Characterization of Wheat Monogenic Lines with Known *Sr* Genes and Wheat Lines with Resistance to the Ug99 Race Group for Resistance to Prevalent Races of *Puccinia graminis* f. sp. *tritici* in China

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Abstract

Wheat stem rust, caused by *Puccinia graminis* f. sp. *tritici*, is one of the most serious fungal diseases in wheat production, seriously threatening the global supply of wheat and endangering food security. The present study was conducted to evaluate wheat monogenic lines with known *Sr* genes to the most prevalent *P. graminis* f. sp. *tritici* races in China. In addition, wheat lines introduced from the International Maize and Wheat improvement Center (CIMMYT) with resistance to the Ug99 race group were also evaluated with the prevalent Chinese *P. graminis* f. sp. *tritici* races. The monogenic lines containing *Sr9e*, *Sr21*, *Sr26*, *Sr31*, *Sr33*, *Sr35*, *Sr37*, *Sr38*, *Sr47*, and *SrTt3* were effective against races 21C3CTTMM, 34C0MRGSM, and 34C3MTGQM at both seedling and adult-plant stages. In contrast,

monogenic lines containing *Sr6*, *Sr7b*, *Sr8a*, *Sr9a*, *Sr9b*, *Sr9d*, *Sr9f*, *Sr9g*, *Sr13*, *Sr16*, *Sr18*, *Sr19*, *Sr20*, *Sr24*, *Sr28*, *Sr29*, and *Sr34* were highly susceptible to these races at both seedling and adult-plant stages. Lines with *Sr5*, *Sr10*, *Sr13*, *Sr14*, *Sr15*, *Sr17*, *Sr21*, *Sr22*, *Sr23*, *Sr25*, *Sr27*, *Sr29*, *Sr30*, *Sr32*, *Sr36*, and *Sr39* were resistant to one or more of the tested races. Among the 123 CIMMYT lines, 38 (30.9%) showed varying levels of susceptibility to Chinese *P. graminis* f. sp. *tritici* races. The results should be useful for breeding wheat cultivars with resistance to stem rust.

Keywords: *Puccinia graminis* f. sp. *tritici*, resistance, *Sr* genes, wheat stem rust

Wheat is among the most important food crops around the world. Despite annual global production of wheat amounting to more than 700 million tons, food shortage is still a global problem due to rapid population growth. According to the data published by the Food and Agriculture Organization (FAO) of the United Nations, nearly 1/9 of the global population suffers long-term hunger (FAO 2017a). Huge yield losses caused by a variety of wheat diseases exacerbate this problem. The biotrophic parasitic pathogen *Puccinia graminis* f. sp. *tritici* Erikss. & E. Henn. causes wheat stem rust that affects wheat stalks, leaf sheaths, and leaves, seriously reducing yield. It has historically caused severe devastation to wheat crops in Asia, Africa, the Americas, Europe, Australia, and New Zealand (Moscou and van Esse 2017; Pardey et al. 2013; Qiu 1982; Saari and Prescott 1985). From 1923 to 1964, nine epidemics occurred in the northeastern spring wheat region of China. The yield losses caused by wheat stem rust amounted to 740 and 560 million kg in 1923 and 1948, respectively. The United States and Canada experienced substantial losses in their wheat production for three consecutive years due to a sudden attack of *P. graminis* f. sp. *tritici* race 15B between 1950 and 1954 (Stakman and Rodenhiser 1959; Wu and Huang 1987).

The implementation of measures, especially breeding resistant cultivars since the 1970s, has effectively controlled wheat stem rust (Li

et al. 2016b; Rouse et al. 2012). In particular, resistance gene *Sr31* from wheat-rye 1BL/1RS translocation has been widely introduced into wheat cultivars. However, *P. graminis* f. sp. *tritici* is a pathogen that can quickly change virulence. For example, race 15B suddenly appeared in North America (Stakman and Rodenhiser 1959). The Ug99 race group, virulent to the *Sr31* gene, was first discovered in Uganda in 1998. Based on the North American system for naming *P. graminis* f. sp. *tritici* races, it was initially named TTKS and later renamed TTKSK (Jin et al. 2007; Pretorius et al. 2000). With a strong virulence variability, the group has evolved to include at least 13 races that have been identified in 13 countries and caused epidemics in African countries, resulting in serious yield losses (FAO 2017b). In 2013 to 2014, a different race, TKTTF, caused epidemics in the Digalu wheat-growing region of approximately 20,000 to 400,000 ha in southern Ethiopia (Olivera et al. 2015). In 2016, a new race, TTTTF, which combines virulence factors against resistance genes *Sr9e* and *Sr13* commonly used in durum wheat, attacked thousands of hectares of durum wheat in Sicily, Italy, causing the largest outbreak of stem rust in Europe since the 1950s (Bhattacharya 2017). These recent outbreaks of wheat stem rust threaten the security of global wheat production. Because of this, plant pathologists and wheat breeders have conducted global monitoring of *P. graminis* f. sp. *tritici* populations and screening wheat germplasm for resistance to stem rust.

Although the Ug99 race group has not been found and the *Sr31* resistance in many Chinese wheat cultivars is still effective against the *P. graminis* f. sp. *tritici* population in China, Chinese scientists have studied changes in the virulence structure of the *P. graminis* f. sp. *tritici* population and screened wheat germplasm from various sources for resistance to stem rust (Cao et al. 2019; Han et al. 2010; Li et al. 2018; Yao et al. 1998). Two *P. graminis* f. sp. *tritici* race groups, 21C3 and 34C0, have been predominant in China for many years (Cao et al. 2016; Yao et al. 1998). In 2008, we obtained monogenic lines with known *Sr* genes for identification of *P. graminis* f. sp. *tritici* race from Dr. Yue Jin, at the United States Department of Agriculture–Agricultural Research Service (USDA-ARS) Cereal Disease Laboratory in Minnesota, the United States, and changed the Chinese *P. graminis* f. sp. *tritici* race naming system from 3 letters (e.g., MKG) to 5 letters (e.g., MKGQM) (Cao et al. 2019; Li et al. 2018). Recently, races 21C3CTTMM and 34C0MRGSM, in addition

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to 34C3MTGQM that was first identified from *Berberis* spp., the alternative host of *P. graminis* f. sp. *tritici*, were predominant in China from 2009 to 2015 (Cao et al. 2019; Li et al. 2018). The breeding of resistant cultivars has been regarded as the most economic, effective, and environmentally friendly strategy for control of stem rust. So far, more than 70 genes for resistance to wheat stem rust have been identified (Chen et al. 2020; Goutam et al. 2015). It has become important to clarify the resistance of monogenic lines with known *Sr* genes at both seedling and adult stages. Not only is this important for the rational deployment of disease-resistant cultivars but it also assists in steering predictive disease resistance breeding programs. Additionally, in order to prevent potential damage caused by the Ug99 race group to wheat production in China, researchers have introduced resistant wheat lines against the race group from the International Wheat and Maize Improvement Center (CIMMYT) to accelerate Ug99 stem-rust-resistance breeding. Therefore, the objectives of this study were to determine the effectiveness of the monogenic lines with known *Sr* genes at the seedling and adult-plant stages against the three predominant Chinese *P. graminis* f. sp. *tritici* races, 21C3CTTTM, 34C0MRGSM, and 34C3MTGQM; and to determine the resistance levels of the CIMMYT wheat lines with resistance to the Ug99 race group to the Chinese predominant races to select lines resistant to both Ug99 and Chinese *P. graminis* f. sp. *tritici* races.

Materials and Methods

Wheat lines. In total, 43 monogenic lines (ISr5-Ra, ISr6-Ra, ISr7b-Ra, ISr8a-Ra, ISr9a-Ra, W2691Sr9b, ISr9d-Ra, W2619Sr9e, CnsSr9f, CnsSr9g, W2691Sr10, ISr11-Ra, W2691Sr13, MQSr14, W2691Sr15, ISr16-Ra, Combination VII, LCSr18, LCSr19, LCSr20, Cns_T_mono_der1, SwSr22T.B., Exchange, LcSr24Ag, Agatha/9*LMPG, Eagle, 73,214,3-1/9*LMPG, W2691Sr28, Pusa4/Edel, BtS30Wst, Sr31/6*LMPG, Federation*4/Kavkaz, CnsSr32, RL5405, Compare, Mq(2)5XG2919, W2691SrTt-1, W2691Sr37, Trident, RL6082, DAS15, CnsSrTtmp, and Fed/SrTt3) were provided by Dr. Yue Jin from the USDA-ARS Cereal Disease Laboratory, University of Minnesota. In total, 123 wheat lines with resistance to the Ug99 race group from CIMMYT were provided by Dr. Zhonghu He, the Crop Institute of the Chinese Academy of Agricultural Sciences.

Isolates of *P. graminis* f. sp. *tritici*. Isolates of *P. graminis* f. sp. *tritici* used in this study included Yt6 (collected from Yanting, Sichuan Province in 2014), Hlm10 (collected from Mingzhu, Heilongjiang Province in 2014), and XN₂₁₋₁ (collected from *Berberis brachypoda* in Tianshui, Gansu Province in 2015). The three isolates

were identified as races 21C3CTTTM, 34C0MRGSM, and 34C3MTGQM, respectively, based on a new compound differential system (3 selected from Stakman's differentials, 5 Chinese supplementary differentials, and 20 single *Sr*-gene lines used for differentiating *P. graminis* f. sp. *tritici* races in North America) (Cao et al. 2019).

Evaluation of resistance to stem rust in the seedling stage. The three *P. graminis* f. sp. *tritici* races (21C3CTTTM, 34C0MRGSM, and 34C3MTGQM) were propagated in a greenhouse and then stored at 4°C. In the greenhouse, seed of the 43 known *Sr* monogenic lines and 123 CIMMYT lines were sown into pots of 10 cm in diameter, 10 seeds per pot for each line. Wheat variety Little Club (LC) was used as a susceptibility check. Inoculation was conducted on seedlings at the one-leaf stage (approximately 8 to 10 days old). Briefly, leaves were sprayed with 0.05% Tween 20 aqueous solution, dust inoculated with urediniospores mixed with talcum at a ratio of 1:20 (vol/vol), then sprayed again with 0.05% Tween 20 aqueous solution to produce a moisturizing film. The inoculated plants were kept at 18 to 20°C for 16 h, then grown in a greenhouse at 20 ± 1°C. The test with each isolate was conducted twice. Infection types (ITs) were recorded approximately 14 days after inoculation, when LC was fully sporulated, using the 0-to-4 scale described by Stakman et al. (1962). ITs of 0, 1-, 1+, 2, and 2+ were classified as resistant and ITs of 3-, 3, 3+, and 4 as susceptible.

Field evaluation. Wheat lines were evaluated for response to stem rust in the experimental field of the College of Plant Protection, Shenyang Agricultural University (latitude 41°49'N, longitude 123°33'E, altitude 67 m) in 2017. Seed of each line were planted in a 100-cm row with a 25-cm space between rows on 25 March 2017. The susceptible check, LC, was planted every 10 rows. The field was inoculated at the jointing stage in the evening of 1 June. Prior to inoculation, the field was irrigated to ensure the maximum soil moisture. Plants were sprayed with 0.05% Tween 20 aqueous solution, then dust inoculated with urediniospores mixed with talcum at the ratio of 1:30. Plants were covered with plastic to maintain moisture for 14 h. Infection response (IR) and severity and were scored for each line starting at 14 days after inoculation, when plants were at the grain-filling stage using a modified Cobb scale, as described by Roelfs et al. (1992). IRs included R for resistant, MR for moderately resistant, MS for moderately susceptible, and S for susceptible. Severity was defined as the percentage of leaf area covered by rust pustules, with each percent representing 0.37% of leaf area covered with uredinia, and recorded as 1, 5, 10, 20, 30, 40, 50, 60, 70, 80, 90, or 100%

Table 1. Infection types (ITs) on seedlings and infection responses (IRs) on adult plants of *Sr* gene lines that are effective against Chinese races 21C3CTTTM, 34C0MRGSM, and 34C3MTGQM of *Puccinia graminis* f. sp. *tritici*

Line	<i>Sr</i> gene	21C3CTTTM		34C0MRGSM		34C3MTGQM		Background
		IT ^a	IR ^b	IT	IR	IT	IR	
W2619Sr9e	9e	1	5R	;	0	;1	0	W2619
Lee	11	;	10R	0	0	1	10R	Lee
Cns_T_mono_der1	21	1	5R	;1 =	0	2+	30MR	Chinese Spring
Eagle	26	0,1+	5R	1+	5R	1+	10R	...
Sr31/6*LMPG	31	0	0	1	5R	1	10R	LMPG-6
Federation*4/Kavkaz	31	0	0	;	5R	;1-	0	-
RL5405	33	0	0	0	0	;	0	Tetra Canthatch
Mq(2)5XG2919	35	1	5R	2	20MR	;1	5R	Marquis
W2691Sr37	37	1+	10R	1+	10R	1	10R	W2691
Trident	38	;1	0	0;	0	;;1-	0	-
DAS15	47	;1	5R	0	0	1	10R	-
Fed/SrTt3	Tt3	0	0	1	5R	1	10R	LMPG-6
Little Club	-	4	100S	4	100S	4	90S	-

^a ITs scored in the greenhouse seedling tests were based on a 0-to-4 scale (Stakman et al. 1962), where ITs 0, 1, or 2 were considered resistant and ITs of 3 or 4 susceptible, and symbols + and - indicated slightly larger and smaller pustule sizes, respectively.

^b IRs in combination with severity were scored at the adult-plant stage in the field tests following the descriptions of Roelfs et al. (1992), where R = resistant, MR = moderately resistant, MS = moderately susceptible, and S = susceptible.

(Peterson et al. 1948). Disease data were recorded three times at 5-day intervals. The highest IT and severity were used to characterize the response of each line.

Results

Responses of monogenic *Sr* gene lines to Chinese *P. graminis* f. sp. *tritici* races. ITs at the seedling stage and IRs in combination with severity values at the adult-plant stage of the 43 monogenic lines with known *Sr* genes tested with Chinese *P. graminis* f. sp. *tritici* races 21C3CTTTM, 34C3MTGQM, and 34C0MRGSM are presented as resistant, susceptible, and with varying reactions in Tables 1, 2, and 3, respectively. Ten lines with *Sr9e*, *Sr11*, *Sr21*, *Sr26*, *Sr33*, *Sr35*, *Sr37*, *Sr38*, *Sr47*, or *SrTt3* plus two lines with *Sr31* had an IT of 0 to 2 at the seedling stage and were considered

R to MR at the adult-plant stage with relatively low severity (Table 1), indicating that those *Sr* genes were effective against the three tested races. Seventeen lines with *Sr6*, *Sr7b*, *Sr8a*, *Sr9a*, *Sr9b*, *Sr9d*, *Sr9f*, *Sr9g*, *Sr13*, *Sr16*, *Sr18*, *Sr19*, *Sr20*, *Sr24*, *Sr28*, *Sr29*, or *Sr34* exhibited high ITs (≥ 3) at the seedling stage and an MS to S response with high severity at the adult-plant stage (Table 2), indicating that those genes were not effective against the three predominant races. The remaining 15 lines with *Sr5*, *Sr10*, *Sr14*, *Sr15*, *Sr17+Sr13*, *Sr21*, *Sr22*, *Sr23*, *Sr25*, *Sr27*, *Sr29*, *Sr30*, *Sr32*, *Sr36*, or *Sr39* were resistant to one or two of the three tested races (Table 3). The line with *Sr8a* exhibited resistance to 34C0MRGSM at the seedling stage (Its = 1) in the greenhouse test but was susceptible to the same race at the adult-plant stage with relatively high severity (60%).

Table 2. Infection types (ITs) on seedlings and infection responses (IRs) on adult plants of *Sr* genes that are ineffective against Chinese races 21C3CTTTM, 34C0MRGSM, and 34C3MTGQM of *Puccinia graminis* f. sp. *tritici*

Line	<i>Sr</i> gene	21C3CTTTM		34C0MRGSM		34C3MTGQM		Background
		IT ^a	IR ^b	IT	IR	IT	IR	
ISr6-Ra	6	4	80S	4	70S	3	70S	Chinese Spring
ISr7b-Ra	7b	4	100S	4	100S	4	90S	Chinese Spring
ISr9a-Ra	9a	4	70S	4	80S	4	80S	Chinese Spring
W2691Sr9b	9b	3	70S	3	80S	4	90S	W2691
ISr9d-Ra	9d	4	80S	4	80S	4	80S	Chinese Spring
CnsSr9f	9f	3+	60S	3+	80S	4	80S	Chinese Spring
CnSr9g	9g	4	80S	3	80S	4	100S	Chinese Spring
ISr11-Ra	11	3	50S	4	80S	3+	60S	Chinese Spring
W2691Sr13	13	4	90S	3	80S	4	80S	W2691
ISr16-Ra	16	3	80S	3+	70S	3	60S	Chinese Spring
LCSr18	18	4	80S	4	90S	3	70S	Little Club
LCSr19	19	3	70S	3	60S	4	80S	Little Club
LCSr20	20	4	80S	4	100S	3	80S	Little Club
LcSr24Ag	24	3+	60MS	3	60MS	4	80S	Little Club
W2691Sr28	28	4	100S	4	90S	4	90S	W2691
Pusa4/Edel	29	4	90S	3+	80S	2+	50MR-MS	...
Compare	34	4	70S	3	60S	4	80S	...
Little Club	-	4	100S	4	100S	4	90S	...

^a ITs scored in the greenhouse seedling tests were based on a 0-to-4 scale (Stakman et al. 1962), where ITs 0, 1, or 2 were considered resistant and ITs 3 or 4 susceptible, and symbols + and - indicated slightly larger and smaller pustule sizes, respectively.

^b IRs were scored at the adult-plant stage in the field tests following the descriptions of Roelfs et al. (1992), where R = resistant, MR = moderately resistant, MS = moderately susceptible, and S = susceptible.

Table 3. Infection types (ITs) on seedlings and infection responses (IRs) on adult plants of *Sr* genes that are effective against at least one of races 21C3CTTTM, 34C0MRGSM, and 34C3MTGQM of *Puccinia graminis* f. sp. *tritici*

Line	<i>Sr</i> gene	21C3CTTTM		34C0MRGSM		34C3MTGQM		Background
		IT ^a	IR ^b	IT	IR	IT	IR	
ISr5-Ra	5	;	10R	4	70S	4	60S	Chinese Spring
ISr8a-Ra	8a	4	60S	1	60MS-S	4	70S	Chinese Spring
W2691Sr10	10	4	70S	3	60S	;	10R	W2691
MQSr14	14	1+	40MR-MS	1	30MR	3	70S	Marquis
W2691Sr15	15	3	70S	4	100S	0;	0	W2691
Combination VII	17+13	3+	60MS-S	0;	10R	0;	10R	W2691
CnS_T_mono_deri	21	1	5R	;1 =	0	2+	30MR	Chinese Spring
SwSr22T.B.	22	2+	40MR-MS	0	0	4	60S	...
Exchange	23	2+	30MR	0	0	4	60S	...
Agatha/9*LMPG	25	3	60MR-MS	3	50MR-MS	2	30MR-MS	LMPG-6
73,214,3-1/9*LMPG	27	2+	20MR	3+	70S	2	30MR	LMPG-6
Pusa4/Edel	29	4	90S	3+	80S	2+	50MR-MS	...
BtS30Wst	30	3+	50S	;	20R-MR	;1	10R-MR	Baart
CnsSr32	32	4	80S	2+	40MR	4	80S	Chinese Spring
W2691SrTt-1	36	3	80S	0	5R	1+	10R-MR	W2691
RL6082	39	1+	10R	4	60S	3+	80S	Thatcher
CnsSrTnp	Tnp	3	30MR-MS	0;,1	10R	;	10R	Chinese Spring
Little Club	...	4	100S	4	100S	4	90S	...

^a ITs were scored in the greenhouse seedling tests based on a 0-to-4 scale (Stakman et al. 1962), where ITs 0, 1, and 2 were considered resistant and ITs 3 and 4 susceptible, and symbols + and - indicated slightly larger and smaller pustule sizes, respectively.

^b IRs were scored at the adult-plant stage in the field tests following the descriptions of Roelfs et al. (1992), where R = resistant, MR = moderately resistant, MS = moderately susceptible, and S = susceptible.

Evaluation of CIMMYT wheat lines resistant to the Ug99 race group with Chinese *P. graminis* f. sp. *tritici* races 21C3CTTMM, 34C3MTGQM, and 34C0MRGSM. The responses of the 123 CIMMYT wheat lines resistant to the Ug99 race group were tested with races 21C3CTTMM, 34C3MTGQM, and 34C0MRGSM. The ITs of all lines are provided in Supplementary Table S1. For individual races, 97 (78.8%) lines were resistant to 21C3CTTMM, 117 (95.1%) lines were resistant to race 34C0MRGSM, and 107 (87.0%) were resistant to 34C3MTGQM (Table 4). Overall, 85 (69.1%) lines were resistant to all tested races.

Discussion

In the present study, 43 monogenic lines were evaluated for their reaction to three Chinese predominant *P. graminis* f. sp. *tritici* races to determine their effectiveness in China. Among these monogenic lines, W2619Sr9e (*Sr9e*), CnS_T_mono_der1 (*Sr21*), Eagle (*Sr26*), Sr31/6*LMPG (*Sr31*), Federation*4/Kavkaz (*Sr31*), RL5405 (*Sr33*), Mq(2)5XG2919 (*Sr35*), W2691Sr37 (*Sr37*), Trident (*Sr38*), DAS15 (*Sr47*), and Fed/SrTt3 (*SrTt3*) exhibited low ITs at the seedling stage in the greenhouse tests and an R or MR response with relatively low disease severity at the adult-plant stage in the field tests. The genes in these lines are effective against the three predominant races (21C3CTTMM, 34C3MTGQM, and 34C0MRGSM) in China. Among these effective resistance genes, *Sr31* and *Sr38* have been widely used in wheat breeding programs for developing cultivars with resistance to stem rust and are present in many wheat cultivars in China (Das et al. 2006; Xu et al. 2017; Zhou et al. 2007). Although these two genes have lost their resistance to the Ug99 race group, *Sr31* and *Sr38* are still effective in China because no *P. graminis* f. sp. *tritici* races virulent to these genes have been found in China (Cao et al. 2019; Li et al. 2018). In the present study, the lines with *Sr31* or *Sr38* had low ITs (0 to 1) in the seedling stage and low IR and severity at the adult-plant stage (0 to 10R). *Sr9e*, *Sr21*, and *Sr33*, which were found in low frequencies in Chinese cultivars (Cao et al. 1996b), exhibited effective resistance against the predominant races in the present study. *Sr26* was transferred from *Agropyron elongatum* to a popular Australian wheat cultivar (Mago et al. 2005; Martin 1971). Because of its excellent resistance to Ug99 and TTTTF, we tested 340 wheat genotypes, including cultivars widely grown in China using molecular markers closely linked to this gene. As expected, *Sr26* was not found in any of the genotypes (Li et al. 2016a; Xu et al. 2017, 2018). *Sr35*, *Sr37*, *Sr47*, and *SrTt3* were reported to be present in few wheat cultivars from Inner Mongolia and the northeastern provinces of China (Cao et al. 1994; Li et al. 2016a). Because of the excellent resistance of *Sr26*, *Sr33*, *Sr35*, *Sr37*, *Sr47*, and *SrTt3* to the predominant Chinese races, and to Ug99, TKTTF, and TTTTF, these genes should be used in breeding programs for developing wheat cultivars with durable resistance to stem rust.

In addition to the 10 *Sr* genes discussed above, the remaining genes displayed varying degrees of susceptibility to the three predominant Chinese *P. graminis* f. sp. *tritici* races. In all, 18 lines with *Sr5*, *Sr8a*, *Sr10*, *Sr13*, *Sr14*, *Sr15*, *Sr17*, *Sr21*, *Sr22*, *Sr23*, *Sr25*, *Sr27*, *Sr29*, *Sr30*, *Sr32*, *Sr36*, *Sr39*, or *SrTmp* were susceptible to one or two of the three races, and 17 lines with *Sr6*, *Sr7b*, *Sr9a*, *Sr9b*, *Sr9d*, *Sr9f*, *Sr9g*, *Sr11*, *Sr13*, *Sr16*, *Sr18*, *Sr19*, *Sr20*, *Sr24*, *Sr28*, *Sr29*, or *Sr34* were susceptible to all three races.

Table 4. Numbers (N) and percentages (%) of resistant and susceptible lines among the 123 CIMMYT wheat lines with resistance to the Ug99 race group tested with Chinese races 21C3CTTMM, 34C0MRGSM, and 34C3MTGQM of *Puccinia graminis* f. sp. *tritici*

Race	Resistant		Susceptible	
	N	%	N	%
21C3CTTMM	97	78.8	26	21.2
34C0MRGSM	117	95.1	6	4.9
34C3MTGQM	107	87.0	16	13.0
All tested races	85	69.1	38	30.9

Among these genes, *Sr5*, *Sr6*, *Sr11*, *Sr13*, *Sr14*, *Sr17*, *Sr21*, *Sr22*, *Sr23*, *Sr24*, *Sr25*, *Sr28*, *Sr32*, *Sr36*, *Sr37*, *Sr39*, and *SrTmp* are commonly present in wheat cultivars singly or in combination in China and many other countries and have played a key role in stabilizing stem rust resistance (Jin et al. 2007; Wu and Huang 1987). *Sr5* has been widely used in wheat breeding programs in China (Cao et al. 2019; Zhang et al. 1987). Wheat cultivars Minn2761, Alondra'S', and Orofen containing *Sr5* have been grown for a long time and continually used in breeding programs (Cao et al. 2019; Zhang et al. 1987). As a differential, the *Sr5* single-gene line, which can distinguish *P. graminis* f. sp. *tritici* races in almost all countries, is especially useful in the identification of *P. graminis* f. sp. *tritici* races in China. Among the tens of thousands of wheat stem rust samples that have been identified to races, the *Sr5* line assists in the classification of Chinese *P. graminis* f. sp. *tritici* isolates into 21 race groups starting with the initial C (e.g., CTHTM, CTQSM, and so on) and 34 race groups with M as the first initial (e.g., MKGSM, MRGQM, and so on) (Li et al. 2018; Wu and Huang 1987; Yao et al. 1994). *Sr11* has been used as a major source of stem rust resistance in the United States, and is also used to differentiate *P. graminis* f. sp. *tritici* races. In the 1950s, *Sr11* was widely used in the United States, resulting in a single source of resistance which caused an outbreak of stem rust caused by race 15B (Stakman and Rodenhiser 1959). From the history of occurrence in wheat stem rust, the races virulent to *Sr11* are mainly distributed in wheat-growing regions such as Central and South America, Europe, and Australia (Jin 2005; Luig 1983). Race 21C3CTR, which is virulent to *Sr11*-containing wheat cultivars (Lee, Gabo, and Line AG), was first discovered in 1993 in Leshan City, Sichuan Province in China (Cao et al. 1996a). Due to wheat breeding for stem rust resistance in China, *Sr13*, *Sr17*, *Sr21*, *Sr22*, *Sr25*, *Sr28*, *Sr32*, *Sr36*, *Sr37*, *Sr39*, and *SrTmp* are distributed widely in different wheat regions of China. However, *Sr24*, a gene widely used in many other countries, is seldom present in spring wheat cultivars in northern China (Xu et al. 2017, 2018).

The international wheat lines for resistance to the Ug99 race group were obtained from CIMMYT after intensive screening in Kenya. CIMMYT has distributed these lines to wheat-growing countries around the world so that they can be used for breeding wheat cultivars with resistance to the Ug99 race group. However, many other races exist in the pathogen population. Thus, the lines resistant to the Ug99 race group may not resistant to other races. The results of the present study showed that 85 of the 123 lines from CIMMYT with resistance to the Ug99 race group are also resistant to the three predominant races in China. These lines can be used in breeding programs for control of stem rust caused by the current races and potentially caused by any Ug99 race if introduced or developed in China.

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