., 2011).

Origin of the A Genome

The two tetraploid wheat species appear to be crucial in understanding the evolution of polyploid wheat. Early cytogenetic research concluded that *T. monococcum* provided the A genome to both tetraploid species (Sax, 1922; Kihara, 1924; Lilienfeld and Kihara, 1934). A reconsideration of the origins of the A genome in polyploid wheats became important when it became evident that Einkorn wheat truly consisted of two species, *T. monococcum* and *T. urartu*. Chapman et al. (1976) revealed that *T. urartu* was the source of the A genome. According to the immunological characteristics of seed-storage proteins, Konařev et al. (1979) determined that *T.*

urartu provided the A genome to the *T. turgidum* lineage, whereas *T. monococcum* contributed the A genome to the *T. timopheevii* lineage. Nishikawa (1983) proposed that the A genome in both lineages originated from *T. urartu*, relying on esterase diversity. Dvorak et al. (1988) demonstrated that variation in repeated nucleotide sequences may be used to investigate the phylogeny of polyploid wheat species, and they also found that the A genome in both tetraploid wheats are related more closely to the A genome of *T. urartu* than to the A genome of *T. monococcum*.

Wheat Rust Diseases

Bread wheat is the most cultivated grain crop in the world and is a very important source of nutrition. Fungal rust diseases are one of the most important diseases of wheat are a cause of great yield loss worldwide (Wellings, 2011). Rust diseases are common, especially in humid areas. The three types of wheat rust disease include stripe rust (*Puccinia striiformis* Westendorp f. sp. *tritici* Eriks.), leaf rust (*Puccinia triticina* Eriks.) and stem rust (*Puccinia graminis* Pers. f. sp. *tritici* Eriks. and E. Henn.) (Samborski, 1985; Wiese, 1985).

The history of rust diseases in cereals is as old as the Torah. In ancient Rome, they had connections with divinities, and were believed that the disaster of rust was a punishment for sinfulness by the special god of rust, Robigus or Rubigo. Aristotle (384-322 BC) writes that rust is produced by "hot vapors" and that rust causes great destruction in the epidemic years (Roelfs, 1992). This has continued to modern times as Dubin and Brennan (2009) reported that the disease has caused epidemics since the first half of the 20th century in many countries, such as the USA, India, Canada, Mexico, Pakistan, Russia, and Chile. The spores of the disease can spread to grain fields at distances of thousands of kilometers under suitable conditions (İren, 1964).

Wheat rust infections have a complex life cycle that includes five spore stages, which are classified as sexual and asexual. Whereas the sexual stage necessitates the use of an alternative host (*Berberis* spp. for stem rust and stripe rust and *Thalictrum* for leaf rust), the asexual phase only requires the use of a primary host (wheat) (Jin et al., 2010). Wind disperses disease-causing spores in the asexual phase that are the primary source of disease. Wheat rusts are damaging to wheat at all stages of growth. As the rust fungus extracts nutrients from the mesophyll cells, they increase transpiration and respiration rates while reducing photosynthesis, resulting in damage to the plant. As a result, the quantity of florets and grain weight are reduced. Wheat stems that are severely infected with stem rust can become lodged, resulting in considerable production losses and yield reduction (Wiese, 1987; Roelfs, 1992; Marsalis and Goldberg, 2006).

The rust diseases can be controlled by applying chemical fungicides, removing alternative hosts, changing cultivation techniques, and using resistant varieties. Costly and potentially damaging to the environment, fungicides are not the best choice for disease control. Sexual aecia production is reduced when the alternate host is removed. Planting early maturing cultivars and early seeding may help wheat avoid infection and eliminating volunteer crops decreases inoculum levels. Because the efficiency of each technique varies by epidemic and location, cultural approaches do not sufficiently control wheat rusts. The most cost-effective and ecologically friendly approach to manage wheat rusts is by growing resistant cultivars (Roelfs, 1992; Roelfs, 1985). A large number of resistance genes are available (McIntosh et al., 1995), and many are now utilized in different wheat cultivars.

Resistance can either be expressed in the seedling stage or as adult-plant resistance (APR) (Chen, 2005). Seedling resistance remains active throughout the plant's lifecycle so is also called all-stage resistance. Generally, seedling resistance requires a gene-for-gene interaction and

is race-specific (Flor, 1971). This form of resistance is not long-lasting, because of the continuous development of virulent races of the pathogen. APR is mainly race-nonspecific and, thus, more durable although it is expressed later in plant growth (Line, 2002). High-temperature adult-plant (HTAP) resistance is a form of APR that is more durable and stable and is race-nonspecific (Line, 2002). At high temperatures, HTAP is expressed in adult plants and is regulated by a number of genes (Qayoum and Line, 1985).

Stripe Rust

Stripe rust, caused by *P. striiformis* f. sp. *tritici* (Pst), is one of the most important and most destructive wheat diseases worldwide (Li et al., 2006). Stripe rust was first described by Gadd in Europe in 1777, but probably existed for a long time (Chen, 2005). Subsequent epidemics recorded in England in 1725 and in Sweden in 1794 are also thought to be stripe rust. More than 60 countries around the world experience stripe rust epidemics to date (Li et al., 2006; Wellings, 2011).

Pst is an obligate biotrophic pathogen that can survive only as a parasite in living host tissue. Belonging to the order *Uredinales* of the *Basidiomycota* clade, stripe rust infects cereal crops and grasses (Roose-Amsaleg et al., 2002). The pathogen has had several name changes, such as *Uredo glumarum* (1827), *Puccinia striaeformis* (1854), *Puccinia straminis* (1860), and *Puccinia glumarum* (1894) before the current species name was established in 1953 (Chen, 2005).

The hosts of Pst include cereals, such as wheat, barley, triticale, rye, and grasses (Curtis et al., 2002). There are different strains of virulence and specialized forms for small grain cereal hosts such as wheat, barley, and rye (Chen, 2005; Roose-Amsaleg et al., 2002). Although the alternative host of the pathogen was unknown before 2010, Jin et al. revealed that sensitive

Berberis spp. was the alternative host of the pathogen and showed that the barberry plays a major role in the development of new strains. These new strains are created from sexual reproduction, mutations, or somatic hybridizations on *Berberis* species (Jin et al., 2010) and infect wheat genotypes known to be resistant.

Stripe rust infects the green plant tissues. Infection can occur at any time from single leaves to maturity. Although this period changes according to seasonal and local climatic conditions, it coincides with an optimum air temperature of 10-15°C and high humidity in the spring. The first symptoms begin as yellow lines (prepustules) on the leaves during the time of infection, followed by the formation of stripe pustules on the upper surfaces of the leaves, on the leaf sheath in the later stages, and on the glumes or awns in the years when the disease is severe (GKGM, 2012). The pustules are yellow or orange in color. As the plant matures, infected tissues may become brownish and dry. In the second week of infection, single-celled, dikaryotic (n+n) urediniospores of 20-30 µm in diameter form inside the pustules. Millions of urediniospores released from pustules in the spring are often transported by wind across countries or even continents. In suitable conditions, Pst infects wheat plants, is transported to neighboring plants or fields where new urediniospores are produced (Broad Institute, 2012).

Nearly 100% relative humidity and precipitation are needed for the new urediniospores produced to germinate and enter the host. The urediniospores are followed by formation of two-celled, dikaryotic teliospores, which are called ‘winter spores’. In the spring, these teliospores germinate to form single-celled, haploid (n) basidiospores (Broad Institute, 2012). After *Berberis* species were determined to be the alternate host, it was thought that basidiospores germinate and infect the leaves of *Berberis* plants, where they form structures called pycnia on the upper surface of the leaf and aecia on the lower surface. Aeciospores, which are formed from aecia, are

carried by the wind, and germinate on their new hosts under suitable conditions, forming uredinia with summer urediniospores. These spores are carried by the wind and spread to infect other plants (Chen, 2005).

The rust fungus grows and reproduces in the host plant, making use of the host plant's water and nutrients. Dry, poor quality grain formation is caused by suppressing photosynthesis in the infected leaves, especially in the flag leaf, which provides the nutrients for grains development in the spike. In this way, Pst restricts plant development and causes yield and quality losses (Chen, 2005; Martinez et al., 2012; Broad Institute, 2012).

Yield and quality losses can be between 30-100% in conducive climatic conditions and especially when using susceptible varieties (Department of Primary Industries, 2008; Bux et al., 2012b). Epidemics of different severity continue to be seen in wheat production areas around the world. Morgounov's study conducted in five central Asian and three Caucasian countries reported that stripe rust is the main biotic factor limiting wheat production in the region and has been affecting the region for the last 5 years (Morgounov et al., 2001). Widespread epidemics of stripe rust have been observed in southwest China almost every year since 1996 (Zhonghu, 2001). In the United States, recent reports indicate that the extent of damage from stripe rust has increased (Martinez et al., 2012). This situation is highly variable due to the frequent mutations of the pathogen, the formation of new virulent pathotypes in a short time and the transport of these new pathotypes by wind between countries and continents. For example, a stripe rust pathotype acting on the stripe rust resistance gene *Yr9* originated in East Africa in 1986 and was carried by air to northern Africa and western and southern Asia and eventually North America by 2000. More than 80 genes have been identified for resistance to stripe rust (*Yr*) (McIntosh et al.,

2011). In the gene-for-gene system, a large percentage of these genes determine race-specific resistance (Flor, 1971).

Stripe rust is a significant historical problem in the United States, but only in the Pacific Northwest and California, where the environment is favorable for disease growth. However, stripe rust was observed in 25 states throughout the country in 2000 (Chen et al., 2002). Due to the introduction of new Pst races, the disease has grown increasingly problematic in the south-central United States and the central Great Plains (Chen, 2005; Markell and Milus, 2008). Because new races of the pathogen have adapted to high temperatures and are more aggressive, stripe rust has become a more significant problem in the United States (Chen, 2005; Milus et al., 2009; Chen et al., 2010).

The molecular biology of *P. striiformis* races is difficult, mostly because of the heterozygous structure and obligate parasites. In recent years, developments in plant biotechnology are mostly directed plant breeding studies. Genome editing technologies, such as clustered regularly interspaced short palindromic repeats (CRISPR-Cas9), transcription activator-like effector nucleases (TALENs) and zinc finger nucleases will further improve the development of better adapted cultivars (Schwessinger and Rathjen, 2017).

Leaf Rust

Bolton et al. (2008) determined that the most common disease in wheat was leaf rust, caused by *P. triticina*. The fungus that causes the disease is a parasite that can produce urediniospores as long as the infected leaf tissue survives. Urediniospores can be transmitted hundreds of kilometers away from the host plant by wind, infecting wheat fields and, thus, spreads over wide areas. The leaf rust fungus *P. triticina* is in *Phylum Basidiomycota,* in the class of *Urediniomycetes*, *Pucciniaceae* family and subfamily *Puccinia* (Bolton et al., 2008).

The leaf rust forms spots or pustules and is classified accordingly. Rust spots can be found scattered over the upper and lower leaf surfaces of the host as 1.5 mm diameter, round, orange, and brown spots (Roelfs, 1992). Rust diseases stand out because of serious yield losses. Because these are the most common and important diseases of wheat, they are among the most studied (Tonk and Yüce, 2007).

The urediniospores, which play the most important role in the spread of rust diseases, occur mostly in spring and summer, and are carried by the wind, causing new infections in other plants. In mild temperatures, the fungus is transmitted in the form of urediniospores and overwinters on other crops or wild wheatgrasses. Urediniospores formed in the spring and spread by wind create new infections under suitable humidity and temperature (10-18^{o}C) conditions (Lipps and Mills, 2006).

The development of a *P. triticina* infection in wheat was first described by Allen (1926) in a cytological study. Urediniospores are single-celled, and their outer wall is covered with a spiny, hydrophobic surface. The fungus infects the host plant with external factors such as wind, attaches by hydrophobic interactions and enters through the stomatal openings. If the urediniospores that settle on the leaf surface come into contact with rain or dew, they absorb water, swell and develop germination tubes. Germination takes place after 4-8 hours under 100% humidity at 20^{o}C. Spores can maintain their vitality for 1-3 days without germination (Bolton et al., 2008). *P. triticina* germination tubes begin to develop and continue to grow until they reach a stomate. When a stomate is found, they differentiate and form an appressorium (Appressorium-A). The appressorium ensures that the plant and the fungus are firmly attached, and also allows the fungus to grow into the host (Allen, 1926).

P. triticina is a macrocyclic and heteroecious rust with five spore stages. The telia and uredia stages occur on bread wheat; durum wheats *T. turgidum* subsps. *durum* (Desf.) Husn., *dicoccum,* and *dicoccoides*; *Ae. speltoides* Tausch, *Ae. cylindrica* Host and *Triticale* (X *Triticosecale*). Pycnia and aecia occur on alternate hosts, *Thalictrum speciosissimum* (=*T. flavum glaucum*) and *Anchusa italica* (Bolton et al., 2008). After overwintering, teliospores germinate in the spring to form basidiospores. Basidiospores reach alternate hosts by wind, germinate, and form primary hyphae. Primary hyphae (haploid) on the leaves produce pycnia (spermagonia). The spermagonia contain spermatia and receptive hyphae. Often, incompatibility between the recipient hyphae and spermatium occurs when they are made up of the same mycelium. The emergence of new strains of rust fungi occurs by spermatization between spermatia of different races and recipient hyphae. Although this is not the only way for race formation, it is of special importance in race formation. Dikaryotic hyphae begin to develop in the host tissue after the first stage of sexual reproduction, i.e., plasmogamy, which takes place between the spermatia and recipient hyphae. Spermagonia form on the upper surface of the leaf, and aecia on the lower. Aeciospores formed in aecia infect the wheat by wind dispersal and the resulting urediniospores cause infection during the summer. Teliospores form towards the end of the season. The rust fungus can be transmitted to autumn crops in the form of urediniospores in temperate regions and coasts, in which case the intermediate host is of no consequence (Bolton et al., 2008).

Because the leaf rust fungus is adapted to different climatic conditions, disease can be found in every region of the world where wheat is grown. Wheat cultivars susceptible to leaf rust show a 5-15% or greater reduction in yield when rust infection occurs. Genetic resistance is the most economical and preferred method to reduce yield losses due to leaf rust (Kolmer, 1996).

If the fungus can survive and reproduce on the plant, the host plant is deemed susceptible, and the pathogen virulent; this is a compatible relationship. If the pathogen lives without causing harm to the plant, the plant is pathogen tolerant. However, if the plant prevents the pathogen from growth and reproduction, the plant is resistant, the pathogen is avirulent; this is an incompatible relationship (Prasad et al., 2020).

Currently, there are over 70 leaf rust (*Lr*) named resistance genes (McIntosh et al., 2011). On a gene-for-gene basis, most of the *Lr* genes determine race-specific resistance (Flor, 1971). Despite being effective, race-specific resistance is not long-lasting because of the continuous development of virulent pathogen races. Every year, around 40-60 pathogen races are identified in the United States. Several of these new races have been able to overcome previously identified resistance genes (Kolmer et al., 2006).

In North America, the alternate host is thought to have a smaller role in the development of new leaf rust races (Samborski, 1985). In the United States, the asexual stage is the primary source of new leaf rust races. In the southern US, leaf rust overwinters on winter wheat. For the northern Great Plains, this acts as a reservoir of inoculum for the disease. The inoculum is wind-blown from the south into the northern Great Plains all the way to Manitoba, Canada, every spring (Samborski, 1985; Kolmer 2005; McMullen et al., 2008). Taking everything into consideration, winter wheat cultivars must be continuously screened for race changes, and new resistance genes must be introduced into local cultivars to manage disease threats.

Stem Rust

Stem rust is a fungal disease known in wheat since ancient times. The first studies on the life cycle of the disease, also called black rust, started in 1767. *Puccinia graminis* Pers. f. sp. *tritici* is a heteroecious rust species, in the *Basidiomycota* division, class *Urediniomycetes*, order

Urediniales and the family *Pucciniaceae*. Stem rust, which has five different stages (pycniospore, aeciospores, urediniospore, teliospore and basidiospore) in its life cycle, passes the aeciospore and pycniospore stages on the alternate host *Berberis* or *Mahonia* plant species. Apart from wheat, the disease can occur on some barley and rye cultivars, wild barley and *Aegilops* species (Knott, 2012).

The optimum temperature for the development of stem rust disease is 26^{o}C; temperatures below 15^{o}C and above 40^{o}C are adversely affecting the fungus. Stem rust, which causes significant yield and quality losses by creating epidemics under suitable conditions, occurs in the advanced stages of plant development, during grain filling, when the air temperature rises. The time of emergence of the disease makes chemical applications difficult (Wiese, 1987). The fungus infects the stem of the plant and limits the transport of nutrients and water also leads to the breakdown of chlorophyll. The rate of photosynthesis in stem rust-infected leaves can decrease by 30% daily compared to that in noninfected leaves (Keutgen et al., 1995). Stem rust also causes wrinkling in the grains and reduces quality.

Berberis species are important as intermediate hosts of stem rust, both as a source of inoculum and for increasing genetic variation. In order to prevent or minimize stem rust epidemics, the destruction of *Berberis* shrubs by burning is also used as a control method (Roelfs, 1982). After the 1916 epidemic in the United States, the eradication of *Berberis* shrubs began in 1918. Until 1967, nearly 100 million *Berberis* bushes were destroyed by burning also poisoning. As a result, *Berberis* shrubs have ceased to be the main source of inoculum and a significant decrease has been observed in the number of stem rust epidemics in the USA. Roelfs (1982) identified three main effects of the eradication of *Berberis* bushes, first, a reduction in the amount of inoculum for first infections in stem rust disease, second, a reduction in the number of

new races that may emerge due to limited sexual reproduction and third, the pathogen population becomes more stable as a result of a decrease in the rate of change of the pathogen population and the number of races emerging each year.

On the other hand, recent regrowth of *Berberis* shrubs in the areas where they have been eliminated in the USA and infection of wheat with stem rust caused by *Berberis* is observed (Kolmer et al., 2007).

In years when climatic conditions are suitable for the development of stem rust, epidemics may cause important yield and quality losses on sensitive genotypes. Stem rust is a problem in North Africa, western and eastern Asia, Australia, and New Zealand, eastern and Western Europe, central parts of North America and southern parts of South America. The disease has caused varying levels of damage in many countries until now. For example, epidemics were observed on genotypes containing the *Sr6* resistance gene in the 1940s and the *Sr9g*, *Sr11* and *Sr16* resistance genes in the mid-1950s. The most severe stem rust epidemics in Europe in the Twentieth Century occurred between 1932 and 1950 (Roelfs, 1992). Losses of 20-30% in western and central Europe in 1932 and 9-33% in Scandinavia in 1951 have occurred (Zadoks, 1963). In 1974, epidemics of high crop losses occurred in the southern parts of Australia (Watson, 1981). In the 1950s, severe stem rust epidemics were seen in Argentina and other South American countries (Germán et al., 2007). Epidemics from 1920 to 1960 in Minnesota and North and South Dakota in the USA caused yield losses from 20% to 50% on average (Leonard, 2001).

The presence of varieties containing the *Sr24* and *Sr31* resistance genes in Argentina, Brazil, Chile, Paraguay, and Uruguay in South America, where nine million ha of wheat is planted, has prevented the occurrence of stem rust epidemics for the last 20 years. Along with

these resistance genes, genotypes containing *Sr22*, *Sr25*, *Sr26*, *Sr32*, *Sr33*, *Sr35*, *Sr39* and *Sr40* resistance genes also were reported to be resistant to stem rust populations, although not yet deployed (Germán et al., 2007).

A new stem rust race was identified in Uganda in 1999. This new race was named Ug99, referring to the place and year it was identified. This race affects many resistance genes and is also virulent on genotypes carrying the *Sr31* resistance gene, which has played an important role in resistance for 30 years (Pretorius et al., 2000). This gene is located on the T1RS·1BL wheat-rye translocation chromosome. The origin of this gene is the rye cultivar Petkus, and Kavkaz, Aurora and Loverin wheat containing this translocation chromosome that are used widely in breeding. The rye segment containing *Sr31* also harbors leaf rust (*Lr26*), stripe rust (*Yr9*) and powdery mildew (*Pm8*) resistance genes (McIntosh et al., 1995). Over time, the emergence of more aggressive races that can overcome these genes led to the breakdown of all these genes except *Sr31* (Jin and Singh, 2006). Recently, the emergence of a new stem rust race virulent on genotypes containing *Sr31* gene also has rendered this gene ineffective (Pretorius et al., 2000). Jin and Singh (2006) reported that 80-90% of the wheat genotypes worldwide are susceptible to Ug99 in test studies conducted in areas where the Ug99 is prevalent.

In the U.S., 50% of winter and 70%-80% of spring wheat varieties are susceptible to Ug99. Moreover, 70-80% of the breeding material is susceptible, and most stem-rust resistance genes used in breeding programs have been defeated by Ug99 (Todorovska et al., 2009). As a result, research on stem rust now is directed on identifying novel resistance genes for Ug99. A number of *Sr* genes have been discovered and inserted into wheat genomes over the last 50 years. There are a number of genes, such as *Sr*2, *Sr*13, *Sr*21, *Sr*22, *Sr*24, *Sr*25, *Sr*26, *Sr*27, *Sr*28, *Sr*32, *Sr*33, *Sr*35, *Sr*36, *Sr*37, *Sr*39, *Sr*40, *Sr*42, *Sr*44, *Sr*45, *Sr*46, *Sr*47, *Sr*51, *Sr*52, *Sr*53, *Sr*55,

*Sr*57, and *Sr*58 that are resistant to Ug99 and derivatives (Dundas et al., 2007; Xu et al., 2008; Qi et al. 2011, Liu et al. 2011a; Liu et al. 2011b ; Rouse and Jin 2011).

Resistance Genes of Wheat Rusts

About 19 percent of the world's major grain crop production comes from wheat (Todorovska et al., 2009). Rust infections cause considerable production losses and are one of the most economically important diseases affecting wheat. The control of rust infections has relied on two methods: genetic and chemical control. Genetic management, or the cultivation of resistant cultivars is the most successful, cost-effective, and ecologically friendly strategy because it minimizes the need for fungicides and reduces production costs. Due to the risk of rust pathogens building resistance to fungicides, farmers in developing countries prefer to use resistant cultivars rather than fungicides. (Oliver, 2014).

The most successful and low-cost management method for rust control, especially in developing countries, is to deploy host genetic resistance (Ellis et al., 2014). There are several types of genetic resistance to rust infections. “Seedling resistance,” which is often conferred by single genes with major phenotypic effects throughout all growth periods of the plant (Flor, 1971), and “adult-plant resistance,” (APR), which is often provided by multiple genes with additional slight phenotypic effects during the later stages of plant development (Knott, 2012). Seedling and adult-plant phenotyping assays, as well as molecular marker assays, if available for particular resistance genes, are used widely in selecting and breeding for rust resistance (Juliana et al., 2017).

Johnson proposed the idea of durable resistance (Johnson, 1984; Johnson, 1988) and described it as 'resistance that stays functional when deployed over large areas and for a long period of time, in an ideal environment'. Minor genes, also known as slow-rusting genes, are

responsible for this form of resistance, which is typically regulated by more than one gene during the adult-plant stage. A single resistance gene in a wheat cultivar is typically less efficient in controlling rust, but a combination of two or more genes improves resistance durability. Pyramiding 4–5 minor genes generated a degree of rust resistance that approached immunity in a collection of CIMMYT germplasm that included 10–12 different genes. The Pakistani cultivar Lyalpur 73 remains resistant to rust practically worldwide, despite being created more than 50 years ago (Khan et al., 2013).

About 70 stem rust resistance genes, 65 stripe rust resistance genes, and 79 leaf rust resistance genes currently are cataloged (McIntosh et al., 2017). When new, aggressive races of the stem, stripe and leaf rust pathogens develop, widely used cultivars with good resistance genes might experience production losses, resulting in "boom and bust" cycles (Pretorius et al., 2000; Huerta-Espino et al., 2011; Wellings, 2011; Solh et al., 2012). A number of commonly used and essential resistance genes recently were overcome by new pathogen races, including *Sr13, Sr24, Sr31, Sr36, Sr38, SrTmp* and *Sr1RSAmigo* for stem rust; *Yr2, Yr6, Yr7, Yr8, Yr9, Yr17* and *Yr27* for stripe rust; and *Lr9, Lr14a, Lr16, Lr17a, Lr21, Lr24, Lr26* and *Lr39* for leaf rust in wheat (Huerta-Espino et al., 2011; Singh et al., 2015; Ali et al., 2017).

Back in the early 1900s, researchers tested the leaf rust resistance of Malakof and Webster wheat varieties (Mains et al., 1926). Later, leaf rust resistance genes *Lr1* and *Lr2* were identified in these cultivars (Ausemus et al., 1946). Soliman et al. (1964) identified the chromosomes that carry the leaf rust resistance genes *Lr1, Lr3* and *Lr11.* In bread wheat, durum wheat and diploid wheat species, about 80 leaf rust resistance genes or alleles (McIntosh et al., 1995) have been discovered and described using several DNA molecular and microsatellite markers, including enzymes and PCR-based markers (McIntosh et al., 2007). In hexaploid

wheat, these genes are present on 20 of the 21 chromosomes (McIntosh et al., 1995; McIntosh et al., 2007; McCallum et al., 2012). The majority of *Lr* genes provide major, seedling or race-specific resistance and operate on a gene-for-gene basis, resulting in a hypersensitive reaction (HR) (Flor, 1942; McIntosh et al., 2008; Samsampour et al., 2010). However, several APR genes, such as *Lr34* and *Lr46*, confer durable, long-term resistance in varied conditions and against numerous fungal pathogens, making them highly valuable for breeding purposes (Schnurbusch et al., 2004).

Several wild wheat and grass cultivars are important sources of resistance genes to major wheat diseases, including *Ae. tauschii* (Gill et al., 1986). From these wild accessions, resistance genes to leaf rust were first transferred into common wheat cultivars. One gene (*Lr9*) was derived from the wild species *Ae. umbellulata* Zhuk.; three (*Lr19, Lr24 and Lr29*) from *Thinopyrum elongatum* (Host) D. R. Dewey; five (*Lr28, Lr35, Lr36, Lr47* and *Lr51*) from *Ae. speltoides*; one (*L37*) from *Ae. ventricosa* Tausch (Todorovska et al., 2009); one (*Lr37*) from *Th. Intermedium* (Host) Barkworth and D. R. Dewey; seven (*Lr21, Lr22a, Lr32, Lr39, Lr42*) from *Ae. tauschii*; one (*Lr65*) from *T. aestivum* subsp. *spelta*, three (*Lr25, Lr26* and *Lr45*) from *Secale* cereale (McIntosh et al., 2003) one (*Lr50*) from *T. monococcum* subsp. *monococcum* (Blaszczyk et al., 2004; Mago et al., 2002) one (*Lr33*) from *T. turgidum* subsp. *dicoccoides* (Blaszczyk et al., 2004) and one (*Lr54*) from Ae. *kotschyi* Boiss.

In order to improve wheat breeding, it is important to understand the genetic basis of durable resistance to stem rust disease (Yu et al., 2014). One of the most efficient resistance gene combinations against stem rust, *Sr2+Sr57+Sr58* is a group of wheat genes that confer resistance to adult plant stem rust (McIntosh, 1988; Singh et al., 2006). *Sr2* was mapped to the short arm of chromosome 3B using SSR markers (Hare and McIntosh, 1979). The *Sr2* gene has been utilized

to increase stem rust resistance in numerous popular International Maize and Wheat Improvement Center (CIMMYT) varieties farmed globally due to its potential to give durable and broad-spectrum resistance (Singh et al., 2007b). *Sr2* gives moderate resistance to Ug99 (about a 30% reduction in disease severity); but, once it is combined with other genes from the *Sr2*-complex, such as the *Sr57* and *Sr58* genes, significant resistance is obtained. These *Sr2*-complex resistance genes are effective against all Pgt isolates in all wheat-growing regions (Sunderwirth and Roelfs, 1980).

First detected in *T. turgidum* subsp. *dicoccum* (Emmer or Khapli wheat), *Sr13* has now been found in numerous *T. turgidum* subsp. *durum* cultivars as well (Huerta-Espino and Roefls, 1992). *Sr13* is located on the long arm of chromosome 6A. *Sr22* is located on the long arm of chromosome 7A (Khan et al., 2005). In certain cases, hexaploid wheat lines containing *Sr22* are successful in developing resistance to Ug99, although they are not completely effective (Olson et al., 2010). *Th. elongatum* has the stem rust resistance genes *Sr25* on 7DL and *Sr26* on 6AL (Dundas et al., 2007; McIntosh et al., 2003; Liu et al., 2010). *Sr35* was initially introduced from *T. monococcum* to hexaploid wheat (Neu et al., 2002) and is effective against the TTKSK (Ug99) race of *P. graminis* f. sp. *tritici*. The long arm of chromosome 3A (3AL) was found to contain this gene. Hexaploid wheat received the *Sr49* gene from *T. timopheevii*, which is located on chromosome arm 2BS (McIntosh et al., 2003; Liu et al., 2011b; Dyck, 1992; Singh et al., 2007a).

A total of 49 resistance genes against stripe rust, *Yr1* to *Yr49*, have been identified in bread, durum wheat and wild species (McIntosh et al., 1995). The majority of the stripe rust resistance genes were derived from common wheat (*T. aestivum* subsp. *aestivum*), but some were derived from other wild species, including *T. aestivum* subsp. *spelta*, *T. turgidum* subsp.

dicoccoides, *S. cereale*, *Ae. comosa* Sm. In Sibth. & Sm., *Ae. ventricosa*, *Ae. tauschii*, and *Dasypyrum villosum* (L.) P. Candargy.

Materials and Methods

Plant Materials

A total of 108 A-genome diploid wheat accessions consisting of 24 *T. monococcum* subsp. *monococcum* (cultivated einkorn), 59 *T. monococcum* subsp. *aegilopoides* (wild einkorn) and 25 *T. urartu* subspecies were obtained from the Wheat Genetics Resource Center (WGRC) at Kansas State University, Manhattan, Kansas, USA. TA10881, an accession previously believed to be *T. urartu*, actually was identified as *T. turgidum* subsp. *dicoccoides*, and was not included in the studies (see Table 1). A mini-core collection of diploid A-genome species covering about 90 percent of the genetic variation of these species spanning their whole area of geographic distribution was established at the WGRC using genotyping-by-sequencing (GBS) (Adhikari et al., 2021). Geographic distributions and allelic diversity helped to identify the mini-core collection from 980 diverse accessions.

Pathogen Isolates

Accessions were screened with stripe rust (*P. striiformis* f. sp. *tritici*), leaf rust (*Puccinia triticina*), and stem rust (*P. graminis* f. sp. *tritici*) cultures. The inoculum consisted of a composite of 12 diverse local field isolates, 5 local field isolates, and pure cultures of race QFCSC for leaf rust, stripe rust, and stem rust, respectively. The pathogen cultures were provided by Dr. Robert L. Bowden, USDA-ARS, Kansas State University.

Disease Evaluation: Seedling Stage

The screening experiments were carried out in the Throckmorton Plant Science Center greenhouses of the Plant Pathology Department at Kansas State University Manhattan, Kansas in Spring 2020, and Autumn 2020. The experiments were planted in a completely randomized design with two replicates. Seeds were planted in germination boxes in the seedling laboratory in order to obtain the highest germination rates. Seeds were treated with a Terraclor solution (PCNB) at 0.25g per liter of solution to control a range of fungal diseases. Germinated seeds were transferred to 3-inch square plastic pots, five plants per pot, in a Sungro 360 soil mix and slow-release commercial fertilizer. Recommended cultural practices, including fertilization and irrigation, were applied during the experiment in a rust-free greenhouse set at 22℃/18℃ (day/night) with 16-hour photoperiod. The same experiment was conducted two times in order to confirm the results. Susceptible checks Morocco (in Spring 2020) and Avery (in Autumn 2020) were provided in each tray.

Plants were ready for inoculation seven to nine days after germination. The key point for inoculation was when the first leaf was fully emerged, and the second leaf was beginning to grow. Ten-day-old plants were inoculated using rust spores. Stripe and leaf rust spores kept at -80°C were heat shocked for 6 min at 42°C for spray inoculation. The rust spores were suspended in Soltrol-170 oil, and the inoculation material was evenly applied by spraying at different times for stripe rust and leaf rust. Plants were air-dried for 15-20 minutes after inoculation.

Stripe Rust

Inoculated seedlings were placed in a dew chamber at 12 ± 2 °C; 16 hours of darkness. For stem rust, darkness followed by 3-5 hours of light in the dew chamber. The dew chamber

period simulated the infection cycle in the field. Incubation continued in the greenhouse at 20°C/15°C (day/night) with a 16-hour photoperiod. Disease response was scored 14-16 days after inoculation on a 0 to 9 scale (McNeal et al., 1971) with "; = no visible signs or symptom; 1 = necrotic and/or chlorotic flecks, no sporulation; 2 = necrotic and/or chlorotic blotches or stripes, no sporulation; 3 = necrotic and/or chlorotic blotches or stripes, trace sporulation; 4 = necrotic and/or chlorotic blotches or stripes, light sporulation; 5 = necrotic and/or chlorotic blotches or stripes, intermediate sporulation; 6 = necrotic and/or chlorotic blotches or stripes, moderate sporulation; 7 = necrotic and/or chlorotic blotches or stripes, abundant sporulation; 8 = chlorosis behind sporulating area, abundant sporulation; and 9 = no necrosis or chlorosis, abundant sporulation". Plants with a score of 0-3 were rated resistant, those with a score of 4-6 were called intermediate, and those with a score of 7-9 were considered susceptible.

Leaf Rust

Seedlings inoculated with the leaf rust pathogen were placed in a dew chamber for 12-14 hours at 22°C. Incubation continued in the greenhouse at 25°C/ 15°C (day/night). Disease response was scored on the 0 to 4 Stakman scale 12-14 days after inoculation with "0 = no macroscopic sign of infection; ; = no uredinia but flecks present; 1 = small uredinia surrounded by necrosis; 2 = small to medium uredinia surrounded by chlorosis or necrosis; 3 = medium sized uredinia with or without chlorosis; and 4 = large uredinia without chlorosis. In the rating, a - indicates smaller than average and a + larger than average pustules". Ratings of 0 to 2 were considered resistant, whereas a 3 was considered moderately susceptible and 4 a highly susceptible reaction.

Disease Evaluation: Adult Plant Stage

Adult-plant reaction to rust was evaluated in the greenhouses of the Plant Pathology Department, Kansas State University in September 2020. Adult-plant experiments were in a completely randomized design with three replicates. Five seeds were sown in 3-inch square plastic pots filled with a sterilized soil-peat mixture. Pots were placed in trays of 32. All recommended cultural practices for fertilization and irrigation were used. At the two to three leaf stage, the plants were moved to vernalization for 6 weeks at 4°C with 8 hours of supplemental fluorescent lighting in a 24-hour period. After vernalization, plants were moved to the greenhouse and transplanted to 1-gallon plastic pots filled with the same sterilized soil-peat mixture and grown to the adult-plant stage.

Greenhouse Experiments

At the adult-plant stage (heading stage), plants were moved to a different greenhouse for each type of rust. For stripe rust, the greenhouse was at 20°C/15°C (day/night); for leaf rust, the greenhouse was at 25°C/15°C (day/night); and for stem rust, which has the warmest temperature requirement, the greenhouse was set at 30°C/18°C (day/night). Supplemental greenhouse lighting of 16 hours was provided for all three experiments. Five to six weeks after moving the plants to the greenhouses, they were inoculated by spraying depending on the experiment and the rate of the growth. The same inoculation procedures used for the seedling stage were used for the adult-plant inoculum. Avery and Morocco were used as susceptible controls and Joe and Kingbird as the resistant control for all three rusts (Figure 1).

Plants inoculated with stripe rust were placed in a dew chamber for 12-14 hours at 17°C. Incubation continued in the greenhouse at 15°C/10°C (day/night) and 16-hour day-length. Fifteen days after inoculation, each plant was rated on a 0-9 scale. The Cobb scale was not used

to rate adult-plant resistance under greenhouse conditions because of the leaf damage encountered following the low-temperature incubation period needed for stripe rust. Inoculation was not as successful compared to that for the leaf and stem rust experiments. Resistance was determined using the 0 to 9 scale of McNeal (1971) described previously.

Plants inoculated with leaf rust were placed in a dew chamber for 12-14 hours at 22°C. Incubation was in the greenhouse at 25°C/15°C (day/night).

For stem rust, inoculated plants were placed in a dew chamber for 12-14 hours at 24°C followed by incubation in the greenhouse at 30°C/18°C (day/night).

Three replications of each accession and the susceptible and resistant checks were included for all rust inoculations. To measure disease response for leaf and stem rust, a modified Cobb scale (Peterson et al., 1948) was used, which included both percent leaf area and/or stem area affected and host response. For the host response, "R (Resistant) = no uredinia present and necrotic areas without pustules; MR (Moderately Resistant) = small uredinia with slight sporulation, chlorosis and/or necrosis surrounding small uredinia as a result of an incomplete reaction; M (Moderate) = small to moderate sized uredinia with moderate to heavy sporulation, some chlorosis may be visible; MS (Moderately Susceptible) = medium size uredinia with moderate to heavy sporulation, some chlorosis may still be possible; and S (Susceptible) = large uredinia with abundant sporulation, uredinia often coalesced to form lesions without any visible chlorosis or necrosis". Disease responses in the greenhouse was scored at least twice during the adult-plant stage.

Field Experiments

For the field experiments conducted in 2020 and 2021, accessions were planted in same plastic pots and soil in the greenhouse. Each pot received 5 seeds followed by the same management as described for greenhouse experiments.

In late March 2020, plants were transplanted with three replications in a randomized complete block design for the field screening. Experiments were conducted at two different locations, the Rocky Ford Experiment Station, Manhattan, and the Rossville Experiment Station, Rossville, KS, USA (Figure 2). Leaf rust and stem rust nurseries were located at the Rocky Ford Experiment Station and the stripe rust nursery was at the Rossville Experiment Station. Experiment locations were chosen for their highest natural infection exposure. To obtain rust epidemics, leaf rust nurseries were surrounded by the leaf rust susceptible spreader cultivar Jagger, stripe rust nurseries were surrounded by KS89180B spreader, and stem rust nurseries were surrounded by PIONEER25R40 spreader. Morocco and Kingbird were included as susceptible and resistant controls, respectively. The field was inoculated as spikes were forming, which is equal to between boot and heading stages, and the climate was favorable. The inoculation process was same as for the greenhouse experiments. National Weather Service data were used to determine the inoculation time. First inoculation began in late April 2020 and the last around the middle of May 2020. These times change depending on weather conditions, specifically humidity, temperature, and rain. At least 10 days after inoculation, disease severity for each accession and their replications was assessed according to the modified Cobb Scale combined with a reaction type. Disease response in the field was scored at least twice during the experiment.

In the second round of evaluations, transplants were made in mid-October 2020 with three replications in a completely randomized design at the Rocky Ford Experiment and Rossville Experiment Stations as previous year. Plants were increased in the wheat growing season, and winter type susceptible (Avery) and resistant (Joe) checks were used, which were different than those used in previous year experiment. One hundred eight different genotypes and their replications, with five plants per entry were available for disease evaluation. All recommended cultural practices, including fertilization, irrigation, and herbicide treatments were followed. Winter-damaged and/or winter-killed plants were noted and replanted if needed. Inoculations began in early May 2021 and the same process was followed as described for the 2020 field experiments. Disease responses were recorded at least twice by using Cobb scale.

Data Analysis

Disease severity score for each accession were collected to determine the overall response to stripe rust, leaf rust, stem rust at the seedling stage and adult plant stage in both greenhouse and field conditions. The PROC MIXED statement in SAS computer software package version 9.3 was used to determine the best linear unbiased predictors (BLUPs) for resistance responses and severity of each accession across three different diseases.

Analysis of variance (ANOVA) was conducted with all effects fixed. To calculate the Best Linear Unbiased Predictors (BLUPs) for stripe rust, leaf rust, and stem rust scores, the following mixed-effect model was used:

$$Y_{ijm} = \mu + E_i + RE_{j(i)} + G_m + GE_{mi} + \varepsilon_{ijm}$$

where Y_{ijm} is the response, E_i is the i^{th} level of year effect, $RE_{j(i)}$ is the effect of j^{th} replicate nested within i^{th} year, G_m is the effect of m^{th} accession, GE_{mi} is the interaction effect

between m^{th} accession and i^{th} year, and ε_{ijm} is the random experimental error effect associated with Y_{ijm}.

The wheat rust data was adjusted to approach near normality using a logit transformation, and the statistical analysis of the experiments was performed on both the logit transformed and non-transformed datasets. The given first order parameters, such as means and figures, were determined from untransformed data, whereas second order statistics (ANOVAs) were obtained using transformed data.

Experiment effects were computed using a combination of accession, year, replication within years (experiments), and accession-by-year (experiment) interaction.

Under greenhouse and field conditions, the coefficient of infection (CI) was determined by multiplying the amount of disease severity with the resistance response at the adult plant stage. The constant values for infection types were used based on; R = 0.2, MR = 0.4, M = 0.6, MS = 0.8, S = 1 (Stubbs et al., 1986).

Results

Seedling Stage

One hundred eight accessions, including 24 *T. monococcum* subsp. *monococcum*, 59 *T. monococcum* subsp. *aegilopoides*, and 25 *T. urartu*, were screened for resistance to stripe rust under greenhouse conditions. Disease reactions (Table 2) are summarized for all 108 accessions.

Stripe Rust

Eighteen (16.6%) accessions were scored as resistant with six highly resistant. Nineteen (17.5%) accessions were scored as intermediate and 71 (65.7%) were susceptible to stripe rust at the seedling stage. Ten (41.6%) accessions of *T. monococcum* subsp. *monococcum* and eight (13.5%) accessions of *T. monococcum* subsp. *aegilopoides* were resistant, however no *T. urartu*

accessions were resistant. Six (25%) *T. monococcum* subsp. *monococcum* accessions, 11 (18.6%) *T. monococcum* subsp. *aegilopoides* accessions and two (8%) *T. urartu* accessions had intermediate reactions. The majority of accessions were scored as susceptible to stripe rust at the seedling stage; eight (33.4%) *T. monococcum* subsp. *monococcum*, 40 (67.7%) *T. monococcum* subsp. *aegilopoides* and 23 (92%) *T. urartu* (Fig. 1). The Stakman 0-4 infection type scale is illustrated using some examples of stripe rust of A-genome diploid wheat at the seedling stage (Figure 3).

Leaf Rust

Twenty-five (23.2%) accessions were scored resistant and 20 were highly resistant. Ten (9.3%) accessions were intermediate, and 73 (67.5%) accessions were susceptible to leaf rust at the seedling stage. Twenty-two (91.6%) accessions of *T. monococcum* subsp. *monococcum* and three (5%) of *T. monococcum* subsp. *aegilopoides* were resistant, however no *T. urartu* accessions was recorded as resistant. Two (8.3%) *T. monococcum* subsp. *monococcum* accessions, 8 (13.5%) *T. monococcum* subsp. *aegilopoides* accessions and zero (0%) *T. urartu* accessions were intermediate. As shown in Figure 3, the majority of accessions were scored as susceptible to leaf rust seedling stage; zero (0%) of *T. monococcum* subsp. *monococcum*, 48 (81.3%) of *T. monococcum* subsp. *aegilopoides*, and twenty-five (100%) of *T. urartu* were scored as susceptible. All *T. monococcum* subsp. *monococcum* were considered either resistant or intermediate, while all *T. urartu* were recorded as susceptible (see Table 2). In Figure 4, the Stakman 0-4 infection type scale was illustrated using some examples of leaf rust on accessions of A-genome diploid wheat at the seedling stage.

Data Analysis

Table 3 shows the combined analysis of variance across experiments for stripe rust and leaf rust. The findings demonstrate that accessions had a highly significant effect ($P < 0.001$) on stripe rust and leaf rust resistance scores. These results showed that all the accession differed in their response to stripe rust and leaf rust disease. Moreover, for leaf rust, the interaction between accessions and experiments was not significant. Stripe rust, on the other hand, showed a strong interaction ($P < 0.001$) between accessions and experiments.

Adult Plant Stage

Greenhouse Evaluations

Stripe Rust

A composite culture pathogen isolates was used for stripe rust inoculation in the greenhouse. Out of 80 A-genome diploid wheat accessions tested, 13.8% showed a susceptible reaction (IT=7-9). Reactions of A-genome, mini-core set and checks at the adult-plant stage are shown in Table 4. About 52% of the accessions exhibited a resistance response (IT=0-3), and 28 (35%) showed intermediate reactions (IT=4-6) (summarized in Figure 6). Out of 80 accessions tested in the greenhouse, *T. monococcum* subsp. *aegilopoides* exhibited the most resistance (65%), followed by *T. monococcum* subsp. *monococcum* (52.6%) and *T. urartu* (23.8%).

Leaf Rust

Leaf rust severities varied greatly, ranging from 0 to 60% in the greenhouse. The final rust severities of the accessions and their infection types are presented in Table 4. Final rust severity represents the cumulative results of all resistance factors. Based on the final rust severity, the accessions were placed into three groups: resistant, moderate, and susceptible

having 0-20%, 20-40% and 40-60%, respectively. During the experiment, 31 accessions had resistant to moderately resistant (R-MR) reactions, whereas 32 accessions were moderately susceptible to susceptible (MS-S) responses, and 17 accessions had moderate (M) response. On the other hand, *T. monococcum* subsp. *monococcum* accessions showed only R (63.2%), MR (31.5%) and M (5.3%) reactions. However, *T. urartu* was scored generally moderately susceptible (57.2%), susceptible (19.1%) and moderate (23.8). No *T. urartu* accessions were resistant and moderately resistant to leaf rust in the greenhouse. In the case of *T. monococcum* subsp. *aegilopoides,* 7.5% were R, 25% were MR, 27.5% were M, 35% were MS and 5% had an S respons (see Figure 5). In addition, Morocco (susceptible check) and Joe (resistant check) wheats were up to 50S and 20 MR, respectively.

Stem Rust

The 80 A-genome accessions tested for adult-plant stem rust under greenhouse conditions were classified into five groups. The first group contained six (7.5%) accessions resistant to stem rust. In the second group, five (60.3%) accessions showed an MR response with a severity between 10%-20%. The third group consisted of 19 (23.8%) accessions that were moderately (M) resistant. In the fourth group, 16 (20%) accessions showed an MS reaction with a severity between 20%-40%. In the fifth group, the remaining 32 (40%) accessions showed S reactions with severity between 20%-80% in all three different species (Table 4). Two (10.6%) accessions of *T. monococcum* subsp. *monococcum* and four (10.3%) accessions of *T. monococcum* subsp. *aegilopoides* were resistant whereas one (5.3%) accession of subsp. *monococcum* and four (10.3%) accessions of subsp. *aegilopoides* were moderately resistant. However, none of the (0%) accessions of *T. urartu* were recorded as resistant. Four (21.1%) accessions of *T. monococcum* subsp. *monococcum,* 13 (33.4%) of *T. monococcum* subsp. *aegilopoides,* and two (10%) of *T.*

urartu exhibited moderate reaction. Seven (36.8%) of subsp. *monococcum*, eight (20.6%) of subsp. *aegilopoides*, and one (5%) of *T. urartu* accession were moderately susceptible. The majority of accessions were scored as susceptible to stem rust at the adult-plant stage; five (26.3%) of *T. monococcum* subsp. *monococcum*, 10 (25.6%) of *T. monococcum* subsp. *aegilopoides*, and 17 (85%) of *T. urartu* (see Figure 5).

Data Analysis

Table 5 shows the combined analysis of variance for stripe rust, leaf rust, and stem rust experiments. The findings demonstrate that accessions had a highly significant effect ($P < 0.001$) on stripe rust, leaf rust, and stem rust severities and resistance responses. These results showed that all the accession differed in their response to stripe rust, leaf rust, and stem rust diseases at the adult plant stage under the greenhouse conditions. Furthermore, for leaf rust, replications and score dates also had significant effect on source of variance.

Field Evaluations

Stripe Rust

Different stripe rust reaction types were observed in the 108 accessions. The final rust severities of the genotypes and their infection types are presented in Figure 6. Based on their final rust severity, the wheat genotypes were placed into three groups: high (0-20%), intermediate (20-40 %) and low (40-100%) resistance. Four accessions were resistant, 42 were moderately resistant, 57 moderate, four moderately susceptible, and one was susceptible (see Table 6). Despite the heavy stripe rust disease pressure, one (4.2%), 10 (41.6%), 13 (54.2%) accessions *T. monococcum* subsp. *monococcum* showed R, MR and M reactions, respectively, and no moderately susceptible or susceptible response was observed. For *T. monococcum* subsp. *aegilopoides*, two (3.4%), 21 (35.6%), 34 (57.6%), 2 (3.4%) accessions exhibited R, MR, M, and

MS reactions, respectively. After the final scoring, one (4%) accession of the 25 *T. urartu* accessions showed resistance, 10 (40%) were MR, 11 (44%) were M, two (8%) were MS and only one accession (4%) was susceptible. In Figure 6, the Cobb scale is illustrated using examples of stripe rust on accessions of A-genome diploid wheat at the adult-plant stage.

Leaf Rust

Field reactions ranging from resistance to susceptibility were observed at the Rocky Ford experiment station in 2020 and 2021. The infection types of all 108 accessions and the checks are presented in Table 6. The diploid wheat accessions were placed into three groups, resistant, moderate, and susceptible levels having 0-20%, 20-40 % and 40-100% resistance, respectively. During the experiment, 32 accessions were resistant to moderately resistant, whereas 11 showed moderately susceptible to susceptible responses, and 65 accessions had a moderate response. On the other hand, *T. monococcum* subsp. *monococcum* accessions showed only MR (62.5%) and M (33.4%) reactions. However, *T. urartu* and *T. monococcum* subsp. *aegilopoides* were scored generally as moderately resistant, moderate, and moderately susceptible (see Figure 6). In addition, the susceptible checks Morocco (2020) and Avery (2021) displayed up to 100 S and 60 S, respectively, whereas the resistant checks Kingbird (2020) and Joe (2021) had 10 MR and 15 MR responses, respectively. In Figure 6, the Cobb scale is illustrated using some examples of leaf rust on accessions of A-genome diploid wheat at the adult plant stage.

Stem Rust

Of the 108 A-genome diploid accessions of wheat tested, moderately resistance to stem rust was detected in nine (8.5%), a moderate response was detected in 17 (16.1%), and moderately susceptible and susceptible reactions were detected 28 (26.4%) and 52 (49.1%) accessions, respectively (see Table 6). Although no highly resistant (R) accession was found, the

response of three different subspecies to stem rust was variable. Five (20.8%) accessions of *T. monococcum* subsp. *monococcum,* three (5.2%) of *T. monococcum* subsp. *aegilopoides,* and one (4.2%) of the *T. urartu* accessions were moderately resistant. Three (12.5%) and three (12.5%) of *T. monococcum* subsp. *monococcum* accessions, 14 (24.2%) and 22 (37.9%) of *T. monococcum* subsp. *aegilopoides* accessions and none (0%) and three (12.5%) of *T. urartu* were moderate and moderately susceptible. The majority of accessions were scored as susceptible to stem rust at the adult-plant stage; 13 (54.2%) *T. monococcum* subsp. *monococcum*, 19 (32.7%) *T. monococcum* subsp. *aegilopoides,* and 20 (83.3%) *T. urartu* were susceptible in the field experiments in 2020 and 2021 (see Figure 6). In addition, the susceptible checks Morocco (2020) and Avery (2021) displayed infection types up to 60 S and 60 S, respectively, whereas the resistant checks King Bird (2020) and Joe (2021) had 10 MR and 10 MR responses, respectively. In Figure 7, the Cobb scale is illustrated using some examples of stem rust on accessions of A-genome diploids at the adult-plant stage.

Data Analysis

Table 7 shows the combined analysis of variance for stripe rust, leaf rust, and stem rust experiments. The findings demonstrate that accessions, the interaction between accessions and years, and replications within years had a highly significant effect ($P < 0.001$) on stripe rust, leaf rust, and stem rust severities and resistance responses. These results showed that all the accession differed in their response to stripe rust, leaf rust, and stem rust diseases at the adult plant stage under the field conditions. Furthermore, for leaf rust and stem rust, score dates also had significant effect on source of variance.

Discussion

Rust infections are a major disease of wheat worldwide and cause nearly 60 percent yield loss for stripe and leaf rust. Yield losses can be up to 100 % for stem rust. The stem rust epidemic in Canada and the United States is a prime example, which caused a loss in productivity (Kolmer, 2001). Infections occur in spring and summer and can frequently reinfect wheat and cause epidemics. A stem rust epidemic in 2008 in North America destroyed a million tons of wheat (Olivera et al., 2008). Rusts affects young wheat crops, but more typical damage is a decrease in foliage, root growth, and yield loss caused by reduced photosynthesis, an increase in the rate of respiration, and a reduced level of carbohydrates. Rust pathogens have a high rate of mutation. Sexual variation in stem rust in the U.S and other countries plays a substantial role (Olivera et al., 2008). Leaf rust reduces light saturation and gross photosynthesis. Subsequently, disease screening focuses on hot spots of the disease. The lines with the lowest rust infections are most likely to have more durable resistance. The main focus of screening wild wheat relatives is to broaden the genetic variability of rust resistance and make them accessible to wheat improvement programs. We analyzed a set of diploid A-genome relatives of wheat for seedling and adult-plant resistance for leaf, stripe, and stem rust, in order to provide breeders with potential new sources of resistance aimed at developing wheat cultivars with superior rust resistance.

Our phenotypic screening achieved reliable outcomes, and rust-resistant and susceptible accessions were effectively distinguished. For stripe rust, the presence of a consistent resistance response in seedlings and adult plants was demonstrated in seven accessions, including both *T. monococcum* subsp. *monococcum* and subsp. *aegilopoides.* The results of seedling and adult plants also showed that the A-genome minicore accessions in *T. monococcum* subspecies

exhibited leaf and stem rust resistance at both seedling and adult-plant stage in the greenhouse and under field conditions. Among the accessions evaluated in this study, *T. monococcum* subsp. *monococcum* showed good number of resistant accessions, followed by *T. monococcum* subsp. *aegilopoides* and *T. urartu*, which generally had a moderate or susceptible response. These findings might indicate that strong pathogen resistance requires too much energy and isn't good for a balanced plant defense and development system (Kazan and Manners, 2009). *T. urartu* is a wild species that does not grow in great densities in nature, thus there is unlikely to be much pressure for it to evolve severe or high wheat rust resistance.

These various responses to A-genome diploid accessions confirmed the findings of other studies. For instance, Vallega (1979) tested up to 102 *T. monococcum* accessions with five different leaf rust races and found that all accessions were resistant to all races of leaf rust. Two separate dominant genes for leaf rust resistance were discovered in a study of 49 accessions from the University of Saskatchewan collection (Bai et al., 1998). At the seedling and adult-plant stages, a *T. monococcum* accession was also shown to be resistant to leaf rust and have adult-plant resistance to stripe rust (Dhaliwal et al., 2005). Furthermore, 78.7% of 1,062 *T. monococcum* gene bank accessions were shown to be resistant to Ug99 stem rust (Rouse and Jin, 2011). Some accessions were resistant to more than one race and several of the resistant accessions were subjected to genetic testing (Rouse and Jin, 2011). In addition to *Sr21*, *Sr22* and *Sr35*, they discovered two additional novel resistant genes against Ug99.

To date, much work identifying sources of novel resistance using wild wheat relatives has been done. *T. monococcum* species, for instance, are recognized to be an important source of resistance to the most common fungal infections and have been integrated into several improved cultivars (Beteselassie et al., 2007). In our study, seedling and adult-plant tests showed that the A

genome mini core set accession TA10622 (*T. monococcum* subsp. *monococcum*), exhibited stripe, leaf, and stem rust resistance at the adult-plant stage in the greenhouse and under field conditions.

Several rust resistant genes have been transferred into several wheat cultivars. More than 200 wheat resistance genes have been discovered so far, including 60 stem, 79 leaf and 83 stripe rust resistance genes (McIntosh et al., 2017). Almost all of them were introduced into wheat cultivars.

Yr5, *Yr8*, *Yr9*, *Yr28*, *Yr37*, *Yr38*, *Yr40*, and *Yr42* are examples of stripe rust resistance genes transferred from wild relatives (Marais et al., 2009). However, no stripe rust resistance genes have been transferred from *T. monococcum* and *T. urartu*.

In general, diploid wheats are resistant to leaf rust (Bai et al., 1998). Several einkorn accessions were discovered by Dorofeev et al. (1987) to be resistant to leaf rust. *T. monococcum* subsp. *monococcum* had a greater number of leaf rust resistant accessions than *T. urartu* and *T. monococcum* subsp. *aegilopoides*, which was confirmed in our study. Einkorn, according to Anker et al. (2001), seems to have a non-host status for this disease. A spring einkorn accession in India has maintained a high-level resistance to many wheat diseases, primarily leaf rust, for many years (Dhaliwal et al., 2005). Einkorn wheat also is the diploid *Triticum* species most resistant to stripe rust, according to Donchev and Mihova (1988). *T. monococcum* subsp. *monococcum* and subsp. *aegilopoides* have been used to transfer leaf rust resistance genes into wheat. Kaur et al. (2007) found a leaf rust resistance gene on chromosome 5A and transferred it from einkorn to bread wheat. The leaf rust resistance gene was shown to be closely associated with the SSR markers BARC57 and BARC321, both of which are found on chromosome 3AS. *T.*

monococcum subsp. *monococcum* has a leaf rust resistance gene known as *Lr63* (Kolmer et al., 2010).

Monneveux et al. (2003) have underlined the potential interest of einkorn wheat as a gene reservoir for wheat improvement. Einkorn has a number of characteristics that make it resistant to fungal infections. Biffen (1907), who proposed its use in developing new cultivated wheats with improved resistance, was the first to recognize this species as a reservoir for most fungal disease resistance genes. Einkorn was described by Vavilov (1957) as a "collector of complicated immunity" and by Soshnikova (1990) as a valuable source of stem rust resistance. *T. monococcum* subsp. *monococcum* has been used to introduce three stem rust resistance genes (*Sr21*, *Sr35* and *Sr22*) into wheat cultivars (Olson et al., 2010). When the *Sr21* gene was introduced from diploid wheat to tetraploid and hexaploid wheat, the level of resistance gradually decreased, suggesting that the genetic background can have an effect on the expression of the resistance (Jin et al., 2008).

We have identified several accessions with seedlings and adult-plant rust resistance; however, it remains to be shown that these accessions harbor novel resistance genes that are different from those that have already been transferred to wheat. Gene postulation, genetic studies, and determining the number and position of genes providing resistance are all used to characterize resistance to rusts. Genetic analysis studies may comprise crossing resistant and susceptible cultivars or crossing different parents with one or more known genes for resistance, as outlined by Roelfs (1992). This is also referred to as a "test of allelism". If the resistance gene is fully expressed in the F1 plant, this may indicate a dominant trait of the gene, and conversely. Tests on F2 populations and F3 families, backcross F1 and F2 families, doubled haploid or RILs of single seed descent populations are used to determine the inheritance of resistance and the

number of genes involved in the expression of the trait in wheat (Roelfs, 1992; Bariana, 2003). Chi-squared analyses are commonly used to estimate the number of genes by comparing observed ratios to theoretically predicted values and calculating the goodness of fit. Almost all of the loci in wheat rust resistance genes that have been identified, mapped, and cataloged have undertaken genetic analysis, followed by chromosomal localization by monosomic cytogenetic analysis, and more recently, bulked segregant analysis or selective genotyping (Lorz and Wenzel, 2018). On the other hand, for identification of the presence or absence of resistant genes in genotypes, molecular marker-based screening of resistance sources with diagnostic or related markers is an alternative to the phenotypic approach (Vanzetti et al., 2011; Goutam et al., 2015). Most of the rust genes in wheat have been linked or diagnosed using a variety of molecular markers (SSR, RFLP, STS, SCAR, CAPS, RAPD, DArt) (Robert et al., 1999; Zhou et al., 2014). Yet, progress in the production of diagnostic/linked KASP based SNP markers for resistance genes has been slow, and they are rare in comparison to SSRs or other marker technologies (Singh et al., 2000; Marchal et al., 2018).

Even though einkorn wheat is a source of resistance to a wide range of pests and diseases, its use in durum and bread wheat breeding has been restricted due to low crossability with hexaploid species. The A genomes of *T. monococcum* subsp. *monococcum* and subsp. *aegilopoides* and *T. urartu* diverged from a common ancestor about 1 million years ago (Brandolini et al., 2006). Most polyploid wheat species, including durum and bread wheat, have *T. urartu* as their A-genome donor (Dubcovsky and Dvorak, 2007). Einkorn wheat, on the other hand, is mainly a genome donor for *T. zhukovskyi* (Baum and Bailey, 2004). The direct transfer of valuable genes from einkorn to cultivated wheat is challenging due to post-syngamic hybridization barriers that result in embryo abortion and lack of endosperm development

(Bhagyalakshmi et al., 2008). Bochev (1983) studied the crossability of *Aegilops* species (as the female parent) and einkorn (as the male parent). When a specific *T. monococcum* subsp. *monococcum* was used as a male parent, hybrid sterility was reduced, suggesting that this accession may be used as a bridge parent to introduce genes from other einkorn accessions into hexaploid wheat.

Traditional breeding methods based on phenotypic evaluations are used to develop resistant cultivars. This method requires intensive labor and is a long process. Today, molecular breeding approaches are considered an important supplement to traditional breeding methods for increasing the efficiency in breeding programs (Collard and Mackill, 2008). Marker-assisted selection (MAS) is widely used as a crucial tool in wheat breeding programs, especially in the transfer of traits determined by single-gene inheritance (Randhawa et al., 2013). These programs are carried out in the form of marker-assisted backcrossing and gene pyramiding, especially in breeding studies for resistance to diseases controlled by a single gene. Gene pyramiding can also be accomplished with traditional breeding methods, but it is often not possible to select plants phenotypically with more than one gene. Many studies show that the combination of more than one gene against strains of a pathogen can provide more durable resistance (Joshi and Nayak, 2010).

For fast release of rust-resistant cultivars, MAS has generated good results by enabling novel gene deployment and gene pyramiding. Gene pyramiding with traditional methods, on the other hand, is complex, time-consuming and involves testing of the same wheat breeding materials with many individual rust races (Haile and Rouml, 2013). Maintaining all the rust isolates required to phenotypically pyramid rust genes is difficult and gene pyramiding can be achieved more effectively by molecular marker analyses. (Wu, 2008). Gene pyramiding, in

which genes found in various genotypes are inserted into a single cultivar that includes the required alleles at several loci, has become more effective with MAS (Joshi and Nayak, 2010). Describing and comparing rust populations is also possible using selectively neutral markers, such as isozymes, or more recently discovered forms of molecular markers, such as random amplified polymorphic DNA (RAPD), SSR (simple sequence repeat) markers and amplified fragment length polymorphism (AFLP) (Chen, 2005). The wheat genome is large (16GB), complicated, and contains a lot of repetitive elements. Reduced-representation libraries, complexity reduction of polymorphic sequences, restriction-site associated DNA sequencing, sequence-based polymorphic marker technology, low coverage multiplexed shotgun genotyping, and genotyping-by-sequencing to reduce complexity have all been described (Yang et al., 2012). In addition, the GBS pathway was created to decrease the wheat genome's complexity. To minimize additional genome redundancy, the RAD-seq and GBS were used to select cutting sites following restriction digestion (Poland et al., 2012). The exact identification of genetic areas supporting rust resistance has been improved thanks to high throughput genotyping technologies and targeted genotyping-by-sequencing (tGBS) (Nsabiyera et al., 2018).

When used over a broader region, pyramiding two or more genes can help to extend the lifespan of the genes. However, only if tightly linked DNA markers are available, can two or more resistance genes be pyramided. Disease resistance genes have more variability in wild species than cultivated germplasm. In recent years, DNA markers has made it convenient to accurately transfer desired genes from unadapted germplasm to elite lines with little or no linkage drag (Young and Tanksley, 1989). As many as 101 genes for resistance to leaf, stripe and stem rust have been transferred from wild species to wheat (Chaudhary et al., 2014).

The stripe rust resistance QTLs in *T. monococcum* are known despite its high adult-plant resistance to *Puccinia sp*. *QYrtbm.pau-2A* was found in *T. monococcum* accession pau14087 and is located between SSR markers *Xwmc407* and *Xwmc170* on chromosome 2A (Chhuneja et al., 2008).

Leaf rust resistance gene *Lr63* is closely associated with SSR markers *Xbarc57* and *Xbarc321*, which were found on chromosome 3AS in *T. monococcum*. This gene can be utilized in wheat improvement programs to improve leaf rust resistance by conditioning low to intermediate infection types to most *P. triticina* isolates (Kolmer et al., 2010).

The *Sr22* gene was first discovered in *T. monococcum* subsp. *aegilopoides* (G-21) and *T. monococcum* (RL5244) (Kerber and Dyck, 1973). Through interspecific hybridization, *Sr22* was then introduced into tetraploid and hexaploid wheat cultivars. In addition, *Sr22* is effective against Ug99. *Sr22* was previously mapped on chromosome 7AL. Yu et al. (2009) utilized three linked markers, *Xcfa2019*, *Xcfa2123* and *Xbarc121*, to haplotype this locus, however *Xcfa2123* was not always polymorphic between *T. monococcum* and *T. aestivum*. *Xwmc633* and *Xcfa2123* were determined to be the closest markers flanking *Sr22* in a new set of lines generated by Olson et al. (2010). After the translocated section was shortened, elements of the deleterious genetic material linked with *Sr22* were eliminated, making it a more attractive source of resistance (Olson et al., 2010). In addition, in 2011, a KASP marker for the qualitative resistance gene was developed. Since the new marker, *cssu22*, can distinguish between the presence and absence of the gene in a variety of genetic backgrounds, it should be possible to combine *Sr22* with other stem rust resistance genes in marker assisted breeding to produce more durable rust resistant germplasm (Periyannan et al., 2011).

The number of cloned wheat rust resistance genes has increased in recent years and researchers need to rethink how to use these newly discovered resistance sources to avoid "boom and bust cycles." A "boom-and-bust" cycle can occur when resistance genes are overused, and a small genetic base is present. Resistant cultivars experience a "boom" in area as producers take advantage of the higher yields that resistant cultivars provide, however, at the same time reducing the genetic variability. As a result, the pathogen population has an increased selection pressure to develop virulence against these genes and that eventually breaks down leading to a “bust”. Kolmer (1996) has conducted the most extensive research on boom-and-bust cycles in cereals. Effective gene stewardship and pyramiding several resistance genes is to be the most reliable method for breaking this cycle.

The careful and responsible care of resistance genes with the goal of extending the resistance effect is referred to as effective resistance gene stewardship. Because they reduce the possibility of the disease developing virulence via mutation, the greatest way to gene stewardship is gene pyramids (Hafeez, 2021). Effective resistance gene stewardship necessitates consideration of the resistance mechanism provided by the available genes as well as their potential to function together (Periyannan et al., 2017). According to Pretorius et al. (2017), gene stewardship is a result of the entire agricultural system. For instance, regardless of how much work the breeding community has gone into building gene pyramids including this gene, an unplanned release of a cultivar with a single resistance gene would be enough to put this gene at danger of being defeated by the pathogen under high selection pressure.

Conclusion

The major goals of wheat breeding projects often comprise developing new cultivars with higher yield, quality, and resistance to abiotic/biotic stresses. The rust diseases of wheat are the most important factor limiting wheat production and cause significant losses in wheat yield and quality. Regardless of the target product in breeding studies, the most critical step in achieving success is the accessibility of a diverse set of germplasm to screen for genes for the traits of interest. Wild wheat relatives are a potential genetic resource for improving abiotic and biotic stress in wheat. The diploid A-genome wheat species have been identified as an important and valuable genetic resource. However, no comprehensive research has uncovered the disease resistance potential of A-genome diploid wheat maintained in gene banks. Here, we evaluated a diverse set of A-genome accessions maintained at the Wheat Genetics Resource Center, Kansas State University, for their seedling and adult plant-rust resistance. Several accessions with single and multiple resistance to different rusts were identified, which can be the starting point of using these genes in wheat improvement.

References

Admassu, B., and Fekadu, E. (2005). Physiological races and virulence diversity of *Puccinia graminis* f. sp. *tritici* on wheat in Ethiopia. Phytopathologia Mediterranea, 44(3), 313-318.

Adhikari, L., Raupp, J., Wu, S., Wilson, D., Evers, B., Koo, D. H., Singh, N., Friebe, B., and Poland, J. (2021). Genetic characterization and curation of diploid A-genome wheat species. bioRxiv. https://doi.org/10.1101/2021.08.20.457122

Ali, S., Rodriguez-Algaba, J., Thach, T., Sørensen, C. K., Hansen, J. G., Lassen, P., Nazari K., Hodson D.P., Justesen AF., and Hovmøller, M. S. (2017). Yellow rust epidemics worldwide were caused by pathogen races from divergent genetic lineages. Frontiers in Plant Science, 8, 1057. https://doi.org/10.3389/fpls.2017.01057

Allen, R. F. (1926). A cytological study of *Puccinia triticina* physiologic form 11 on Little Club wheat. Journal of Agricultural Research. 33, 201– 222.

Anker, C. C., Buntjer, J. B., and Niks, R. E. (2001). Morphological and molecular characterisation confirm that *Triticum monococcum* ss is resistant to wheat leaf rust. Theoretical and Applied Genetics, 103(6), 1093-1098. https://doi.org/10.1007/s001220100667

Ausemus, E. R., Harrington, J. B., Reitz, L. P., and Worzella, W. W. (1946). Summary of genetic studies in hexaploid and tetraploid wheats. Journal of the American Society Agronomy, 38(12), 1082-1099.

Bai, D., Knott, D. R., and Zale, J. M. (1998). The inheritance of leaf and stem rust resistance in *Triticum monococcum* L. Canadian Journal of Plant Science, 78(2), 223-226. https://doi.org/10.4141/P97-069

Bariana, H. S. (2003). Breeding for disease resistance. Encyclopedia of applied plant sciences. (Thomas, B., Murphy, D. J., Murray, B. G., Eds.). Academic Press, Harcourt, UK, 244–253.

Baum, B. R., and Bailey, L. G. (2004). The origin of the A genome donor of wheats (*Triticum*: *Poaceae*)–a perspective based on the sequence variation of the 5S DNA gene units. Genetic Resources and Crop Evolution, 51(2), 183-196. https://doi.org/10.1023/B:GRES.0000020861.96294.f4

Beddow, J. M., Pardey, P. G., Chai, Y., Hurley, T. M., Kriticos, D. J., Braun, H. J., Park, R.F., Cuddy, W.S., and Yonow, T. (2015). Research investment implications of shifts in the global geography of wheat stripe rust. Nature Plants, 1(10), 1-5. https://doi.org/10.1038/nplants.2015.132

Beteselassie, N., Fininsa, C., and Badebo, A. (2007). Sources of stem rust resistance in Ethiopian tetraploid wheat accessions. African Crop Science Journal, 15(1). https://doi.org/10.4314/acsj.v15i1.54417

Bhagyalakshmi, K., Vinod, K. K., Kumar, M., Arumugachamy, S., Prabhakaran, A. J., and Raveendran, T. S. (2008). Interspecific hybrids from wild types cultivated *Triticum* crosses. A Study on the Cytological Behaviour and Molecular Relations. Journal of Crop Science and Biotechnology, 11(4), 257-262.

Biffen, R. H. (1907). Studies in the inheritance of disease-resistance. The Journal of Agricultural Science, 2(2), 109-128.

Blaszczyk, L., Chelkowski, J., Korzun, V., Kraic, J., Ordon, F., Ovesná, J., Purnhauser L., Tar M., and Vida, G. (2004). Verification of STS markers for leaf rust resistance genes of wheat by seven European laboratories. Cellular and Molecular Biology Letters, 9(4b), 805-817.

Bochev, B., Hristova, I., and Doncheva, V. (1983). Genus *Aegilops*--possibilities and perspectives of utilization in the breeding of high-quality wheat cultivars. Developments in Food Science. 5a, 237-242.

Bolton, M. D., Kolmer, J. A., and Garvin, D. F. (2008). Wheat leaf rust caused by *Puccinia triticina*. Molecular Plant Pathology, 9(5), 563-575. https://doi.org/10.1111/j.1364-3703.2008.00487.x

Brandolini, A., Vaccino, P., Boggini, G., Özkan, H., Kilian, B., and Salamini, F. (2006). Quantification of genetic relationships among A-genomes of wheats. Genome, 49(4), 297-305. https://doi.org/10.1139/g05-110

Bux, H., Ashraf, M., Hussain, F., Rattu, A. U. R., and Fayyaz, M. (2012a). Characterization of wheat germplasm for stripe rust ('Puccini striiformis f. sp.'tritici') resistance. Australian Journal of Crop Science, 6(1), 116-120. https://doi/10.3316/informit.053671199428626

Bux, H., Ashraf, M., and Chen, X. (2012b). Expression of high-temperature adult-plant (HTAP) resistance against stripe rust (Puccinia striiformis f. sp. tritici) in Pakistan wheat landraces. Canadian Journal of Plant Pathology, 34(1), 68-74. https://doi.org/10.1080/07060661.2012.662998

Broad Institute, (2012). “What is Puccinia striiformis?”, Puccinia Group Database, http://www.broadinstitute.org/annotation/genome/puccinia_group/MultiHome.html. (Accessed: September, 2021).

Chapman, V., Miller, T. E., and Riley, R. (1976). Equivalence of the A genome of bread wheat and that of *Triticum urartu*. Genetics Research, 27(1), 69-76. https://doi.org/10.1017/S0016672300016244

Chaudhary, H. K., Kalia, V., Rather, S. A., Badiyal, A., Hussain, W., and Jamwal, N. S. (2014). Wheat. Alien gene transfer in crop plants. (Pratap, A., and Kumar, J., Eds.). Achievements and Impacts, 2, 1-26.

Chen, X. M. (2005). Epidemiology and control of stripe rust [*Puccinia striiformis* f. sp. *tritici*] on wheat. Canadian Journal of Plant Pathology, 27(3), 314-337. https://doi.org/10.1080/07060660509507230

Chen, X., Moore, M., Milus, E. A., Long, D. L., Line, R. F., Marshall, D., and Jackson, L. (2002). Wheat stripe rust epidemics and races of *Puccinia striiformis* f. sp. *tritici* in the United States in 2000. Plant Disease, 86(1), 39-46. https://doi.org/10.1094/PDIS.2002.86.1.39

Chen, X., Penman, L., Wan, A., and Cheng, P. (2010). Virulence races of *Puccinia striiformis* f. sp. *tritici* in 2006 and 2007 and development of wheat stripe rust and distributions, dynamics, and evolutionary relationships of races from 2000 to 2007 in the United States. Canadian Journal of Plant Pathology, 32(3), 315-333. https://doi.org/10.1080/07060661.2010.499271

Chhuneja, P., Kaur, S., Garg, T., Ghai, M., Kaur, S., Prashar, M., Bains, N. S., Goel, N. K., Keller, B., Dhaliwal, H. S., and Singh, K. (2008). Mapping of adult plant stripe rust resistance genes in diploid A genome wheat species and their transfer to bread wheat. Theoretical and Applied Genetics, 116(3), 313-324. https://doi.org/10.1007/s00122-007-0668-0

Collard, B. C., and Mackill, D. J. (2008). Marker-assisted selection: an approach for precision plant breeding in the twenty-first century. Philosophical Transactions of the Royal Society B: Biological Sciences, 363(1491), 557-572. https://doi.org/10.1098/rstb.2007.2170

Curtis, B. C., Rajaram, S., and Gómez Macpherson, H. (2002). Bread wheat: improvement and production. Food and Agriculture Organization of the United Nations (FAO), Roma, 1-18.

De Candolle, A. (1886). Plants Cultivated for Their Seeds. Origin of Cultivated Plants, 2nd Edition. International Scientific Series Vol. XLIX, Kegan Paul Trench & Co., London, 376-384.

Department of Primary Industries, (2008). Stripe Rust of Wheat, http://www.dpi.vic.gov.au/agriculture/pests-diseases-and-weeds/plant-diseases/grains-pulses-cereals/stripe-rust-of-wheat. (Accessed: September, 2021).

Dhaliwal HS, Chhuneja P, Singh I, Ghai M, Goel RK, Garg M, Keller B, Roder M, and Singh K (2005). *Triticum monococcum* a novel source of transfer and exploitation of disease resistance in wheat. In: Pogna NE, Romeno M, Pogna EA, Galterio G (eds.), Proceedings of the 10th International Wheat Genetics Symposium, Paestum, Italy, 346–349. https://doi.org/10.1007/978-3-319-23494-6_8

Donchev, N., and Mihova, S. (1988). Possibilities for survival over the summer of the pathogen of yellow rust (*Puccinia striiformis* West. f. sp. *tritici*). Rasteniev'dni Nauki, 25(3), 102-107.

Dorofeev V.F., R.A. Udachin and L.V. Semenova, 1987. Wheats of the world. "Agropromisdat" (in Russian), Leningrad, 559.

Dubcovsky, J., and Dvorak, J. (2007). Genome plasticity a key factor in the success of polyploid wheat under domestication. Science, 316(5833), 1862-1866. https://doi.org/10.1126/science.1143986

Dubin, H. J., and Brennan, J. P. (2009). Combating stem and leaf rust of wheat: Historical perspective, impacts, and lessons learned. Proven successes in agricultural development: A technical compendium to millions fed. Washington: International Food Policy Research Institute. (Spielman, D.J. and Pandya-Lorch, R., Eds.), 910.

Dundas, I. S., Anugrahwati, D. R., Verlin, D. C., Park, R. F., Bariana, H. S., Mago, R., and Islam, A. K. M. R. (2007). New sources of rust resistance from alien species: meliorating linked defects and discovery. Australian Journal of Agricultural Research, 58(6), 545-549. https://doi.org/10.1071/AR07056

Dvorak, J. (1988). Cytogenetical and molecular inferences about the evolution of wheat. 7th International Wheat Genetics Symposium, (Miller, T. E., and Koebner, R. M. D., Eds.), 1, 187-192.

Dvorak, J., McGuire, P. E., and Cassidy, B. (1988). Apparent sources of the A genomes of wheats inferred from polymorphism in abundance and restriction fragment length of repeated nucleotide sequences. Genome, 30(5), 680-689. https://doi.org/10.1139/g88-115

Dyck, P. L. (1992). Transfer of a gene for stem rust resistance from *Triticum araraticum* to hexaploid wheat. Genome, 35(5), 788-792. https://doi.org/10.1139/g92-120

Ellis, J. G., Lagudah, E. S., Spielmeyer, W., and Dodds, P. N. (2014). The past, present, and future of breeding rust resistant wheat. Frontiers in Plant Science, 5, 641. https://doi.org/10.3389/fpls.2014.00641

Flor, H. H. (1942). Inheritance of pathogenicity in Melampsora lini. Phytopathology, 32, 653-669.

Flor, H. H. (1971). Current status of the gene-for-gene concept. Annual Review of Phytopathology, 9(1), 275-296.

Germán, S., Barcellos, A., Chaves, M., Kohli, M., Campos, P., and de Viedma, L. (2007). The situation of common wheat rusts in the Southern Cone of America and perspectives for control. Australian Journal of Agricultural Research, 58(6), 620-630. https://doi.org/10.1071/AR06149

Gill, B. S., Friebe, B., Raupp, W. J., Wilson, D. L., Cox, T. S., Sears, R. G., Brown-Guedira, G. L., and Fritz, A. K. (2006). Wheat genetics resource center: the first 25 years. *Advances in Agronomy*, *89*, 73-136. https://doi.org/10.1016/S0065-2113(05)89002-9

Gill, B. S., Raupp, W. J., Sharma, H. C., Browder, L. E., & Hatchett, J. H. (1986). Resistance in *Aegilops squarrosa* to wheat leaf rust, wheat powdery mildew, greenbug, and Hessian fly. Plant Disease, 70(6), 553-556.

GKGM, (2012). Buğday Pas Hastalıkları, Zirai Mücadele Teknik Talimatı, http://www.gkgm.gov.tr/birim/bitki_karantina/faaliyet/teknik_talimat/hububat/bugday_pas_hast.pdf . (Accessed: September, 2021).

Goutam, U., Kukreja, S., Yadav, R., Salaria, N., Thakur, K., and Goyal, A. K. (2015). Recent trends and perspectives of molecular markers against fungal diseases in wheat. Frontiers in Microbiology, 6, 861. https://doi.org/10.3389/fmicb.2015.00861

Gupta, P. K., Mir, R. R., Mohan, A., and Kumar, J. (2008). Wheat genomics: present status and future prospects. International Journal of Plant Genomics, 2008, 1-36. https://doi.org/10.1155/2008/896451

Hafeez, A. N., Arora, S., Ghosh, S., Gilbert, D., Bowden, R. L., and Wulff, B. B. (2021). Creation and judicious application of a wheat resistance gene atlas. Molecular Plant. 14(7), 1053-1070. https://doi.org/10.1016/j.molp.2021.05.014

Haile, J. K., and Rouml, M. S. (2013). Status of genetic research for resistance to Ug99 race of *Puccinia graminis* f. sp. *tritici*: A review of current research and implications. African Journal of Agricultural Research, 8(50), 6670-6680. https://doi.org/10.5897/AJAR2013.7257

Hare, R. A., and McIntosh, R.A. (1979). Genetic and cytogenetic studies of durable adult-plant resistances in" Hope" and related cultivars to wheat rusts. Zeitschrift Fur Pflanzenzuchtung. 83(4), 350–367.

He, D., Li, H., Xu, S., Duan, X., Zhou, Y., and Li, L. (2007). Reaction to powdery mildew and stripe rust in related species and landraces of wheat. Genetic Resources and Crop Evolution, 54(2), 213-219. https://doi.org/10.1007/s10722-006-9117-1

Heun, M., Schäfer-Pregl, R., Klawan, D., Castagna, R., Accerbi, M., Borghi, B., and Salamini, F. (1997). Site of einkorn wheat domestication identified by DNA fingerprinting. Science, 278(5341), 1312-1314. https://doi.org/10.1126/science.278.5341.1312

Huerta-Espino, J., and Roelfs, A. P. (1992). Leaf rust on durum wheats. Vortraege Fuer Pflanzenzuechtung (Germany). 24, 100–102.

Huerta-Espino, J., Singh, R. P., German, S., McCallum, B. D., Park, R. F., Chen, W. Q., Bhardwaj S.C., and Goyeau, H. (2011). Global status of wheat leaf rust caused by

Puccinia triticina. Euphytica, 179(1), 143-160. https://doi.org/10.1007/s10681-011-0361-x

Hussien, T., Bowden, R. L., Gill, B. S., and Cox, T. S. (1998). Chromosomal locations in common wheat of three new leaf rust resistance genes from *Triticum monococcum*. Euphytica, 101(1), 127-131. https://doi.org/10.1023/A:1018376315133

İren, S. (1964). Türkiye'de 1963 yılı hububat pas türleri ve zarar ve yayılışları üzerinde araştırmalar. Bitki Koruma Bülteni, 4, 141-159.

Jin, Y., and Singh, R. P. (2006). Resistance in US wheat to recent eastern African isolates of *Puccinia graminis* f. sp. *tritici* with virulence to resistance gene Sr31. Plant Disease, 90(4), 476-480. https://doi.org/10.1094/PD-90-0476

Jin, Y., Szabo, L. J., and Carson, M. (2010). Century-old mystery of *Puccinia striiformis* life history solved with the identification of Berberis as an alternate host. Phytopathology, 100(5), 432-435. https://doi.org/10.1094/PHYTO-100-5-0432

Jin, Y., Szabo, L. J., and Pretorius, Z. A. (2008). Virulence variation within the Ug99 lineage. In: Proceedings of the 11th International Wheat Genet Symposium, Sydney University Press, Sydney, Australia. (Appels, R., Eastwood, R., Lagudah, E., Langridge, P., Mackay, M., McIntye, L., Sharp, P., Eds.), 4–6.

Johnson, R. (1984). A critical analysis of durable resistance. Annual Review of Phytopathology, 22(1), 309-330.

Johnson, R. (1988). Durable resistance to yellow (stripe) rust in wheat and its implications in plant breeding. Breeding Strategies for Resistance to the Rusts of Wheat, El Batan, Mexico (Mexico), 29 Jun-1 Jul 1987. CIMMYT. (Simmonds, N.W. and Rajaram, S., Eds.), 63-75.

Joshi, R. K., and Nayak, S. (2010). Gene pyramiding-A broad spectrum technique for developing durable stress resistance in crops. Biotechnology and Molecular Biology Reviews, 5(3), 51-60. https://doi.org/10.5897/BMBR2010.0006

Juliana, P., Singh, R. P., Singh, P. K., Crossa, J., Huerta-Espino, J., Lan, C., Bhavani, S., Rutroski J.E., Poland, J.A., Bergstorm M.E., and Sorrells, M. E. (2017). Genomic and pedigree-based prediction for leaf, stem, and stripe rust resistance in wheat. Theoretical and Applied Genetics, 130(7), 1415-1430. https://doi.org/10.1007/s00122-017-2897-1

Kaur, N., Street, K., Mackay, M., Yahiaoui, N., and Keller, B. (2007). Molecular approaches for characterization and use of natural disease resistance in wheat. Sustainable disease management in a European context. Springer, Dordrecht. (Collinge, D.B., Munk, L., Cooke, B.M., Eds), 121, 387-397. https://doi.org/10.1007/978-1-4020-8780-6_18

Kazan, K., and Manners, J. M. (2009). Linking development to defense: auxin in plant–pathogen interactions. *Trends in plant science*, 14(7), 373-382. https://doi.org/10.1016/j.tplants.2009.04.005

Kerber, E. R., and Dyck, P. L. (1973). Inheritance of stem rust resistance transferred from diploid wheat (*Triticum monococcum*) to tetraploid and hexaploid wheat and chromosome location of the gene involved. Canadian Journal of Genetics and Cytology, 15(3), 397-409. https://doi.org/10.1139/g73-050

Keutgen, N., Roeb, G. W., Fuehr, F., and Reisener, H. J. (1995). Accumulation of assimilates in stem-rust-infected wheat leaves. Journal of Agronomy and Crop Science (Germany). 17(5), 297-305.

Khan, R. R., Bariana, H. S., Dholakia, B. B., Naik, S. V., Lagu, M. D., Rathjen, A. J., Bhavani, S., and Gupta, V. S. (2005). Molecular mapping of stem and leaf rust resistance in wheat. Theoretical and Applied Genetics, 111(5), 846-850. https://doi.org/10.1007/s00122-005-0005-4

Khan, M. H., Bukhari, A., Dar, Z. A., and Rizvi, S. M. (2013). Status and strategies in breeding for rust resistance in wheat. Agricultural Sciences, 4(6), 292-301. http://dx.doi.org/10.4236/as.2013.46042

Kihara, H. (1924). Cytologische und genetische Studien bei wichtigen Getreidearten mit besonderer Rücksicht auf das Verhalten der Chromosomen und die Sterilität in den Bastarden. Memoirs of the College of Science, Kyoto Imperial University. 1(1), 1-200.

Kilian, B., Mammen, K., Millet, E., Sharma, R., Graner, A., Salamini, F., Hammer, K., and Ozkan, H. (2011). *Aegilops*, wild crop relatives, genomic and breeding resources. Cereal. (Kole, C., Eds), 1-76.

Kimber, G. and Feldman, M. (1987). Wild wheat. An introduction. Special Report 353. College of Agriculture, University of Missouri, Columbia, MO, USA, 1-142.

Knott, D. R. (2012). The wheat rusts—breeding for resistance. Springer Science & Business Media, 12.

Kolmer, J. A. (1996). Genetics of resistance to wheat leaf rust. Annual Review of Phytopathology, 34(1), 435-455. https://doi.org/10.1146/annurev.phyto.34.1.435

Kolmer, J. A. (2001). Early research on the genetics of *Puccinia graminis* and stem rust resistance in wheat in Canada and the United States. Stem Rust of Wheat: From Ancient Enemy to Modern Foe. (Peterson, P.D., Eds.), 51-82.

Kolmer, J. A. (2005). Tracking wheat rust on a continental scale. Current Opinion in Plant Biology, 8(4), 441-449. https://doi.org/10.1016/j.pbi.2005.05.001

Kolmer, J. A., Anderson, J. A., and Flor, J. M. (2010). Chromosome location, linkage with simple sequence repeat markers, and leaf rust resistance conditioned by gene *Lr63* in wheat. Crop Science, 50(6), 2392-2395. https://doi.org/10.2135/cropsci2010.01.0005

Kolmer, J. A., Jin, Y., and Long, D. L. (2007). Wheat leaf and stem rust in the United States. Australian Journal of Agricultural Research, 58(6), 631-638. https://doi.org/10.1071/AR07057

Kolmer, J. A., Long, D. L., and Hughes, M. E. (2006). Physiologic specialization of *Puccinia triticina* on wheat in the United States in 2004. Plant Disease, 90(9), 1219-1224. https://doi.org/10.1094/PD-90-1219

Konařev, V. G., Gavrilyuk, I. P., Gubareva, N. K., and Peneva, T. I. (1979). About nature and origin of wheat genomes on the biochemistry and immunochemistry of grains. Cereal Chemistry, 56, 272-278.

Konvalina, P., Capouchová, I., Stehno, Z., and Moudry, J. (2010). Agronomic characteristics of the spring forms of the wheat landraces (einkorn, emmer, spelt, intermediate bread wheat) grown in organic farming. Journal of Agrobiology, 27(1), 9-17. https://doi.org/10.2478/s10146-009-0002-3

Kovács, Z., Simon-Sarkadi, L., Vashegyi, I., and Kocsy, G. (2012). Different accumulation of free amino acids during short-and long-term osmotic stress in wheat. The Scientific World Journal, 2012. https://doi.org/10.1100/2012/216521

Leonard, K. J. (2001). Stem rust-future enemy? Stem Rust of Wheat: From Ancient Enemy to Modern Foe, APS Press, St. Paul. (Peterson, P.D., Eds), 119–146.

Li, G. Q., Li, Z. F., Yang, W. Y., Zhang, Y., He, Z. H., Xu, S. C., Sing, R.P., Qu, Y.Y., and Xia, X. C. (2006). Molecular mapping of stripe rust resistance gene YrCH42 in Chinese wheat cultivar Chuanmai 42 and its allelism with *Yr24* and *Yr26*. Theoretical and Applied Genetics, 112(8), 1434-1440. https://doi.org/10.1007/s00122-006-0245-y

Lilienfeld, F., and Kihara, H. (1934). Genomanalyse bei Triticum und Aegilops. Cytologia, 6(1), 87-122. https://doi.org/10.1508/cytologia.6.87

Line, R. F. (2002). Stripe rust of wheat and barley in North America: a retrospective historical review. Annual Review of Phytopathology, 40(1), 75-118. https://doi.org/10.1146/annurev.phyto.40.020102.111645

Lipps, P. E., and Mills, D. (2006). Ohio State University, Extension FactSheet. Plant Pathology, http://ohioline.osu.edu./ac-fact/0006.html (Accessed: September, 2021).

Liu, S., Yu, L. X., Singh, R. P., Jin, Y., Sorrells, M. E., and Anderson, J. A. (2010). Diagnostic and co-dominant PCR markers for wheat stem rust resistance genes *Sr25* and *Sr26*. Theoretical and Applied Genetics, 120(4), 691-697. https://doi.org/10.1007/s00122-009-1186-z

Liu, W., Jin, Y., Rouse, M., Friebe, B., Gill, B., and Pumphrey, M. O. (2011a). Development and characterization of wheat-*Ae. searsii* Robertsonian translocations and a recombinant chromosome conferring resistance to stem rust. Theoretical and Applied Genetics, 122(8), 1537-1545. https://doi.org/10.1007/s00122-011-1553-4

Liu, W., Rouse, M., Friebe, B., Jin, Y., Gill, B., and Pumphrey, M. O. (2011b). Discovery and molecular mapping of a new gene conferring resistance to stem rust, *Sr53*, derived from Aegilops geniculata and characterization of spontaneous translocation stocks with reduced alien chromatin. Chromosome Research, 19(5), 669-682. https://doi.org/10.1007/s10577-011-9226-3

Lorz, H., and Wenzel, G. (Eds.) (2018). Molecular Marker Systems in Plant Breeding and Crop Improvement: Biotechnology in Agriculture and Forestry 55. Springer.

Ma, H., and Singh, R. P. (1996). Contribution of adult plant resistance gene Yr18 in protecting wheat from yellow rust. Plant Disease (USA), 80(1), 66-69.

Mago, R., Spielmeyer, W., Lawrence, G., Lagudah, E., Ellis, J., and Pryor, A. (2002). Identification and mapping of molecular markers linked to rust resistance genes located on chromosome 1RS of rye using wheat-rye translocation lines. Theoretical and Applied Genetics, 104(8), 1317-1324. https://doi.org/10.1007/s00122-002-0879-3

Mains, E. B., Leighty, C. E., and Johnson, C. O. (1926). Inheritance of resistance to leaf rust, Puccinia triticina Erikss in crosses of common wheat, *Triticum vulgare* VIII. Journal of Agricultural Research, 32, 931-972.

Marais, F., Marais, A., McCallum, B., and Pretorius, Z. (2009). Transfer of leaf rust and stripe rust resistance genes *Lr62* and *Yr42* from *Aegilops neglecta* Req. ex Bertol. to common wheat. Crop Science, 49(3), 871-879. https://doi.org/10.2135/cropsci2008.06.0317

Marchal, C., Zhang, J., Zhang, P., Fenwick, P., Steuernagel, B., Adamski, N. M., Boyd, L., McIntosh, R., Wulff, B.B.H., Berry, S., Lagudah, E., and Uauy, C. (2018). BED-domain-containing immune receptors confer diverse resistance spectra to yellow rust. Nature Plants, 4(9), 662-668. https://doi.org/10.1038/s41477-018-0236-4

Markell, S. G., and Milus, E. A. (2008). Emergence of a novel population of *Puccinia striiformis* f. sp. tritici in eastern United States. Phytopathology, 98(6), 632-639. https://doi.org/10.1094/PHYTO-98-6-0632

Marsalis, M. A., and Goldberg, N. P. (2006). Leaf, Stem and Stripe Rust Diseases of Wheat, New Mexico State University, College of Agriculture and Home Economics, Guide A-415. http://www.cahe.nmsu.edu/ (Accessed: September, 2021).

Martinez, A., Youmans, J., and Buck, J., (2012). “Stripe Rust (Yellow Rust) of Wheat”, The University of Georgia College of Agricultural and Environmental Sciences Publications, 960.

Matsuoka, Y. (2011). Evolution of polyploid *Triticum* wheats under cultivation: the role of domestication, natural hybridization, and allopolyploid speciation in their diversification. Plant and Cell Physiology, 52(5), 750-764. https://doi.org/10.1093/pcp/pcr018

McCallum, B.D., Hiebert, C., Huerta-Espino, J., and Cloutier, S., (2012). Wheat leaf rust. Disease resistance in wheat. Wallingford. (Sharma, I., Eds.). CAB International, 33-62.

McFadden, E. S. (1930). A successful transfer of emmer characters to vulgare wheat. Journal of the American Society of Agronomy, 22, 1020-34.

McIntosh, R. A. (1988). The role of specific genes in breeding for durable stem rust resistance in wheat and triticale. Breeding strategies for resistance to the rusts of wheat. CIMMYT, Mexico. (Simmonds, N.W., and Rajaram, S., Eds), 1-9.

McIntosh, R. A., Devos, K.M., Dubcovsky, J., Rogers, W. J., Morris, C.F., Appels, R., Somers, D.J., and Anderson, O.A. (2007). Catalogue of gene symbols for wheat: 2007 supplement. https://wheat.pw.usda.gov/ggpages/awn/53/Textfile/WGC.html (Accessed: September, 2021).

McIntosh, R. A., Devos, K.M., Dubcovsky, J., Rogers, W. J., Morris, C.F., Appels, R., Somers, D.J., and Anderson, O.A. (2008). Catalogue of gene symbols for wheat: 2008 supplement, 54, 209-225.

McIntosh, R. A., Dubcovsky, J., Rogers, W. J., Morris, C., Appels, R., Xia, X. C., and Azul, B. (2011). Catalogue of gene symbols for wheat: 2011 supplement, 56, 273-282.

McIntosh, R. A., Dubcovsky, J., Rogers, W. J., Morris, C., and Xia, X. C. (2017). Catalogue of gene symbols for wheat: 2017 supplement. (Yokohama, Japan Komugi Wheat Genetic Resources Database).

McIntosh, R. A., Dyck, P. L., Cusick, J., and Milne, D. L. (1984). Cytogenetical studies in wheat. XIII: Sr 35—a third gene from *Triticum monococcum* for resistance to *Puccinia graminis tritici*. Zeitschrift für Pflanzenzüchtung, 92(1), 1-14.

McIntosh, R. A., Wellings, C. R., and Park, R. F. (1995). Wheat rusts: an atlas of resistance genes. CSIRO, Melbourne, Australia.

McIntosh, R. A., Yamazaki, Y., Devos, K.M., Dubcovsky, J., Rogers, W. J., and Appels, R., Somers, (2003). Catalogue of gene symbols for wheat: 2003 supplement. Proceedings of the 10th International Wheat Genetics Symposium; 2003 Sep 1-6; Istituto Sperimentale per la Cerealicoltura; Paestum, Italy.

McMullen, M., Markell, S. G., and Rasmussen, J. B. (2008). Rust diseases of wheat in North Dakota. North Dakota State University Extension Bulletin, 1361.

McNeal, F. H., Konzak, C. F., Smith, E. P., Tate, W. S., and Russell, T. S. (1971). A uniform system for recording and processing cereal research data. USDA-ARS Bull, Washington, 34–121.

Milus, E. A., Kristensen, K., and Hovmøller, M. S. (2009). Evidence for increased aggressiveness in a recent widespread strain of *Puccinia striiformis* f. sp. *tritici* causing

stripe rust of wheat. Phytopathology, 99(1), 89-94. https://doi.org/10.1094/PHYTO-99-1-0089

Monneveux, P., Reynolds, M. P., Aguilar, J. G., Singh, R. P., and Weber, W. E. (2003). Effects of the 7DL. 7Ag translocation from *Lophopyrum elongatum* on wheat yield and related morphophysiological traits under different environments. Plant Breeding, 122(5), 379-384. https://doi.org/10.1046/j.1439-0523.2003.00856.x

Morgounov, A. I., Karabayev, M., Bedoshvili, D., and Braun, H. J. (2001). Improving wheat production in Central Asia and the Caucasus. Research Highlights of the CIMMYT Wheat Program 1999-2000, CIMMYT, 65-68.

Murray, G. M., and Brennan, J. P. (2009). The current and potential costs from diseases of wheat in Australia. Australian Grains Research and Development Corporation Report, 69. http://www.grdc.com.au (Accessed: September, 2021).

Neu, C., Stein, N., and Keller, B. (2002). Genetic mapping of the *Lr20 Pm1* resistance locus reveals suppressed recombination on chromosome arm 7AL in hexaploid wheat. Genome, 45(4), 737-744. https://doi.org/10.1139/g02-040

Nesbitt, M. (1996). From staple crop to extinction? The archaeology and history of hulled wheat. Hulled Wheats, Promoting the Conservation and Use of Underutilized and Neglected Crops 4: Proceedings of the First International Workshop on Hulled Wheats. Castelvecchio Pascoli, Tuscany, Italy. (Padulosi, S., Hammer K., and Heller, J., Eds.), 41-100.

Nishikawa, K. (1983). Species relationship of wheat and its putative ancestors as viewed from isozyme variation. Sixth International Wheat Genetics Symposium; Plant Germplasm Institute, Kyoto University. Kyoto, Japan. (Sakamoto, S. Eds), 59-63.

Nsabiyera, V., Bariana, H. S., Qureshi, N., Wong, D., Hayden, M. J., and Bansal, U. K. (2018). Characterisation and mapping of adult plant stripe rust resistance in wheat accession Aus27284. Theoretical and Applied Genetics, 131(7), 1459-1467. https://doi.org/10.1007/s00122-018-3090-x

Oliver, R. P. (2014). A reassessment of the risk of rust fungi developing resistance to fungicides. Pest Management Science, 70(11), 1641-1645. https://doi.org/10.1002/ps.3767

Olivera, P. D., Millet, E., Anikster, Y., and Steffenson, B. J. (2008). Genetics of resistance to wheat leaf rust, stem rust, and powdery mildew in *Aegilops sharonensis*. Phytopathology, 98(3), 353-358. https://doi.org/10.1094/PHYTO-98-3-0353

Olson, E. L., Brown-Guedira, G., Marshall, D., Stack, E., Bowden, R. L., Jin, Y., Rouse, M., and Pumphrey, M. O. (2010). Development of wheat lines having a small introgressed segment carrying stem rust resistance gene Sr22. Crop Science, 50(5), 1823-1830. https://doi.org/10.2135/cropsci2009.11.0652

Özkan, H., Brandolini, A., Torun, A., Altintas, S., Eker, Kilian, B., Braun, H.J., Salamini, F., and Cakmak, I. (2007). Natural variation and identification of microelements content in seeds of einkorn wheat (Triticum monococcum). Wheat production in stressed environments. Springer, Dordrecht. (Buck, H.T., Nisi, J.E., Salomón, N. Eds.), 12, 455-462. https://doi.org/10.1007/1-4020-5497-1_55

Özkan, H., Willcox, G., Graner, A., Salamini, F., and Kilian, B. (2011). Geographic distribution and domestication of wild emmer wheat (Triticum dicoccoides). Genetic Resources and Crop Evolution, 58(1), 11-53. https://doi.org/10.1007/s10722-010-9581-5

Paull, J. G., Pallotta, M. A., and Langridge, P. (1994). RFLP markers associated with *Sr22* and recombination between chromosome 7A of bread wheat and the diploid species *Triticum boeoticum*. Theoretical and Applied Genetics, 89(7), 1039-1045. https://doi.org/10.1007/BF00224536

Peng, J. H., Sun, D., and Nevo, E. (2011). Domestication evolution, genetics, and genomics in wheat. Molecular Breeding, 28(3), 281-301. https://doi.org/10.1007/s11032-011-9608-4

Periyannan, S. K., Bansal, U. K., Bariana, H. S., Pumphrey, M., and Lagudah, E. S. (2011). A robust molecular marker for the detection of shortened introgressed segment carrying the stem rust resistance gene *Sr22* in common wheat. *Theoretical and Applied Genetics*, *122*(1), 1-7. https://doi.org/10.1007/s00122-010-1417-3

Periyannan, S., Milne, R. J., Figueroa, M., Lagudah, E. S., and Dodds, P. N. (2017). An overview of genetic rust resistance: from broad to specific mechanisms. PLoS Pathogens, 13(7). https://doi.org/10.1371/journal.ppat.1006380

Peterson, R. F., Campbell, A. B., & Hannah, A. E. (1948). A diagrammatic scale for estimating rust intensity on leaves and stems of cereals. Canadian Journal of Research, 26(5), 496-500. https://doi.org/10.1139/cjr48c-033

Poland, J. A., Brown, P. J., Sorrells, M. E., and Jannink, J. L. (2012). Development of high-density genetic maps for barley and wheat using a novel two-enzyme genotyping-by-sequencing approach PLoS One 7(2). https://doi.org/10.1371/journal.pone.0032253

Prasad, P., Savadi, S., Bhardwaj, S. C., & Gupta, P. K. (2020). The progress of leaf rust research in wheat. Fungal Biology, 124(6), 537-550. https://doi.org/10.1016/j.funbio.2020.02.013

Pretorius, Z. A., Ayliffe, M., Bowden, R. L., Boyd, L. A., DePauw, R. M., Jin, Y., Knox, R., McIntosh, R., Park, R., Prins, R., and Lagudah, E. (2017). Advances in control of wheat rusts. Achieving Sustainable Cultivation of Wheat. (Langridge, P., Eds.), Volume 1, part 3, chapter 12.

Pretorius, Z. A., Singh, R. P., Wagoire, W. W., and Payne, T. S. (2000). Detection of virulence to wheat stem rust resistance gene *Sr31* in *Puccinia graminis*. f. sp. *tritici* in Uganda. Plant Disease, 84(2), 203. https://doi.org/10.1094/PDIS.2000.84.2.203B

Qayoum, A., and Line, R. F. (1985). High-temperature, adult-plant resistance to stripe rust of wheat. Phytopathology, 75(10), 1121-1125.

Qi, L. L., Pumphrey, M. O., Friebe, B., Zhang, P., Qian, C., Bowden, R. L., Rouse, M. N., Jin, Y., and Gill, B. S. (2011). A novel Robertsonian translocation event leads to transfer of a stem rust resistance gene (Sr52) effective against race Ug99 from *Dasypyrum villosum* into bread wheat. Theoretical and Applied Genetics, 123(1), 159-167. https://doi.org/10.1007/s00122-011-1574-z

Randhawa, H.S., Asif, M., Pozniak, C., Clarke, J.M., Graf, R.J., Fox, S.L., Humphreys, D.G., Knox, R.E., DePauw, R.M., Singh, A.K., Cuthbert, R.D., Hucl, P. and Spaner, D. (2013), Application of molecular markers to wheat breeding in Canada. Plant Breeding, 132: 458-471. https://doi.org/10.1111/pbr.12057

Robert, O., Abelard, C., and Dedryver, F. (1999). Identification of molecular markers for the detection of the yellow rust resistance gene Yr17 in wheat. Molecular Breeding, 5(2), 167-175. https://doi.org/10.1023/A:1009672021411

Roelfs, A. P. (1982). Effects of Barberry eradication. Plant Disease, 66(2), 177-181. https://doi.org/10.1094/PD-66-177

Roelfs, A. P. (1985). Wheat and rye stem rust. Diseases, Distribution, Epidemiology, and Control. (Roelfs, A. P., and Bushnell, W. R., Eds.). Academic Press, 3-37. https://doi.org/10.1016/B978-0-12-148402-6.50009-2

Roelfs, A. P. (1992). Rust diseases of wheat: concepts and methods of disease management. CIMMYT, Mexico, D.F. (Roelfs, A. P., Singh, R.P., Saari E.E., Eds.).

Roose-Amsaleg, C., Brygoo, Y., and Levis, C. (2002). Characterisation of a length polymorphism in the two intergenic spacers of ribosomal RNA in *Puccinia striiformis* f. sp. *tritici*, the causal agent of wheat yellow rust. Mycological Research, 106(8), 918-924. https://doi.org/10.1017/S0953756202006251

Rouse, M. N., and Jin, Y. (2011). Stem rust resistance in A-genome diploid relatives of wheat. Plant Disease, 95(8), 941-944. https://doi.org/10.1094/PDIS-04-10-0260

Salamini, F., Özkan, H., Brandolini, A., Schäfer-Pregl, R., & Martin, W. (2002). Genetics and geography of wild cereal domestication in the near east. Nature Reviews Genetics, 3(6), 429-441. https://doi.org/10.1038/nrg817

Samborski, D. J. (1985). Wheat leaf rust. Cereal rusts. Vol. I. (Roelfs, A. P., and Bushnell, W. R., Eds.), Academic Press, Orlando, 39–59.

Samsampour, D., Zanjani, B. M., Pallavi, J. K., Singh, A., Charpe, A., Gupta, S. K., and Prabhu, K. V. (2010). Identification of molecular markers linked to adult plant leaf rust resistance gene *Lr48* in wheat and detection of *Lr48* in the Thatcher near-isogenic line with gene *Lr25*. Euphytica, 174(3), 337-342. https://doi.org/10.1007/s10681-009-0114-2

Sax, K. (1922). Sterility in wheat hybrids. II. Chromosome behavior in partially sterile hybrids. Genetics, 7(6), 513.

Schnurbusch, T., Paillard, S., Schori, A., Messmer, M., Schachermayr, G., Winzeler, M., and Keller, B. (2004). Dissection of quantitative and durable leaf rust resistance in Swiss winter wheat reveals a major resistance QTL in the Lr34 chromosomal region. Theoretical and Applied Genetics, 108(3), 477-484. https://doi.org/10.1007/s00122-003-1444-4

Schwessinger, B., and Rathjen, J. P. (2017). Extraction of high molecular weight DNA from fungal rust spores for long read sequencing. Wheat rust diseases. (Periyannan, S., Eds). Methods in Molecular Biology, 1659, 49-57. https://doi.org/10.1007/978-1-4939-7249-4_5

Shewry, P. R. (2009). Wheat. Journal of Experimental Botany, 60(6), 1537-1553. https://doi.org/10.1093/jxb/erp058

Singh, K., Ghai, M., Garg, M., Chhuneja, P., Kaur, P., Schnurbusch, T., Keller, B., and Dhaliwal, H. S. (2007a). An integrated molecular linkage map of diploid wheat based on a *Triticum boeoticum*× *T. monococcum* RIL population. Theoretical and Applied Genetics, 115(3), 301-312. https://doi.org/10.1007/s00122-007-0543-z

Singh, R. P., Hodson, D. P., Jin, Y., Huerta-Espino, J., Kinyua, M. G., Wanyera, R., Njau, P., and Ward, R. W. (2006). Current status, likely migration and strategies to mitigate the threat to wheat production from race Ug99 (TTKS) of stem rust pathogen. CAB Reviews: Perspectives in Agriculture, Veterinary Science, Nutrition and Natural Resources, 1(54), 1-13. https://doi.org/10.1079/PAVSNNR20061054

Singh, R. P., Hodson, D. P., Jin, Y., Lagudah, E. S., Ayliffe, M. A., Bhavani, S., Rouse, M.N., Pretorius, Z.A., Szabo, L.J., Huerta-Espino, J., Basnet, B.R., and Hovmøller, M. S. (2015). Emergence and spread of new races of wheat stem rust fungus: continued threat to food security and prospects of genetic control. Phytopathology, 105(7), 872-884. https://doi.org/10.1094/PHYTO-01-15-0030-FI

Singh, R. P., Kinyua, M. G., Wanyera, R., Njau, P., Jin, Y., and Huerta-Espino, J. (2007b). Spread of a highly virulent race of Puccinia graminis tritici in Eastern Africa. Wheat Production in Stressed Environments, Springer, Dordrecht. (Buck, H. T., Nisi, E., Salomon, N., Eds.). Developments in Plant Breeding, 12, 51-57.

Singh, R. P., Nelson, J. C., and Sorrells, M. E. (2000). Mapping *Yr28* and other genes for resistance to stripe rust in wheat. Crop Science, 40(4), 1148-1155. https://doi.org/10.2135/cropsci2000.4041148x

Solh, M., Nazari, K., Tadesse, W., and Wellings, C. R. (2012, September). The growing threat of stripe rust worldwide. Borlaug Global Rust Initiative (BGRI) conference, Beijing, China, 1-4.

Soliman, A. S., Heyne, E. G., and Johnston, C. O. (1964). Genetic Analysis for leaf rust resistance in the eight differential varieties of wheat 1. Crop Science, 4(3), 246-248. https://doi.org/10.2135/cropsci1964.0011183X000400030002x

Soshnikova, E. A. (1990). Promising species of Triticum for the production of donors of resistance to stem rust of wheat. Nauchno-Tekhnicheskiĭ Byulleten'Vsesoyuznogo Ordena Lenina i Ordena Druzhby Narodov Nauchno-Issledovatel'skogo Instituta Rastenievodstva Imeni NI Vavilova, (197), 4-5.

Stakman, E. C., Stewart, D. M., and Loegering, W. Q. (1962). Identification of physiologic races of *Puccinia graminis* var. *tritici*. USDA, Washington, DC).

Stubbs, R. W., Prescott, J. M., Saari, E. E., & Dubin, H. J. (1986). Cereal disease methodology manual. El Batan, Mexico, CIMMYT.

Sunderwirth, S. D., and Roelfs, A. P. (1980). Greenhouse evaluation of the adult plant resistance of *Sr2* to wheat stem rust. Phytopathology, 70(7), 634-637.

Tanno, K., and Willcox, G. (2012). Distinguishing wild and domestic wheat and barley spikelets from early Holocene sites in the Near East. Vegetation History and Archaeobotany. 21, 107–115. https://doi.org/10.1007/s00334-011-0316-0

Todorovska, E., Christov, N., Slavov, S., Christova, P., and Vassilev, D. (2009). Biotic stress resistance in wheat—breeding and genomic selection implications. Biotechnology & Biotechnological Equipment, 23(4), 1417-1426. https://doi.org/10.2478/V10133-009-0006-6

Tonk, F., and Yüce, S. (2007). Ekmeklik Buğday İzmir 85 Çeşidinde ve Thatcher Yakın İzogenik Hatlarında Kahverengi Pas Dayanıklılık Geni Lr13'ün SSR Markörleriyle İncelenmesi. Ege Üniversitesi Ziraat Fakültesi Dergisi, 44(3), 13-25.

Vallega, V. (1979). Field performance of varieties of *Triticum monococcum*, *T. durum*, and *Hordeum vulgare* grown at two locations. Genetic Agriculture, 33, 363-370.

Van Slageren, M. W. (1994). Wild wheats: a monograph of *Aegilops* L. and *Amblyopyrum* (Jaub. & Spach) Eig (Poaceae). Wageningen: Agricultural University, 513.

Vanzetti, L. S., Campos, P., Demichelis, M., Lombardo, L. A., Aurelia, P. R., Vaschetto, L. M., Bainotti, C.T., and Helguera, M. (2011). Identification of leaf rust resistance genes in selected Argentinean bread wheat cultivars by gene postulation and molecular markers. Electronic Journal of Biotechnology, 14(3), 9-9.

Vavilov, N. I. (1957). World resources of cereals, grain, leguminous crops and flax and their utilization in plant breeding. Agroecological Survey of the Principal Field Crops. Moscow, Russia.

Watson, I. A. (1981). Wheat and its rust parasites in Australia. Wheat science-today and tomorrow. (Evans, L.T., and Peacock, W.J., Eds). Cambridge University Press, London, 129-147.

Wellings, C. R. (2011). Global status of stripe rust: a review of historical and current threats. Euphytica, 179(1), 129-141. https://doi.org/10.1007/s10681-011-0360-y

Wiese, M. V. (1985). Compendium of Wheat Diseases. The American Phytopathological Society, St. Paul, MN, USA, 39.

Wiese, M. V. (1987). Compendium of Wheat Diseases. The American Phytopathological Society, St. Paul, MN, USA, 1-124.

Wu, S. (2008). Molecular mapping of stem rust resistance genes in wheat [M Sc Thesis]. Kansas State University, Manhattan, KS, USA.

Xu, S. S., Dundas, I. S., Pumphrey, M. O., Jin, Y., Faris, J. D., Cai, X., Qi, L.L., Friebe, B.R., and Gill, B. S. (2008). Chromosome engineering to enhance utility of alien-derived stem rust resistance. Proceedings of the 11th International Wheat Genet Symposium, Sydney University Press, Sydney, Australia. (Appels, R., Eastwood, R., Lagudah, E., Langridge, P., Mackay, M., McIntye, L., Sharp, P., Eds.), 12–14.

Yang, H., Tao, Y., Zheng, Z., Li, C., Sweetingham, M. W., and Howieson, J. G. (2012). Application of next generation sequencing for rapid marker development in molecular plant breeding: a case study on anthracnose disease resistance in Lupinus angustifolius L. BMC Genomics, 13(1), 1-12. https://doi.org/10.1186/1471-2164-13-318

Yao, G., Zhang, J., Yang, L., Xu, H., Jiang, Y., Xiong, L., Zhang, Z., Ma, Z., and Sorrells, M. E. (2007). Genetic mapping of two powdery mildew resistance genes in einkorn (Triticum monococcum L.) accessions. Theoretical and Applied Genetics, 114(2), 351-358. https://doi.org/10.1007/s00122-006-0438-4

Young, N. D., and Tanksley, S. D. (1989). RFLP analysis of the size of chromosomal segments retained around the Tm-2 locus of tomato during backcross breeding. Theoretical and Applied Genetics, 77(3), 353-359. https://doi.org/10.1007/BF00305828

Yu, L. X., Abate, Z., Anderson, J. A., Bansal, U. K., Bariana, H. S., Bhavani, S., Dubcovsky, J., Lagudah, E. S., Liu, S., Sambasivam, P. K., Singh, R. P., and Sorrells, M. E. (2009). Developing and optimizing markers for stem rust resistance in wheat. Proceedings Oral Papers, 117.

Yu, L. X., Barbier, H., Rouse, M. N., Singh, S., Singh, R. P., Bhavani, S., Huerta-Espino, J., and Sorrells, M. E. (2014). A consensus map for Ug99 stem rust resistance loci in wheat. Theoretical and Applied Genetics, 127(7), 1561-1581. https://doi.org/10.1007/s00122-014-2326-7

Yürür, N. (1998). Serin iklim tahılları-I. Uludağ Üniversitesi Yayınları., Yayın, (7), 250.

Zadoks, J.C. (1963). Epidemiology of wheat rusts in Europe. FAO Plant Protection Bull, 13, 97–108.

Zaharieva, M., Ayana, N. G., Al Hakimi, A., Misra, S. C., and Monneveux, P. (2010). Cultivated emmer wheat (*Triticum dicoccon* Schrank), an old crop with promising future: a review. Genetic Resources and Crop Evolution, 57(6), 937-962. https://doi.org/10.1007/s10722-010-9572-6

Zaharieva, M., and Monneveux, P. (2014). Cultivated einkorn wheat (*Triticum monococcum* L. subsp. *monococcum*): the long life of a founder crop of agriculture. Genetic Resources and Crop Evolution, 61(3), 677-706. https://doi.org/10.1007/s10722-014-0084-7

Zhonghu, H. (2001). Chinese wheat production and the CIMMYT-China partnership. Research Highlights of the CIMMYT Wheat Program 1999-2000, 61-64.

Zhou, X. L., Wang, M. N., Chen, X. M., Lu, Y., Kang, Z. S., and Jing, J. X. (2014). Identification of Yr59 conferring high-temperature adult-plant resistance to stripe rust in wheat germplasm PI 178759. Theoretical and Applied Genetics, 127(4), 935-945. https://doi.org/10.1007/s00122-014-2269-z

Zohary, D., and Hopf, M. (2000). Domestication of plants in the Old World: The origin and spread of cultivated plants in West Asia, Europe, and the Nile Valley. Oxford University Press, 45-316.

Table 1.

List of 108 A-genome diploid wheats collected from different countries and evaluated for wheat rusts in this study.

#TA Number	Description	Origin
TA136	*T. monococcum* subsp. *monococcum*	Sweden
TA177	*T. monococcum* subsp. *aegilopoides*	Iraq
TA190	*T. monococcum* subsp. *aegilopoides*	Iran
TA249	*T. monococcum* subsp. *aegilopoides*	Iraq
TA250	*T. monococcum* subsp. *aegilopoides*	Iraq
TA252	*T. monococcum* subsp. *aegilopoides*	Iraq
TA261	*T. monococcum* subsp. *aegilopoides*	Turkey
TA278	*T. monococcum* subsp. *aegilopoides*	Iraq
TA284	*T. monococcum* subsp. *aegilopoides*	Iraq
TA285	*T. monococcum* subsp. *aegilopoides*	Iraq
TA299	*T. monococcum* subsp. *aegilopoides*	Iraq
TA306	*T. monococcum* subsp. *aegilopoides*	Iraq
TA309	*T. monococcum* subsp. *aegilopoides*	Iraq
TA316	*T. monococcum* subsp. *aegilopoides*	Iraq
TA346	*T. monococcum* subsp. *aegilopoides*	Iraq
TA362	*T. monococcum* subsp. *aegilopoides*	Iraq
TA366	*T. monococcum* subsp. *aegilopoides*	Iraq
TA394	*T. monococcum* subsp. *aegilopoides*	Iraq
TA396	*T. monococcum* subsp. *aegilopoides*	Iraq
TA408	*T. monococcum* subsp. *aegilopoides*	Iraq
TA412	*T. monococcum* subsp. *aegilopoides*	Iraq
TA438	*T. monococcum* subsp. *aegilopoides*	Iraq
TA443	*T. monococcum* subsp. *aegilopoides*	Iraq
TA447	*T. monococcum* subsp. *aegilopoides*	Iraq
TA466	*T. monococcum* subsp. *aegilopoides*	Iraq

TA473	*T. monococcum* subsp. *aegilopoides*	Iraq
TA479	*T. monococcum* subsp. *aegilopoides*	Iraq
TA488	*T. monococcum* subsp. *aegilopoides*	Iraq
TA502	*T. monococcum* subsp. *aegilopoides*	Iraq
TA526	*T. monococcum* subsp. *aegilopoides*	Turkey
TA534	*T. monococcum* subsp. *aegilopoides*	Turkey
TA544	*T. monococcum* subsp. *aegilopoides*	Turkey
TA580	*T. monococcum* subsp. *aegilopoides*	United Kingdom
TA585	*T. monococcum* subsp. *aegilopoides*	Turkey
TA590	*T. monococcum* subsp. *aegilopoides*	Turkey
TA593	*T. monococcum* subsp. *aegilopoides*	Turkey
TA632	*T. monococcum* subsp. *aegilopoides*	Turkey
TA647	*T. monococcum* subsp. *aegilopoides*	Turkey
TA661	*T. monococcum* subsp. *aegilopoides*	Turkey
TA686	*T. monococcum* subsp. *aegilopoides*	Turkey
TA709	*T. urartu*	Turkey
TA721	*T. urartu*	Turkey
TA724	*T. urartu*	Turkey
TA748	*T. monococcum* subsp. *aegilopoides*	Turkey
TA756	*T. monococcum* subsp. *aegilopoides*	Turkey
TA790	*T. urartu*	Lebanon
TA792	*T. urartu*	Lebanon
TA800	*T. urartu*	Lebanon
TA810	*T. urartu*	Turkey
TA827	*T. urartu* subsp. *binartulutriru*	Turkey
TA832	*T. urartu*	Turkey
TA834	*T. urartu*	Turkey
TA841	*T. urartu*	Turkey
TA850	*T. urartu* subsp. *spontaneorubrum*	Russian Federation
TA1212	*T. monococcum* subsp. *aegilopoides*	Iraq
TA1254	*T. monococcum* subsp. *aegilopoides*	Turkey

TA1266	*T. monococcum* subsp. *aegilopoides*	Turkey
TA1282	*T. urartu*	Lebanon
TA1313	*T. urartu*	Lebanon
TA1314	*T. urartu*	Lebanon
TA1315	*T. urartu*	Lebanon
TA2012	*T. monococcum* subsp. *aegilopoides*	Turkey
TA2022	*T. monococcum* subsp. *aegilopoides*	Turkey
TA2021	*T. monococcum* subsp. *aegilopoides*	Turkey
TA2025	*T. monococcum* subsp. *monococcum*	Turkey
TA2032	*T. monococcum* subsp. *monococcum*	Spain
TA2035	*T. monococcum* subsp. *monococcum*	Hungary
TA2716	*T. monococcum* subsp. *monococcum*	United Kingdom
TA2719	*T. monococcum* subsp. *monococcum*	Germany
TA2720	*T. monococcum* subsp. *monococcum*	Balkans
TA2723	*T. monococcum* subsp. *monococcum*	Germany
TA2724	*T. monococcum* subsp. *monococcum*	United Kingdom
TA10418	*T. monococcum* subsp. *monococcum*	Turkey
TA10546	*T. monococcum* subsp. *aegilopoides*	Serbia & Montenegro
TA10569	*T. monococcum* subsp. *monococcum*	Germany
TA10573	*T. monococcum* subsp. *aegilopoides*	Asia Minor
TA10574	*T. monococcum* subsp. *monococcum*	Belgium
TA10581	*T. monococcum* subsp. *monococcum*	Austria
TA10587	*T. monococcum* subsp. *monococcum*	Montenegro
TA10588	*T. monococcum* subsp. *monococcum*	Turkey
TA10593	*T. monococcum* subsp. *aegilopoides*	Turkey
TA10595	*T. monococcum* subsp. *aegilopoides*	Turkey
TA10603	*T. monococcum* subsp. *aegilopoides*	Turkey
TA10612	*T. monococcum* subsp. *monococcum*	Albania
TA10622	*T. monococcum* subsp. *monococcum*	Albania
TA10629	*T. monococcum* subsp. *monococcum*	Balkans
TA10630	*T. monococcum* subsp. *monococcum*	Unknown

TA10634	*T. monococcum* subsp. *monococcum*	Italy
TA10636	*T. monococcum* subsp. *monococcum*	Georgia
TA10642	*T. monococcum* subsp. *monococcum*	Unknown
TA10652	*T. monococcum* subsp. *monococcum*	Turkey
TA10873	*T. urartu*	Jordan
TA10876	*T. urartu*	Lebanon
TA10878	*T. urartu*	Iran
TA10879	*T. urartu*	Iraq
TA10884	*T. urartu*	Syrian Arab Republic
TA10887	*T. urartu*	Turkey
TA10888	*T. urartu*	Turkey
TA10889	*T. urartu*	Turkey
TA10891	*T. urartu*	Turkey
TA10896	*T. monococcum* subsp. *monococcum*	Italy
TA10900	*T. monococcum* subsp. *aegilopoides*	Iran
TA10902	*T. monococcum* subsp. *aegilopoides*	Iran
TA10904	*T. monococcum* subsp. *aegilopoides*	Iraq
TA10907	*T. monococcum* subsp. *aegilopoides*	Turkey
TA10909	*T. monococcum* subsp. *aegilopoides*	Turkey
TA10916	*T. monococcum* subsp. *aegilopoides*	Ukraine
TA11012	*T. monococcum* subsp. *aegilopoides*	Azerbaijan

Note. TA refers to *Triticum* accessions number at Wheat Genetics Resource Center Gene Bank, Kansas State University, Manhattan, Kansas, USA.

Table 2.

Disease reactions recorded here are the average infection types for two experiments with two replicates of each disease at the seedling stage.

		Stripe Rust				Leaf Rust			
		Exp 1		Exp 2		Exp 1		Exp 2	
TA Number	Description	Rep 1	Rep 2	Rep 1	Rep 2	Rep 1	Rep 2	Rep 1	Rep 2
TA 136	*T. monococcum* subsp. *monococcum*	3-	3-	1+	2-	;	;	;	;
TA 177	*T. monococcum* subsp. *aegilopoides*	3+	3	3	3+	3	3	NA	3
TA 190	*T. monococcum* subsp. *aegilopoides*	2+	2	3	2	1	1	2+	3-
TA 249	*T. monococcum* subsp. *aegilopoides*	3	3-	2+	3-	3	3	3	NA
TA 250	*T. monococcum* subsp. *aegilopoides*	NA	NA	3-	3	NA	NA	2+	3
TA 252	*T. monococcum* subsp. *aegilopoides*	3+	3+	3+	3+	3+	3	3	3

TA 261	*T. monococcum* subsp. *aegilopoides*	3	3	2+	3-	3	3+	3	3
TA 278	*T. monococcum* subsp. *aegilopoides*	NA	NA	3+	3+	NA	NA	3	3
TA 284	*T. monococcum* subsp. *aegilopoides*	3	3+	3	2-	3+	3+	3+	3
TA 285	*T. monococcum* subsp. *aegilopoides*	3	3-	2+	;	2+	3-	3	3
TA 299	*T. monococcum* subsp. *aegilopoides*	3+	3+	3	3	3	3	3	NA
TA 306	*T. monococcum* subsp. *aegilopoides*	3	3	3	3	2+	3	3	3
TA 309	*T. monococcum* subsp. *aegilopoides*	NA	NA	3	3	NA	NA	3+	3+
TA 316	*T. monococcum* subsp. *aegilopoides*	3-	2+	1-	1+	3	3-	2+	3
TA 346	*T. monococcum* subsp. *aegilopoides*	3	2	2+	3-	3	3	3	3
TA 362	*T. monococcum* subsp. *aegilopoides*	3	3	2+	2+	3+	3	3	3
TA 366	*T. monococcum* subsp. *aegilopoides*	NA	NA	1-	1+	NA	NA	3+	3+

TA 394	*T. monococcum* subsp. *aegilopoides*	2+	2	3+	3+	3+	3+	3	NA
TA 396	*T. monococcum* subsp. *aegilopoides*	2-	1+	1-	;	2+	2	NA	3
TA 408	*T. monococcum* subsp. *aegilopoides*	1+	1+	1	1-	2+	3	3	3
TA 412	*T. monococcum* subsp. *aegilopoides*	3+	3	3+	3	3	3	3	3
TA 438	*T. monococcum* subsp. *aegilopoides*	NA	NA	3	3	NA	NA	2+	3
TA 443	*T. monococcum* subsp. *aegilopoides*	NA	NA	3+	3+	NA	NA	3	3+
TA 447	*T. monococcum* subsp. *aegilopoides*	3+	3+	3	3+	3	3	2+	3
TA 466	*T. monococcum* subsp. *aegilopoides*	3	3	2+	1	2	2	2+	1+
TA 473	*T. monococcum* subsp. *aegilopoides*	3	3	3	3	4	3	3	3
TA 479	*T. monococcum* subsp. *aegilopoides*	NA	NA	3	3	NA	NA	3+	3+
TA 488	*T. monococcum* subsp. *aegilopoides*	NA	NA	1+	2	NA	NA	3	3+

TA 502	*T. monococcum* subsp. *aegilopoides*	3	3-	2+	3	3	3	NA	3
TA 526	*T. monococcum* subsp. *aegilopoides*	NA	NA	3	3	NA	NA	3+	3+
TA 534	*T. monococcum* subsp. *aegilopoides*	3	3-	2	1	2+	2	1+	1+
TA 544	*T. monococcum* subsp. *aegilopoides*	3+	3+	3+	3+	3	3-	3	3
TA 580	*T. monococcum* subsp. *aegilopoides*	1	;	1	1-	1	1	;	;
TA 585	*T. monococcum* subsp. *aegilopoides*	3+	2+	1+	2	2+	2+	3	3
TA 590	*T. monococcum* subsp. *aegilopoides*	NA	NA	1-	1+	NA	NA	3+	3
TA 593	*T. monococcum* subsp. *aegilopoides*	3+	3+	3	3	3	3-	3	3
TA 632	*T. monococcum* subsp. *aegilopoides*	NA	NA	1-	1-	NA	NA	3	3
TA 647	*T. monococcum* subsp. *aegilopoides*	NA	NA	2-	2-	NA	NA	1+	2
TA 661	*T. monococcum* subsp. *aegilopoides*	3	3	3-	3	3-	3	3	3

TA 686	*T. monococcum* subsp. *aegilopoides*	1-	1	1-	;	3-	3	3	3
TA 709	*T. urartu*	3+	3+	3+	3+	3+	3+	3	3
TA 721	*T. urartu*	3	3	3-	2	3	3	3	3
TA 724	*T. urartu*	3	3	3+	3+	3+	3	3	3
TA 748	*T. monococcum* subsp. *aegilopoides*	NA	NA	1+	2-	NA	NA	3	3
TA 756	*T. monococcum* subsp. *aegilopoides*	NA	NA	3	3	NA	NA	2+	3+
TA 790	*T. urartu*	NA	NA	2+	2	NA	NA	3+	3
TA 792	*T. urartu*	3+	3	3	3-	3	3	NA	3
TA 800	*T. urartu*	3+	3	3+	3+	3	3	3	3
TA 810	*T. urartu*	3	3+	3+	3	3	3+	3	NA
TA 827	*T. urartu* subsp. *binartulutriru*	3-	3-	3	3-	3+	3+	2+	3
TA 832	*T. urartu*	3	3+	3+	3+	3	3+	3	3
TA 834	*T. urartu*	NA	NA	3+	3+	NA	NA	3+	3+
TA 841	*T. urartu*	3	3	3	3	3	3	3	NA
TA 850	*T. urartu* subsp. *spontaneorubrum*	3	3+	3+	3+	3+	3+	3	3
TA 1212	*T. monococcum* subsp. *aegilopoides*	3+	NA	2+	3-	3	3	3	3

TA 1254	*T. monococcum* subsp. *aegilopoides*	NA	NA	3-	2+	NA	NA	3+	3+
TA 1266	*T. monococcum* subsp. *aegilopoides*	3-	3	3-	1-	3	3	3	3
TA 1282	*T. urartu*	3	3	2	2+	3	3	NA	NA
TA 1313	*T. urartu*	3+	3+	3+	3	2+	3-	3	3
TA 1314	*T. urartu*	3+	3	3+	3+	3	3	NA	NA
TA 1315	*T. urartu*	3	2+	NA	NA	2+	3-	NA	3
TA 2012	*T. monococcum* subsp. *aegilopoides*	3-	2+	1	2	2	2	2-	2+
TA 2021	*T. monococcum* subsp. *aegilopoides*	NA	NA	1-	1-	NA	NA	3+	3+
TA 2022	*T. monococcum* subsp. *aegilopoides*	2	1+	2+	NA	3	3-	3	NA
TA 2025	*T. monococcum* subsp. *monococcum*	2+	1+	1	1	;	;	;	NA
TA 2032	*T. monococcum* subsp. *monococcum*	NA	NA	1+	1+	NA	NA	;	;
TA 2035	*T. monococcum* subsp. *monococcum*	2+	2	2	2+	;	1	;	;
TA 2716	*T. monococcum* subsp. *monococcum*	3+	3+	3	2	1-	;	;	;

TA 2719	*T. monococcum* subsp. *monococcum*	3	3	2-	2-	1	1+	2	2-
TA 2720	*T. monococcum* subsp. *monococcum*	2	3-	2-	2+	1+	1	2	2+
TA 2723	*T. monococcum* subsp. *monococcum*	3+	3	2	1+	1-	;	1-	2+
TA 2724	*T. monococcum* subsp. *monococcum*	3	3	3	3-	1	1-	;	;
TA 10418	*T. monococcum* subsp. *monococcum*	2-	1	1-	;	;	;	;	;
TA 10546	*T. monococcum* subsp. *aegilopoides*	NA	NA	3	3	NA	NA	;	;
TA 10569	*T. monococcum* subsp. *monococcum*	2	1+	1-	1	1-	1-	1	1-
TA 10573	*T. monococcum* subsp. *aegilopoides*	3	3	3	3	2-	2	2+	2+
TA 10574	*T. monococcum* subsp. *monococcum*	1+	1	;	;	;	;	;	;
TA 10581	*T. monococcum* subsp. *monococcum*	NA	NA	1-	1-	NA	NA	;	;
TA 10587	*T. monococcum* subsp. *monococcum*	3	2+	3-	3-	1	1-	1+	1

TA 10588	*T. monococcum* subsp. *monococcum*	1	1-	1+	NA	;	;	NA	NA
TA 10593	*T. monococcum* subsp. *aegilopoides*	3	3	3	3+	3+	3+	3	3
TA 10595	*T. monococcum* subsp. *aegilopoides*	3+	3+	3+	3+	3	3	3	3
TA 10603	*T. monococcum* subsp. *aegilopoides*	3	3	NA	3	3+	3+	NA	NA
TA 10612	*T. monococcum* subsp. *monococcum*	NA	NA	3	3-	NA	NA	;	1-
TA 10622	*T. monococcum* subsp. *monococcum*	NA	NA	1+	2	NA	NA	;	1-
TA 10629	*T. monococcum* subsp. *monococcum*	3	3-	2	3-	1	1-	;	2+
TA 10630	*T. monococcum* subsp. *monococcum*	1	1	;	1-	1	1	3	;
TA 10634	*T. monococcum* subsp. *monococcum*	3+	3	3-	2+	1	1	;	;
TA 10636	*T. monococcum* subsp. *monococcum*	NA	NA	1-	1-	NA	NA	1	1
TA 10642	*T. monococcum* subsp. *monococcum*	1+	1-	;	;	;	;	;	;

TA 10652	*T. monococcum* subsp. *monococcum*	3	2+	3-	2+	1+	1+	1+	2-
TA 10873	*T. urartu*	NA	NA	3	3-	NA	NA	3	3
TA 10876	*T. urartu*	3-	3-	3	3	3+	3+	3	3
TA 10878	*T. urartu*	3+	3+	3	3	3+	3+	NA	NA
TA 10879	*T. urartu*	NA	NA	2-	2+	NA	NA	2+	3+
TA 10884	*T. urartu*	2+	3-	NA	3	3	3	NA	3-
TA 10887	*T. urartu*	3	3	3+	NA	3	3+	3	3
TA 10888	*T. urartu*	2+	2+	NA	2	3-	3	3	3-
TA 10889	*T. urartu*	3	3	3	3	3	3	3	3
TA 10891	*T. urartu*	3-	3	3-	3-	3	3	3	NA
TA 10896	*T. monococcum* subsp. *monococcum*	NA	NA	2+	3-	NA	NA	;	;
TA 10900	*T. monococcum* subsp. *aegilopoides*	2	2	3-	2+	3-	3	3	3
TA 10902	*T. monococcum* subsp. *aegilopoides*	3-	3-	1+	2-	3-	3	3	3
TA 10904	*T. monococcum* subsp. *aegilopoides*	3-	3-	3	3	3-	3	3	NA
TA 10907	*T. monococcum* subsp. *aegilopoides*	NA	NA	3-	3-	NA	NA	3	3+

TA 10909	*T. monococcum* subsp. *aegilopoides*	NA	NA	3	3	NA	NA	3	3+
TA 10916	*T. monococcum* subsp. *aegilopoides*	3	3	3-	3-	;	;	;	NA
TA 11012	*T. monococcum* subsp. *aegilopoides*	3	3	2	3	3	3	3	3-
Morocco	*T. aestivum* - Susceptible Check	3+	3+	3+	3+	4	4	3+	4
Avery	*T. aestivum* - Susceptible Check	NA	NA	3+	3+	NA	NA	;	0
Joe	*T. aestivum* - Resistant Check	NA	NA	3	3	NA	NA	1+	1+

Note. Stakman scale (0-4 infection type) was used for seedling evaluations and Resistant: from ; to 1+, Intermediate: from 2- to 2+, Table 2. Disease reactions recorded here are the average infection types for two experiments with two replicates of each disease.

Table 3.

ANOVA for stripe rust and leaf rust scores of 108 accessions evaluated at the seedling stage.

Stripe Rust					
	Source of variation	df	Sum of Squares	F-value	p-value
	Accession	78	1619.3684	24.5088	<.0001*
	Replication within experiment	2	8.5654	5.0558	0.0073
	Accession x Experiment	78	287.4259	4.3501	<.0001*
	Error	177	149.9346		
Leaf Rust					
	Source of variation	df	Sum of Squares	F-value	p-value
	Accession	74	2444.1078	46.8647	<.0001*
	Replication within exp	2	1.919	1.3615	0.2592
	Accession x Experiment	74	102.8732	1.9726	0.0002
	Error	164	115.581		

Note. Significant codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Table 4.

Disease reactions recorded here are the median infection types and coefficient of infection (CI) values for the greenhouse experiment with three replicates of each disease at the adult plant stage.

		Stripe Rust	**Leaf Rust**		**Stem Rust**	
TA Number	Description	Greenhouse Response	Greenhouse Response	CI	Greenhouse Response	CI
TA 136	*T. monococcum* subsp. *monococcum*	7	10MR	4	60S	60
TA 177	*T. monococcum* subsp. *aegilopoides*	2	1R	0.2	25S	25
TA 190	*T. monococcum* subsp. *aegilopoides*	4	20M	12	20M	12
TA 249	*T. monococcum* subsp. *aegilopoides*	2	5M	3	50MS	40
TA 252	*T. monococcum* subsp. *aegilopoides*	6	10M	6	30MS	24

TA 261	*T. monococcum* subsp. *aegilopoides*	2	5MR	2	10R	2
TA 284	*T. monococcum* subsp. *aegilopoides*	1	5MR	2	20M	12
TA 285	*T. monococcum* subsp. *aegilopoides*	1	1R	0.2	30M	18
TA 299	*T. monococcum* subsp. *aegilopoides*	7	5M	3	30M	18
TA 306	*T. monococcum* subsp. *aegilopoides*	1	20MR	8	20M	12
TA 316	*T. monococcum* subsp. *aegilopoides*	3	30M	18	50S	50
TA 346	*T. monococcum* subsp. *aegilopoides*	2	10M	6	15M	9
TA 362	*T. monococcum* subsp. *aegilopoides*	3	1M	0.6	NA	NA

TA 394	*T. monococcum* subsp. *aegilopoides*	1	10M	6	40S	40
TA 396	*T. monococcum* subsp. *aegilopoides*	3	10MR	4	15S	15
TA 408	*T. monococcum* subsp. *aegilopoides*	3	25MR	10	15S	15
TA 412	*T. monococcum* subsp. *aegilopoides*	4	10M	6	30S	30S
TA 447	*T. monococcum* subsp. *aegilopoides*	6	10MR	4	10M	6
TA 466	*T. monococcum* subsp. *aegilopoides*	3	5MR	2	20MS	16
TA 473	*T. monococcum* subsp. *aegilopoides*	3	1MS	0.8	50S	50
TA 502	*T. monococcum* subsp. *aegilopoides*	2	5M	3	15MR	6

TA 534	*T. monococcum* subsp. *aegilopoides*	2	20MR	8	10MR	4
TA 544	*T. monococcum* subsp. *aegilopoides*	5	5R	1	30MS	24
TA 580	*T. monococcum* subsp. *aegilopoides*	2	30MR	12	10M	6
TA 585	*T. monococcum* subsp. *aegilopoides*	2	10M	6	30M	18
TA 593	*T. monococcum* subsp. *aegilopoides*	2	10M	6	30M	18
TA 661	*T. monococcum* subsp. *aegilopoides*	6	20M	12	40S	40
TA 686	*T. monococcum* subsp. *aegilopoides*	1	10M	6	20MS	16
TA 709	*T. urartu*	8	20MS	16	60S	60
TA 721	*T. urartu*	3	10M	6	20M	12

TA 724	*T. urartu*	7	50S	50	50S	50
TA 792	*T. urartu*	4	20MS	16	50S	50
TA 800	*T. urartu*	7	60MS	48	40S	40
TA 810	*T. urartu*	6	10MS	8	40S	40
TA 827	*T. urartu* subsp. *binartulutriru*	2	25MS	20	40S	40
TA 832	*T. urartu*	7	20MS	16	30S	30
TA 841	*T. urartu*	3	20M	12	40S	40
TA 850	*T. urartu* subsp. *spontaneorubrum*	7	15S	15	30S	30
TA 1212	*T. monococcum* subsp. *aegilopoides*	1	20MS	16	30M	18
TA 1266	*T. monococcum* subsp. *aegilopoides*	3	20M	12	40S	40
TA 1282	*T. urartu*	6	20M	12	40S	40
TA 1313	*T. urartu*	7	15MR	6	50S	50

TA 1314	*T. urartu*	8	20MR	8	30S	30
TA 1315	*T. urartu*	4	10M	6	NA	NA
TA 2012	*T. monococcum* subsp. *aegilopoides*	1	20MR	8	10R	2
TA 2022	*T. monococcum* subsp. *aegilopoides*	2	10MS	8	30MS	24
TA 2025	*T. monococcum* subsp. *monococcum*	2	5R	1	20M	12
TA 2035	*T. monococcum* subsp. *monococcum*	6	1R	0.2	30MS	24
TA 2716	*T. monococcum* subsp. *monococcum*	5	10R	2	40S	40
TA 2719	*T. monococcum* subsp. *monococcum*	6	1R	0.2	10R	2
TA 2720	*T. monococcum* subsp. *monococcum*	4	1R	0.2	30S	30

TA 2723	*T. monococcum* subsp. *monococcum*	2	20MR	8	20MS	16
TA 2724	*T. monococcum* subsp. *monococcum*	8	20R	4	10M	6
TA 10418	*T. monococcum* subsp. *monococcum*	3	5R	1	20MS	16
TA 10569	*T. monococcum* subsp. *monococcum*	2	10MR	4	30S	30
TA 10573	*T. monococcum* subsp. *aegilopoides*	7	5M	3	10R	2
TA 10574	*T. monococcum* subsp. *monococcum*	3	5R	1	20MS	16
TA 10587	*T. monococcum* subsp. *monococcum*	6	50M	30	10MS	8
TA 10588	*T. monococcum* subsp. *monococcum*	2	20R	4	40S	40

TA 10593	*T. monococcum* subsp. *aegilopoides*	6	40S	40	20M	12
TA 10595	*T. monococcum* subsp. *aegilopoides*	6	20MS	16	40S	40
TA 10603	*T. monococcum* subsp. *aegilopoides*	5	50MS	40	50S	50
TA 10622	*T. monococcum* subsp. *monococcum*	3	10R	2	20MR	8
TA 10629	*T. monococcum* subsp. *monococcum*	6	30R	6	20R	4
TA 10630	*T. monococcum* subsp. *monococcum*	2	1R	0.2	20S	20
TA 10634	*T. monococcum* subsp. *monococcum*	3	1R	0.2	30MS	24
TA 10642	*T. monococcum* subsp. *monococcum*	3	5R	1	25MS	20

TA 10652	*T. monococcum* subsp. *monococcum*	2	20MR	8	20MS	16
TA 10876	*T. urartu*	3	20MS	16	50S	50
TA 10878	*T. urartu*	5	30S	30	80S	80
TA 10884	*T. urartu*	3	10M	6	50S	50
TA 10887	*T. urartu*	6	10S	10	50S	50
TA 10888	*T. urartu*	2	20M	12	10M	6
TA 10889	*T. urartu*	2	15MR	6	40S	40
TA 10891	*T. urartu*	6	10MS	8	50S	50
TA 10900	*T. monococcum* subsp. *aegilopoides*	2	15MS	12	10MS	8
TA 10902	*T. monococcum* subsp. *aegilopoides*	3	20M	12	15MR	6
TA 10904	*T. monococcum* subsp. *aegilopoides*	2	1M	0.6	20M	12

TA 10916	*T. monococcum* subsp. *aegilopoides*	3	10MR	4	15R	3
TA 11012	*T. monococcum* subsp. *aegilopoides*	5	10M	6	20MS	16
Morocco	*T. aestivum* – Susceptible Check	9	40S	40	60S	60
Joe	*T. aestivum* – Resistant Check	6	30MR	12	NA	NA

Note. McNeal scale (0-9 infection type) was used for adult plant evaluations of stripe rust in the greenhouse and Resistant: from 0 to 3, Intermediate: from 4 to 6, Susceptible: from 7 to 9. Cobb scale was used for adult plant evaluations of leaf rust and stem rust in the greenhouse and R: Resistant, MR: Moderately Resistant, M: Moderate, MS: Moderately Susceptible, S: Susceptible. CI: Coefficient of infection.

Table 5.

ANOVA for stripe rust, leaf rust and stem rust scores of 80 accessions evaluated at the adult plant stage in the greenhouse conditions.

Stripe Rust			Resistance Response						
	Source of variation	df	Sum of Squares	F-value	p-value				
	Accession	79	1586.605	14.2219	<.0001*				
	Replication	2	11.6279	4.1171	0.017				
	Score-Date	1	0.2273	0.1609	0.6885				
	Error	388	547.9176						
Leaf Rust		Severity				Resistance Response			
	Source	df	Sum of Squares	F-value	p-value	df	Sum of Squares	F-value	p-value
	Accession	79	41170.07	5.0662	<.0001*	79	494.98616	9.5238	<.0001*
	Replication	2	2023.852	9.8373	<.0001*	2	2.86363	2.1764	0.1149
	Score-Date	1	1943.216	18.8906	<.0001*	1	1.3174	2.0025	0.1579
	Error	368	37854.953			368	242.10462		

Stem Rust		Severity				Resistance Response			
	Source	df	Sum of Squares	F-value	p-value	df	Sum of Squares	F-value	p-value
	Accession	77	38868.171	3.7353	<.0001*	77	432.35239	12.6468	<.0001*
	Replication	1	18.344	0.1357	0.7129	1	0.02797	0.063	0.8021
	Score-Date	1	519.733	3.8459	0.0512	1	0.1272	0.2865	0.593
	Error	211	28514.285			211	93.68037		

Note. Significant codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Table 6.

Disease reactions recorded here are the median infection types and coefficient of infection (CI) values for two field experiments with three replicates of each disease at the adult plant stage.

		Stripe Rust				Leaf Rust				Stem Rust			
		2020		2021		2020		2021		2020		2021	
TA Number	Description	Field Score	CI	Field Score	CI	Field Score	CI	Field Score	CI	Field Score	CI	Field Score	CI
TA 136	*T. monococcum* subsp. *monococcum*	20M	12	15MR	6	10MR	4	15MR	6	15S	15	1MS	0.8
TA 177	*T. monococcum* subsp. *aegilopoides*	25M	15	15M	9	20MR	8	20M	12	20MS	16	30S	30
TA 190	*T. monococcum* subsp. *aegilopoides*	20M	12	15MR	6	20MR	8	20MR	8	20MS	16	5MS	4
TA 249	*T. monococcum* subsp. *aegilopoides*	15MR	6	10MR	4	20MR	8	20MR	8	15M	9	15MS	12

TA 250	*T. monococcum* subsp. *aegilopoides*	NA	NA	5R	1	NA	NA	20MR	8	NA	NA	10MR	4
TA 252	*T. monococcum* subsp. *aegilopoides*	25M	15	10MR	4	10MR	4	20MR	8	10M	6	10MR	4
TA 261	*T. monococcum* subsp. *aegilopoides*	20M	12	10MR	4	20MR	8	20M	12	10MR	4	5MR	2
TA 278	*T. monococcum* subsp. *aegilopoides*	NA	NA	30MS	24	NA	NA	20M	12	NA	NA	30S	30
TA 284	*T. monococcum* subsp. *aegilopoides*	15M	9	10M	6	30M	18	15M	9	20M	12	50S	50
TA 285	*T. monococcum* subsp. *aegilopoides*	20M	12	5MR	2	20MR	8	15MR	6	20MS	16	10MS	8
TA 299	*T. monococcum* subsp. *aegilopoides*	30M	18	20M	12	20MR	8	15MR	6	20M	12	15S	15
TA 306	*T. monococcum* subsp. *aegilopoides*	15MR	6	10MR	4	15MR	6	10M	6	15M	9	25S	25

TA 309	*T. monococcum* subsp. *aegilopoides*	NA	NA	10MR	4	NA	NA	15M	9	NA	NA	10M	6
TA 316	*T. monococcum* subsp. *aegilopoides*	20MR	8	15MR	6	20MR	8	20M	12	30MS	24	30S	30
TA 346	*T. monococcum* subsp. *aegilopoides*	20M	12	15M	9	20MR	8	20M	12	20M	12	5M	3
TA 362	*T. monococcum* subsp. *aegilopoides*	20M	12	15MR	6	30MR	12	15M	9	30MS	24	5MS	4
TA 366	*T. monococcum* subsp. *aegilopoides*	NA	NA	15MR	6	NA	NA	20M	12	NA	NA	10M	6
TA 394	*T. monococcum* subsp. *aegilopoides*	20M	12	10MR	4	20M	12	15M	9	30MS	24	30S	30
TA 396	*T. monococcum* subsp. *aegilopoides*	15M	9	10M	6	20MR	8	15M	9	20MS	16	5MS	4
TA 408	*T. monococcum* subsp. *aegilopoides*	20M	12	10MR	4	20M	12	20MR	8	10MS	8	5M	3

TA 412	*T. monococcum* subsp. *aegilopoides*	15MR	6	10MR	4	25M	15	20M	12	10MS	8	5M	3
TA 438	*T. monococcum* subsp. *aegilopoides*	NA	NA	20MR	8	NA	NA	20M	12	NA	NA	10M	6
TA 443	*T. monococcum* subsp. *aegilopoides*	NA	NA	15MR	6	NA	NA	20M	12	NA	NA	10MS	8
TA 447	*T. monococcum* subsp. *aegilopoides*	25M	15	25M	15	20MR	8	15MR	6	20MS	16	10MS	8
TA 466	*T. monococcum* subsp. *aegilopoides*	15M	9	15M	9	30MR	12	20M	12	20MS	16	10MS	8
TA 473	*T. monococcum* subsp. *aegilopoides*	10MR	4	5MR	2	10MR	4	15M	9	30MS	24	10M	6
TA 479	*T. monococcum* subsp. *aegilopoides*	NA	NA	15MS	12	NA	NA	20M	12	NA	NA	15MS	12
TA 488	*T. monococcum* subsp. *aegilopoides*	NA	NA	15M	9	NA	NA	20M	12	NA	NA	30S	30

TA 502	*T. monococcum* subsp. *aegilopoides*	20M	12	15MR	6	20MR	8	15MR	6	15MS	12	10MS	8
TA 526	*T. monococcum* subsp. *aegilopoides*	NA	NA	15M	9	NA	NA	20M	12	NA	NA	10M	6
TA 534	*T. monococcum* subsp. *aegilopoides*	20MR	8	20MR	8	10MR	4	20MR	8	20MS	16	10MS	8
TA 544	*T. monococcum* subsp. *aegilopoides*	10MR	4	10M	6	10MR	4	15M	9	15MR	6	10MS	8
TA 580	*T. monococcum* subsp. *aegilopoides*	20MR	8	5MR	2	10R	2	10MR	4	25MS	20	10M	6
TA 585	*T. monococcum* subsp. *aegilopoides*	10MR	4	20MR	8	20MR	8	20M	12	15M	9	5MS	4
TA 590	*T. monococcum* subsp. *aegilopoides*	NA	NA	30M	18	NA	NA	20M	12	NA	NA	5M	3
TA 593	*T. monococcum* subsp. *aegilopoides*	20M	12	10MR	4	30MR	12	20M	12	20MS	16	10M	6

TA 632	*T. monococcum* subsp. *aegilopoides*	NA	NA	25MR	10	NA	NA	15M	9	NA	NA	5M	3
TA 647	*T. monococcum* subsp. *aegilopoides*	NA	NA	25M	15	NA	NA	20M	12	NA	NA	10M	6
TA 661	*T. monococcum* subsp. *aegilopoides*	30M	18	25M	15	20MR	8	20M	12	20MS	16	20MS	16
TA 686	*T. monococcum* subsp. *aegilopoides*	15MR	6	10MR	4	25M	15	10M	6	15MS	12	15MS	12
TA 709	*T. urartu*	15MR	6	40MS	32	20MS	16	25M	15	30MS	24	40S	40
TA 721	*T. urartu*	15MR	6	10MR	4	25M	15	25M	15	20MS	16	10M	6
TA 724	*T. urartu*	10MR	4	20M	12	20MS	16	15M	9	20MS	16	40S	40
TA 748	*T. monococcum* subsp. *aegilopoides*	NA	NA	20M	12	NA	NA	20M	12	NA	NA	10M	6
TA 756	*T. monococcum* subsp. *aegilopoides*	NA	NA	15M	9	NA	NA	20M	12	NA	NA	20M	12
TA 790	*T. urartu*	NA	NA	20M	12	NA	NA	15M	9	NA	NA	30S	30

TA 792	*T. urartu*	10MR	4	5MR	2	15MR	6	20M	12	30S	30	20MS	16
TA 800	*T. urartu*	20M	12	20M	12	20MR	8	15M	9	30MS	24	20S	20
TA 810	*T. urartu*	15MR	6	30M	18	20MS	16	20M	12	30MS	24	25S	25
TA 827	*T. urartu* subsp. *binartulutriru*	5R	1	5R	1	20MS	16	20MS	16	15MS	12	20MS	16
TA 832	*T. urartu*	10M	6	25M	15	20MS	16	10M	6	30MS	24	40S	40
TA 834	*T. urartu*	NA	NA	30MS	24	NA	NA	20M	12	NA	NA	25MS	20
TA 841	*T. urartu*	10MR	4	25MR	10	20M	12	20M	12	30MS	24	25S	25
TA 850	*T. urartu* subsp. *spontaneorubrum*	10MS	8	20MS	16	30MS	24	40MS	32	20MS	16	10M	6
TA 1212	*T. monococcum* subsp. *aegilopoides*	15M	9	10R	2	20MR	8	10M	6	20M	12	10M	6
TA 1254	*T. monococcum* subsp. *aegilopoides*	NA	NA	15MR	6	NA	NA	20M	12	NA	NA	15M	9
TA 1266	*T. monococcum* subsp. *aegilopoides*	10M	6	10MR	4	15MR	6	15M	9	25MS	20	20S	20

TA 1282	*T. urartu*	5R	1	15MR	6	15MR	6	15M	9	20MS	16	50S	50
TA 1313	*T. urartu*	20M	12	20M	12	20M	12	15MR	6	20MS	16	50S	50
TA 1314	*T. urartu*	10MR	4	30M	18	15MS	12	20M	12	25MS	20	40S	40
TA 1315	*T. urartu*	15MR	6	20MR	8	30MR	12	15M	9	20MS	16	40S	40
TA 2012	*T. monococcum* subsp. *aegilopoides*	15MR	6	5MR	2	20MR	8	20MR	8	10MR	4	5MR	2
TA 2021	*T. monococcum* subsp. *aegilopoides*	NA	NA	25M	15	NA	NA	20M	12	NA	NA	10MR	4
TA 2022	*T. monococcum* subsp. *aegilopoides*	20M	12	20M	12	20MR	8	15M	9	10M	6	15M	9
TA 2025	*T. monococcum* subsp. *monococcum*	25M	15	10MR	4	20MR	8	20MR	8	10MS	8	10MR	4
TA 2032	*T. monococcum* subsp. *monococcum*	NA	NA	20MR	8	NA	NA	20MR	8	NA	NA	20MR	8
TA 2035	*T. monococcum* subsp. *monococcum*	20M	12	10MR	4	20MR	8	20M	12	15MS	12	5M	3

TA 2716	*T. monococcum* subsp. *monococcum*	10MR	4	15M	9	10MR	4	20MR	8	25MS	20	10MS	8
TA 2719	*T. monococcum* subsp. *monococcum*	5R	1	20MR	8	20MR	8	15MR	6	15MR	6	5R	1
TA 2720	*T. monococcum* subsp. *monococcum*	30M	18	10MR	4	30M	18	10M	6	20S	20	5M	3
TA 2723	*T. monococcum* subsp. *monococcum*	30M	18	10MR	4	20M	12	15MR	6	25MS	20	5MS	4
TA 2724	*T. monococcum* subsp. *monococcum*	30M	18	10MR	4	15MR	6	15MR	6	30MS	24	10MS	8
TA 10418	*T. monococcum* subsp. *monococcum*	20MR	8	10MR	4	20MR	8	20MR	8	10MS	8	10M	6
TA 10546	*T. monococcum* subsp. *aegilopoides*	NA	NA	15MR	6	NA	NA	20MR	8	NA	NA	5M	3
TA 10569	*T. monococcum* subsp. *monococcum*	15MR	6	10MR	4	25MR	10	20M	12	40MS	32	20S	20

TA 10573	*T. monococcum* subsp. *aegilopoides*	25M	15	5MR	2	15MR	6	20M	12	10MR	4	5M	3
TA 10574	*T. monococcum* subsp. *monococcum*	15MR	6	5R	1	10R	2	15MR	6	20MS	16	10S	10
TA 10581	*T. monococcum* subsp. *monococcum*	NA	NA	15MR	6	NA	NA	20MR	8	NA	NA	15MR	6
TA 10587	*T. monococcum* subsp. *monococcum*	10MR	4	5MR	2	10MR	4	15MR	6	20MS	16	5M	3
TA 10588	*T. monococcum* subsp. *monococcum*	20M	12	1R	0.2	15MR	6	15M	9	10MS	8	10MR	4
TA 10593	*T. monococcum* subsp. *aegilopoides*	15M	9	10MR	4	30M	18	25M	15	20MS	16	20M	12
TA 10595	*T. monococcum* subsp. *aegilopoides*	15M	9	10MR	4	30MS	24	20MS	16	30S	30	20S	20
TA 10603	*T. monococcum* subsp. *aegilopoides*	10MR	4	10MR	4	30MS	24	15M	9	25MS	20	15MS	12

TA 10612	*T. monococcum* subsp. *monococcum*	NA	NA	10R	2	NA	NA	20MR	8	NA	NA	10MR	4
TA 10622	*T. monococcum* subsp. *monococcum*	NA	NA	5MR	2	NA	NA	15M	9	NA	NA	5MR	2
TA 10629	*T. monococcum* subsp. *monococcum*	20M	12	20MR	8	20MR	8	20M	12	15MR	6	10MR	4
TA 10630	*T. monococcum* subsp. *monococcum*	15MR	6	5MR	2	10R	2	20MR	8	25MS	20	15S	15
TA 10634	*T. monococcum* subsp. *monococcum*	20M	12	10MR	4	20MR	8	20MR	8	20MS	16	5MS	4
TA 10636	*T. monococcum* subsp. *monococcum*	NA	NA	15M	9	NA	NA	15M	9	NA	NA	20S	20
TA 10642	*T. monococcum* subsp. *monococcum*	10MR	4	5R	1	10MR	4	20MR	8	20S	20	5MS	4
TA 10652	*T. monococcum* subsp. *monococcum*	20M	12	5MR	2	30MR	12	25M	15	15MR	6	10MR	4

TA 10873	*T. urartu*	NA	NA	10MR	4	NA	NA	15M	9	NA	NA	NA	NA
TA 10876	*T. urartu*	5R	1	10MR	4	25MR	10	20M	12	20MS	16	50S	50
TA 10878	*T. urartu*	10MR	4	25M	15	40MS	32	40MS	32	20MS	16	25S	25
TA 10879	*T. urartu*	NA	NA	5MR	2	NA	NA	20M	12	NA	NA	25MS	20
TA 10884	*T. urartu*	15M	9	5R	1	10M	6	20M	12	30MS	24	25S	25
TA 10887	*T. urartu*	20M	12	5MR	2	15MR	6	15MR	6	25MS	20	15S	15
TA 10888	*T. urartu*	30M	18	5R	1	15M	9	15M	9	10MR	4	5MR	2
TA 10889	*T. urartu*	15MR	6	5MR	2	10MR	4	15MR	6	20MS	16	20MS	16
TA 10891	*T. urartu*	10MR	4	5R	1	15MR	6	20M	12	40S	40	30S	30
TA 10896	*T. monococcum* subsp. *monococcum*	NA	NA	25M	15	NA	NA	20MR	8	NA	NA	10M	6
TA 10900	*T. monococcum* subsp. *aegilopoides*	10MR	4	10MR	4	10MR	4	20M	12	20MS	16	5MS	4
TA 10902	*T. monococcum* subsp. *aegilopoides*	5MR	2	30M	18	20MR	8	20M	12	20M	12	15M	9

TA 10904	*T. monococcum* subsp. *aegilopoides*	20M	12	15M	9	15MR	6	20M	12	30MS	24	10S	10
TA 10907	*T. monococcum* subsp. *aegilopoides*	NA	NA	25MR	10	NA	NA	20M	12	NA	NA	10MS	8
TA 10909	*T. monococcum* subsp. *aegilopoides*	NA	NA	5R	1	NA	NA	20MR	8	NA	NA	NA	NA
TA 10916	*T. monococcum* subsp. *aegilopoides*	5R	1	15MR	6	10MR	4	15M	9	10MR	4	10MR	4
TA 11012	*T. monococcum* subsp. *aegilopoides*	10MR	4	10MR	4	10MR	4	15MR	6	20MS	16	10MS	8
Morocco	*T. aestivum* - Susceptible Check	60S	60	NA	NA	100S	100	NA	NA	60S	60	NA	NA
Avery	*T. aestivum* - Susceptible Check	NA	NA	70S	70	NA	NA	60S	60	NA	NA	50S	50
King Bird	*T. aestivum* - Susceptible Check	15MR	6	NA	NA	15MR	6	NA	NA	10MR	4	NA	NA

Joe	*T. aestivum* - Resistant Check	NA	NA	20MR	8	NA	NA	15M	9	NA	NA	10MR	4

Note. Cobb scale was used for adult plant evaluations in the field and R: Resistant, MR: Moderately Resistant, M: Moderate, MS: Moderately Susceptible, S: Susceptible. CI: Coefficient of infection.

Table 7.

ANOVA for stripe rust, leaf rust, and stem rust scores of 108 accessions evaluated at the adult plant stage in the field conditions during 2020 and 2021.

Stripe Rust		Severity				Resistance Response			
	Source of variation	df	Sum of Squares	F-value	p-value	df	Sum of Squares	F-value	p-value
	Accession	79	18690.456	5.1415	<.0001*	79	170.78845	4.9915	<.0001*
	Accession x Year	79	16906.462	4.6507	<.0001*	79	141.28507	4.1292	<.0001*
	Replication within year	4	3376.431	18.3439	<.0001*	4	10.52057	6.0726	<.0001*
	Score-Date	1	103.857	2.257	0.1334	1	2.51751	5.8126	0.0161
	Eror	867	88691.877			867	375.50995		cc

Leaf Rust		Severity				Resistance Response			
	Source of variation	df	Sum of Squares	F-value	p-value	df	Sum of Squares	F-value	p-value
	Accession	79	13786.401	8.439	<.0001*	79	250.20394	14.6654	<.0001*
	Accession x Year	79	6945.285	4.2514	<.0001*	79	92.58646	5.4268	<.0001*
	Replication within year	4	2766.483	33.4453	<.0001*	4	4.7811	5.5347	0.0002
	Score-Date	1	3660.024	176.9911	<.0001*	1	6.47204	29.9687	<.0001*
	Error	899	18590.555			899	194.14788		

Stem Rust		Severity				Resistance Response			
	Source of variation	df	Sum of Squares	F-value	p-value	df	Sum of Squares	F-value	p-value
	Accession	79	62769.095	19.1309	<.0001*	79	665.08443	18.0798	<.0001*
	Accession x Year	79	29872.547	9.1046	<.0001*	79	151.7676	4.1257	<.0001*
	Replication within year	4	2392.794	14.4033	<.0001*	4	23.12963	12.418	<.0001*
	Score-Date	1	4181.389	100.6787	<.0001*	1	36.02668	77.369	<.0001*
	Error	871	36174.37			871	405.5787		

Note. Significant codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' '

Figure 1.

Pictures show the A-genome diploid relatives of wheat at different adult plant stages under greenhouse conditions.

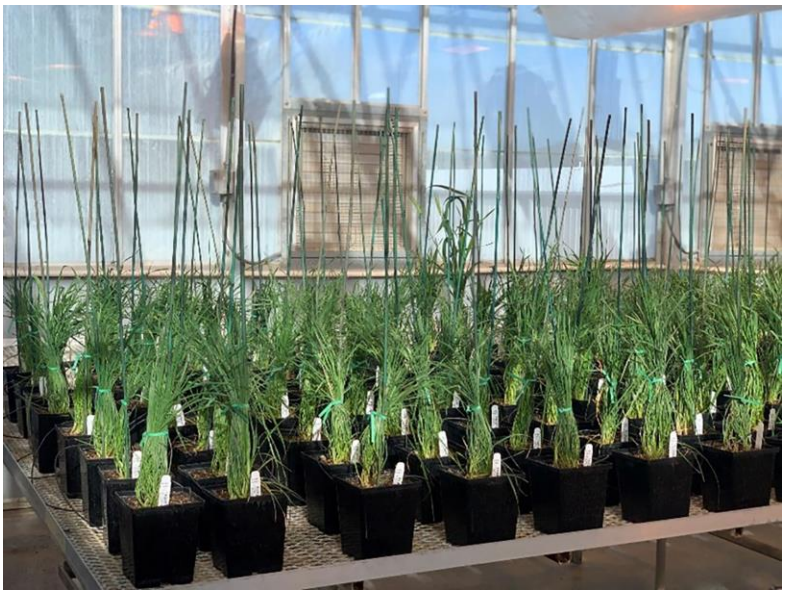


Figure 2.

Examples of stripe rust (A), leaf rust (B), and stem rust (C) nurseries in Rocky Ford (leaf rust and stem rust) and Rossville Experiment Stations (stripe rust), 2021.

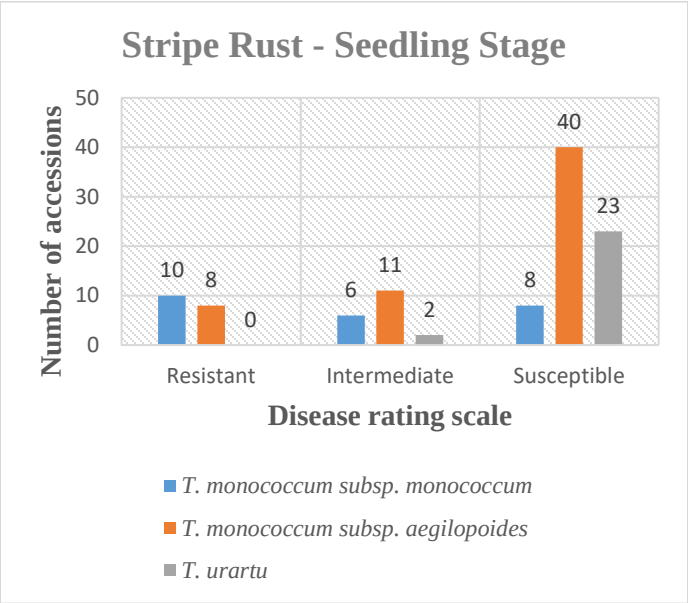
A)

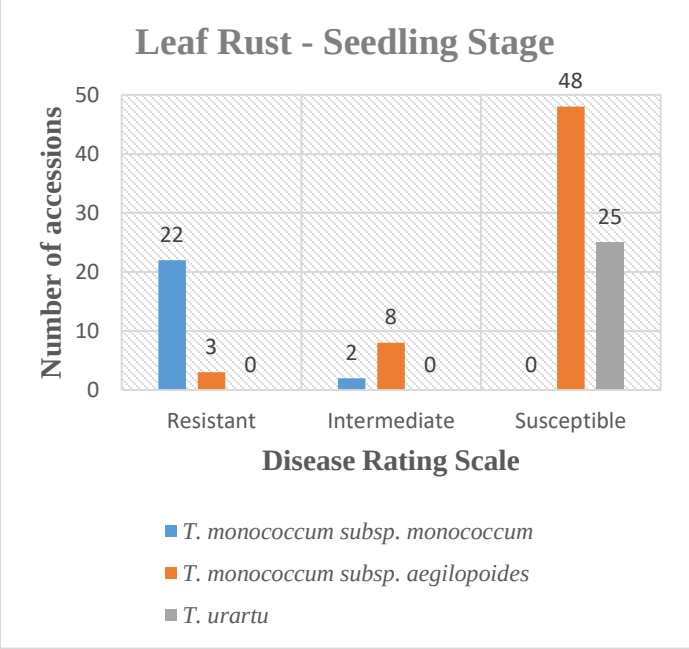
B)

C)

Figure 3.

Distribution of infection types of 108 accessions evaluated for seedling resistance stripe rust and leaf rust under greenhouse conditions.

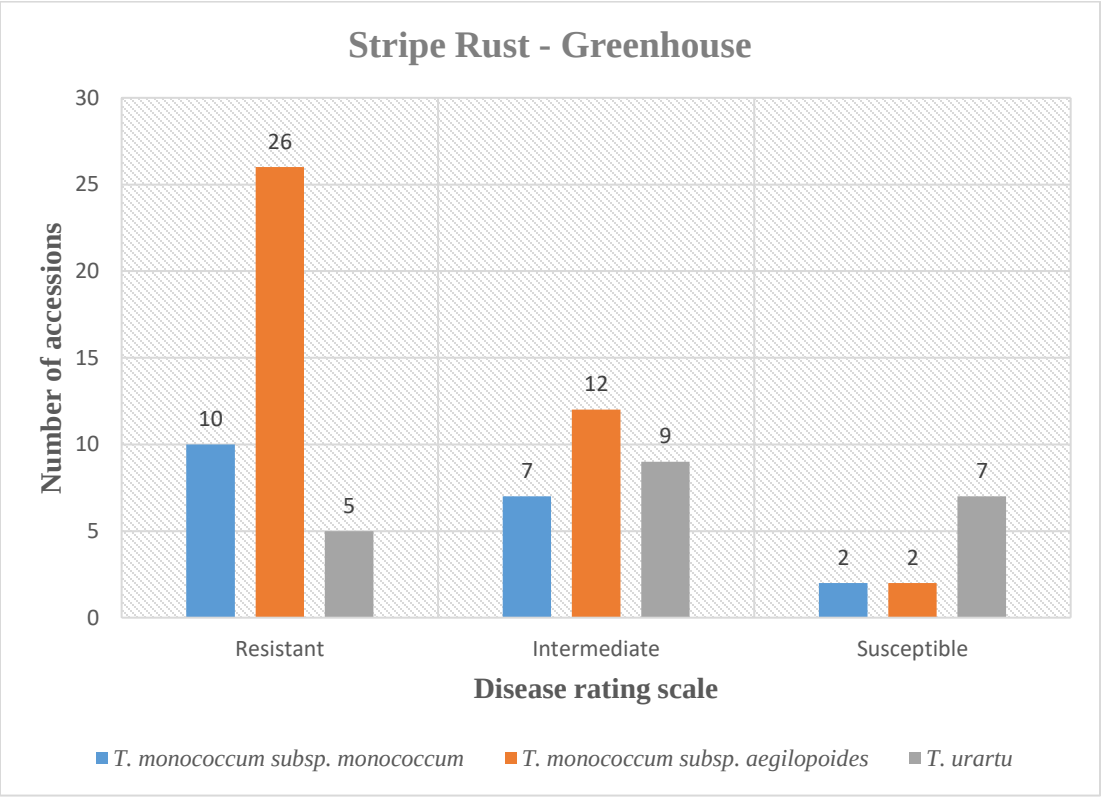




Note. Stakman scale (0-4 infection type) was used for seedling evaluations and Resistant: from ; to 1+, Intermediate: from 2- to 2+, Susceptible: from 3- to 4.

Figure 4.

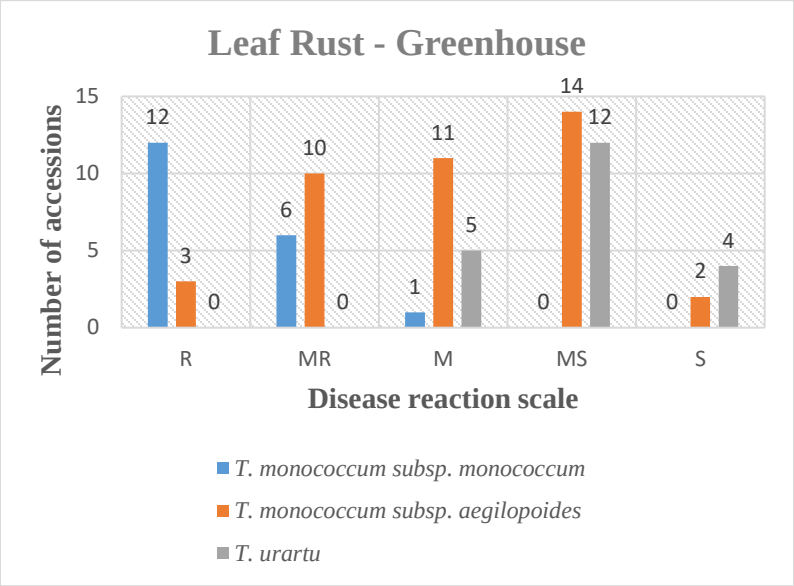
Distribution of infection types of 80 accessions evaluated for stripe rust at the adult plant stage under greenhouse conditions.

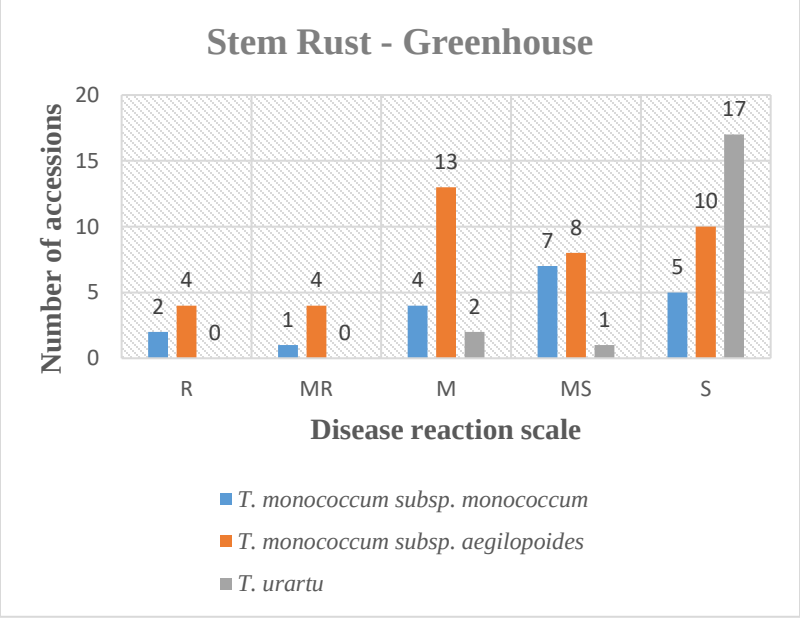


Note. McNeal scale (0-9 infection type) was used for adult plant evaluations in the greenhouse and Resistant: from 0 to 3, Intermediate: from 4 to 6, Susceptible: from 7 to 9.

Figure 5.

Frequency distribution of 80 accessions evaluated for leaf rust and stem rust at the adult plant stage under greenhouse conditions.

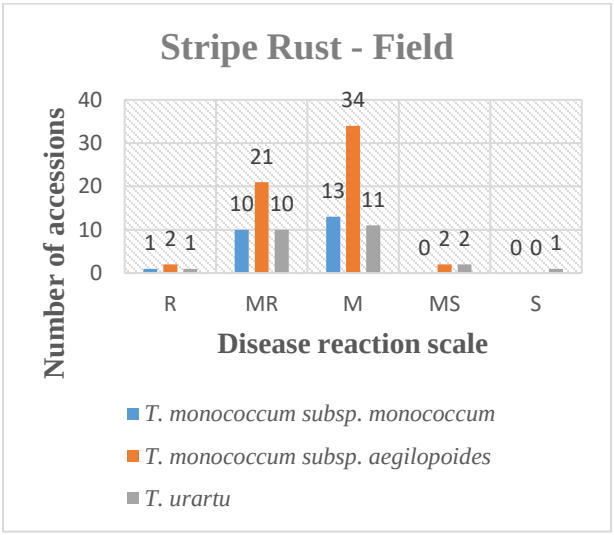


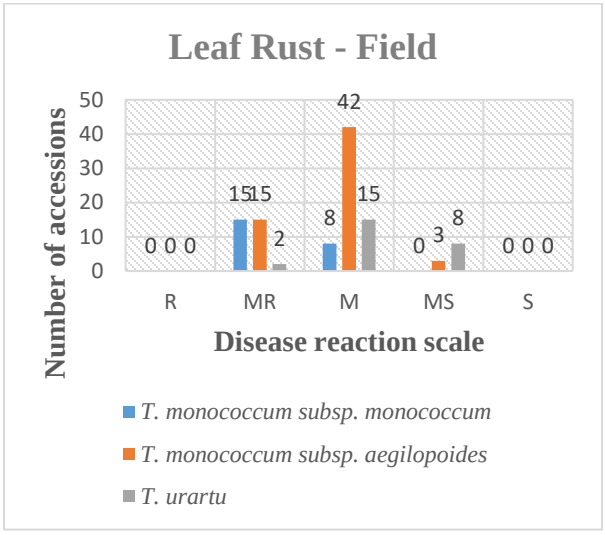


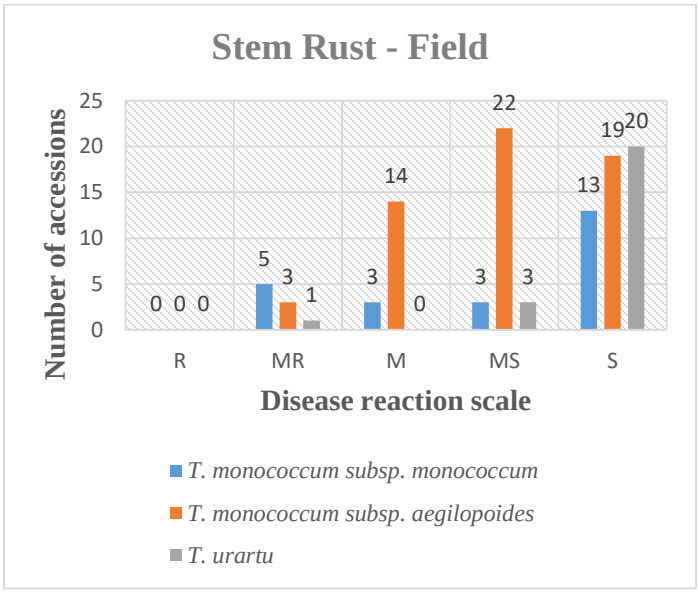
Note. Cobb scale was used for adult plant evaluations in the greenhouse and R: Resistant, MR: Moderately Resistant, M: Moderate, MS: Moderately Susceptible, S: Susceptible.

Figure 6.

Frequency distribution of 108 accessions evaluated for stripe rust, leaf rust, and stem rust at the adult plant stage under field conditions.



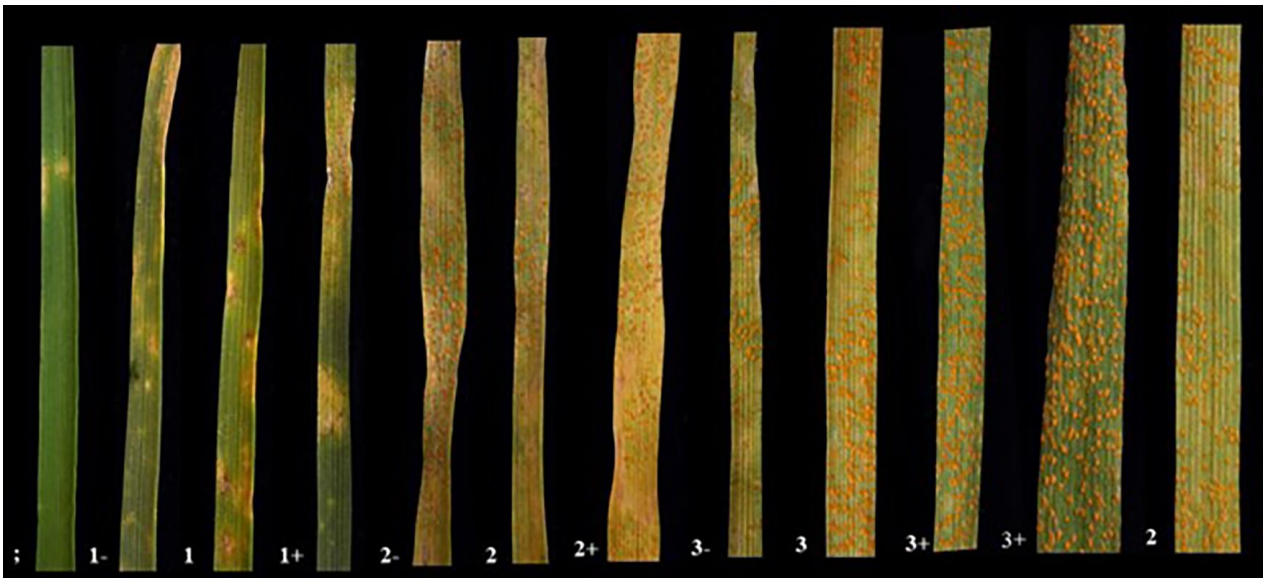




Note. Cobb scale was used for adult plant evaluations in the field and R: Resistant, MR: Moderately Resistant, M: Moderate, MS: Moderately Susceptible, S: Susceptible.

Figure 7.

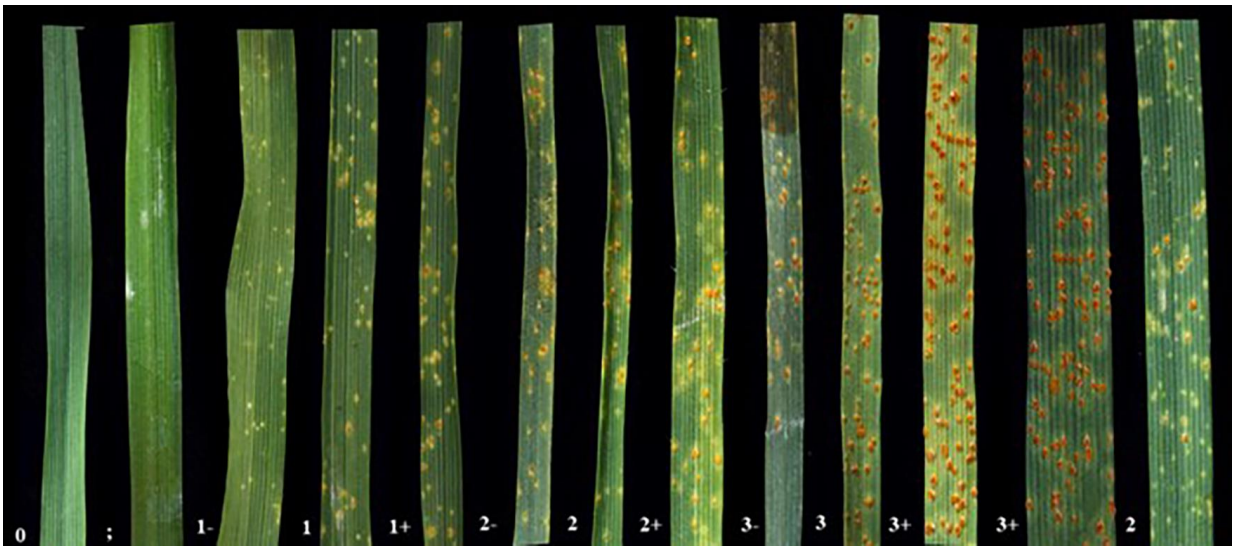
Illustration of the Stakman 0-4 infection-type scale using stripe rust on accessions of A genome diploid wheat at the seedling stage.



Note. ; = TA2025 (*T. monococcum* subsp. *monococcum*); 1- = TA408 (*T. monococcum* subsp. *aegilopoides*); 1 = TA580 (*T. monococcum* subsp. *aegilopoides*); 1+= TA10642 (*T. monococcum* subsp. *monococcum*); 2- = TA10622 (*T. monococcum* subsp. *monococcum*); 2 = TA2719 (*T. monococcum* subsp. *monococcum*); 2+ = TA2035 (*T. monococcum* subsp. *monococcum*); 3- = TA10891 (*T. urartu*); 3 = TA306 (*T. monococcum* subsp. *aegilopoides*); 3+ = TA544 (*T. monococcum* subsp. *aegilopoides*); 3+ = Morocco (Susceptible Check); 2 = Joe (Resistant Check). ITs ranging from 0 to 2 are considered resistant and from 3 to 3+ susceptible.

Figure 8.

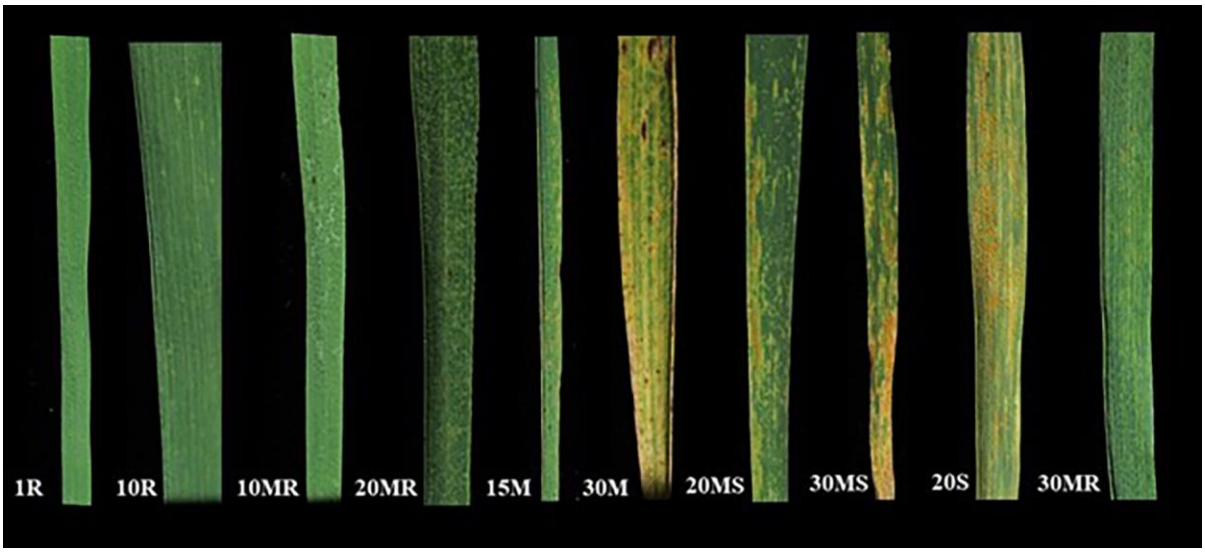
Illustration of the Stakman 0-4 infection type scale using leaf rust on accessions of A genome diploid wheat at the seedling stage.



Note. 0 = TA136 (*T. monococcum* subsp. *monococcum*); ; = TA136 (*T. monococcum* subsp. *monococcum*); 1- = TA10587 (*T. monococcum* subsp. *monococcum*); 1 = TA10573 (*T. monococcum* subsp. *aegilopoides*); 1+ = TA10652 (*T. monococcum* subsp. *monococcum*); 2- = TA2719 (*T. monococcum* subsp. *monococcum*); 2 = TA466 (*T. monococcum* subsp. *aegilopoides*); 2+ = TA250 (*T. monococcum* subsp. *aegilopoides*); 3- = TA748 (*T. monococcum* subsp. *aegilopoides*); 3 = TA346 (*T. monococcum* subsp. *aegilopoides*); 3+ = TA284 (*T. monococcum* subsp. *aegilopoides*); 3+ = Morocco (Susceptible Check); 2 = Joe (Resistant Check). ITs ranging from 0 to 2 are considered resistant and from 3 to 3+ susceptible.

Figure 9.

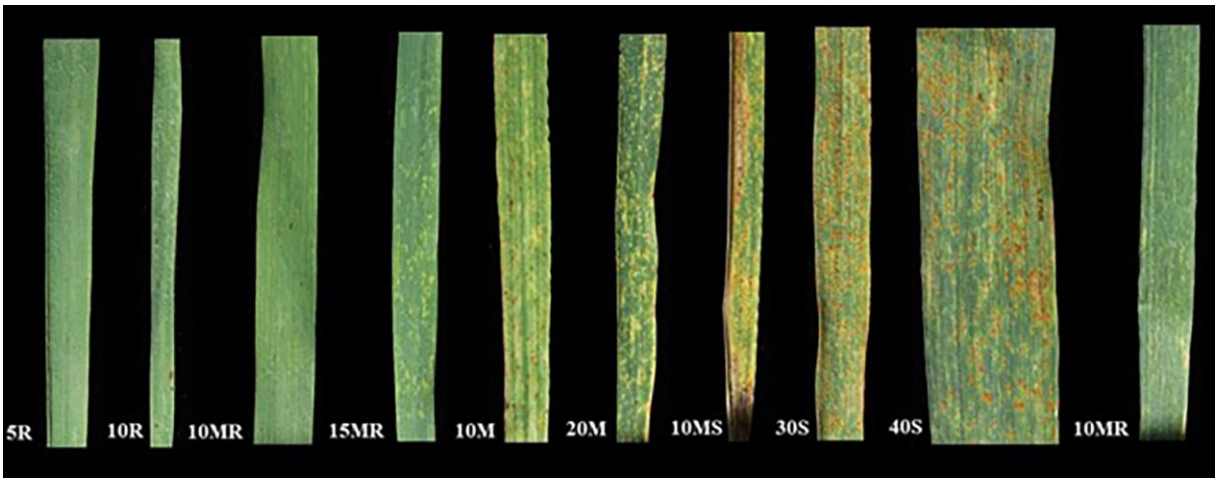
Illustration of the Cobb scale using stripe rust on accessions of A genome diploid wheat at the adult plant stage from field experiments.



Note. 1R = TA250 (*T. monococcum* subsp. *aegilopoides*); 10R = TA10569 (*T. monococcum* subsp. *monococcum*); 10MR = TA479 (*T. monococcum* subsp. *aegilopoides*); 20MR = TA2032 (*T. monococcum* subsp. *monococcum*); 15M = TA10887 (*T. urartu*); 30M = TA632 (*T. monococcum* subsp. *aegilopoides*); 20MS = TA850 (*T. urartu*); 30MS = TA834 (*T. urartu*); 20S =Avery (Susceptible Check); 30 MR = Joe (Resistant Check). R = Resistant, MR = Moderately Resistant, M = Moderate, MS = Moderately Susceptible, S = Susceptible. In the case of severity levels: 20%< = Resistant, 20-40% = Intermediate, 40%> = Susceptible.

Figure 10.

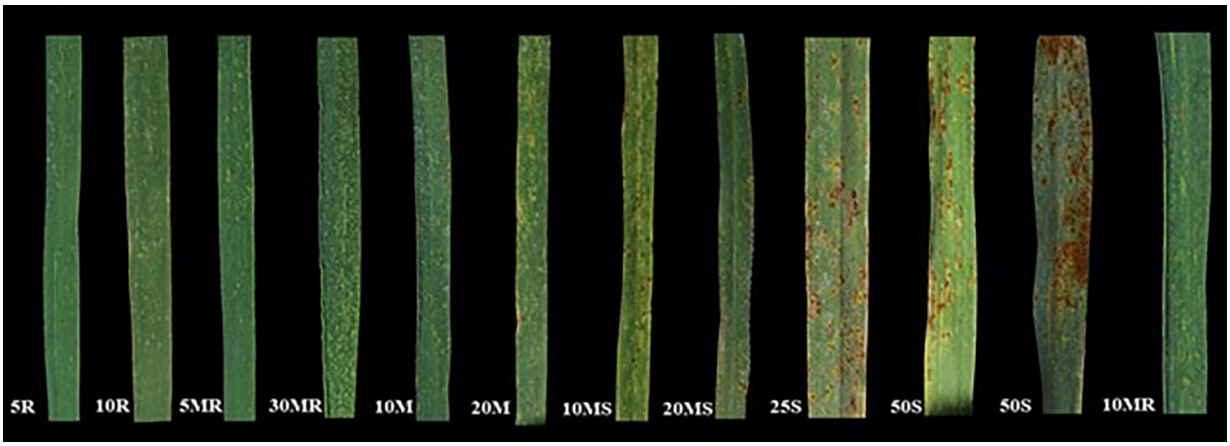
Illustration of the Cobb scale using leaf rust on accessions of A genome diploid wheat at the adult plant stage from field experiments.



Note. 5R = TA299 (*T. monococcum* subsp. *aegilopoides*); 10R = TA261 (*T. monococcum* subsp. *aegilopoides*); 10MR = TA136 (*T. monococcum* subsp. *monococcum*); 15MR = TA177 (*T. monococcum* subsp. *aegilopoides*); 10M = TA316 (*T. monococcum* subsp. *aegilopoides*); 20M = TA10593 (*T. monococcum* subsp. *aegilopoides*); 10MS = TA1314 (*T. urartu*); 30S = TA10878 (*T. urartu*); 40S =Avery (Susceptible Check); 10 MR = Joe (Resistant Check). R = Resistant, MR = Moderately Resistant, M = Moderate, MS = Moderately Susceptible, S = Susceptible. In the case of severity levels: 20%< = Resistant, 20-40% = Intermediate, 40%> = Susceptible.

Figure 11.

Illustration of the Cobb scale using stem rust on accessions of A genome diploid wheat at the adult plant stage from field experiments.



Note. 5R = TA2719 (*T. monococcum* subsp. *monococcum*); 10R = TA2025 (*T. monococcum* subsp. *monococcum*); 5MR = TA2025 (*T. monococcum* subsp. *monococcum*); 30MR = TA10629 (*T. monococcum* subsp. *monococcum*); 10M = TA190 (*T. monococcum* subsp. *aegilopoides*); 20M = TA10593 (*T. monococcum* subsp. *aegilopoides*); 10MS = TA2724 (*T. monococcum* subsp. *monococcum*); 20MS = TA661 (*T. monococcum* subsp. *aegilopoides*); 25S = TA394 (*T. monococcum* subsp. *aegilopoides*); 50S = TA1282 (*T. urartu*); 50S = Avery (Susceptible Check); 10 MR = Joe (Resistant Check). R = Resistant, MR = Moderately Resistant, M = Moderate, MS = Moderately Susceptible, S = Susceptible. In the case of severity levels: 20%< = Resistant, 20-40% = Intermediate, 40%> = Susceptible.

Appendix A - Supplementary Material

Table A. 1. Stripe rust seedling and adult plant resistance responses under greenhouse and field conditions for 2020 and 2021.

		Seedling Response		2021	2020		2021	
TA Number	Description	Exp 1	Exp 2	Greenhouse - Adult	Field Response	CI	Field Response	CI
TA 136	*T. monococcum* subsp. *monococcum*	3-	2-	7	20M	12	15MR	6
TA 177	*T. monococcum* subsp. *aegilopoides*	3+	3+	2	25M	15	15M	9
TA 190	*T. monococcum* subsp. *aegilopoides*	2+	3	4	20M	12	15MR	6
TA 249	*T. monococcum* subsp. *aegilopoides*	3	3-	2	15MR	6	10MR	4
TA 250	*T. monococcum* subsp. *aegilopoides*	NA	3	NA	NA	NA	5R	1
TA 252	*T. monococcum* subsp. *aegilopoides*	3+	3+	6	25M	15	10MR	4
TA 261	*T. monococcum* subsp. *aegilopoides*	3	3-	2	20M	12	10MR	4
TA 278	*T. monococcum* subsp. *aegilopoides*	NA	3+	NA	NA	NA	30MS	24

TA 284	*T. monococcum* subsp. *aegilopoides*	3+	3	1	15M	9	10M	6
TA 285	*T. monococcum* subsp. *aegilopoides*	3	2+	1	20M	12	5MR	2
TA 299	*T. monococcum* subsp. *aegilopoides*	3+	3	7	30M	18	20M	12
TA 306	*T. monococcum* subsp. *aegilopoides*	3	3	1	15MR	6	10MR	4
TA 309	*T. monococcum* subsp. *aegilopoides*	NA	3	NA	NA	NA	10MR	4
TA 316	*T. monococcum* subsp. *aegilopoides*	3-	1+	3	20MR	8	15MR	6
TA 346	*T. monococcum* subsp. *aegilopoides*	3	3-	2	20M	12	15M	9
TA 362	*T. monococcum* subsp. *aegilopoides*	3	2+	3	20M	12	15MR	6
TA 366	*T. monococcum* subsp. *aegilopoides*	NA	1+	NA	NA	NA	15MR	6
TA 394	*T. monococcum* subsp. *aegilopoides*	2+	3+	1	20M	12	10MR	4
TA 396	*T. monococcum* subsp. *aegilopoides*	2-	1-	3	15M	9	10M	6

TA 408	*T. monococcum* subsp. *aegilopoides*	1+	1	3	20M	12	10MR	4
TA 412	*T. monococcum* subsp. *aegilopoides*	3+	3+	4	15MR	6	10MR	4
TA 438	*T. monococcum* subsp. *aegilopoides*	NA	3	NA	NA	NA	20MR	8
TA 443	*T. monococcum* subsp. *aegilopoides*	NA	3+	NA	NA	NA	15MR	6
TA 447	*T. monococcum* subsp. *aegilopoides*	3+	3+	6	25M	15	25M	15
TA 466	*T. monococcum* subsp. *aegilopoides*	3	2+	3	15M	9	15M	9
TA 473	*T. monococcum* subsp. *aegilopoides*	3	3	3	10MR	4	5MR	2
TA 479	*T. monococcum* subsp. *aegilopoides*	NA	3	NA	NA	NA	15MS	12
TA 488	*T. monococcum* subsp. *aegilopoides*	NA	2	NA	NA	NA	15M	9
TA 502	*T. monococcum* subsp. *aegilopoides*	3	3	2	20M	12	15MR	6
TA 526	*T. monococcum* subsp. *aegilopoides*	NA	3	NA	NA	NA	15M	9

TA 534	*T. monococcum* subsp. *aegilopoides*	3	2	2	20MR	8	20MR	8
TA 544	*T. monococcum* subsp. *aegilopoides*	3+	3+	5	10MR	4	10M	6
TA 580	*T. monococcum* subsp. *aegilopoides*	1	1	2	20MR	8	5MR	2
TA 585	*T. monococcum* subsp. *aegilopoides*	3+	2	2	10MR	4	20MR	8
TA 590	*T. monococcum* subsp. *aegilopoides*	NA	1+	NA	NA	NA	30M	18
TA 593	*T. monococcum* subsp. *aegilopoides*	3+	3	2	20M	12	10MR	4
TA 632	*T. monococcum* subsp. *aegilopoides*	NA	1-	NA	NA	NA	25MR	10
TA 647	*T. monococcum* subsp. *aegilopoides*	NA	2-	NA	NA	NA	25M	15
TA 661	*T. monococcum* subsp. *aegilopoides*	3	3	6	30M	18	25M	15
TA 686	*T. monococcum* subsp. *aegilopoides*	1	1-	1	15MR	6	10MR	4
TA 709	*T. urartu*	3+	3+	8	15MR	6	40MS	32
TA 721	*T. urartu*	3	3-	3	15MR	6	10MR	4

TA 724	*T. urartu*	3	3+	7	10MR	4	20M	12
TA 748	*T. monococcum* subsp. *aegilopoides*	NA	2-	NA	NA	NA	20M	12
TA 756	*T. monococcum* subsp. *aegilopoides*	NA	3	NA	NA	NA	15M	9
TA 790	*T. urartu*	NA	2+	NA	NA	NA	20M	12
TA 792	*T. urartu*	3+	3	4	10MR	4	5MR	2
TA 800	*T. urartu*	3+	3+	7	20M	12	20M	12
TA 810	*T. urartu*	3+	3+	6	15MR	6	30M	18
TA 827	*T. urartu* subsp. *binartulutriru*	3-	3	2	5R	1	5R	1
TA 832	*T. urartu*	3+	3+	7	10M	6	25M	15
TA 834	*T. urartu*	NA	3+	NA	NA	NA	30MS	24
TA 841	*T. urartu*	3	3	3	10MR	4	25MR	10
TA 850	*T. urartu* subsp. *spontaneorubrum*	3+	3+	7	10MS	8	20MS	16
TA 1212	*T. monococcum* subsp. *aegilopoides*	3+	3-	1	15M	9	10R	2
TA 1254	*T. monococcum* subsp. *aegilopoides*	NA	3-	NA	NA	NA	15MR	6
TA 1266	*T. monococcum* subsp. *aegilopoides*	3	3-	3	10M	6	10MR	4

TA 1282	*T. urartu*	3	2+	6	5R	1	15MR	6
TA 1313	*T. urartu*	3+	3+	7	20M	12	20M	12
TA 1314	*T. urartu*	3+	3+	8	10MR	4	30M	18
TA 1315	*T. urartu*	3	NA	4	15MR	6	20MR	8
TA 2012	*T. monococcum* subsp. *aegilopoides*	3-	2	1	15MR	6	5MR	2
TA 2021	*T. monococcum* subsp. *aegilopoides*	NA	1-	NA	NA	NA	25M	15
TA 2022	*T. monococcum* subsp. *aegilopoides*	2	2+	2	20M	12	20M	12
TA 2025	*T. monococcum* subsp. *monococcum*	2+	1	2	25M	15	10MR	4
TA 2032	*T. monococcum* subsp. *monococcum*	NA	1+	NA	NA	NA	20MR	8
TA 2035	*T. monococcum* subsp. *monococcum*	2+	2+	6	20M	12	10MR	4
TA 2716	*T. monococcum* subsp. *monococcum*	3+	3	5	10MR	4	15M	9
TA 2719	*T. monococcum* subsp. *monococcum*	3	2-	6	5R	1	20MR	8
TA 2720	*T. monococcum* subsp. *monococcum*	3-	2+	4	30M	18	10MR	4

TA 2723	*T. monococcum* subsp. *monococcum*	3+	2	2	30M	18	10MR	4
TA 2724	*T. monococcum* subsp. *monococcum*	3	3	8	30M	18	10MR	4
TA 10418	*T. monococcum* subsp. *monococcum*	2-	1-	3	20MR	8	10MR	4
TA 10546	*T. monococcum* subsp. *aegilopoides*	NA	3	NA	NA	NA	15MR	6
TA 10569	*T. monococcum* subsp. *monococcum*	2	1	2	15MR	6	10MR	4
TA 10573	*T. monococcum* subsp. *aegilopoides*	3	3	7	25M	15	5MR	2
TA 10574	*T. monococcum* subsp. *monococcum*	1+	;	3	15MR	6	5R	1
TA 10581	*T. monococcum* subsp. *monococcum*	NA	1-	NA	NA	NA	15MR	6
TA 10587	*T. monococcum* subsp. *monococcum*	3	3-	6	10MR	4	5MR	2
TA 10588	*T. monococcum* subsp. *monococcum*	1	1+	2	20M	12	1R	0.2
TA 10593	*T. monococcum* subsp. *aegilopoides*	3	3+	6	15M	9	10MR	4

TA 10595	*T. monococcum* subsp. *aegilopoides*	3+	3+	6	15M	9	10MR	4
TA 10603	*T. monococcum* subsp. *aegilopoides*	3	3	5	10MR	4	10MR	4
TA 10612	*T. monococcum* subsp. *monococcum*	NA	3	NA	NA	NA	10R	2
TA 10622	*T. monococcum* subsp. *monococcum*	NA	2	3	NA	NA	5MR	2
TA 10629	*T. monococcum* subsp. *monococcum*	3	3-	6	20M	12	20MR	8
TA 10630	*T. monococcum* subsp. *monococcum*	1	1-	2	15MR	6	5MR	2
TA 10634	*T. monococcum* subsp. *monococcum*	3+	3-	3	20M	12	10MR	4
TA 10636	*T. monococcum* subsp. *monococcum*	NA	1-	NA	NA	NA	15M	9
TA 10642	*T. monococcum* subsp. *monococcum*	1+	;	3	10MR	4	5R	1
TA 10652	*T. monococcum* subsp. *monococcum*	3	3-	2	20M	12	5MR	2
TA 10873	*T. urartu*	NA	3	NA	NA	NA	10MR	4
TA 10876	*T. urartu*	3-	3	3	5R	1	10MR	4

TA 10878	*T. urartu*	3+	3	5	10MR	4	25M	15
TA 10879	*T. urartu*	NA	2+	NA	NA	NA	5MR	2
TA 10884	*T. urartu*	3-	3	3	15M	9	5R	1
TA 10887	*T. urartu*	3	3+	6	20M	12	5MR	2
TA 10888	*T. urartu*	2+	2	2	30M	18	5R	1
TA 10889	*T. urartu*	3	3	2	15MR	6	5MR	2
TA 10891	*T. urartu*	3	3-	6	10MR	4	5R	1
TA 10896	*T. monococcum* subsp. *monococcum*	NA	3-	NA	NA	NA	25M	15
TA 10900	*T. monococcum* subsp. *aegilopoides*	2	3-	2	10MR	4	10MR	4
TA 10902	*T. monococcum* subsp. *aegilopoides*	3-	2-	3	5MR	2	30M	18
TA 10904	*T. monococcum* subsp. *aegilopoides*	3-	3	2	20M	12	15M	9
TA 10907	*T. monococcum* subsp. *aegilopoides*	NA	3-	NA	NA	NA	25MR	10
TA 10909	*T. monococcum* subsp. *aegilopoides*	NA	3	NA	NA	NA	5R	1
TA 10916	*T. monococcum* subsp. *aegilopoides*	3	3-	3	5R	1	15MR	6

TA 11012	*T. monococcum* subsp. *aegilopoides*	3	3	5	10MR	4	10MR	4
Morocco	*T. aestivum* - Susceptible Check	3+	3+	9	60S	60	NA	NA
Avery	*T. aestivum* - Susceptible Check	NA	3+	NA	NA	NA	70S	70
Kingbird	*T. aestivum* - Resistant Check	NA	NA	NA	15MR	6	NA	NA
Joe	*T. aestivum* - Resistant Check	NA	3	6	NA	NA	20MR	8

Table A. 2. Leaf rust seedling and adult plant resistance responses under greenhouse and field conditions for 2020 and 2021.

		Seedling Response		2021		2020		2021	
TA Number	Description	Exp 1	Exp 2	Greenhouse-Adult	CI	Field Response	CI	Field Response	CI
TA 136	*T. monococcum* subsp. *monococcum*	;	;	10MR	4	10MR	4	15MR	6
TA 177	*T. monococcum* subsp. *aegilopoides*	3	3	1R	0.2	20MR	8	20M	12
TA 190	*T. monococcum* subsp. *aegilopoides*	1	3-	20M	12	20MR	8	20MR	8
TA 249	*T. monococcum* subsp. *aegilopoides*	3	3	5M	3	20MR	8	20MR	8
TA 250	*T. monococcum* subsp. *aegilopoides*	NA	3	NA	NA	NA	NA	20MR	8
TA 252	*T. monococcum* subsp. *aegilopoides*	3+	3	10M	6	10MR	4	20MR	8
TA 261	*T. monococcum* subsp. *aegilopoides*	3+	3	5MR	2	20MR	8	20M	12
TA 278	*T. monococcum* subsp. *aegilopoides*	NA	3	NA	NA	NA	NA	20M	12

TA 284	*T. monococcum* subsp. *aegilopoides*	3+	3+	5MR	2	30M	18	15M	9
TA 285	*T. monococcum* subsp. *aegilopoides*	3-	3	1R	0.2	20MR	8	15MR	6
TA 299	*T. monococcum* subsp. *aegilopoides*	3	3	5M	3	20MR	8	15MR	6
TA 306	*T. monococcum* subsp. *aegilopoides*	3	3	20MR	8	15MR	6	10M	6
TA 309	*T. monococcum* subsp. *aegilopoides*	NA	3+	NA	NA	NA	NA	15M	9
TA 316	*T. monococcum* subsp. *aegilopoides*	3	3	30M	18	20MR	8	20M	12
TA 346	*T. monococcum* subsp. *aegilopoides*	3	3	10M	6	20MR	8	20M	12
TA 362	*T. monococcum* subsp. *aegilopoides*	3+	3	1M	0.6	30MR	12	15M	9
TA 366	*T. monococcum* subsp. *aegilopoides*	NA	3+	NA	NA	NA	NA	20M	12
TA 394	*T. monococcum* subsp. *aegilopoides*	3+	3	10M	6	20M	12	15M	9
TA 396	*T. monococcum* subsp. *aegilopoides*	2+	3	10MR	4	20MR	8	15M	9

TA 408	*T. monococcum* subsp. *aegilopoides*	3	3	25MR	10	20M	12	20MR	8
TA 412	*T. monococcum* subsp. *aegilopoides*	3	3	10M	6	25M	15	20M	12
TA 438	*T. monococcum* subsp. *aegilopoides*	NA	3	NA	NA	NA	NA	20M	12
TA 443	*T. monococcum* subsp. *aegilopoides*	NA	3+	NA	NA	NA	NA	20M	12
TA 447	*T. monococcum* subsp. *aegilopoides*	3	3	10MR	4	20MR	8	15MR	6
TA 466	*T. monococcum* subsp. *aegilopoides*	2	2+	5MR	2	30MR	12	20M	12
TA 473	*T. monococcum* subsp. *aegilopoides*	4	3	1MS	0.8	10MR	4	15M	9
TA 479	*T. monococcum* subsp. *aegilopoides*	NA	3+	NA	NA	NA	NA	20M	12
TA 488	*T. monococcum* subsp. *aegilopoides*	NA	3+	NA	NA	NA	NA	20M	12
TA 502	*T. monococcum* subsp. *aegilopoides*	3	3	5M	3	20MR	8	15MR	6
TA 526	*T. monococcum* subsp. *aegilopoides*	NA	3+	NA	NA	NA	NA	20M	12

TA 534	*T. monococcum* subsp. *aegilopoides*	2+	1+	20MR	8	10MR	4	20MR	8
TA 544	*T. monococcum* subsp. *aegilopoides*	3	3	5R	1	10MR	4	15M	9
TA 580	*T. monococcum* subsp. *aegilopoides*	1	;	30MR	12	10R	2	10MR	4
TA 585	*T. monococcum* subsp. *aegilopoides*	2+	3	10M	6	20MR	8	20M	12
TA 590	*T. monococcum* subsp. *aegilopoides*	NA	3+	NA	NA	NA	NA	20M	12
TA 593	*T. monococcum* subsp. *aegilopoides*	3	3	10M	6	30MR	12	20M	12
TA 632	*T. monococcum* subsp. *aegilopoides*	NA	3	NA	NA	NA	NA	15M	9
TA 647	*T. monococcum* subsp. *aegilopoides*	NA	2	NA	NA	NA	NA	20M	12
TA 661	*T. monococcum* subsp. *aegilopoides*	3	3	20M	12	20MR	8	20M	12
TA 686	*T. monococcum* subsp. *aegilopoides*	3	3	10M	6	25M	15	10M	6
TA 709	*T. urartu*	3+	3	20MS	16	20MS	16	25M	15
TA 721	*T. urartu*	3	3	10M	6	25M	15	25M	15

TA 724	*T. urartu*	3+	3	50S	50	20MS	16	15M	9
TA 748	*T. monococcum* subsp. *aegilopoides*	NA	3	NA	NA	NA	NA	20M	12
TA 756	*T. monococcum* subsp. *aegilopoides*	NA	3+	NA	NA	NA	NA	20M	12
TA 790	*T. urartu*	NA	3+	NA	NA	NA	NA	15M	9
TA 792	*T. urartu*	3	3	20MS	16	15MR	6	20M	12
TA 800	*T. urartu*	3	3	60MS	48	20MR	8	15M	9
TA 810	*T. urartu*	3+	3	10MS	8	20MS	16	20M	12
TA 827	*T. urartu* subsp. *binartulutriru*	3+	3	25MS	20	20MS	16	20MS	16
TA 832	*T. urartu*	3+	3	20MS	16	20MS	16	10M	6
TA 834	*T. urartu*	NA	3+	NA	NA	NA	NA	20M	12
TA 841	*T. urartu*	3	3	20M	12	20M	12	20M	12
TA 850	*T. urartu* subsp. *spontaneorubrum*	3+	3	15S	15	30MS	24	40MS	32
TA 1212	*T. monococcum* subsp. *aegilopoides*	3	3	20MS	16	20MR	8	10M	6
TA 1254	*T. monococcum* subsp. *aegilopoides*	NA	3+	NA	NA	NA	NA	20M	12
TA 1266	*T. monococcum* subsp. *aegilopoides*	3	3	20M	12	15MR	6	15M	9

TA 1282	*T. urartu*	3	NA	20M	12	15MR	6	15M	9
TA 1313	*T. urartu*	3-	3	15MR	6	20M	12	15MR	6
TA 1314	*T. urartu*	3	NA	20MR	8	15MS	12	20M	12
TA 1315	*T. urartu*	3-	3	10M	6	30MR	12	15M	9
TA 2012	*T. monococcum* subsp. *aegilopoides*	2	2+	20MR	8	20MR	8	20MR	8
TA 2021	*T. monococcum* subsp. *aegilopoides*	NA	3+	NA	NA	NA	NA	20M	12
TA 2022	*T. monococcum* subsp. *aegilopoides*	3	3	10MS	8	20MR	8	15M	9
TA 2025	*T. monococcum* subsp. *monococcum*	;	;	5R	1	20MR	8	20MR	8
TA 2032	*T. monococcum* subsp. *monococcum*	NA	;	NA	NA	NA	NA	20MR	8
TA 2035	*T. monococcum* subsp. *monococcum*	1	;	1R	0.2	20MR	8	20M	12
TA 2716	*T. monococcum* subsp. *monococcum*	1-	;	10R	2	10MR	4	20MR	8
TA 2719	*T. monococcum* subsp. *monococcum*	1+	2	1R	0.2	20MR	8	15MR	6
TA 2720	*T. monococcum* subsp. *monococcum*	1+	2+	1R	0.2	30M	18	10M	6

TA 2723	*T. monococcum* subsp. *monococcum*	1-	2+	20MR	8	20M	12	15MR	6
TA 2724	*T. monococcum* subsp. *monococcum*	1	;	20R	4	15MR	6	15MR	6
TA 10418	*T. monococcum* subsp. *monococcum*	;	;	5R	1	20MR	8	20MR	8
TA 10546	*T. monococcum* subsp. *aegilopoides*	NA	;	NA	NA	NA	NA	20MR	8
TA 10569	*T. monococcum* subsp. *monococcum*	1-	1	10MR	4	25MR	10	20M	12
TA 10573	*T. monococcum* subsp. *aegilopoides*	2	2+	5M	3	15MR	6	20M	12
TA 10574	*T. monococcum* subsp. *monococcum*	;	;	5R	1	10R	2	15MR	6
TA 10581	*T. monococcum* subsp. *monococcum*	NA	;	NA	NA	NA	NA	20MR	8
TA 10587	*T. monococcum* subsp. *monococcum*	1	1+	50M	30	10MR	4	15MR	6
TA 10588	*T. monococcum* subsp. *monococcum*	;	NA	20R	4	15MR	6	15M	9
TA 10593	*T. monococcum* subsp. *aegilopoides*	3+	3	40S	40	30M	18	25M	15

TA 10595	*T. monococcum* subsp. *aegilopoides*	3	3	20MS	16	30MS	24	20MS	16
TA 10603	*T. monococcum* subsp. *aegilopoides*	3+	NA	50MS	40	30MS	24	15M	9
TA 10612	*T. monococcum* subsp. *monococcum*	NA	1-	NA	NA	NA	NA	20MR	8
TA 10622	*T. monococcum* subsp. *monococcum*	NA	1-	10R	2	NA	NA	15M	9
TA 10629	*T. monococcum* subsp. *monococcum*	1	2+	30R	6	20MR	8	20M	12
TA 10630	*T. monococcum* subsp. *monococcum*	1	3	1R	0.2	10R	2	20MR	8
TA 10634	*T. monococcum* subsp. *monococcum*	1	;	1R	0.2	20MR	8	20MR	8
TA 10636	*T. monococcum* subsp. *monococcum*	NA	1	NA	NA	NA	NA	15M	9
TA 10642	*T. monococcum* subsp. *monococcum*	;	;	5R	1	10MR	4	20MR	8
TA 10652	*T. monococcum* subsp. *monococcum*	1+	2-	20MR	8	30MR	12	25M	15
TA 10873	*T. urartu*	NA	3	NA	NA	NA	NA	15M	9
TA 10876	*T. urartu*	3+	3	20MS	16	25MR	10	20M	12

TA 10878	*T. urartu*	3+	NA	30S	30	40MS	32	40MS	32
TA 10879	*T. urartu*	NA	3+	NA	NA	NA	NA	20M	12
TA 10884	*T. urartu*	3	3-	10M	6	10M	6	20M	12
TA 10887	*T. urartu*	3+	3	10S	10	15MR	6	15MR	6
TA 10888	*T. urartu*	3	3	20M	12	15M	9	15M	9
TA 10889	*T. urartu*	3	3	15MR	6	10MR	4	15MR	6
TA 10891	*T. urartu*	3	3	10MS	8	15MR	6	20M	12
TA 10896	*T. monococcum* subsp. *monococcum*	NA	;	NA	NA	NA	NA	20MR	8
TA 10900	*T. monococcum* subsp. *aegilopoides*	3	3	15MS	12	10MR	4	20M	12
TA 10902	*T. monococcum* subsp. *aegilopoides*	3	3	20M	12	20MR	8	20M	12
TA 10904	*T. monococcum* subsp. *aegilopoides*	3	3	1M	0.6	15MR	6	20M	12
TA 10907	*T. monococcum* subsp. *aegilopoides*	NA	3+	NA	NA	NA	NA	20M	12
TA 10909	*T. monococcum* subsp. *aegilopoides*	NA	3+	NA	NA	NA	NA	20MR	8
TA 10916	*T. monococcum* subsp. *aegilopoides*	;	;	10MR	4	10MR	4	15M	9

TA 11012	*T. monococcum* subsp. *aegilopoides*	3	3	10M	6	10MR	4	15MR	6
Morocco	*T. aestivum* - Susceptible Check	4	4	40S	40	100S	100	NA	NA
Avery	*T. aestivum* - Susceptible Check	NA	;	NA	NA	NA	NA	60S	60
Kingbird	*T. aestivum* - Resistant Check	NA	NA	NA	NA	15MR	6	NA	NA
Joe	*T. aestivum* - Resistant Check	NA	1+	30MR	12	NA	NA	15M	9

Table A. 3. Stem rust adult plant resistance responses under greenhouse and field conditions for 2020 and 2021.

		2021		2020		2021	
TA Number	Description	Greenhouse-Adult	CI	Field Response	CI	Field Response	CI
TA 136	*T. monococcum* subsp. *monococcum*	60S	60	15S	15	1MS	0.8
TA 177	*T. monococcum* subsp. *aegilopoides*	25S	25	20MS	16	30S	30
TA 190	*T. monococcum* subsp. *aegilopoides*	20M	12	20MS	16	5MS	4
TA 249	*T. monococcum* subsp. *aegilopoides*	50MS	40	15M	9	15MS	12
TA 250	*T. monococcum* subsp. *aegilopoides*	NA	NA	NA	NA	10MR	4
TA 252	*T. monococcum* subsp. *aegilopoides*	30MS	24	10M	6	10MR	4
TA 261	*T. monococcum* subsp. *aegilopoides*	10R	2	10MR	4	5MR	2
TA 278	*T. monococcum* subsp. *aegilopoides*	NA	NA	NA	NA	30S	30
TA 284	*T. monococcum* subsp. *aegilopoides*	20M	12	20M	12	50S	50
TA 285	*T. monococcum* subsp. *aegilopoides*	30M	18	20MS	16	10MS	8
TA 299	*T. monococcum* subsp. *aegilopoides*	30M	18	20M	12	15S	15
TA 306	*T. monococcum* subsp. *aegilopoides*	20M	12	15M	9	25S	25

TA 309	*T. monococcum* subsp. *aegilopoides*	NA	NA	NA	NA	10M	6
TA 316	*T. monococcum* subsp. *aegilopoides*	50S	50	30MS	24	30S	30
TA 346	*T. monococcum* subsp. *aegilopoides*	15M	9	20M	12	5M	3
TA 362	*T. monococcum* subsp. *aegilopoides*	NA	NA	30MS	24	5MS	4
TA 366	*T. monococcum* subsp. *aegilopoides*	NA	NA	NA	NA	10M	6
TA 394	*T. monococcum* subsp. *aegilopoides*	40S	40	30MS	24	30S	30
TA 396	*T. monococcum* subsp. *aegilopoides*	15S	15	20MS	16	5MS	4
TA 408	*T. monococcum* subsp. *aegilopoides*	15S	15	10MS	8	5M	3
TA 412	*T. monococcum* subsp. *aegilopoides*	30S	30S	10MS	8	5M	3
TA 438	*T. monococcum* subsp. *aegilopoides*	NA	NA	NA	NA	10M	6
TA 443	*T. monococcum* subsp. *aegilopoides*	NA	NA	NA	NA	10MS	8
TA 447	*T. monococcum* subsp. *aegilopoides*	10M	6	20MS	16	10MS	8
TA 466	*T. monococcum* subsp. *aegilopoides*	20MS	16	20MS	16	10MS	8
TA 473	*T. monococcum* subsp. *aegilopoides*	50S	50	30MS	24	10M	6
TA 479	*T. monococcum* subsp. *aegilopoides*	NA	NA	NA	NA	15MS	12
TA 488	*T. monococcum* subsp. *aegilopoides*	NA	NA	NA	NA	30S	30

TA 502	*T. monococcum* subsp. *aegilopoides*	15MR	6	15MS	12	10MS	8
TA 526	*T. monococcum* subsp. *aegilopoides*	NA	NA	NA	NA	10M	6
TA 534	*T. monococcum* subsp. *aegilopoides*	10MR	4	20MS	16	10MS	8
TA 544	*T. monococcum* subsp. *aegilopoides*	30MS	24	15MR	6	10MS	8
TA 580	*T. monococcum* subsp. *aegilopoides*	10M	6	25MS	20	10M	6
TA 585	*T. monococcum* subsp. *aegilopoides*	30M	18	15M	9	5MS	4
TA 590	*T. monococcum* subsp. *aegilopoides*	NA	NA	NA	NA	5M	3
TA 593	*T. monococcum* subsp. *aegilopoides*	30M	18	20MS	16	10M	6
TA 632	*T. monococcum* subsp. *aegilopoides*	NA	NA	NA	NA	5M	3
TA 647	*T. monococcum* subsp. *aegilopoides*	NA	NA	NA	NA	10M	6
TA 661	*T. monococcum* subsp. *aegilopoides*	40S	40	20MS	16	20MS	16
TA 686	*T. monococcum* subsp. *aegilopoides*	20MS	16	15MS	12	15MS	12
TA 709	*T. urartu*	60S	60	30MS	24	40S	40
TA 721	*T. urartu*	20M	12	20MS	16	10M	6
TA 724	*T. urartu*	50S	50	20MS	16	40S	40
TA 748	*T. monococcum* subsp. *aegilopoides*	NA	NA	NA	NA	10M	6

TA 756	*T. monococcum* subsp. *aegilopoides*	NA	NA	NA	NA	20M	12
TA 790	*T. urartu*	NA	NA	NA	NA	30S	30
TA 792	*T. urartu*	50S	50	30S	30	20MS	16
TA 800	*T. urartu*	40S	40	30MS	24	20S	20
TA 810	*T. urartu*	40S	40	30MS	24	25S	25
TA 827	*T. urartu* subsp. *binartulutriru*	40S	40	15MS	12	20MS	16
TA 832	*T. urartu*	30S	30	30MS	24	40S	40
TA 834	*T. urartu*	NA	NA	NA	NA	25MS	20
TA 841	*T. urartu*	40S	40	30MS	24	25S	25
TA 850	*T. urartu* subsp. *spontaneorubrum*	30S	30	20MS	16	10M	6
TA 1212	*T. monococcum* subsp. *aegilopoides*	30M	18	20M	12	10M	6
TA 1254	*T. monococcum* subsp. *aegilopoides*	NA	NA	NA	NA	15M	9
TA 1266	*T. monococcum* subsp. *aegilopoides*	40S	40	25MS	20	20S	20
TA 1282	*T. urartu*	40S	40	20MS	16	50S	50
TA 1313	*T. urartu*	50S	50	20MS	16	50S	50
TA 1314	*T. urartu*	30S	30	25MS	20	40S	40

TA 1315	*T. urartu*	NA	NA	20MS	16	40S	40
TA 2012	*T. monococcum* subsp. *aegilopoides*	10R	2	10MR	4	5MR	2
TA 2021	*T. monococcum* subsp. *aegilopoides*	NA	NA	NA	NA	10MR	4
TA 2022	*T. monococcum* subsp. *aegilopoides*	30MS	24	10M	6	15M	9
TA 2025	*T. monococcum* subsp. *monococcum*	20M	12	10MS	8	10MR	4
TA 2032	*T. monococcum* subsp. *monococcum*	NA	NA	NA	NA	20MR	8
TA 2035	*T. monococcum* subsp. *monococcum*	30MS	24	15MS	12	5M	3
TA 2716	*T. monococcum* subsp. *monococcum*	40S	40	25MS	20	10MS	8
TA 2719	*T. monococcum* subsp. *monococcum*	10R	2	15MR	6	5R	1
TA 2720	*T. monococcum* subsp. *monococcum*	30S	30	20S	20	5M	3
TA 2723	*T. monococcum* subsp. *monococcum*	20MS	16	25MS	20	5MS	4
TA 2724	*T. monococcum* subsp. *monococcum*	10M	6	30MS	24	10MS	8
TA 10418	*T. monococcum* subsp. *monococcum*	20MS	16	10MS	8	10M	6
TA 10546	*T. monococcum* subsp. *aegilopoides*	NA	NA	NA	NA	5M	3
TA 10569	*T. monococcum* subsp. *monococcum*	30S	30	40MS	32	20S	20
TA 10573	*T. monococcum* subsp. *aegilopoides*	10R	2	10MR	4	5M	3

TA 10574	*T. monococcum* subsp. *monococcum*	20MS	16	20MS	16	10S	10
TA 10581	*T. monococcum* subsp. *monococcum*	NA	NA	NA	NA	15MR	6
TA 10587	*T. monococcum* subsp. *monococcum*	10MS	8	20MS	16	5M	3
TA 10588	*T. monococcum* subsp. *monococcum*	40S	40	10MS	8	10MR	4
TA 10593	*T. monococcum* subsp. *aegilopoides*	20M	12	20MS	16	20M	12
TA 10595	*T. monococcum* subsp. *aegilopoides*	40S	40	30S	30	20S	20
TA 10603	*T. monococcum* subsp. *aegilopoides*	50S	50	25MS	20	15MS	12
TA 10612	*T. monococcum* subsp. *monococcum*	NA	NA	NA	NA	10MR	4
TA 10622	*T. monococcum* subsp. *monococcum*	20MR	8	NA	NA	5MR	2
TA 10629	*T. monococcum* subsp. *monococcum*	20R	4	15MR	6	10MR	4
TA 10630	*T. monococcum* subsp. *monococcum*	20S	20	25MS	20	15S	15
TA 10634	*T. monococcum* subsp. *monococcum*	30MS	24	20MS	16	5MS	4
TA 10636	*T. monococcum* subsp. *monococcum*	NA	NA	NA	NA	20S	20
TA 10642	*T. monococcum* subsp. *monococcum*	25MS	20	20S	20	5MS	4
TA 10652	*T. monococcum* subsp. *monococcum*	20MS	16	15MR	6	10MR	4
TA 10873	*T. urartu*	NA	NA	NA	NA	NA	NA

TA 10876	*T. urartu*	50S	50	20MS	16	50S	50
TA 10878	*T. urartu*	80S	80	20MS	16	25S	25
TA 10879	*T. urartu*	NA	NA	NA	NA	25MS	20
TA 10884	*T. urartu*	50S	50	30MS	24	25S	25
TA 10887	*T. urartu*	50S	50	25MS	20	15S	15
TA 10888	*T. urartu*	10M	6	10MR	4	5MR	2
TA 10889	*T. urartu*	40S	40	20MS	16	20MS	16
TA 10891	*T. urartu*	50S	50	40S	40	30S	30
TA 10896	*T. monococcum* subsp. *monococcum*	NA	NA	NA	NA	10M	6
TA 10900	*T. monococcum* subsp. *aegilopoides*	10MS	8	20MS	16	5MS	4
TA 10902	*T. monococcum* subsp. *aegilopoides*	15MR	6	20M	12	15M	9
TA 10904	*T. monococcum* subsp. *aegilopoides*	20M	12	30MS	24	10S	10
TA 10907	*T. monococcum* subsp. *aegilopoides*	NA	NA	NA	NA	10MS	8
TA 10909	*T. monococcum* subsp. *aegilopoides*	NA	NA	NA	NA	NA	NA
TA 10916	*T. monococcum* subsp. *aegilopoides*	15R	3	10MR	4	10MR	4
TA 11012	*T. monococcum* subsp. *aegilopoides*	20MS	16	20MS	16	10MS	8

Morocco	*T. aestivum* - Susceptible Check	60S	60	60S	60	NA	NA
Avery	*T. aestivum* - Susceptible Check	NA	NA	NA	NA	50S	50
Kingbird	*T. aestivum* - Resistant Check	NA	NA	10MR	4	NA	NA
Joe	*T. aestivum* - Resistant Check	NA	NA	NA	NA	10MR	4

Table A. 4. The greenhouse data at the adult plant stage with all replication values for stripe rust, leaf rust, and stem rust in the experiment in 2021.

		Stripe Rust			**Leaf Rust**			**Stem Rust**	
TA Number	Description	Rep 1	2	Rep 3	Rep 1	Rep 2	Rep 3	Rep 1	Rep 2
TA 136	*T. monococcum* subsp. *monococcum*	7	7	7	10MR	10MR	15MR	60S	5MS
TA 177	*T. monococcum* subsp. *aegilopoides*	4	2	2	1R	5R	1R	40MS	25S
TA 190	*T. monococcum* subsp. *aegilopoides*	3	4	4	5MS	20M	10MR	20M	10M
TA 249	*T. monococcum* subsp. *aegilopoides*	2	3	2	5M	10M	5M	20MS	50MS
TA 252	*T. monococcum* subsp. *aegilopoides*	6	7	4	5R	10M	30MS	30MS	30MS
TA 261	*T. monococcum* subsp. *aegilopoides*	3	2	2	1M	5MR	1R	5R	10R
TA 284	*T. monococcum* subsp. *aegilopoides*	1	1	2	5MR	1R	5M	20M	10R
TA 285	*T. monococcum* subsp. *aegilopoides*	1	1	2	1R	5MR	1R	30M	15M

TA 299	*T. monococcum* subsp. *aegilopoides*	8	7	7	1R	5M	30MS	30M	15M
TA 306	*T. monococcum* subsp. *aegilopoides*	1	1	2	30MS	1R	20MR	20M	5M
TA 316	*T. monococcum* subsp. *aegilopoides*	3	3	2	10M	30M	20MS	50S	40S
TA 346	*T. monococcum* subsp. *aegilopoides*	2	2	6	10M	25MS	10M	15M	15MR
TA 362	*T. monococcum* subsp. *aegilopoides*	3	2	3	NA	5R	1M	NA	NA
TA 394	*T. monococcum* subsp. *aegilopoides*	1	1	1	10M	1R	5MS	40S	40S
TA 396	*T. monococcum* subsp. *aegilopoides*	3	3	3	20MR	10MR	10MR	20MS	15S
TA 408	*T. monococcum* subsp. *aegilopoides*	2	3	3	25MR	30MR	10M	10MS	15S
TA 412	*T. monococcum* subsp. *aegilopoides*	6	4	3	10M	20MR	20MS	30S	25MS
TA 447	*T. monococcum* subsp. *aegilopoides*	6	6	4	5MS	1R	10MR	10M	NA
TA 466	*T. monococcum* subsp. *aegilopoides*	4	3	2	1R	20MR	5MR	20MS	15MR

TA 473	*T. monococcum* subsp. *aegilopoides*	1	4	3	1R	20MS	1MS	50S	30S
TA 502	*T. monococcum* subsp. *aegilopoides*	2	3	2	NA	5MR	5M	15MR	10MR
TA 534	*T. monococcum* subsp. *aegilopoides*	1	3	2	NA	20MR	5MR	10MR	NA
TA 544	*T. monococcum* subsp. *aegilopoides*	4	5	6	5R	10M	1R	30MS	15MR
TA 580	*T. monococcum* subsp. *aegilopoides*	2	2	3	15R	30MR	NA	30MR	10M
TA 585	*T. monococcum* subsp. *aegilopoides*	1	4	2	NA	10MR	10M	30M	NA
TA 593	*T. monococcum* subsp. *aegilopoides*	4	2	2	NA	10M	10MR	30M	15M
TA 661	*T. monococcum* subsp. *aegilopoides*	7	6	5	20MS	20M	1R	40S	10MS
TA 686	*T. monococcum* subsp. *aegilopoides*	1	1	3	10M	20MR	5M	20M	20MS
TA 709	*T. urartu*	8	8	6	20MS	10MS	20MS	50S	60S
TA 721	*T. urartu*	3	3	2	10M	10M	10MS	20M	20M
TA 724	*T. urartu*	1	7	7	50S	50S	5S	50S	30S
TA 792	*T. urartu*	3	4	4	30MS	20MS	5M	50S	50S

TA 800	*T. urartu*	8	7	7	60MS	10S	5M	40S	25S
TA 810	*T. urartu*	3	8	6	10MS	10MS	5MS	40S	40S
TA 827	*T. urartu* subsp. *binartulutriru*	2	1	3	40MS	20MS	25MS	15S	40S
TA 832	*T. urartu*	8	7	5	40MS	15M	20MS	30S	15S
TA 841	*T. urartu*	3	3	4	20M	20MS	5MR	40S	30S
TA 850	*T. urartu* subsp. *spontaneorubrum*	7	NA	5	50MS	15S	NA	30S	30MS
TA 1212	*T. monococcum* subsp. *aegilopoides*	1	1	1	30MS	5MR	20MS	30M	NA
TA 1266	*T. monococcum* subsp. *aegilopoides*	1	3	4	20M	5MR	20MS	40S	10MR
TA 1282	*T. urartu*	7	6	5	20M	1M	20MS	20S	40S
TA 1313	*T. urartu*	8	7	7	15MR	5R	20MS	50S	30S
TA 1314	*T. urartu*	7	8	8	10MS	20MR	5R	30S	30S
TA 1315	*T. urartu*	8	4	3	10M	10M	10MR	NA	NA
TA 2012	*T. monococcum* subsp. *aegilopoides*	1	1	2	10MR	20MR	1M	10R	10R
TA 2022	*T. monococcum* subsp. *aegilopoides*	2	2	1	10MS	20MS	1R	30MS	15M
TA 2025	*T. monococcum* subsp. *monococcum*	5	2	2	10R	1R	5R	15M	20M

TA 2035	*T. monococcum* subsp. *monococcum*	7	6	4	1R	1R	1R	40M	30MS
TA 2716	*T. monococcum* subsp. *monococcum*	3	5	4	10R	5R	10R	40S	10MS
TA 2719	*T. monococcum* subsp. *monococcum*	3	6	NA	1R	1R	5R	5R	10R
TA 2720	*T. monococcum* subsp. *monococcum*	4	3	4	5R	1R	1R	30S	30S
TA 2723	*T. monococcum* subsp. *monococcum*	1	2	3	30MR	10MR	20MR	20MS	10MR
TA 2724	*T. monococcum* subsp. *monococcum*	8	6	NA	10R	20R	20MR	15MR	10M
TA 10418	*T. monococcum* subsp. *monococcum*	2	3	3	1R	5R	10R	20MS	15M
TA 10569	*T. monococcum* subsp. *monococcum*	4	2	2	10MR	10MR	10MR	30S	40MS
TA 10573	*T. monococcum* subsp. *aegilopoides*	6	7	7	10M	5M	10R	5R	10R
TA 10574	*T. monococcum* subsp. *monococcum*	3	3	2	1R	5R	20R	15MS	20MS
TA 10587	*T. monococcum* subsp. *monococcum*	7	6	6	50M	1R	1R	10MS	20M

TA 10588	*T. monococcum* subsp. *monococcum*	3	2	2	20R	5R	NA	5M	40S
TA 10593	*T. monococcum* subsp. *aegilopoides*	1	7	6	40S	40S	60S	10R	20M
TA 10595	*T. monococcum* subsp. *aegilopoides*	2	6	7	40MS	10MS	20MS	40S	40S
TA 10603	*T. monococcum* subsp. *aegilopoides*	6	5	5	40S	40MS	50MS	50S	NA
TA 10622	*T. monococcum* subsp. *monococcum*	2	3	3	5R	10R	30MR	15MR	20MR
TA 10629	*T. monococcum* subsp. *monococcum*	7	6	5	20MR	30R	5R	20R	NA
TA 10630	*T. monococcum* subsp. *monococcum*	2	2	2	1R	1R	1R	5R	20S
TA 10634	*T. monococcum* subsp. *monococcum*	4	3	2	5R	1R	1R	5M	30MS
TA 10642	*T. monococcum* subsp. *monococcum*	3	3	2	5R	1R	5R	5M	25MS
TA 10652	*T. monococcum* subsp. *monococcum*	2	2	2	10MR	20MR	20MR	15MS	20MS
TA 10876	*T. urartu*	3	2	3	25MS	10M	20MS	40S	50S
TA 10878	*T. urartu*	4	5	6	30S	40S	30S	5S	80S

TA 10884	*T. urartu*	3	6	2	10M	1M	10M	5R	50S
TA 10887	*T. urartu*	4	6	NA	25S	5R	10S	30S	50S
TA 10888	*T. urartu*	2	2	2	30M	20M	5M	10MR	10M
TA 10889	*T. urartu*	1	7	2	15MR	10M	1R	20S	40S
TA 10891	*T. urartu*	7	6	5	10MS	5M	10MS	25S	50S
TA 10900	*T. monococcum* subsp. *aegilopoides*	2	2	2	40M	15MS	10MS	10MS	30M
TA 10902	*T. monococcum* subsp. *aegilopoides*	3	3	4	30MS	20M	5M	15MR	NA
TA 10904	*T. monococcum* subsp. *aegilopoides*	4	2	2	1M	1M	5MR	10M	20M
TA 10916	*T. monococcum* subsp. *aegilopoides*	2	3	3	1R	10MR	10MR	10R	15R
TA 11012	*T. monococcum* subsp. *aegilopoides*	6	5	4	30MS	10M	10M	10MR	20MS
Morocco	*T. aestivum* – Susceptible Check	8	9	9	40S	70S	30S	60S	50S
Joe	*T. aestivum* – Resistant Check	6	6	4	20MR	30MR	30MR	NA	NA

Table A. 5. Field data at the adult plant stage with all replication values for stripe rust, leaf rust, and stem rust in the experiments in 2020 and 2021.

		Stripe Rust						Leaf Rust						Stem Rust					
		2020			2021			2020			2021			2020			2021		
TA Number		Rep 1	Rep 2	Rep 3	Rep 1	Rep 2	Rep 3	Rep 1	Rep 2	Rep 3	Rep 1	Rep 2	Rep 3	Rep 1	Rep 2	Rep 3	Rep 1	Rep 2	Rep 3
TA 136	subsp. *monococcum*	30 MR	5MR	20 MR	25 MR	10 MR	15 MR	10 MR	20 MR	10R	15 MR	10 MR	15 MR	70S	20 MS	15S	10 MS	1MS	5MR
TA 177	subsp. *aegilopoides*	25 M	10R	10 MR	10 MR	15 M	1R	30 MR	20 MR	20 MR	20 M	15 M	20 M	NA	20 MS	20 M	40S	30 MS	30S
TA 190	subsp. *aegilopoides*	20 M	10R	10 MR	15 MR	15 MR	10 MR	20 MR	20 MR	15 MR	20 MR	20 MR	20 MR	NA	15 MS	20 MS	15S	5MS	15 M
TA 249	subsp. *aegilopoides*	15 MR	1R	10R	5R	10 MR	10 MR	15 MR	10 MR	10R	20 M	10 MR	20 MR	20 M	15 M	10 M	20 MS	10 M	15 MS

TA	subsp.	20	25	25	10	10	20	30	10	10	15	15	20	10	10	20	10	10	10
252	*aegilopoides*	MR	M	M	MR	MR	M	M	MR	MR	M	MR	MR	M	MR	MS	M	MR	MR
TA	subsp.	10	5M	20	15	5M	10	20	10	20	20	20	20	10	10	15	10	5M	10
261	*aegilopoides*	MR	R	M	MR	R	MR	MR	MR	MR	M	MR	M	MR	MR	MR	MR	R	M
TA	subsp.	15	15	30	10	20	10	30	20	25	15	15	15	NA	20	10	60S	10	50S
284	*aegilopoides*	MR	M	M	M	M	MR	M	MR	MS	M	M	M		M	M		MS	
TA	subsp.	20	10	20	10R	5M	5M	20	20	15	15	15	15	20	20	20	10	5M	20
285	*aegilopoides*	MR	MR	M		R	R	MR	MR	MR	M	MR	MR	MS	MR	MS	MS		MS
TA	subsp.	30	15	10	30	20	10	25	20	20	15	20	15	NA	15	20	15S	15	30S
299	*aegilopoides*	M	MR	MR	MS	M	MR	MR	MR	M	MR	MR	MR		M	M		M	
TA	subsp.	20	5M	15	10	5R	5R	10	15	20	10	10	10	30	15	10	10	1M	25S
306	*aegilopoides*	MR	R	MR	MR			MR	MR	MR	M	M	M	MS	M	MR	MR		
TA	subsp.	30	5R	20	15	5M	15	30	20	15	15	10	20	40S	30	20	30S	30S	20S
316	*aegilopoides*	M		MR	M	R	MR	MR	MR	MR	MS	MS	M		MS	M			

TA	subsp.	20	5M	15	15	15	10	20	20	20	20	20	20	30	20	15	5M	10	10
346	*aegilopoides*	M	R	MR	M	M	MR	MR	MR	MR	M	M	M	M	M	M		MR	M
TA	subsp.	20	15	10	25	15	10	30	20	30	15	15	20	30S	30	20	10	5M	5M
362	*aegilopoides*	M	MR	MR	M	MR	MR	M	MR	MR	MR	M	M		MS	MS	MS		S
TA	subsp.	30	20	10	20	10	1R	25	20	25	15	15	15	30S	30	20	30S	30S	30S
394	*aegilopoides*	M	M	MR	M	MR		MR	M	M	M	M	MR		MS	MS			
TA	subsp.	NA	15	5R	5M	10	5R	20	10	20	15	20	20	20	25	15	10	5M	50S
396	*aegilopoides*		M		R	M		MR	MR	MR	M	M	MR	MS	MS	MS	M	S	
TA	subsp.	20	20	5R	5M	5R	10	30	20	20	20	15	20	10	15	15	5M	5M	10R
408	*aegilopoides*	M	M		R		MR	M	MR	M	MR	M	MR	MS	MS	MR			
TA	subsp.	15	5R	5R	20	5R	10	30	25	20	20	20	20	10	10	10	5M	10	10
412	*aegilopoides*	MR			MR		MR	M	M	MR	M	M	MR	MR	MS	MR		MS	MR
TA	subsp.	25	10	5R	25	10	30	30	20	20	15	10	15	30S	20	15	5M	25S	10
447	*aegilopoides*	M	MR		M	M	M	M	MR	MR	MR	MR	M		MS	MS	S		MS

TA	subsp.	25	5R	15	25	15	10	30	20	25	20	20	20	30	20	20	10	15	10
466	*aegilopoides*	M		M	M	M	MR	MR	MR	M	M	M	MR	MS	MS	MS	MS	MS	M
TA	subsp.	10R	10	10	10	5R	5M	30	10	10	10	20	15	40	30	20	5M	15	10
473	*aegilopoides*		MR	MR	MR		R	MR	MR	MR	M	M	M	MS	MS	MS	S	M	M
TA	subsp.	20	20	10	15	10	15	20	20	10R	15	15	20	15	15	10R	5M	15S	10
502	*aegilopoides*	M	M	MR	MR	MR	MR	MR	M		MR	MR	MR	MR	MS		S		MS
TA	subsp.	20	20	5R	20	20	20	20	10	10	15	20	20	15	20	20	5M	10	10
534	*aegilopoides*	M	MR		MR	MR	MR	M	MR	MR	MR	MR	M	MS	MS	MS		MR	MS
TA	subsp.	10	10	10	20	5R	10	20	10	10	25	15	15	15	10	10	5M	10	10
544	*aegilopoides*	MR	MR	MR	M		M	M	MR	MR	M	MR	M	MR	MR	M		MR	MS
TA	subsp.	30	10	20	10	1R	5M	30	10R	5R	10	10	15	25	25	15	1M	5R	10
580	*aegilopoides*	M	MR	MR	MR		R	MR			MR	MR	MR	MS	MS	MS	R		M
TA	subsp.	10	30	10	25	5R	20	30	10	20	20	20	15	15	20	15	5M	5M	10
585	*aegilopoides*	MR	M	MR	M		MR	M	MR	MR	M	M	MR	M	MS	MR	S	R	MS

TA	subsp.	20	30	5R	20	10	10	30	30	15	20	20	20	10	20	20	10	10	20
593	*aegilopoides*	M	M		M	MR	MR	MR	M	MR	M	M	MR	MS	MS	MS	M	MR	MS
TA	subsp.	30	40	10R	25	NA	10	25	20	10	25	20	20	30S	20	20	30S	20	30
661	*aegilopoides*	M	M		M		MR	MR	MR	MR	MS	M	M		MS	MS		MS	MS
TA	subsp.	NA	15	10	25	5R	10	15	30	25	15	10	15	20	15	20	10	20	15
686	*aegilopoides*		MR	MR	M		MR	MR	M	M	M	M	MR	MR	MS	MS	MS	MS	MS
TA	*T. urartu*	NA	15	NA	50	30	40	30	20	20	25	NA	20	30S	30	30	30S	40S	40S
709			MR		MS	MS	MS	MS	M	MS	M		M		MS	MS			
TA	*T. urartu*	15	5R	5R	20	5R	10	30	25	25	25	20	25	20	30	15	10	20	10
721		MR			MR		MR	MS	M	M	M	M	M	MS	MS	MS	M	M	MS
TA	*T. urartu*	20	10	5R	20	30	5M	30	20	15	20	20	15	30S	20	20	40S	40S	30S
724		M	MR		M	MS	R	MS	MS	M	M	MR	M		MS	MS			
TA	*T. urartu*	5R	10	NA	5R	10	5M	15	15	20	20	20	20	50S	30S	20	15	20S	20
792			MR			MR	R	MR	MR	M	M	M	M			MS	MS		MS
TA	*T. urartu*	20	10	5R	25	20	20	20	20	15	15	20	10	30	30	20	20S	30	15S
800		M	MR		M	MR	M	MR	MR	M	M	M	M	MS	MS	M		MS	
TA	*T. urartu*	20	15	10	30	30	20	25	20	15	20	20	20	30	30	30S	40S	25S	20
810		MR	MR	MR	MS	M	M	MS	MS	MS	M	MR	M	MS	MS				M

TA	*T. urartu*	1R	5R	NA	10R	5R	5R	30	20	20	30	20	15	15	30	15	25S	20	10
827								MS	MS	M	MS	MS	M	MS	M	MS		MS	M
TA	*T. urartu*	10	10	5R	25	20	50	25	20	20	10	15	15	40S	30	20	50S	30S	40S
832		M	MR		M	M	MS	M	MS	MS	M	M	MR		MS	MS			
TA	*T. urartu*	10	5R	5R	25	10	30	20	20	15	15	10	20	30S	30	20	40S	30	25S
841		MR			MR	MR	M	M	MS	M	M	MS	M		MS	MS		MS	
TA	*T. urartu*	20	10	5R	20	20	30	40	30	30	40S	25	40	30	20	20	NA	15	10
850		M	MS		MS	M	MS	MS	MS	MS		MS	MS	MS	MS	M		MR	M
TA	subsp.	10	5R	15	10R	5R	10	20	20	15	10	15	20	20	20	10	15S	5M	10
1212	*aegilopoides*	MR		M			MR	MR	MR	MR	M	M	MR	MS	M	M			M
TA	subsp.	20	10	10	20	10	5R	20	15	10	15	20	15	25	30	20	20S	10	20S
1266	*aegilopoides*	M	MR	M	M	MR		MR	MR	MR	M	M	M	MS	MS	MS		MS	
TA	*T. urartu*	5R	5R	5R	15	25	5R	15	15	15	15	15	15	20	20	20	60S	40S	50S
1282					MR	M		MR	MR	MR	M	M	M	MS	MS	MS			
TA	*T. urartu*	20	NA	5R	20	10	30	20	20	20	10	10	15	20	25	20	50S	40S	50S
1313		M			M	MR	MS	M	M	M	M	MR	MR	M	MS	MS			
TA	*T. urartu*	10	10	NA	20	30	25	30	15	20	15	15	20	30	20	25	50S	40S	30S
1314		MR	MR		MR	M	MS	M	MS	MS	MS	MR	M	MS	MS	MS			
TA	*T. urartu*	20	15	5R	20	10	NA	30	30	20	20	15	15	20	20	20	50S	30	40S
1315		MR	MR		MR	MR		MR	MR	M	M	M	M	MS	MS	MS		MS	

TA 2012	subsp. *aegilopoides*	15 MR	1R	5R	5R	10 MR	5M R	25 MR	20 MR	20 MR	15 MR	20 MR	20 MR	5M R	10 MR	15 MR	5M R	10 M	5M R
TA 2022	subsp. *aegilopoides*	25 M	20 M	15 MR	20 M	10 MR	20 M	15 MR	25 M	20 MR	15 M	20 M	25 MR	15 MR	10 M	20 MS	10 M	15 M	15 M
TA 2025	subsp. *monococcum*	30 M	25 M	20 M	20 M	10 MR	10 MR	20 MR	20 MR	20 MR	25 MR	20 MR	20 MR	15 M	20 MS	10 MS	10 MR	10 MR	15 MR
TA 2035	subsp. *monococcum*	20 M	30 M	10 MR	15 M	10 MR	10 MR	20 MR	20 MR	20 MR	20 M	25 MR	20 M	20 M	20 MS	15 MS	5M	20S	5M R
TA 2716	subsp. *monococcum*	10R	20 M	10 MR	15 M	5R	NA	30 M	10 MR	10 MR	15 MR	20 MR	20 MR	25 MS	30S	30 MS	10S	20 MS	10 MS
TA 2719	subsp. *monococcum*	5R	5R	5R	15 M	20 MR	10 MR	20 MR	15 MR	20 MR	10 MR	15 MR	15 MR	10 MR	15 MR	15 MR	5R	5R	5R
TA 2720	subsp. *monococcum*	30 M	30 M	NA	20 MR	10 MR	10R	30 M	30 M	15 MR	10 M	15 MR	15 M	25S	5M S	20S	1S	5M	5M R

TA	subsp.	20	30	NA	10	10	5M	30	30	20	15	15	15	20S	20	25	5M	5M	5M
2723	*monococcum*	MR	M		MR	MR	R	M	MR	M	MR	M	MR		MS	MS	S	S	
TA	subsp.	30	30	10	5M	10	10	15	15	15	10	15	15	30	30	30	10	10	10
2724	*monococcum*	M	M	MR	R	MR	M	MR	MR	MR	MR	MR	MR	MS	MS	MS	MS	MS	MS
TA	subsp.	25	20	10	15	10	1R	20	25	10	20	20	25	10	15	10	10	10	10
10418	*monococcum*	M	MR	MR	M	MR		MR	MR	MR	MR	MR	MR	MS	MS	MR	M	MR	M
TA	subsp.	10	20	15	10	5R	10	25	20	25	30	20	20	60S	20	40	20S	10	40S
10569	*monococcum*	MR	M	MR	MR		MR	MR	MR	MR	M	M	MR		MS	MS		MS	
TA	subsp.	NA	25	1R	5R	10	5M	15	20	15	25	20	20	10	15	10	5M	5M	10
10573	*aegilopoides*		M			MR	R	MR	MR	MR	M	M	MR	MR	MS	MR			MR
TA	subsp.	15	10	15	5R	5R	5M	10	10R	10R	15	15	15	25	20	15	10S	5M	10S
10574	*monococcum*	MR	MR	M			R	MR			M	MR	MR	MS	MS	MS		S	
TA	subsp.	5R	10	5R	5M	5M	5R	15	10	10	10	15	15R	15	30S	20	1M	5R	5M
10587	*monococcum*		MR		R	R		MR	MR	MR	MR	MR		MS		MS			

TA	subsp.	20	15	20	5R	1R	1R	15	15R	15	15	25	15	10	10	15	10	10	10R
10588	*monococcum*	M	MR	M				MR		MR	M	MR	M	MS	MS	M	MR	M	
TA	subsp.	10	15	10	10	10	30	20	30	20	40	25	20	10	20	20	20	10	10
10593	*aegilopoides*	MR	M	MR	MR	MR	MR	MS	M	M	MS	M	M	M	MS	MS	M	M	MS
TA	subsp.	20	15	5R	5M	15	10	30	20	30	25	20	25	30S	30S	10	20	20S	20S
10595	*aegilopoides*	M	M		R	MR	MR	MS	MS	MS	MS	MS	M			MS	MS		
TA	subsp.	5R	10	5R	20	1R	10	30	30	20	20	15	25	20	25	25	30	15	10
10603	*aegilopoides*		MR		MR		MR	MS	MS	MS	MS	M	M	MS	MS	MS	MS	MS	M
TA	subsp.	10	30	20	5M	25	20	20	20	10	20	25	20	10	20	15	30	10	10
10629	*monococcum*	MR	M	M	R	M	MR	MR	MR	MR	M	MR	M	MR	MR	MR	MR	MR	MR
TA	subsp.	20	15	10	5M	10	10R	25	10R	5R	15	20	20	40S	20	25	15S	10	5M
10630	*monococcum*	M	MR	MR	R	MR		M			MR	MR	MR		MS	MS		MR	R
TA	subsp.	20	15	20	10	5M	NA	20	10	20	20	15	20	20S	20	15	5M	5M	10
10634	*monococcum*	M	MR	M	MR	R		MR	MR	MR	MR	MR	MR		MS	MS	S	R	MR

TA	subsp.	20	5M	10	5M	5R	5R	10	30	5R	15	15	20	15	20S	30S	5M	10R	5M
10642	*monococcum*	MR	R	MR	R			MR	MR		M	MR	MR	MS			S		R
TA	subsp.	50	10	20	5M	5M	20R	30	30	20	20	25	25	10	10	15	10	10	15
10652	*monococcum*	M	MR	M	R	R		MR	MR	MR	M	M	M	M	MR	MR	MR	MR	MR
TA	*T. urartu*	5R	5R	5R	10	5R	10	25	20	20	25	20	15	20	30S	20	50S	50S	30S
10876					MR		MR	MR	M	MR	M	M	M	MS		MS			
TA	*T. urartu*	10	10	5R	15	25	20	60	30	40	20	30S	40	40S	20	10	25S	20S	50S
10878		MR	MR		M	M	MS	MS	MS	MS	M		MS		MS	M			
TA	*T. urartu*	15	10	10	5R	5R	5R	20	10	10R	20	20	20	30	30	25	20	30S	25S
10884		M	MR	MR				M	M		M	M	MR	MS	MS	MS	MS		
TA	*T. urartu*	20	5R	5R	5M	10	1R	10	15	20	15	15	20	30	25	20	15S	15	20S
10887		M			R	M		MR	MR	M	MR	MR	M	MS	MS	MS		MS	
TA	*T. urartu*	30	10	NA	5R	5R	10R	20	20	15	15	20	15	5M	NA	10	5M	5M	10
10888		M	MR					MR	M	M	M	M	M	R		MR	R	R	MR
TA	*T. urartu*	15	1R	NA	5M	5R	10	10	10	15	15	15R	20	20	20	30	10	25S	20
10889		MR			R		MR	MR	MR	MR	MR		MR	MS	MS	MS	MS		MS
TA	*T. urartu*	10	1R	5R	5M	1R	5R	15	10	20	20	15	30S	40S	20S	40S	15	30S	30S
10891		MR			R			MR	MR	M	M	MR					MS		

TA	subsp.	30	10	10	5M	NA	10	10	10	10	20	20	20	20	20	20	5M	5M	10
10900	*aegilopoides*	M	MR	MR	R		MR	MR	MR	MR	MR	M	M	MS	MS	MS	S	S	M
TA	subsp.	30	5M	5R	30	20	20	20	20	10	20	20	25	30	20	20	15	10	15
10902	*aegilopoides*	M	R		M	MS	M	M	MR	MR	M	M	M	M	M	M	M	M	MS
TA	subsp.	20	20	NA	25	10	15	20	15	10	20	15	20	40S	25	30	10S	25S	10
10904	*aegilopoides*	MR	M		M	M	M	M	MR	MR	M	M	M		MS	MS			M
TA	subsp.	1R	5R	5R	15	15	5M	10	15	10	20	15	15	10R	20	10	10	10	15
10916	*aegilopoides*				MR	MR	R	MR	MR	MR	M	M	M		MR	MR	MR	MR	MR
TA	subsp.	10	5R	10	10	15	10	10	15	10R	15	20	15	30	20	20	10	10	5M
11012	*aegilopoides*	MR		MR	MR	MR	MR	MR	MR		MR	MR	MR	MS	MS	MS	MS	MS	
TA	subsp.	NA	NA	NA	5M	5R	5M	NA	NA	NA	15	10	20	NA	NA	NA	5M	10	5M
10622	*monococcum*				R		R				M	MR	M				R	MR	R
TA	subsp.	NA	NA	NA	5R	1R	5R	NA	NA	NA	15	20	20	NA	NA	NA	NA	5M	10
250	*aegilopoides*										MR	MR	M					R	MR

TA 278	subsp. *aegilopoides*	NA	NA	NA	20 MR	30 MS	30 MS	NA	NA	NA	NA	20 M	20 M	NA	NA	NA	30S	20S	NA
TA 309	subsp. *aegilopoides*	NA	NA	NA	10 MR	5R	10 MR	NA	NA	NA	20 MR	20 M	15 M	NA	NA	NA	15 M	10 MR	10 M
TA 366	subsp. *aegilopoides*	NA	NA	NA	NA	20 MR	15 MR	NA	NA	NA	20 M	20 M	20 MR	NA	NA	NA	10 M	5M	10 MR
TA 438	subsp. *aegilopoides*	NA	NA	NA	5R	20 MR	25 MR	NA	NA	NA	NA	NA	20 M	NA	NA	NA	25 MR	10 M	NA
TA 443	subsp. *aegilopoides*	NA	NA	NA	15 MR	20 MR	15 MR	NA	NA	NA	20 M	10 M	NA	NA	NA	NA	10 M	15 M	10 MS
TA 479	subsp. *aegilopoides*	NA	NA	NA	10 MR	15 MS	10 MR	NA	NA	NA	20 M	20 M	20 M	NA	NA	NA	10 MS	NA	15 MS
TA 488	subsp. *aegilopoides*	NA	NA	NA	10 MR	10 MR	15 M	NA	NA	NA	15 M	20 M	NA	NA	NA	NA	5M	30S	10 MS

TA 526	subsp. *aegilopoides*	NA	NA	NA	15 MR	15 M	NA	NA	NA	NA	20 M	15 M	20 M	NA	NA	NA	NA	10 M	15 MR
TA 590	subsp. *aegilopoides*	NA	NA	NA	20 MR	NA	30 M	NA	NA	NA	20 M	20 M	25 M	NA	NA	NA	5M	15 M	5M
TA 632	subsp. *aegilopoides*	NA	NA	NA	25 MR	5R	30 M	NA	NA	NA	20 MR	15 M	NA	NA	NA	NA	10 MR	NA	5M
TA 647	subsp. *aegilopoides*	NA	NA	NA	10 MR	NA	25 M	NA	NA	NA	20 M	20 MR	20 M	NA	NA	NA	10 M	NA	10 M
TA 748	subsp. *aegilopoides*	NA	NA	NA	20 M	NA	25 M	NA	NA	NA	20 MR	20 M	20 M	NA	NA	NA	10 M	NA	10 M
TA 756	subsp. *aegilopoides*	NA	NA	NA	15 M	15 MR	25 M	NA	NA	NA	15 M	20 M	20 M	NA	NA	NA	10 MR	20 M	5M S
TA 790	*T. urartu*	NA	NA	NA	20 M	10 MR	20 M	NA	NA	NA	15 M	15 M	15 M	NA	NA	NA	NA	30S	10 MS
TA 834	*T. urartu*	NA	NA	NA	30 MS	20 M	60 MS	NA	NA	NA	15 MR	20 M	NA	NA	NA	NA	15 MS	20S	25 MS

TA 1254	subsp. *aegilopoides*	NA	NA	NA	15 MR	10 M	5R	NA	NA	NA	20 M	20 M	20 M	NA	NA	NA	5M	15 M	NA
TA 2021	subsp. *aegilopoides*	NA	NA	NA	25 M	NA	25 MR	NA	NA	NA	20 M	20 M	20 M	NA	NA	NA	5M R	10 MR	10 MR
TA 2032	subsp. *monococcum*	NA	NA	NA	25 M	20 MR	30 MR	NA	NA	NA	20 MR	20 MR	NA	NA	NA	NA	10 MR	20 MR	5M
TA 10546	subsp. *aegilopoides*	NA	NA	NA	15 MR	NA	25 MR	NA	NA	NA	25 M	15 MR	20 MR	NA	NA	NA	5M	10 M	10 MR
TA 10581	subsp. *monococcum*	NA	NA	NA	15 MR	15R	15 MR	NA	NA	NA	20 MR	20 MR	20 M	NA	NA	NA	10R	15 MR	15 MR
TA 10612	subsp. *monococcum*	NA	NA	NA	15 MR	10R	5R	NA	NA	NA	20 MR	20 MR	20 MR	NA	NA	NA	5M R	10 MR	5M
TA 10636	subsp. *monococcum*	NA	NA	NA	20 M	15 M	15R	NA	NA	NA	15 M	20 M	15 MR	NA	NA	NA	10S	25S	20S

TA 10873	*T. urartu*	NA	NA	NA	10 MR	NA	10 MR	NA	NA	NA	NA	NA	15 M	NA	NA	NA	NA	NA	NA
TA 10879	*T. urartu*	NA	NA	NA	10 MR	5MR	5R	NA	NA	NA	15 M	20 M	20 M	NA	NA	NA	10S	10 MS	25 MS
TA 10896	subsp. *monococcum*	NA	NA	NA	25 M	NA	NA	NA	NA	NA	20 MR	NA	20 MR	NA	NA	NA	NA	10 M	10 M
TA 10907	subsp. *aegilopoides*	NA	NA	NA	25 MR	NA	NA	NA	NA	NA	20 M	20 MS	20 M	NA	NA	NA	5MS	10 MS	10 M
TA 10909	subsp. *aegilopoides*	NA	NA	NA	5R	5R	5MR	NA	NA	NA	15 M	20 MR	20 MR	NA	NA	NA	NA	NA	NA
Morocco	*T. aestivum* - Susceptible Check	80S	60S	60S	NA	NA	NA	100S	100S	100S	NA	NA	NA	60S	70S	60S	NA	NA	NA
Avery	*T. aestivum* -	NA	NA	NA	70S	70S	60S	NA	NA	NA	70S	60S	60S	NA	NA	NA	50S	50S	60S

	Susceptible Check																	
King Bird	*T. aestivum* - Susceptible Check	20 MR	15 MR	15 MR	NA	NA	NA	15 MR	15 MR	20 MR	NA	NA	NA	5MR	10R	10 MR	NA	NA	NA
Joe	*T. aestivum* - Resistant Check	NA	NA	NA	15 MR	30 MS	20 MR	NA	NA	NA	20 M	15 M	20 MR	NA	NA	NA	10 MR	10 MR	5M