# Evaluation of a Collection of Wild Timopheevi Wheat for Resistance to Disease and Arthropod Pests

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**ABSTRACT**

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Wild relatives of wheat (*Triticum aestivum*) are important sources of genes for resistance to disease and insect pests. A collection of the wild tetraploid wheat species *Triticum timopheevii* var. *araraticum* was evaluated for reaction to Hessian fly (*Mayetiola destructor*), wheat curl mite (*Eriophyes tulipae*), and six foliar diseases: leaf rust (caused by *Puccinia recondita* f. sp. *tritici*), stem rust (caused by *Puccinia graminis* f. sp. *tritici*), stripe rust (caused by *Puccinia striiformis*), powdery mildew (caused by *Blumeria graminis* f. sp. *tritici*), tan spot (caused by *Pyrenophora tritici-repentis*), and Septoria blotch (caused by *Septoria tritici*). All accessions tested were resistant to Septoria blotch and a very high percentage were resistant to tan spot. Resistance was detected to four obligate fungal pathogens, although accessions with leaf rust resistance were more frequent in the collection than those with resistance to stripe rust, stem rust, or powdery mildew. Resistance to Hessian fly biotype D and wheat curl mite was detected in 91 and 27% of the tested accessions, respectively. Variation was noted in reaction of a subset of accessions when tested with biotype L of Hessian fly. Thirty-one accessions with intermediate to high levels of resistance to at least five pests each were identified. Accessions from northern Iraq had the highest frequency of resistances. This collection of wild timopheevi wheat represents a diverse gene pool that may be useful for improvement of common wheat.

Breeding for resistance to a wide range of disease and insect pests is a major emphasis for most wheat (*Triticum aestivum* L. emend. Thell) improvement programs. However, the agricultural deployment of genetic resistance frequently places selection pressure on the pathogen or insect population, resulting in the loss of effective crop resistance. Schemes directed at increasing the durability of genetic resistance, such as gene deployment or gene pyramiding, require that a sufficient number of diverse resistance genes be available. The wild and domestic relatives of common wheat are important sources of additional genes for resistance to disease and insect pests (18).

There are two groups of tetraploid wheats, the emmer wheats, *Triticum turgidum* L. (2n = 28, AABB), and the timopheevi wheats, *Triticum timopheevii* (Zhuk.) Zhuk., (2n = 28, $A^tA^tGG$), which consist of two forms, the domesticated form frequently referred to as either *Triticum timopheevii* (Zhuk.) Zhuk. var. *timopheevii* or T. *timopheevii* (Zhuk.) Zhuk. subsp. *timopheevii* and the wild form known as *Triticum timopheevii* (Zhuk.) Zhuk. var. *araraticum* (Jakubz.), synonymous with *T. araraticum* (Jakubz.) and *T. timopheevii* (Zhuk.) Zhuk. subsp. *armeniacum* (Jakubz.) van Slageran. The $A^t$ and G genomes of the timopheevi wheats are closely related to the A and B genomes, respectively, of emmer wheat and common wheat (2n = 42, AABBDD). *T. timopheevii* may be directly hybridized with common wheat; however, fertility of hybrids is low because of differences in chromosome number and incomplete chromosome pairing. Wild *T. timopheevii* has not been widely used in wheat improvement, but the cultivated form of the species has been used to a greater extent (18). Two named genes conferring resistance to stem rust (caused by *Puccinia graminis* Pers.:Pers. f. sp. *tritici* Eriks. & E. Henn.), *Sr*36 and *Sr*37, were transferred to common wheat from *T. timopheevii* var. *timopheevii*, and *Sr*40 was transferred from *T. timopheevii* var. *araraticum* (1,2,9,19,22). Genes for resistance to powdery mildew (caused by *Blumeria graminis* (DC. ) E. O. Speer f. sp. *tritici* Em. Marchal [syn. *Erysiphe graminis* f. sp. *tritici*]) and leaf rust (caused by *Puccinia recondita* Roberge ex Desmasz. f. sp. *tritici*), *Pm*6 and *Lr*18, also were transferred to common wheat from cultivated *T. timopheevii* (1,10,14).

Cultivated *T. timopheevii* was domesticated in a restricted region of western Georgia and has a very narrow distribution in nature (4). The species is thought to have existed for a historically short period of time, and little diversity in morphology, karyotype, or seed storage proteins has been observed in cultivated *T. timopheevii* (4,13). It was concluded by McIntosh and Gyarfus (19) that cultivated *T. timopheevii* may have as few as three genes for stem rust resistance (*Sr*36, *Sr*37, and possibly a third, unnamed gene present in the common wheat derivative C.I. 13005) (2). Alternatively, the wild form of the species is found throughout the Middle East and surrounding areas, including eastern Turkey, northern Iraq, northeastern Iran, Armenia, and Azerbaijan (27). Wild timopheevi is characterized by a high degree of C-banding polymorphism and karyotypic rearrangements (3). Because the wild *T. timopheevii* var. *araraticum* is found in more ecologically diverse areas than *T. timopheevii* var. *timopheevii*, this form of the species may have more diverse genes for pest resistance.

Gill et al. (12) reported reactions to leaf rust, Hessian fly (*Mayetiola destructor* Say), greenbug (*Schizaphis graminum* (Rond.)), and wheat streak mosaic virus of a portion of the wild timopheevi wheat collection maintained by the Wheat Genetics

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Resource Center (WGRC) in Manhattan, Kansas. Resistance to Hessian fly and *P. recondita tritici* was detected; however, no *T. timopheevii* var. *araraticum* accessions resistant to greenbug or wheat streak mosaic virus were identified. Since that time, additional leaf rust and Hessian fly screening was conducted, and screening for resistance to a range of economically important wheat pathogens and insect and mite pests has been done by the WGRC and cooperators at other institutions. Our objective was to evaluate the collection for resistance to biotic stresses in order to facilitate its use. In this paper, we report the results of screening the WGRC *T. timopheevii* var. *araraticum* collection for resistance to six foliar diseases of wheat, Hessian fly, and wheat curl mite.

## MATERIALS AND METHODS

Seeds of the 301 *T. timopheevii* var. *araraticum* accessions used in this study are maintained by the WGRC at Kansas State University in Manhattan. Accessions were contributed by the University of California, Riverside, Kyoto University, Japan, and the Vavilov Institute, Russia. Geographic origin of the accessions is shown in Figure 1. While accessions are available from all countries where wild timopheevi wheat occurs, only northern Iraq is well represented in the collection. Over 80% of the accessions were collected from three regions covering the area of distribution of *T. timopheevii* var. *araraticum* in northern Iraq (Table 1). Fifteen percent of accessions were collected in Armenia and Azerbaijan, whereas only five and nine accessions were collected in Turkey and Iran, respectively.

Screening of accessions for resistances to leaf rust and tan spot (caused by *Pyrenophora tritici-repentis* (Died.) Drechs.), Septoria blotch (caused by *Septoria tritici* Roberge in Desmasz.), and Hessian fly was at the WGRC in cooperation with the Departments of Plant Pathology and Entomology and the USDA-ARS at Kansas State University, Manhattan. Accessions were screened for reaction to powdery mildew at the USDA-ARS/North Carolina State University facilities at Raleigh. Stem rust testing was done at the USDA-ARS/University of Nebraska facilities at Lincoln and screening for stripe rust reaction was carried out at the Oregon State University Columbia Basin Field Station in Pendleton. Testing of accessions for reaction to the wheat curl mite was done at the Agriculture and Agrifood Canada Research Station at Lethbridge, Alberta.

Leaf and stem rust screenings were carried out by inoculating five to 10 seedlings with *P. recondita* f. sp. *tritici* culture PRT US6 (avirulence/virulence formula *Lr*2a, 9, 16, 18, 19, 24 / *Lr*1, 2c, 2d, 3a, 10, 11, 17) and *P. graminis* f. sp. *tritici* culture TMN (avirulence/virulence formula *Sr*8a, 9, 17, 30 / *Sr*5, 6, 7b, 9e, 11, 21, 36), respectively.


**Fig. 1.** Geographic distribution and collection sites of *Triticum timopheevii* var. *araraticum*. Shaded areas indicate distribution of the species. Collection sites of accessions maintained at the Wheat Genetics Resource Center are indicated by diamonds.

**Table 1.** Numbers of *Triticum timopheevii* var. *araraticum* accessions with resistant (R), moderately resistant (MR), heterogeneous (H), or susceptible (S) reactions to five leaf diseases, wheat curl mite, and Hessian fly

| Geographic origin | No. of accessions | Leaf rust PRTUS6[a] | | | Stem rust TMN[b] | | | Stripe rust CDL-43[c] | | | Powdery mildew isolate 9[d] | | | Tan spot[e] | | Wheat curl mite | | | Hessian fly | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | R | MR | S | R | MR | S | R | MR | S | R | MR | S | R | S | R | MR | S | R | H[f] | S |
| Armenia | 18 | 1 | 3 | 14 | 0 | 1 | 13 | 0 | 1 | 5 | 1 | 8 | 9 | 10 | 1 | 0 | 5 | 11 | 0 | 2 | 1 |
| Azerbaijan | 28 | 0 | 4 | 23 | 3 | 0 | 20 | 0 | 9 | 4 | 0 | 8 | 17 | 9 | 3 | 1 | 2 | 20 | 3 | 1 | 1 |
| Iran | 8 | 1 | 2 | 6 | 1 | 0 | 5 | 0 | 0 | 2 | 0 | 0 | 6 | 4 | 1 | 0 | 1 | 5 | 0 | 1 | 3 |
| Iraq (regions) | | | | | | | | | | | | | | | | | | | | | |
| Sawarah Tuka | 56 | 21 | 23 | 12 | 0 | 2 | 28 | 0 | 3 | 12 | 0 | 24 | 26 | 16 | 1 | 0 | 2 | 46 | 18 | 15 | 3 |
| Shaqlala | 148 | 72 | 37 | 39 | 3 | 4 | 70 | 0 | 30 | 23 | 11 | 70 | 50 | 46 | 3 | 17 | 30 | 64 | 32 | 38 | 5 |
| Sulaymaniyah | 38 | 13 | 18 | 7 | 1 | 3 | 21 | 0 | 7 | 8 | 7 | 15 | 14 | 9 | 4 | 1 | 4 | 24 | 9 | 5 | 0 |
| Turkey | 5 | 0 | 2 | 3 | 3 | 1 | 0 | 0 | 2 | 2 | 0 | 2 | 2 | 3 | 0 | 2 | 0 | 3 | 1 | 2 | 0 |
| Total | 301 | 108 | 89 | 104 | 11 | 11 | 157 | 0 | 52 | 56 | 19 | 127 | 124 | 97 | 13 | 21 | 44 | 173 | 63 | 64 | 13 |
| No. tested | ... | | 301 | | | 179 | | | 108 | | | 270 | | | | | 110 238 | | | 140 | |

[a] R ≤ 23X, MR ≤ 78X, and S >78X where first and second digits indicate relative amount of sporulation and lesion size, respectively, and X = mixed damage.
[b] R ≤ 1, MR ≤ 2 and S ≥ 3 on a scale of 0 to 4, where 0 = lowest infection.
[c] R ≤ 3, MR ≤ 6 and S ≥ 7 on a scale of 0 to 9, where 0 = lowest infection.
[d] R ≤ 2, MR ≤ 4 and S ≥ 5 on a scale of 0 to 9, where 0 = lowest infection.
[e] Accessions with mean infected leaf area similar to the resistant check were scored as R.
[f] Heterogeneous; accessions contain resistant and susceptible plants.

Seedlings were inoculated with an oil suspension of urediniospores according to the procedure of Browder (5). Stem rust ratings were on a scale of 0 to 4 according to Stakman et al. (25).

Leaf rust ratings were coded by using the system of Browder and Young (6). The first digit of each code indicates the relative amount of sporulation and the second digit indicates the relative lesion size, both on a scale of 0 to 9. A letter following the digits describes the appearance of the tissue surrounding the lesion (C = chlorotic, P = pale, and X = mixed). Fifteen accessions giving low infection type (≤14×) when inoculated with PRTUS6 had been crossed to local wheat cultivars. These accessions were screened for resistance to PRTUS3 (avirulence/virulence formula *Lr*1, 2a, 2b, 2c, 2d, 3b, 3c, 9, 11, 16, 17, 19, 24 / *Lr*3a, 10, 18) to determine if they had a gene(s) for leaf rust resistance different from *Lr*18.

For stripe rust screening, up to 10 seedlings were inoculated with two pathotypes of *P. striiformis*, CDL-43 (avirulence/virulence formula *Yr*Tye / *Yr*2, 6, 10, 20, 21, 25, 27, 28, 29) and CDL-45 (avirulence/virulence formula *Yr*10, 27, 29 / *Yr*Tye, 2, 6, 20, 21, 25, 28) using a talc-urediniospore mixture. Seedlings were placed in a chamber maintained at 7°C and 100% relative humidity for 36 h, then transferred to a growth chamber at 15°C for 32 days. Readings were recorded on a scale of 0 to 9 as described by Zwer and Qualset (31).

Powdery mildew evaluations were made using a method similar to that described by Cox et al. (8). Five seeds of each accession were planted for evaluation. Inoculations were made 7 days after planting with *B. graminis tritici* isolate no. 9 (avirulence/virulence formula *Pm*8, 17 / *Pm*2, 3a, 3b, 3c, 4a, 4b, 5, 6, 7), that is virulent to the *T. timopheevii*-derived gene *Pm*6. Powdery mildew was scored 11 and 16 days after inoculation and ratings were made on a scale of 0 to 9. Additional seed of accessions with a score of 4 or less were planted and seedlings were inoculated with the *Pm*4 Axminster composite culture (avirulence/virulence formula *Pm*2, 3a, 3b, 4a, 4b, 6, 17 / *Pm*1, 3a, 5, 7, 8, *MA*). Powdery mildew was scored 13 days after inoculation.

For Septoria blotch and tan spot screenings, rows of five seeds per accession were planted in racks holding 18 accessions each along with the wheat cultivars Newton and Karl as susceptible and resistant checks, respectively. Seven sets of accessions were tested. Each experiment included 20 entries and was run as a randomized complete block with three replications.

Inoculations with spores of *S. tritici* were done when seedlings had five fully expanded leaves. After inoculation, plants were placed in a mist chamber that provided continual wetness for 96 h, after which they were moved to the greenhouse where they were kept under a shade cloth to provide low light conditions. The bottom five leaves of each plant were rated for percentage of chlorosis and necrosis 16 to 21 days after inoculation. Each leaf was placed in one of the following categories: 0, 1, 5, 10, 25, 50, 75, or 100% of leaf area affected. Statistical analysis of the data used the analysis of variance (ANOVA) procedure of SAS (SAS Institute, Cary, NC). Accessions with a mean significantly lower than or not significantly different from that of the resistant check Karl were classified as resistant to Septoria blotch. To compare accessions tested in different experiments, a disease severity score, $S$, was calculated for each accession as follows: $S = (\bar{X}_{Ai} / \bar{X}_{Ni})\ \bar{X}_N$, where $\bar{X}_{Ai}$ = mean leaf area affected of accession A in experiment $i$, $\bar{X}_{Ni}$ = mean leaf area affected of Newton in experiment $i$, and $\bar{X}_N$ = mean leaf area of Newton affected in all experiments.

For tan spot screening, seedlings at the three-leaf stage were inoculated with conidia of *P. tritici-repentis* by means of the method of Riaz et al. (23). The top three fully expanded leaves of each plant were rated for percent leaf area affected by tan spot 5 to 7 days after inoculation. Disease ratings, statistical analysis, and calculation of disease severity scores were as described for Septoria blotch. Accessions with a mean leaf area affected significantly lower than Karl, the resistant check, were classified as very resistant. Those with means not significantly different from that of Karl were classified as resistant.

Reaction to the *Ptr* necrosis toxin produced by the tan spot fungus was evaluated by means of the method of Tomás and Bockus (29). One fully expanded leaf on three seedlings per accession was infiltrated with culture filtrate of *P. tritici-repentis* isolate Pt-1c. Symptoms of necrosis were recorded as either present or absent 5 days after infiltration.

The method described by Thomas and Conner (28) was used to determine the reaction of accessions to wheat curl mite. Six seeds of each accession were planted and infested with nonviruliferous mites. Ratings were taken 10 to 14 days after planting. Accessions were classified as susceptible, moderately susceptible, moderately resistant, or resistant based on curling and trapping of the leaves.

Reaction to Hessian fly was determined by means of a method similar to that described by Cartwright and LaHue (7). First-leaf-stage seedlings were infested with eggs of Hessian fly biotype D and plant reaction to larval feeding was assessed 15 to 20 days after infestation. Susceptible plants were stunted and dark green. Plants that were not stunted and that retained their light green color were examined for the presence of dead or live larvae to detect escapes. Accessions with only resistant plants were scored as resistant and accessions with a mixture of resistant and susceptible plants were classified as heterogeneous. Fifteen seed of 15 accessions that were crossed to wheat and were initially scored as resistant, heterogeneous, or susceptible were planted and infested with Hessian fly biotype L. Reaction was scored 15 days following infestation.

## RESULTS

All accessions were screened for reaction to *P. recondita* f. sp. *tritici*. Most of the collection was tested for resistance to *B. graminis* f. sp. *tritici* and wheat curl mite, and more than a third of the lines were screened for stem rust, stripe rust, Hessian fly, tan spot, and Septoria blotch reaction. Resistance was detected to each of the pathogens and pests screened (Table 1). However, the range of reaction types differed among pathogens. Most striking was the lack of variation in the reaction type to *S. tritici* and to the *Ptr* necrosis toxin. All accessions tested had significantly less leaf area affected by Septoria blotch ($P = 0.05$) than Karl, the resistant check. When the Septoria blotch disease rating of each accession was converted to a disease severity score, the *T. timopheevii* var. *araraticum* accessions had scores from 7 to 45% of leaf area affected by Septoria blotch, while Karl averaged 60% of leaf area damaged.

A high percentage of accessions screened from all geographic regions were resistant to tan spot (Table 1). Five of the 97 resistant accessions had ratings lower than Karl and were classified as very resistant. Tan spot disease severity of *T. timopheevii* var. *araraticum* ranged from 2 to 98% of leaf area damaged. Regardless of whether accessions were scored as resistant or susceptible to the tan spot pathogen, none exhibited damage when infiltrated with the necrosis-causing *Ptr* toxin.

There was a wide range of reaction types to the powdery mildew and the rust pathogens. Over half of the accessions had a powdery mildew reaction type of 4 or lower when tested with *B. graminis* f. sp. *tritici* isolate 9 (Table 1). All accessions resistant to isolate 9 also were resistant when tested with the *Pm*4 Axminster composite culture. Accessions highly resistant to *B. graminis* f. sp. *tritici* (rating ≤2 when tested with isolate 9) originated mainly from the region near Sulaymaniyah in northern Iraq. No powdery mildew resistance was detected in the accessions from Iran, while only intermediate levels of resistance were present in accessions from Azerbaijan, Turkey, and the northernmost region of Iraq.

Moderate resistance to *P. recondita* f. sp. *tritici* was widespread in the collection; however, no accessions from Azerbaijan or Turkey were highly resistant (Table 1). The highest frequency of resistance was detected in accessions from northern Iraq. All

15 selected accessions from Iraq that had a low infection type when inoculated with PRTUS6 also had low infection types when tested with PRTUS3, which is virulent on *Lr18*, a gene transferred from the cultivated form of *T. timopheevii* (10).

Resistance to *P. graminis* f. sp. *tritici* was present in the collection at a lower frequency than resistance to *B. graminis* f. sp. *tritici* and *P. recondita* f. sp. *tritici* (Table 1). It is noteworthy that the four accessions tested from Turkey were all resistant to race TMN. Variation within accessions for reaction to *P. graminis* f. sp. *tritici* was noted in 11 of the 27 accessions in which resistance was identified.

While 47% of the tested accessions had intermediate levels of resistance to *P. striiformis* culture CDL-43 (rating ≤6), none exhibited a low infection type (Table 2). When inoculated with culture CDL-45, only 8 of the 108 tested accessions had low or intermediate reactions. Three accessions were highly resistant to CDL-45 but were susceptible to CDL-43. There was little correspondence of reactions to the two *P. striiformis* cultures.

Resistance was detected to both arthropod pests screened. Accessions classified as resistant or moderately resistant to the wheat curl mite were detected from all geographic regions. Though resistance was most frequent in accessions collected in Turkey, the majority of accessions resistant to the wheat curl mite were collected from the Shaqlala region of northern Iraq (Table 1).

Hessian fly resistance was present in accessions from all geographic regions (Table 1). Of the 127 accessions in which Hessian fly resistance was detected, only 63 were uniformly resistant. The others were heterogeneous, containing susceptible as well as resistant plants. Additional testing of 15 selected accessions, originally classified as resistant, heterogeneous, or susceptible gave conflicting results. All accessions were heterogeneous when retested, i.e., containing plants that were stunted and dark green as well as plants that retained their light green color. Dead larvae and live larvae were found on all resistant plants.

Because of differences in the amount of resources necessary to screen seedlings for reaction to different pests and differences in the availability and germination of seed of different accessions, not all lines were screened for reaction to all pests. More than 50% of the collection was tested for reaction to at least five different pests, with 12% of the accessions screened for at least seven different pests. Given that all accessions tested were resistant to Septoria blotch and a large percentage of tested accessions were resistant to Hessian fly and tan spot, accessions of wild timopheevi wheat with multiple pest resistance were expected. Accessions that had some level of resistance to at least three or four pests were frequent (54 and 29% of the collection, respectively). Thirty-one accessions with low or intermediate reactions to at least five pests were identified (Table 2). Of the 39 accessions tested for reaction to seven different pests, three were resistant or moderately resistant to all seven. Accessions with high levels of resistance to multiple pests were also detected. Sixty-one, 25, and 11 accessions were identified having low reactions to three, four, and five different pests, respectively.

## DISCUSSION

The full geographic range of distribution of wild *T. timopheevii* is not well represented by accessions in the WGRC collection. While the collection from northern Iraq is comprehensive, there are few accessions from Armenia, Azerbaijan, Turkey, and Iran. Thus, the entire range of diversity of the species probably has not been tested and patterns of variation may not be representative of the entire species. It appears that the two southernmost collection sites in Iraq possess a higher frequency of resistance to the wheat curl mite, leaf rust, and powdery mildew than do other regions. These two regions also have the greatest karyotypic diversity (3). *Triticum timopheevii* var. *araraticum* is characterized by a high degree of C-banding polymorphism and extensive chromosomal rearrangements, mainly in the form of translocations. Badaeva et al. (3) found the largest number of karyotypic variants in the Shaqlala and Sulaymaniyah regions of Iraq. Our data support the conclusions of these authors that Iraq is the center of diversity of wild timopheevi wheat.

*Triticum timopheevii* var. *araraticum* has at least one gene for resistance to *B. gra-*

**Table 2.** Reactions to leaf, stem, and stripe rust, powdery mildew, tan spot, Septoria blotch, wheat curl mite, and Hessian fly of 31 *Triticum timopheevii* var. *araraticum* accessions with low or intermediate reactions to at least five pests each

| Accession no. | Leaf rust PRTUS6[a] | Stem rust TMN[b] | Stripe rust CDL-43[c] | Powdery mildew isolate 9[c] | Tan spot[d] | Septoria blotch[d] | Wheat curl mite[e] | Hessian fly biotype D[f] |
|---|---|---|---|---|---|---|---|---|
| TA 11 | 17X | 4 | NT[g] | 4 | 27 | 12 | S | R |
| TA 13 | 78X | 4 | NT | 8 | 24 | 12 | R | H |
| TA 34 | 56X | 1 | 5 | 4 | NT | NT | S | R |
| TA 35 | 78X | 4 | NT | 4 | 22 | 7 | S | R |
| TA 38 | 78X | 4 | NT | 6 | 23 | 22 | MR | H |
| TA 40 | 78X | 4 | NT | 3 | 20 | 13 | S | H |
| TA 161 | 78X | 2 | NT | 4 | 11 | 17 | S | NT |
| TA 861 | 56X | 2 | NT | 4 | 26 | 30 | R | H |
| TA 878 | 03C | 4 | 6 | 4 | 7 | 24 | MR | H |
| TA 895 | 03C | 4 | 5 | 4 | 13 | 7 | S | R |
| TA 909 | 02C | 4 | NT | 0 | 15 | 13 | NT | R |
| TA 912 | 02C | 4 | H | NT | 2 | 23 | S | R |
| TA 914 | 03C | 4 | NT | NT | 18 | 23 | R | R |
| TA 917 | 88P | 4 | NT | 4 | 20 | 23 | R | R |
| TA 919 | 78X | 4 | NT | 1 | 23 | 22 | R | R |
| TA 924 | 23X | 4 | NT | 4 | 12 | 13 | NT | R |
| TA 926 | 23X | NT | 6 | 3 | NT | NT | MR | H |
| TA 935 | 78X | 3 | 6 | 4 | NT | NT | MR | R |
| TA 940 | 03C | H | NT | 4 | 16 | 17 | S | H |
| TA 942 | 03C | 4 | 6 | 4 | NT | NT | R | H |
| TA 943 | 03C | 4 | NT | 4 | 26 | 17 | S | R |
| TA 946 | 23X | 4 | NT | 4 | 30 | 17 | S | H |
| TA 956 | 23X | 4 | NT | 4 | 20 | 22 | S | R |
| TA 960 | 03C | 4 | NT | 4 | 30 | 18 | S | R |
| TA 967 | 78X | 4 | NT | NT | 25 | 36 | S | H |
| TA 976 | 78X | 1 | NT | 4 | 20 | 32 | R | H |
| TA 1486 | 03C | 2+ | NT | 1 | 12 | 11 | R | NT |
| TA 1489 | 23C | 1+ | 5 | 3 | NT | NT | R | NT |
| TA 1497 | 03C | 4 | NT | 3 | 18 | 18 | MR | NT |
| TA 1518 | 45X | 4 | NT | 3 | 13 | 22 | R | NT |
| TA 1520 | 14C | H | 5 | 3 | 11 | 18 | MR | NT |
| Newton | NT | NT | NT | NT | 63 | 83 | NT | NT |
| Karl 92 | NT | NT | NT | NT | 23 | 60 | NT | NT |

[a] First and second digits indicate amount of sporulation and relative lesion size, respectively. C = chlorosis, P = pale green tissue, X = mixed damage.

[b] Rated on a scale of 0 to 4, where 0 = lowest infection. H = heterogeneous; accessions contain both resistant and susceptible plants.

[c] Rated on a scale of 0 to 9, where 0 = lowest infection. H = heterogeneous; accessions contain both resistant and susceptible plants.

[d] Percent leaf area affected, expressed as disease severity score (*S*). $S = (\overline{X}_{Ai} / \overline{X}_{Ni})\ \overline{X}_{N}$, where $\overline{X}_{Ai}$ = mean leaf area affected of accession A in experiment *i*, $\overline{X}_{Ni}$ = mean leaf area affected of Newton in experiment *i*, and $\overline{X}_{N}$ = mean leaf area of Newton affected in all experiments.

[e] R = resistant, MR = moderately resistant, S = susceptible.

[f] R = resistant, S = susceptible, H = heterogeneous; accessions contain both resistant and susceptible plants.

[g] Not tested.

*minis tritici* different from *Pm6* from cultivated *T. timopheevii*. Accessions were identified with resistance to *B. graminis tritici* isolate 9, which is virulent on *Pm6*. Wild timopheevi wheat also possesses at least one leaf rust resistance gene different from *Lr18* from cultivated *T. timopheevii*, because lines resistant to a culture virulent on *Lr18* were identified. Backcross derivatives from crosses between wheat and *T. timopheevii* var. *araraticum* that are resistant to powdery mildew in seedling tests or resistant to leaf rust under natural and artificial inoculations were identified, indicating that these resistance genes are expressed in a common wheat background (G. L. Brown-Guedira et al., unpublished data).

Whereas *P. graminis* f. sp. *tritici* culture TMN is virulent to *Sr36*, cultures were not available that would allow us to determine if stem rust resistance was conditioned by a gene different from *Sr37* or *Sr40*. Infection type would indicate that an additional gene(s) for resistance to stem rust may be present in the collection because lines with either *Sr37* or *Sr40* give an intermediate reaction when inoculated with TMN and *T. timopheevii* var. *araraticum* accessions were identified with low infection types.

No accessions had a low reaction type to both the cultures of *P. striiformis* used in the screening tests. Accessions with intermediate reactions, and perhaps susceptible ones as well, should be screened as adult plants. Adult plant resistance has played an important role in protection against stripe rust (26).

All accessions tested were more resistant to Septoria blotch in a seedling test than was Karl, one of the Great Plains wheat cultivars most resistant to Septoria blotch. However, there was variability among accessions in the amount of leaf area affected by Septoria blotch, and no accessions were free of disease symptoms. It is not known if transfer of resistance to Septoria blotch from *T. timopheevii* var. *araraticum* into wheat will be feasible because the genetic control of resistance in wild timopheevi wheat is undetermined.

All *T. timopheevii* var. *araraticum* accessions were insensitive to the necrosis-causing *Ptr* toxin produced by *P. tritici-repentis*. Lamari and Bernier (15) have shown, in studies of hexaploid wheat, that insensitivity to the *Ptr* necrosis toxin is conferred by a single recessive gene. *Ptr* necrosis toxin insensitivity transferred from wild timopheevi wheat to bread wheat at our laboratory also appears to be due to a single recessive gene (G. L. Brown-Guedira et al., unpublished data). Resistance to *P. tritici-repentis* in wheat requires a *Ptr* necrosis toxin insensitivity gene in addition to another major gene for resistance to the extensive chlorosis disease symptom, also thought to be caused by a fungal toxin (15). Other studies have reported that tan spot resistance in wheat is quantitatively inherited (11,20), suggesting there may be genes of small effect involved in resistance as well. As is the case in common wheat, *Ptr* necrosis toxin insensitivity in *T. timopheevii* var. *araraticum* is not sufficient to prevent *P. tritici-repentis* colonization; many toxin- insensitive accessions were susceptible to tan spot in the seedling screen. While it seems that wild timopheevi wheat does not contain the gene specifying sensitivity to the *Ptr* necrosis toxin, variation may exist at loci influencing sensitivity to the postulated chlorosis-inducing toxin and for minor genes influencing resistance.

Conflicting results were obtained in our Hessian fly screening. These may be explained by differences in resistance of the tested *T. timopheevii* var. *araraticum* accessions to biotype L and biotype D of Hessian fly. It is also possible that expression of the Hessian fly resistance in *T. timopheevi* var. *araraticum* is dependent on factors such as larval population level or temperature. Environmentally sensitive Hessian fly resistance genes were identified in *T. aestivum*, *T. turgidum,* and *T. tauschii* (16,21,24,30). Further study is needed to determine if biotype or environment is a factor in expression of Hessian fly resistance in wild timopheevi wheat.

Several accessions carrying resistance to multiple pests were identified in this collection; however, the actual number of accessions carrying multiple resistances was probably underestimated. Not all accessions were tested for reaction to all disease, insect, and mite pests. Because introgression of genes from *T. timopheevii* var. *araraticum* into common wheat requires a good deal of effort, use of accessions that have multiple resistance genes as parents for crossing would be advantageous.

Our results suggest that wild timopheevi wheat represents a vast gene pool that may be a valuable source of diverse genes for wheat improvement. Collection and evaluation of *T. timopheevii* var. *araraticum* accessions from areas underrepresented in the WGRC collection is needed, particularly in Iran and Turkey. Currently, work is being done to characterize the genes for resistance to the powdery mildew and leaf rust fungi that were transferred from wild *T. timopheevii* to wheat and to evaluate the diversity of resistance genes present in the collection.

**Seed requests.** Wheat workers interested in obtaining complete screening results and/or small quantities of seed of individual *T. timopheevii* var. *araraticum* accessions may do so by contacting the WGRC, Department of Plant Pathology, Throckmorton Hall, Manhattan, KS 66506.

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