Seedling and Slow Rusting Resistance to Stripe Rust in Chinese Common Wheats

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ABSTRACT

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Identification of seedling and slow stripe rust resistance genes is important for gene pyramiding, gene deployment, and developing slow-rusting wheat cultivars to control the disease. A total of 98 Chinese lines were inoculated with 26 pathotypes of *Puccinia striiformis* f. sp. *tritici* for postulation of stripe rust resistance genes effective at the seedling stage. A total of 135 wheat lines were planted at two locations to characterize their slow rusting responses to stripe rust in the 2003–2004 and 2004–2005 cropping seasons. Genes *Yr2*, *Yr3a*, *Yr4a*, *Yr6*, *Yr7*, *Yr9*, *Yr26*, *Yr27*, and *YrSD*, either singly or in combinations, were postulated in 72 lines, whereas known resistance genes were not identified in the other 26 accessions. The resistance genes *Yr9* and *Yr26* were found in 42 and 19 accessions, respectively. *Yr3a* and *Yr4a* were detected in two lines, and four lines may contain *Yr6*. Three lines were postulated to possess *YrSD*, one carried *Yr27*, and one may possess *Yr7*. Thirty-three lines showed slow stripe rusting resistance at two locations in both seasons.

Additional keywords: bread wheat, gene-for-gene specificity, yellow rust

Stripe rust, caused by *Puccinia striiformis* f. sp. *tritici*, is an important disease in many wheat-growing regions of the world. Epidemics of stripe rust have occurred periodically in China and, in some years, have caused destructive yield losses in the major wheat production regions, particularly in northwestern and southwestern China (35). The most recent widespread epidemic, in 2002, was caused by Chinese *P. striiformis* f. sp. *tritici* pathotype CYR32, which is virulent to almost all Chinese wheat cultivars except those with resistance genes *Yr5*, *Yr10*, *Yr15*, *Yr24*, or *Yr26* (11,16,35,44).

Following the gene-for-gene hypothesis proposed by Flor (7), Zadoks (45) found a gene-for-gene interaction between wheat cultivars and pathotypes of *P. striiformis* f. sp. *tritici*. Based on the gene-for-gene

concept, Loegering and Burton (14) reported that race-specific resistance genes in wheat cultivars could be identified by comparing their reactions to different pathotypes of *Puccinia graminis tritici* with those of lines with known resistance genes. Perwaiz and Johnson (24) tested seedlings of 26 wheat cultivars from Pakistan with 18 British *P. striiformis* f. sp. *tritici* pathotypes and postulated *Yr2*, *Yr6*, *Yr7*, and/or *Yr9* to be present in the cultivars. Bartos et al. (2) postulated *Yr1*, *Yr2*, *Yr3a+Yr4a*, *Yr9*, and *Yr32* (*YrCV*) in 17 Czechoslovakian and two Russian wheat cultivars following tests with 18 *P. striiformis* f. sp. *tritici* pathotypes. Singh et al. (28) found *Yr2* and *Yr7* in a seedling test of 11 Indian wheat cultivars using 17 pathotypes and confirmed the presence of *Yr2* in three cultivars by testing the F_1 and F_2 generations of crosses between these cultivars and Heines VII, a cultivar that contains *Yr2*. Sharma et al. (26) inoculated seedlings of 38 wild emmer derivatives and 53 advanced wheat lines from Nepal with 18 *P. striiformis* f. sp. *tritici* pathotypes and found 28 wild emmer derivatives were resistant to all pathotypes with unidentified resistance genes, and five resis-

tance genes (*Yr2*, *Yr6*, *Yr7*, *Yr9*, and *YrA*) were present in Nepalese wheat cultivars and advanced lines tested. In China, Wang et al. (36,37) identified eight resistance genes (*Yr1*, *Yr2*, *Yr3*, *Yr7*, *Yr9*, *Yr10*, *YrSu*, and *YrSD*) in 39 Chinese wheat cultivars and 20 important resistant germ plasm lines from the provinces of Shaanxi, Gansu, and Sichuan, using 20 *P. striiformis* f. sp. *tritici* pathotypes. Niu et al. (21) screened 50 Chinese wheat cultivars from the provinces of Henan, Shandong, and Anhui with 26 pathotypes, and found that *Yr9* was the most frequent resistance gene. However, no information is available about the identity of stripe rust resistance genes in current leading cultivars, newly released cultivars, and advanced breeding lines in China. Therefore, characterization of stripe rust resistance genes in widely grown Chinese wheats is extremely important for breeding new resistant cultivars and for gene deployment schemes (35).

In general, seedling resistance is race-specific and thus short-lived due to frequent changes of virulence in the pathogen population (13,31). In contrast, resistance at the adult plant stage, such as high-temperature adult-plant (HTAP) resistance or slow rusting, is considered more durable than seedling resistance (5,6,13,18,32). Wheat cultivars with slow rusting genes are often susceptible at the seedling stage, but may be moderately to highly resistant to all pathotypes at the adult plant stage in the field (4,31). The components of slow rusting include a longer latent period, low infection frequency, smaller uredial size, and reduced duration and quantity of spore production (4). Three currently named stripe rust resistance genes, *Yr18*, *Yr29*, and *Yr30*, confer slow rusting (29,33,40), and many more are suspected. Singh (29,30) and McIntosh (18) found the slow rusting resistance gene *Yr18* in Anza and Bezostaja, and this gene confers a moderate level of resistance when present alone. However, combinations of *Yr18* with two to four additional slow rusting genes resulted in high resistance in most environments (31). William et al. (40) identified

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slow rusting gene *Yr29* on chromosome 1B. This gene was closely linked with slow leaf rusting gene *Lr46*. Suenaga et al. (33) reported resistance gene *Yr30* closely linked with durable adult plant stem rust resistance gene *Sr2*.

From the early 1970s, the 1B/1R translocation with *Yr9* was introduced to Chinese wheat breeding programs through introductions such as Lovrin 10, Lovrin 13, Predgoraia 2, Kavkaz, and Neuzucht (9,22). The widespread growing of cultivars with *Yr9* resulted in major epidemics in 1990 and 2002, since the stripe rust resistance was overcome by the new race of the pathogen CYR 32, which has forced Chinese wheat breeders to focus on the development of cultivars with durable resistance. Although breeders are using slow rusting resistance and major genes for durable control of stripe rust, very little information is available on sources and efficacy of resistance in Chinese wheat cultivars.

A total of 145 widely grown Chinese wheat cultivars, newly released cultivars, and advanced lines from 12 provinces in the major wheat production regions were investigated in this study. The objectives were to identify probable genes conferring resistance to stripe rust at the seedling stage and to investigate the likelihood of slow rusting resistance from adult plant tests in the field.

MATERIALS AND METHODS

Wheat germ plasm. The wheat lines comprised 145 Chinese leading cultivars, newly released cultivars, and advanced lines from major breeding programs across the autumn-sown wheat regions of China, including the provinces of Hebei, Henan, Shandong, Shaanxi, Gansu, Anhui, Hubei, Jiangsu, Chongqing, Guizhou, Sichuan, and Yunnan. Ninety-eight lines were tested for seedling response to 26 *P. striiformis* f. sp. *tritici* pathotypes in the greenhouse, and 135 were tested for slow stripe rusting resistance in the field (Table 1).

Seedling testing. A set of 25 differential lines with known stripe rust resistance genes (20) were included in the seedling tests, and the infection types displayed by them were used as a basis for postulating resistance genes in the Chinese lines. The seedling tests for the 98 cultivars and lines were conducted in 2004 and 2005, respectively, using 26 pathotypes with the method described by Bariana and McIntosh (1) and Niu et al. (21) (Table 2). Six to eight plants of each line tested were grown in a growth chamber. Seedling inoculations were performed by brushing urediniospores of pathotypes from a fully infected susceptible cultivar onto the test seedlings when the first leaf was fully expanded. Inoculated seedlings were subsequently placed in plastic-covered cages and incubated at 9°C and 100% RH for 24 h. Seedlings were then transferred to

growth chambers with the day/night regime of 14 h of light (22,000 lux) at 17°C and 10 h of darkness at 12°C, with 70% RH. Infection types (ITs) were scored 15 to 16 days after inoculation based on a 0 to 4 scale (1) when rust was fully developed on the susceptible check, Mingxian 169. Plants with IT 0 to 2+ were considered to be resistant, and those with IT of 3– to 4, susceptible.

Identification of 1B/1R status. 1B/1R translocation lines were identified according to the method described by Fransis et al. (8).

Field testing. Of the 145 cultivars and lines employed in this study, 135 lines and slow rusting check Lantian 12 and highly susceptible check Tiaogan 601 were planted in a randomized complete block design with three replicates, in Beijing and Tianshui in the 2003–2004 and 2004–2005 cropping seasons for the test of adult-plant resistance (Table 1). Each plot consisted of a 2-m row spaced 25 cm apart with 150 seeds. Beijing is the location of the main winter wheat breeding program. Tianshui, located in Gansu province, is considered a hot spot for stripe rust (42,47). Cultivar Lantian 12, with typical slow rusting (47), and highly susceptible line Tiaogan 601 were used as slow rusting and susceptible checks, respectively. Spreader rows of Tiaogan 601 were planted perpendicular and adjacent to the rows of tested cultivars. Stripe rust epidemics were initiated by spraying aqueous suspensions of urediospores of *P. striiformis* f. sp. *tritici* pathotype CYR32, to which a few drops of Tween 20 (0.03%) had been added, onto the spreader rows at tillering. The stripe rust severity was assessed for the first time 4 weeks after inoculation and then at weekly intervals with four times in total using the modified Cobb scale (25), and infection types were scored using a 0 to 4 scale (1). The disease severity data were used to calculate the area under the disease progress curve (AUDPC) based on the method described by Broers et al. (3). AUDPC was calculated as:

$$\text{AUDPC} = \sum_{i=1}^n [(X_i + X_{i+1}) / 2] (T_{i+1} - T_i)$$

where T_i = number of days after inoculation and X_i = disease severity. Relative AUDPC (rAUDPC), calculated using the actual AUDPC divided by the AUDPC of susceptible check Tiaogan 601 (15,17), and final disease severity (FDS), when the susceptible check (Tiaogan 601) displayed maximum disease severity, were used for statistical analyses. The field data obtained in Beijing during the 2004–2005 cropping season was excluded from analysis due to inadequate infection.

Statistical analysis. The Statistical Analysis System (SAS) procedural PROC GLM was used to conduct analysis of variance with lines, environments that were the combination of location and year, and their interaction effects as fixed, and

replicates nested in environments as random. Fisher's *F* protected least significant difference (LSD) was used to separate the means for AUDPC and FDS among the lines tested. Lines that were seedling susceptible to CYR32 and showed lower or not significantly higher values of FDS and AUDPC than those of the slow rusting check in field trials were considered to be slow rusting lines of potential use for crop protection and breeding.

RESULTS

Seedling reaction. The reactions of the standard differential lines with known resistance genes to the 26 pathotypes are included in Table 2. Line *Yr15/6**Avocet S displayed high resistance to all pathotypes tested. Lines *Yr24/3**Avocet S and *Yr26/3**Avocet S showed a moderately susceptible reaction only to pathotype P4 (75078). Moro with *Yr10* gave high infection types to pathotypes P4 (75078) and P10 (72107). Thus, *Yr10*, *Yr15*, *Yr24*, and *Yr26* confer effective resistance against prevailing Chinese pathotypes (P22 to 26), whereas lines with *Yr1* and *Yr6* were susceptible to them.

The resistance genes *Yr2*, *Yr3a*, *Yr4a*, *Yr6*, *Yr7*, *Yr9*, *Yr26*, *Yr27*, and *YrSD*, either independently or in certain combinations, were postulated in 72 lines, whereas 26 accessions did not contain any known stripe rust resistance genes.

Eighteen lines possessed only *Yr9*, whereas another 24 lines possessed *Yr9* plus one or more unknown resistance genes according to their reaction patterns (Table 2). All lines postulated to have *Yr9* also amplified a SCAR marker for rye chromatin (8) (Tables 1 and 2).

Fifteen lines were postulated to have *Yr26* on the basis that only P4 (75078) was virulent. Pedigree information (Table 1) indicated that four additional lines (L107 = LB 0438, L115 = Mian 2000-8, L125 = Nei 2938, and L134 = Xike 01015), highly resistant to all pathotypes, probably carry *Yr26* and one more unknown gene.

Four lines (L133 = W7, L41 = Shaan 512, L52 = Xinong 914, and L106 = LB 0288) carried *Yr6* based on their responses to the pathotypes avirulent to *Yr6/6**Avocet S (Table 2). L133 conferred resistance to pathotypes lacking pathogenicity for *Yr2*, indicating that it contained *Yr2* and *Yr6*. Two lines (L82 = 351-15, L130 = R88) displayed low infection types to pathotypes avirulent to differentials Vil-morin 23 and Nord Desprez, indicating they may contain *Yr3a* and *Yr4a*. In addition, line L82 also carried *Yr2*, being resistant to pathotypes lacking virulence for *Yr2*. Three lines (L64 = Annong 98005, L72 = An 96-8, and L109 = Lemai 3) carried *YrSD*, displaying low ITs to the pathotypes avirulent to *YrSD*. L92 (CD 1485-6) conferred resistance to all pathotypes avirulent to *Yr7* and some pathotypes virulent for *Yr7*, indicating it carried *Yr7* and unknown resistance genes.

Table 1. Pedigrees of 145 Chinese wheat cultivars and lines tested for stripe rust response and arranged according to province of origin

Line no.	Line	Pedigree	Origin	1B/1R status ^a	Stripe rust test ^b
1	Han 3475	Peixian30421/Han 4162	Hebei	-	S and A
2	Han 4564	88-6012/Shi 5144	Hebei	+	S* and A
3	Han 4599	Han 4032/85Zhong47	Hebei	+	S and A
4	Han 5316	Han 7808/CA 8059/85Zhong47	Hebei	+	S* and A
5	Han 6172	Han 4032/Zhongyin 1	Hebei	-	S* and A
6	Lankao 52-24	Triticale 84-184/Yumai 2//90 Xuan	Henan	+	S* and A
7	Lankao 411	893B25/Lankao 906	Henan	+	S* and A
8	Lankao 8	84(184)/90 Selection	Henan	+	S* and A
9	Lankao 906-4	84(184)/Yumai 2//90 Selection	Henan	+	S* and A
10	Luohan 2	Luoyang 78 (111) /Jinmai 33	Henan	-	S* and A
11	Neixiang 188	Mianyang 84-27/Neixiang 82C6/Yumai 17	Henan	+	S* and A
12	Neixiang 991	87C27/Zhengzhou 84115// Yumai 13	Henan	+	S* and A
13	Xinmai 11	Zhou 8826/Xinxiang 3577	Henan	-	S* and A
14	Xinmai 9	Baiquan 3047-3/Neixiang 82C6	Henan	-	S* and A
15	Yanzhan 4110	C39/Xibei 78(6)9-2//FR 81-3/Aizao 781-4/3/Aizao 781-4	Henan	-	S* and A
16	Yumai 18	Zhengzhou 761/Yanshi 4	Henan	-	S* and A
17	Yumai 34	Aifeng 3 //Meng 201/ Neuzucht /3/Yumai 2	Henan	-	S* and A
18	Yumai 49	Bainong 791//Wenxuan 1/Zhengzhou 761/3/Yumai 2	Henan	-	S* and A
19	Yumai 62	Zhou 8425B/SWP73295	Henan	+	S and A
20	Zhengmai 9023	(Xiaoyan 6/Xinong 65//8323-3/8443)/Shaan 213	Henan	+	S* and A
21	Zhou 8425B	Guangmai 74/Lianfeng 1//Predgornayi 2/3/Annong 7959	Henan	+	S
22	Zhou 88114	Zhou 8425B/ Yumai 17	Henan	+	S
23	Zhoumai 11	Zhou 8425B/Yumai 17	Henan	+	S* and A
24	Zhoumai 16	Zhou 9/Zhou 8425B	Henan	+	S* and A
25	Jinan 16	Tal Shannongfu 63/AimengniuV	Shandong	+	S* and A
26	Lumai 21	Lumai 13/Yumai 2	Shandong	-	S* and A
27	Yannong 19	Yan 1933/Shan 82-29	Shandong	-	S* and A
28	Yanyou 361	Yan 1933/Shan 82-29	Shandong	-	S* and A
29	Zimai 12	917065/910292	Shandong	-	S* and A
30	(95).18	? ^c	Shaanxi	+	S* and A
31	1718	Xinong 242//84G6/Shaan 167	Shaanxi	+	S and A
32	2208	Shaan 229//Shaan 213/Xinong 8623	Shaanxi	+	S and A
33	2611	Xinong 881/Shaan 229	Shaanxi	-	S and A
34	953	Xinong 918/Zhi 87-135	Shaanxi	-	S and A
35	N139	Xiaoyan 22//94156/N9134	Shaanxi	-	S
36	99104	9434/9527	Shaanxi	-	S
37	H-46	?	Shaanxi	?	S* and A
38	N95175	92R/Yuancal 142//Xiaoyan 6	Shaanxi	-	S
39	Nonglin 9823	Xiaoyan 4/73 (36) //Baofeng 7228	Shaanxi	-	S and A
40	Qinnong 151	Zhengzi R84019-0-7-5/Xinong 1376	Shaanxi	+	S* and A
41	Shaan 512	Shaan 150/Shaan 354	Shaanxi	-	S and A
42	Shaanzi 1869	Shaan 354/Shaanmai 898	Shaanxi	+	S and A
43	Shaan 715	Shaan 354/Yanmai 8911	Shaanxi	+	S* and A
44	Shaannong 981	Derived from Shaanyou 225	Shaanxi	-	S* and A
45	Xiaoyan 143	87C332/Xiaoyan 135	Shaanxi	-	S* and A
46	Xiaoyan 22	Xiaoyan 6/775-1//Xiaoyan 107	Shaanxi	-	S* and A
47	Xiaoyan 921	?	Shaanxi	-	S and A
48	Xinong 1163-4	84Jia79/Xinong 1376	Shaanxi	+	S and A
49	Xinong 1376	Xinong 84G6/Bi 16	Shaanxi	+	S
50	Xinong 291	?	Shaanxi	+	S and A
51	Xinong 8925-13	Xiaoyan 168/Zhi 763	Shaanxi	-	S and A
52	Xinong 914	Xinong 1376/2611	Shaanxi	?	S
53	Yunfeng 988	?	Shaanxi	-	S and A
54	90-99-5	?	Gansu	+	S* and A
55	93-23-13	83-44-29/Guinong 90-21-7	Gansu	-	S* and A
56	94t-133	Hybrid 46/Xian 4//Tao 157	Gansu	-	S* and A
57	95-108	92R137/Lantian 6	Gansu	-	S* and A
58	95-111-6-3-10	92R137/87-121-2	Gansu	+	S and A
59	953111-13	Mega/Lantian10	Gansu	-	S and A
60	95-3-5-1	Mega/Lantian 10	Gansu	-	S* and A
61	9562-1	Ibis/Lantian 10	Gansu	+	S and A
62	96-22-2-3	Cappelle Desprez/935	Gansu	-	S* and A
63	Lantian 9	Xifeng 16/76-89-13	Gansu	+	S* and A
64	Annong 98005	Yumai 18/Wanmai 19	Anhui	-	S and A
65	Een 1	Lovrin 10/761//Sumai 3	Hubei	+	S* and A
66	Emai 14	Fan 6/Yanda 72-629	Hubei	-	S and A
67	Huaimai 18	Zhengzhou 891/Yan 1604	Jiangsu	+	S* and A
68	Yangfu 2	Yangmai 158/101-90	Jiangsu	-	S and A
69	Yangmai 10	Yuma/8' Cc//Yangmai 5/3/4*Yang 85-85/4/2*Yangmai 158	Jiangsu	-	S and A
70	Yangmai 158	Yangmai 4/ST 1472/506	Jiangsu	-	S and A

(continued on next page)^a + = Presence of 1B/1R translocation, - = nonpresence of 1B/1R translocation, identified according to the method described by Fransis et al. (8).^b S, seedling tests with 26 PST pathotypes including CYR32, S*, seeding tests only with the pathotype CYR32, A, adult-plant tests.^c Unknown.

Table 1. (continued from previous page)

Line no.	Line	Pedigree	Origin	1B/1R status ^a	Stripe rust test ^b
71	Yu 94-7	Chuanyu 84-2/91-125	Chongqing	+	S and A
72	An 96-8	L9288022-21/Xingnong 5	Guizhou	-	S and A
73	Bi 2002-2	8513-1624/Ji 1002	Guizhou	+	S and A
74	Guizhou 98-18	Sumai 3/C39//Qing 30	Guizhou	+	S and A
75	01-018	Chuannong 21/89-8//89-107	Sichuan	+	S and A
76	01-10251	73A/RI	Sichuan	-	S* and A
77	01-3570	96Xia440/Guinong 21	Sichuan	-	S* and A
78	01-DH689	94-D.H-375/Mianyang 26	Sichuan	+	S and A
79	298-1	Mianyang 4/45590	Sichuan	-	S and A
80	323-2	Zhongzhi 3586/50609	Sichuan	-	S and A
81	3472	YanzhanA11/Yiyuan 2	Sichuan	-	S and A
82	351-15	Mian 99-310/GansuM180	Sichuan	-	S and A
83	58512-2	Mian 90-309/92R171	Sichuan	-	S and A
84	58749	SW 3243/35050//21530	Sichuan	+	S and A
85	58769-6	30220/8619-10	Sichuan	-	S* and A
86	93Xia032-1	93-38-1/93-35	Sichuan	+	S and A
87	98-1266	Chuanyu 12/87-429	Sichuan	+	S and A
88	99-0502	911/MY86-51	Sichuan	+	S and A
89	99422	Mianyang 87-19/R1301	Sichuan	-	S and A
90	99-607	Syn-CD769/SW 3243//Chuan 6415	Sichuan	-	S and A
91	C2001-2	P92/P88	Sichuan	+	S and A
92	CD 1485-6	98718/Chuanyu 12	Sichuan	-	S and A
93	Chen 98-18	Mianyang 26/Zixuan 1	Sichuan	-	S and A
94	Chuanmai 42	Syn-CD768/SW3243//Chuan6415	Sichuan	-	S and A
95	Chuanmai 43	Syn-CD768/SW 3243//Chuan 6415	Sichuan	-	S* and A
96	Chuanmai 44	96Xia440/Guinong 21	Sichuan	+	S
97	Chuannong 16	Chuanyu 12/87-429	Sichuan	+	S and A
98	Chuannong 17	91S-23/A302	Sichuan	+	S and A
99	Chuannong 21	91S-23/Qianhui 3	Sichuan	-	S and A
100	Chuan 5436	Cereta/Ae. <i>tauschii</i> //Mianyang 26	Sichuan	?	S
101	Chuanyu 18	Chuanyu 5 /Mo 460//94F2-4	Sichuan	-	S and A
102	Chuanyu 19	Chuanyu 5/Mo 460//Mianyang 26	Sichuan	-	S and A
103	GY 96-35	?	Sichuan	+	S and A
104	Jinfeng 626	9481/93N1001	Sichuan	-	S and A
105	Kefeng 14	8420//Neixiang 82C6F1/Yumai 17	Sichuan	-	S and A
106	LB 0288	Mianyang 90-310/M180	Sichuan	-	S and A
107	LB 0438	Mian 95-339/92R178	Sichuan	-	S and A
108	LB 0458	Mianyang 90-310/M180	Sichuan	-	S and A
109	Lemai 3	Mianyang 89-224/7705	Sichuan	-	S and A
110	Liangmai 2	94-2/Miannong 4	Sichuan	+	S and A
111	Mian 2000-13	Mianyang 01821/90Zhong165//Guinong 19-4	Sichuan	+	S and A
112	Mian 2000-18	Mianyang 96-5/Liaochun 10	Sichuan	-	S and A
113	Mian 2000-34	Mianyang 01821/903//95-14426	Sichuan	-	S and A
114	Mian 2000-36	Mian92-8/Mian88-304//Guinong 19-4	Sichuan	+	S and A
115	Mian 2000-8	Mianyang86-78/Guinong21-1	Sichuan	-	S and A
116	Mian 99-3	Mianyang 87-24/81026-0-1-2//053638-1	Sichuan	+	S and A
117	Mianmai 37	96EW37/Mianyang 90-100	Sichuan	-	S and A
118	Mianyang 4	75-21-4/76-19//Miannong 1	Sichuan	+	S* and A
119	Mianyang 11	70-5858/Fan 6	Sichuan	-	S* and A
120	Mianyang 26	Chuanyu 9/Mianyang 20	Sichuan	-	S* and A
121	Mianyang 28	T79350-1-4-1-2/Mianyang 11	Sichuan	+	S and A
122	Mianyang 29	Mianyang 11/Jiangyou 83-5	Sichuan	-	S and A
123	N1621-19-4	Mianyang 26/Yiyuan 2	Sichuan	+	S and A
124	N711	92-4/Mianyang 4	Sichuan	+	S and A
125	Nei 2938	Mianyang 26/92R178	Sichuan	-	S and A
126	Neimai 9	Mianyang 26/92R178	Sichuan	-	S and A
127	R111	961-225/91S-5-4	Sichuan	-	S and A
128	R122	96I-22/133-3//Mianyang 26	Sichuan	-	S and A
129	R25	91S-23/A302	Sichuan	+	S and A
130	R88	1104A/R935	Sichuan	-	S and A
131	R97	Mianyang 92-8/91S-5-7	Sichuan	+	S and A
132	SW8588	Milan's/SW 5193	Sichuan	-	S and A
133	W7	Durum/Xianyang large spike//W7268	Sichuan	-	S and A
134	Xike 01015	Mianyang 26/Zhi 39060-4	Sichuan	-	S and A
135	Xike0106-1	Chuanyu 11/9310-6	Sichuan	+	S and A
136	Xingmai 2	Mianyang 26/92R178	Sichuan	-	S and A
137	Yi 99-49	Chuanyu 12/85-5	Sichuan	+	S and A
138	Yi 99-81	90036-5-1/89-311	Sichuan	+	S and A
139	9021	Fengmai 10/Mo 120//110-75/3/Zhongkangai 2 /4/04835/5/882 -182	Yunnan	+	S and A
140	Fengmai 24	Yunmai 36/Mo 965	Yunnan	-	S and A
141	Jing 035-1	?	Yunnan	+	S and A
142	Jing 9308	TB78-212/Yin 48/092-1	Yunnan	+	S and A
143	Yin 11-12	NG8319//SHA4/LIRA	Yunnan	-	S and A
144	Yumai 3	81-2/8334	Yunnan	+	S and A
145	3S857	Bai//108/Flaminio-IDO2229/3/BT 881	Beijing	?	S

Table 2. Seedling infection types produced by 25 differentials (bold) with known resistance genes and 98 wheat cultivars and lines when infected with 26 pathotypes of *Puccinia striiformis* f. sp. *tritici* collected from China and other countries^a

Line number	Yr gene	Infection types to <i>Puccinia striiformis</i> f. sp. <i>tritici</i> pathotypes										
		61009 (P1)	78028 (P2)	58893 (P3)	75078 (P4)	60105 (P5)	59791 (P6)	82517 (P7)	78080 (P8)	86094 (P9)	72107 (P10)	74187 (P11)
Clement	<i>Yr9, YrCle</i>	0	0	0	0	0	0	0	0	3	0	0
19	<i>Yr9</i>	0	0	0	0	0;	0	0	0	4	0	0
42	<i>Yr9</i>	0	0	0	0	0	0	0	0;	2	0;	0
71	<i>Yr9</i>	0	0	0	0	0	0	0	0;	4	0	0
78	<i>Yr9</i>	0, 0;	0	0	0	0;	0;	0, 0;	0;	3	0	0;
84	<i>Yr9</i>	0	0	0	0;	0;	0	0	0	3, 4	0;	0
91	<i>Yr9</i>	0	0	0, 0;	0;	0	0;	0;	0;	3	0;	0
110	<i>Yr9</i>	0	0;	0;	0;	0;	0;	0	0;	4	0;	0
116	<i>Yr9</i>	0	0	0;	0;	0;	0	0	0;	4	0	0
121	<i>Yr9</i>	0	0	0	0;	0;	0	0	0;	3	0;	0
123	<i>Yr9</i>	0	0;	0	0;	0;	0;	0	0	3	0	0;
135	<i>Yr9</i>	0, 0;	-	0	0	0	0	0	0	4	0	0
137	<i>Yr9</i>	0	0	0	0	0	0	0	0	4	0	0
138	<i>Yr9</i>	0	0;	0	0;	0;	0;	0;	0	4	0	0
139	<i>Yr9</i>	0;	0	0	0	0;	0	0;	0	3	0;	0
141	<i>Yr9</i>	0	0	0, 0;	0	0	0	0	0	3	0	0
142	<i>Yr9</i>	0	0	0	0;	0, 0;	0	0;	0	4	0;	0
143	<i>Yr9</i>	0	0	0	0;	0	0	0;	0;	3	0	0
144	<i>Yr9</i>	0, 0;	0	0	0	0	0	0	0	4	0;	0
3	<i>Yr9, +</i>	0	0	0	0	0	0	0	0	0	0	0
48	<i>Yr9, +</i>	0	0	0	0	0	0	0	0;	0	0	0
50	<i>Yr9, +</i>	0	0	0	0	0	0	0	0	0	0	0
73	<i>Yr9, +</i>	0, 0;	0	0	0	0	0, 0;	0	0	0	0	0
75	<i>Yr9, +</i>	0	0	0	0, 0;	0	0;	0	0	0	0	0
97	<i>Yr9, +</i>	0	0	0	0	0	0, 0;	0	0;	0, 0;	0	0
98	<i>Yr9, +</i>	0	0	0	0	0	0;	0	0;	0, 0;	0	0
131	<i>Yr9, +</i>	0	0	0, 0;	0	0	0	0	0	0, 0;	0	0
129	<i>Yr9, +</i>	0	0	0	0	0	0	0, 0;	0;	0, 0;	0	0
74	<i>Yr9, +</i>	0	0	0	0	0	0;	0	0	0;	0	0, 0;
88	<i>Yr9, +</i>	0, 0;	0	0	0	0	0;	0	0	0;	0	0
111	<i>Yr9, +</i>	0	0, 0;	0	0	0	0	0	0	0;	0	0, 0;
124	<i>Yr9, +</i>	0	0, 0;	0	0	0	0	0	0;	0;	0	0
61	<i>Yr9, +</i>	0	0;	0	0	0	0	0	0;	0;	0	0
87	<i>Yr9, +</i>	0;	0	0	0	0	0;	0	0;	0;	0	0;
21	<i>Yr9, +</i>	0	0, 0;	0	0	0	0	0	0	2	0	0
49	<i>Yr9, +</i>	0	0;	0	0	0	0, 0;	0	0	2	0;	0
22	<i>Yr9, +</i>	0	0, 0;	0	0	0	0	0	0	3	0	0
31	<i>Yr9, +</i>	0	0	0;	0;	0	0	0;	0;	3	0	0
114	<i>Yr9, +</i>	0	0	0	0	0	0	0	0;	3	0	0
32	<i>Yr9, +</i>	0	0;	0;	0	0	0;	0;	0;	4	0;	0
59	<i>Yr9, +</i>	0	0	0	0;	0;	0	0	0	4	0;	0, 0;
86	<i>Yr9, +</i>	0	0;	0	0;	0;	0	0	0	4	0	0;
103	<i>Yr9, +</i>	0, 0;	0	0	0;	0;	0	0	0	4	0;	0
Yr24/3*Avocet	Yr24	0;	0;	0;	2+	0;	0;	0;	0;	0;	0;	0;
Yr26/3*Avocet	Yr26	0;	0;	0;	2+, 3	0;	0;	0;	0;	0;	0;	0;
36	<i>Yr26</i>	0;	0	0;	2+, 3	0, 0;	0, 0;	0, 1+	0;	0	2	0
38	<i>Yr26</i>	0, 0;	0;	0;	3	0;	0, 0;	0;	0;	0, 0;	2+	0;
58	<i>Yr26</i>	0;	0	0;	3	0;	0	0;	0;	0;	0;	0;
83	<i>Yr26</i>	0;	0;	0;	3, 4	0;	0;	0;	0;	0;	0, 1	0;
90	<i>Yr26</i>	0;	0, 0;	0;	2+, 3	0, 0;	0;	0;	0;	0;	2	0;
94	<i>Yr26</i>	0, 0;	0, 0;	0;	2+, 3	0;	0	0;	0;	0;	0, 1	0;
96	<i>Yr26</i>	0;	0;	0;	2	0	0;	0;	0;	0;	0, 1	0;
100	<i>Yr26</i>	0, 0;	0, 0;	0;	2+, 3	0;	0;	0;	0;	0;	0, 1	0;
104	<i>Yr26</i>	0	0	0;	3	0	0;	0, 0;	0;	0	0;	0, 0;
113	<i>Yr26</i>	0;	0	0, 0;	2	0;	0;	0;	0;	0;	0;	0;
117	<i>Yr26</i>	0	0	0;	3	0;	0	0, 0;	0;	0, 0;	0;	0
126	<i>Yr26</i>	0;	0	0;	2, 3	0;	0;	0;	0;	0;	0;	0
127	<i>Yr26</i>	0, 0;	0	0;	3	0, 0;	0;	0;	0;	0, 0;	0, 1	0
128	<i>Yr26</i>	0, 0;	0, 0;	0;	3	0;	0;	0;	0;	0, 0;	0, 1	0
136	<i>Yr26</i>	0, 0;	0	0;	3	0;	0;	0;	0;	0;	1	0, 0;
107	<i>Yr26, +</i>	0;	0	0;	0;	0;	0;	0;	0, 1	0;	0;	0
115	<i>Yr26, +</i>	0;	0, 0;	0;	0;	0;	0	0;	0;	0, 0;	0;	0, 0;
125	<i>Yr26, +</i>	0;	0;	0;	0+	0;	0;	0;	0;	0;	0;	0
134	<i>Yr26, +</i>	0, 0;	0	0;	0, 1, 2	0;	0;	0;	0;	0;	1, 1+	0, 0;
Maris	<i>Yr2, Yr3a, Yr4a,</i>	0;	0;	0, 1+	3	0, 1+	3	4	4	0;	0;	3
Huntsman	<i>Yr13</i>											
82	<i>Yr2, Yr3a, Yr4a, +</i>	0, 0;	0	0;	0;	0	0	0;	0, 2	0, 0;	1	0;
Heines VII	<i>Yr2</i>	0, 1	1, 2+	0, 1+	3, 3+	0, 2+	4	4	3	0	0, 1	0

^a Lines are arranged in groups according to postulated *Yr* genes. + = unknown gene(s); - = untested.

Infection types to <i>Puccinia striiformis</i> f. sp. <i>tritici</i> pathotypes														
86036 (P12)	76088 (P13)	76093 (P14)	86106 (P15)	68009 (P16)	86107 (P17)	82061 (P18)	80551 (P19)	85019 (P20)	PE92 (P21)	CYR26 (P22)	CYR27 (P23)	CYR29 (P24)	CYRSu- 1 (P25)	CYR32 (P26)
0	0	0	0	0	4	4	4	0;	0	0	0	4	0;	4
0;	0, 0;	0	0	0	4	4	4	0;	0	0	0	4	0	4
0	0	0	0	0;	3	2	3	0;	0	0	0;	4	0	4
0	0	0, 0;	0	0;	4	3	4	0;	0	0	0	4	0	4
0, 0;	0;	0	0	0;	3	4	4	0, 0;	0;	0	0	2, 2+	0	3
0	0;	0;	0	0;	4	3	3	0;	0	0	0	4	0	4
0, 0;	0	0;	0	0;	3	3	3	0;	0;	0, 0;	0;	3	0	4
0;	0	0	0	0;	3	3	4	0;	0;	0, 0;	0;	4	0	3
0;	0;	0, 0;	0	0;	4	4	4	0	0	0	0;	4	0	4
0, 0;	0	0, 0;	0	0	4	3	4	0	0;	0	0	4	0	4
0;	0;	0	0;	0;	3	4	2	0, 0;	0;	0	0;	3	0	3
0	0	0;	0	0;	4	4	4	0, 0;	0;	0	0	4	0	4
0	0	0	0	0	3	4	4	0	0	0	0;	4	0	4
0;	0;	0;	0	0	3	3	3	0;	0	0	0;	3+	0	4
0	0	0	0	0;	3	4	4	0;	0	0, 0;	0	4	0	3
0;	0, 0;	0, 0;	0	0	3	4	4	0, 0;	0	0	0	3	0	4
0;	0;	0;	0, 0;	0	3	3	4	0, 0;	0	0	0	4	0	4
0	0, 0;	0	0	0;	3	3	4	0	0	0, 0;	0;	4	0	4
0	0	0	0;	0;	4	4	4	0;	0;	0, 0;	0	4	0	3
0	0	0	0	0;	3	0;	3	0;	0	0, 0;	0;	4	0, 0;	4
0	0	0	0	0	0, 1	3	3	0	0	0	0;	0	0	4
0, 0;	0	0	0	0	3	0	0, 1	0	0	0	0;	4	0	3+
0	0, 0;	0	0	0	1, 2	0;	0, 2	0	0	0	0	3+	0	3
0	0	0;	0	0;	0	3	0, 0;	0	0	0	0	0	0	3
0	0	0	0	0	0, 1	3	0;	0;	0, 0;	0	0	1+, 2+	0	3, 4
0	0	0	0	0;	0, 1	3	0	0	0	0	0	0;	0	3
0;	0	0	0	0;	0	3	0	0;	0, 1+	0	0;	0	0	3
0	0	0	0	0	0, 1	3	0, 0;	0	0	0	0	0	0	2, 2+
0	0	0	0	0;	3	2	3+	0	0	0, 0;	0	4	0	3
0	0	0	0	0;	0;	3	0	0	0	0	0	0	0	4
0	0	0	0	0	1, 2	0, 2	0, 1	0	0	0	0;	0	0	4
0	0	0	0	0	0;	0;	0, 1	0	0	0	0	4	0	4
0	0	0	0	0	2	0;	3, 3+	0	0, 0;	0	0	0;	0	2
0	0	0	0	0;	1	3	0, 0;	0;	0	0	0;	0, 2+	0	2+
0	0	0	0	0	2	3	3+, 4	0;	0	0	0;	1+, 2	0	1+, 2
0	0	0	0	0	2+	0, 0;	0;	0, 0;	0;	0, 0;	0	4	0	4
0	0	0	0	0	2	3	3+, 4	0	0	0	0;	1+, 2	0	1+, 2
0;	0	0	0	0	4	0, 0;	0;	0	0	0	0;	4	0	4
0;	0	0, 0;	0	0;	4	0, 2	0, 1	0	0	0	0	4	0	4
0;	0	0	0	0;	4	0	4	0	0	0;	0;	3	0	4
0;	0;	0	0	0;	4	0;	1, 2	0	0	0	0;	4	0	4
0;	0	0;	0, 0;	0	0;	3	4	0;	0	0	0;	2, 2+	0	3
0;	0, 0;	0;	0	0	3	0	4	0;	0;	0	0	3	0	3, 4
0;	0	0, 1+	0;	0;	0;	0;	0;	0, 1	0;	0;	0;	0;	0;	0;
0;	0	0;	0, 2	0;	0;	0;	0;	0, 1	0;	0;	0;	0;	0;	0;
0;	0	0, 0;	0;	0;	0, 0;	0	0;	0;	0;	0	0	0	0	0;
0;	0	0;	0;	0	0	0	0;	0;	0;	0	0;	0;	0, 0;	0;
0;	0, 0;	0, 0;	0;	0;	0;	0;	0;	0;	0;	0	0;	0;	0	0, 0;
0;	0, 0;	0;	0, 1+	0;	0;	0;	0;	0, 1	0;	0, 0;	0;	0, 0;	0	0;
0;	0;	0;	0;	0;	0;	0;	0;	0;	0;	0	0	0;	0;	0;
0;	0;	0;	0;	0;	0;	0;	0;	0;	0;	0	0, 0;	0;	0;	0;
0;	0;	0;	0	0;	0;	0;	0;	0;	0;	0	0;	0;	0, 0;	0;
0;	0;	0;	0	0;	0;	0;	0;	0;	0;	0	0;	0;	0;	0;
0	0, 0;	0;	0;	0;	0	0;	0	0;	0	0	0;	0;	0, 0;	0;
0;	0	0;	0, 0;	0, 1	0;	0;	0;	0;	0;	0	0;	0	0;	0;
0	0	0, 0;	0;	0	0;	0;	0;	0;	0;	0	0	0, 0;	0	0, 0;
0;	0;	0;	0;	0;	0, 0;	0	0;	0, 1	0;	0	0	0;	0;	0;
0, 0;	0, 0;	0;	0, 0;	0;	0;	0;	0;	0;	0;	0	0;	0	0	0, 1+
0;	0;	0, 0;	0, 1+	0;	0;	0;	0;	0;	0;	0	0;	0;	0	0;
0;	0;	0;	0, 2	0	0, 0;	0;	0;	0;	0;	0	0	0;	0	0;
0	0;	0;	0;	0;	0;	0;	0;	0;	0, 0;	0	0;	0;	0;	0;
0;	0, 0;	0;	0, 1	0;	0, 0;	0, 1	0;	0	0;	0	0	0;	0, 0;	0;
0;	0, 0;	0;	0;	0;	0;	0;	0	0;	0	0	0	0;	0	0;
0, 0;	0, 0;	0, 0;	0;	0;	0;	0;	0;	0;	0;	0	0;	0	0	0;
0;	0;	0;	0;	0;	0;	0;	0;	0;	0;	0	0;	0	0	0;
0;	0, 0;	0;	0, 1	0;	0, 0;	0, 1	0;	0	0;	0	0	0;	0, 0;	0;
0;	0, 0;	0;	0;	0;	0;	0;	0	0;	0	0	0	0;	0	0;
0, 0;	0, 0;	0, 0;	0;	0;	0;	0;	0;	0;	0;	0	0;	0	0	0;
0;	0	0;	0, 1+	4	0;	4	3	4	1+, 2+	3+	3	4	0;	3+, 4
0;	0	0;	0;	0;	0	2	0;	3	0;	3	3	0, 1	0;	4
0;	0;	1+	4	4	3	4	3	2	2	3	3	4	1	4

(continued on next page)

Table 2. (continued from previous page)

		Infection types to <i>Puccinia striiformis</i> f. sp. <i>tritici</i> pathotypes										
Line number	Yr gene	61009 (P1)	78028 (P2)	58893 (P3)	75078 (P4)	60105 (P5)	59791 (P6)	82517 (P7)	78080 (P8)	86094 (P9)	72107 (P10)	74187 (P11)
Yr6/6*Avocet S	Yr6	3	4	1, 1+	3	0;	0;	1+, 2	4	4	2+	4
133	Yr2, Yr6, +	0;	0	0;	0, 0;	0;	0;	0;	2, 0;	0	1+	0;, 1
41	Yr6, +	3	0;	0;, 2	4	0;	0	0;, 1+	3	3	3	0
52	Yr6, +	0;	2	0;, 1	0;	0;	0;	0;	0;	4	0;	0;
106	Yr6, +	0;	3	0, 0;	0;, 1, 2	0, 0;	0;	0;	0;, 1	0, 0;	1	0
Vilmorin 23	Yr3a, Yr4a,	4	0;	0;	3	0;, 2+	1	4	4	1	0;	3
Nord Desprez	Yr3a, Yr4a,	4	1, 2	0;, 1+	3	0;, 1	2+	4	4	2	0;	3
130	Yr3a, Yr4a, +	2	0;, 1	1, 1+	2+	1, 2+	0;	3+	0;	2	0;, 1	3
Lee*	Yr7, Yr22	0;	4	0;	2+, 3	0;, 1	0;	0;, 1	0;	4	4	0;
Reichersberg 42	Yr7	0;	4	0;	1+	0;, 1	0;	0;, 1	0;	2+	0;	0;, 1
92	Yr7, +	2	2+, 3	0;, 1+	3+	2	0;	2	0;	1, 2	3+	0;, 1
Yr15/6*Avocet S	Yr15	0;	0	0	0	0	0	0	0	0	0	0
35	Yr15 or others	0;	0	0;	0	0, 0;	0	0;	0;	0	0;	0
80	Yr15 or others	0	0, 0;	0	0	0	0;	0	0;	0	0	0
145	Yr15 or others	0	0	0;	0;	0;	0;	0;	0;	0	0	0;
Selkirk	Yr27	0	2, 2+	3	3	3	0;	2	2	2	4	3
112	Yr27, +	0	0, 0;	0	3	0, 0;	0;	0;	0;	0, 0;	4	0
Strubes	YrSD	4	0;, 1+	4	3	4	4	4	4	3	0;, 1	0
Dickkopf												
64	YrSD, +	3	0;, 1+	1+, 2	3	1, 2	2	4	0;	3	0;	0
72	YrSD, +	4	0;, 1	0;, 2	3	1, 2	0;	3	3	4	0;	0;
109	YrSD, +	3	0, 0;	0;	0, 2	1, 2	0;, 1, 2	3	3	0, 0;	1, 1+	0, 0;
Chinese 166	Yr1	0;	0, 0;	0;	0;	3+	0;	4	0	0	3	0
Hybrid 46	Yr3b, Yr4b,	0;	0;	0;, 1	3, 3+	0;	0;	2+, 3	4	0;	0;	0, 1
Compair	Yr8	0;	4	0, 0;	4	0	0	0, 0;	0	3	4	0;
Moro	Yr10	0	0	0, 0;	3+, 4	0	0	0	0	0	4	0
VPM	Yr17	0;	2+, 3	0;	1, 2	1, 2	0;, 1	1+, 2	2	0;	0	0
Funo	YrA	3	3+, 4	0;	3, 3+	0;, 1	3	2+	3	4	1, 1+	3
Alba*	YrAlba	3	0;	0;, 1+	3, 3+	3	3, 4	3+	4	2	0;	0;, 1
Carstens V	YrCV	3	0	2+	3	4	0;	3	3	4	2+	4
Gaby	YrGaby	0;	2+	0;	0;	0;	0;	0;	4	3	0;	0;
Resulka	YrRes	0	0	0	0;	0;	0	0	0	0	0	0
Spaldings	YrSpp	0	0;	0;, 1	2+, 3	2, 3	0	0;	1	0	0	3
Prolific												
Suwon 92/Omar	YrSu	0, 0;	0;	0;	4	0;	0	0;, 1+	4	0	4	4
1	+	3	3	4	3	1, 2	3	4	4	3	4	3
33	+	3	3	3, 3+	3	3	0;	3+	0;	0	2+	3
34	+	0	0	2, 2+	2	3	0, 0;	3	0;	4	3	3
39	+	0;, 2	0	3	3	2+	0, 0;	3	3	3	3	3
47	+	4	3	4	4	4	4	4	3	4	3	4
51	+	3	0;	3	4	3	2, 3	4	3	2+	3	1
53	+	4	4	4	3	3	4	3	0;	3	4	3
66	+	3	3	4	3	4	3	3	3	3	3	3
68	+	4	3	4	4	4	3	4	4	4	4	4
69	+	4	3	4	4	4	4	4	3	4	4	4
70	+	4	3	4	4	4	4	4	4	4	4	4
79	+	4	0;, 1+	3, 3+	3+	3+, 4	0;	3	3	3	1+, 2	4
81	+	1, 2	3	3	3	0;, 1	0	3	3	0;, 2	0;	3
89	+	4	4	4	4	4	4	3	3	3	4	4
93	+	0;, 2	3	3	2	1, 2	0	3	3	2	0;	2
99	+	3, 4	0	4	4	3	0	0, 2	1, 2	3	3	3
101	+	4	4	3	4	3	1, 2	3	3	4	3	3
102	+	4	3	3	4	3	3	3	3	4	3	4
105	+	4	4	4	4	4	4	4	4	4	4	4
108	+	3	4	4	3+	0;	0;	0;, 1	0;, 1	3	3	4
122	+	4	3	3	4	3	3	4	3+	2+	4	4
132	+	0, 0;	0;	0, 0;	0, 0;	0	0;	0;	0	0, 0;	4	0
140	+	3	0	4	3+	0;, 2	3	3	4	2	3	0;, 2

Low infection types produced by L112 (Mian 2000-18) to pathotypes avirulent to Selkirk (Yr27) and some pathotypes virulent to Yr27 indicated the presence of Yr27 and other unidentified resistance genes.

Six lines (L47 = Xiaoyan 921, L68 = Yangfu 2, L69 = Yangmai 10, L70 = Yangmai 158, L89 = 99422, and L102 = Chuanyu 19) showed high infection types to all pathotypes tested, indicating they did not have any detectable stripe rust resistance genes present in the reference differ-

entials. The reactions of 17 lines (L1 = Han 3475, L33 = 2611, L34 = 953, L39 = Nonglin 9823, L51 = Xinong 8925-13, L53 = Yunfeng 988, L66 = Emai 14, L79 = 298-1, L81 = 3472, L93 = Chen 98-18, L99 = Chuannong 21, L101 = Chuanyu 18, L105 = Kefeng 14, L108 = LB 0458, L122 = Mianyang 29, L132 = SW8588, and L140 = Fengmai 24) were not consistent with those of any known resistance genes. Hence, more work is needed to identify the resistance genes in these lines.

Three lines, L35 (N139), L80 (323-2), and L145 (3S857), conferred resistance to all pathotypes tested, indicating they possess either Yr15, a gene combination, or one or more unidentified resistance genes.

Slow rusting resistance in field tests. Highly significant differences were found for genotypes and environments for relative AUDPC and FDS in the field trials (Table 3). The genotype-environment interaction was also significant, but its effect

Infection types to <i>Puccinia striiformis</i> f. sp. <i>tritici</i> pathotypes														
86036 (P12)	76088 (P13)	76093 (P14)	86106 (P15)	68009 (P16)	86107 (P17)	82061 (P18)	80551 (P19)	85019 (P20)	PE92 (P21)	CYR26 (P22)	CYR27 (P23)	CYR29 (P24)	CYRSu- 1 (P25)	CYR32 (P26)
0;	3	3+, 4	4	4	4	3	2+	4	3+, 4	3+	4	4	3	4
0;	0;	0;	3	0;	0;	2	0;	2	0;	4	3	4	0;	4
0;, 1+	3	3+, 4	0;	0;	3	4	2+	3	0;	4	4	0;	4	4
0;	0;	2, 2+	4	4	4	0;	2+	0;	0;	0;	4	4	2	4
0	0;	0;	0;	0;	3	0;	2+	2	3	2+	0;	1+, 2	3	4
0;, 2+	0;	0;	0;	2	0, 1	4	3	3	0;	1, 2	4	4	0	2+
0;	0;	1, 1+	0;	2	2	4	3	4	0;	4	4	4	1	4
1, 2	0;	2, 2+	2+	0;	0;	0;	2, 2+	0;	0;	3	4	3+, 4	0;	4
0;	4	4	4	3+	4	0;	2+	0;	3	4	0;	4	4	4
0;	1+, 2	2+	4	4	4	0;	1+	0;	2, 2+	2+	0;	4	3	2+
0;	3	3	0;	0;	3	0;	2+	0;	1+, 2	3	0;	4	4	4
0	0	0	0	0;	0;	0;	0	0;	0	0	0;	0	0	0, 0;
0	0	0;	0;	0	0, 0;	0	0;	0;	0;	0	0;	0, 0;	0	0;
0, 0;	0	0	0	0	0	0	0	0;	0	0	0;	0	0	0, 0;
0;	0	0	0;	0;	0	0;	0	0;	0;	0	0;	0	0	0;
0;	3	3	0;	0;	2	0;	3	0;	3	3	2	3+	2+	4
0, 0;	0, 2+	1+	0;	0;	0	0;	2+	0;	0;	3	0	0	1, 2	3
4	0;	1+	4	4	2	4	3	3	0;	0;	3	4	2	3
3	0	2	4	2	0;	4	3	3	0;	1, 2	4	4	0;	2+, 3
2+	0;	0;	2	2	0;	3	0;	3	0;	0	3	3+, 4	0;	0;
2+	0;	0;	0, 0;	3	0;	3	2+	3+	0;	0;	0;	0	0;	1+, 2
0;	0	4	3+	4	0	0;	4	4	0, 0;	4	4	4	4	4
0;	0;	0;	0;	0;	1	4	1, 2	4	0;	0;	0;	3	0;	3
0;	3+	4	3	0	3	0;	4	0	4	0;	3	0;	3	0;
0, 0;	0	0	0	0	0	0	0	0	0;	0	0;	0	0	0
0, 0;	0	2+	2	0;	0;	0;	3	0;	0;	0;	0;	4	2	4
0;	2+	1+	0;	2+	4	2	2+	2	4	4	4	4	0;	4
0;, 1+	0, 0;	0;	3, 4	0;	2	0;	2	3	2+	4	4	4	1	3+
0;	0;	0;	0;	3	1	4	0;	4	0;	0;	2	4	0;	3
0;	0;	3	4	4	2+	3	0;	4	3	0;	4	4	2	2+
-	0	-	0	0	0;	-	3	0	0;	0	-	4	0	3
0;	0, 0;	0	2+	0;	0;	3	0;	3	0, 0;	0	4	0	0	4
0	0;	2+	0;	0	0	3	3	0	0	0, 2	0	0;	4	4
3	0;	0	3	4	3	3	4	0;	3	4	4	0;	1, 2	4
3, 4	0;	2+	3	0;	3	4	3	0;	3, 3	0	3	4	4	4
0;	0, 0;	0;	0	0	0	4	0;	3	0;	0	4	4	0	4
0;, 1	0;	0;	1, 2	0;	3	0	4	3	3	4	3	2+	1, 2	3
3	4	3	4	4	4	4	4	4	4	4	4	3	3	4
3	3	2	3	3	3	4	3	3	3	4	3	4	3	4
4	2+	3, 4	4	3	3	3	4	4	4	3	4	3	3	4
0;	0, 0;	0, 0;	3	2	4	4	4	4	4	4	4	3, 4	1, 2	4
4	4	4	4	4	4	4	4	4	4	4	4	4	4	4
4	3	4	4	4	4	4	4	4	4	4	4	4	4	4
4	3	3	4	3	4	4	4	4	4	3	4	4	3	4
0, 0;	3	0	0	0;	3	1	3, 3+	4	0;	3	3	3+	3	4
3	0	3	0	1, 2	3	4	4	4	0	0	3	3, 4	4	4
4	3	4	4	3	3	3	4	4	4	4	4	3	4	3
3	3	2+	0, 1	3	3	4	4	4	4	4	4	4	3	4
4	3	0;	1, 2	1, 2	0;	1	4	3	4	0;	3	4	4	3
3	3	0;	0;	0;	3	0;	4	3	4	0;	2	4	3	4
4	4	4	3	3+	4	3	4	4	4	4	3	4	3	4
4	4	4	4	4	3	4	4	4	0	0;	4	4	4	4
3	3	4	0;	3	2	0;	3	3	4	2	3	4	0;	3
3	1, 2	4	0;	3	4	3	4	4	3	4	4	3	3	3
0, 0;	0;	0;	0;	0	0, 0;	0;	0;	0;	0;	0;	0;	3+	0;	4
3	2	3	0;	0;	3	3	4	4	3	2	4	3	4	4

on variation was much lower than that for genotype differences.

FDS of susceptible check, Tiaogan 601, was 90 to 100 in Beijing and Tianshui (Table 4), indicating disease developed well at both locations. The FDS of the slow rusting check, Lantian 12, was 13 and 19, respectively, while its relative AUDPC was 0.17 and 0.16, respectively, at the two locations (Table 4).

Twenty-six lines, including L23 (Zhoumai 11), L55 (93-23-13), L57 (95-108),

L58 (95-111-6-3-10), L60 (95-3-5-1), L61 (9562-1), L72 (An 96-8), L77 (01-3570), L80 (323-2), L83 (58512-2), L90 (99-607), L94 (Chuanmai 42), L95 (Chuanmai 43), L104 (Jinfeng 626), L107 (LB 0438), L109 (Lemai 3), L113 (Mian 2000-34), L115 (Mian 2000-8), L117 (Mianmai 37), L125 (Nei 2938), L126 (Neimai 9), L127 (R111), L128 (R122), L129 (R25), L134 (Xike 01015), and L136 (Xingmai 2), were identified as highly resistant cultivars with high resistance to the pathotype CYR32 at

both seedling and adult stages. Thirty-three lines (Table 4) showed slow rusting resistance at two locations, exhibiting high infection types at seedling stage, but low FDS and AUDPC in the field tests.

The correlations of FDS and relative AUDPC between Beijing and Tianshui were 0.88 and 0.80, respectively, indicating a high consistency of the test in two locations for slow rusting resistance. The correlation between relative AUDPC and FDS at the two locations varied from 0.91

to 0.98, indicating that FDS could be used as a reliable indicator of AUDPC.

DISCUSSION

Seedling test for stripe rust. In the present study, *Yr9* was identified in 42 of 98 (43%) lines, which is consistent with the results reported by Niu et al. (21) and Wu et al. (43). *Yr26* was postulated to be present in 19 lines. This gene was derived from Chinese line γ 80-1 (*Triticum turgidum* L.) and its derivatives such as

92R137, 92R171, and 92R178 from Nanjing Agricultural University (Table 1) (16). The lines possessing *Yr26* are grown over a large area in Gansu and Sichuan provinces where climatic conditions are favorable to stripe rust development. If a new race of *P. striiformis* f. sp. *tritici* virulent to *Yr26* appears, a new epidemic could again cause severe losses as the case in 1990 and with the Fan 6-derived resistance in 2002. The danger of using limited sources of resistance has become a great concern to

wheat breeders and pathologists. It is imperative that new stripe rust resistance genes be identified and utilized in breeding programs. Although *Yr26* currently provides effective resistance in China, breeding programs should anticipate its downfall by improving the genetic diversity of breeding materials.

The *Yr26*-virulent race (P4 = 75078) originated from Egypt (22). Apart from its *Yr26* virulence, it is probably not a threatening pathotype. This culture was also virulent on the line *Yr24/3**Avocet S, indicating that *Yr26* and *Yr24* are likely the same gene, which is in agreement with our previous study (10). Although *Yr24* was also derived from *T. turgidum* (19), its origin and naming was independent of that for *Yr26*.

Near-isogenic lines (NIL) with one resistance gene were often utilized in the postulation of resistance genes to wheat leaf rust (23,34). Nevertheless, in the postulation of stripe rust resistance genes, differential lines with one or more genes were often employed (24,26). In the present study, 8 of 25 differential lines contain more than one resistance gene, leading to some difficulties in gene postulation in

Table 3. Analysis of variance of relative area under the disease progress curve (AUDPC) and final disease severity (FDS) in 137 wheat lines including slow rusting and susceptible checks tested in Beijing in 2003–2004, and in Tianshui in 2003–2004 and 2004–2005 cropping seasons

Parameter	Source of variation	df	MS	F value	P > F
AUDPC	Line	136	0.92	106.89	<0.0001
	Env	2	1.36	157.51	<0.0001
	Replicate	6	0.0094	1.10	0.36
	Lines $\times$ env	272	0.062	7.15	<0.0001
	Error	816	0.0086		
FDS	Line	136	9,972.99	207.46	<0.0001
	Env	2	13,181.77	274.21	<0.0001
	Replicate	6	35.90	0.75	0.61
	Lines $\times$ env	272	416.60	8.67	<0.0001
	Error	816	48.07		

Table 4. Wheat lines with slow rusting resistance to stripe rust identified by using Fisher's *F* protected LSD (LSD alpha = 0.05) test in Beijing in 2003–2004, and in Tianshui in 2003–2004 and 2004–2005 cropping seasons

Line number	Seedling IT to CYR32	Beijing (2003–2004)			Tianshui (2003–2004)			Tianshui (2004–2005)		
		IT	FDS	rAUDPC	IT	FDS	rAUDPC	IT	FDS	rAUDPC
Lantian 12 ^a	4	1, 2	13	0.17	1, 2	17	0.14	3	21	0.18
Tiaogan 601 ^b	4	4	90	1	4	95	1	4	100	1
Lankao 906-4 (L9)	4	3, 4	25	0.24	3, 4	12	0.12	4	12	0.1
Xinong 291 (L50)	4	0;	1	0.01	2	1	0.01	0;, 2	1	0.01
Shaannong 981 (L44)	4	2, 3	12	0.19	2, 3	15	0.1	2, 3	25	0.21
90-99-5 (L54)	4	3, 4	3	0.11	3, 4	7	0.09	4	17	0.21
94t-133 (L56)	3+	0;	1	0.01	1, 2	3	0.06	1, 2	2	0.07
96-22-2-3 (L62)	4	1, 2	6	0.07	2, 3	10	0.07	2, 3	6	0.09
Lantian 9 (L63)	4	2, 3	6	0.06	0;, 1	1	0.02	1, 2	5	0.1
Guizhou 98-18 (L74)	3	2, 3	6	0.15	3, 4	24	0.15	3, 4	24	0.25
01-018 (L78)	3	1, 2	4	0.1	3, 3+	15	0.14	3, 4	1	0.05
01-10251 (L76)	4	1, 2	19	0.25	2, 3	16	0.13	2, 3	8	0.1
351-15 (L82)	4	1	2	0.02	2	2	0.03	2	11	0.12
58749 (L84)	4	3, 4	9	0.11	3, 4	4	0.04	3, 4	4	0.1
93Xia032-1 (L86)	3	3, 3+	18	0.21	3, 3+	8	0.08	3, 3+	7	0.11
99422 (L89)	3	2, 3	16	0.2	2, 3	4	0.07	2, 3	4	0.07
Bi 2002-2 (L73)	3	2, 3	14	0.1	3	8	0.07	3	12	0.11
Chen 98-18 (L93)	4	2, 3	16	0.26	2, 3	22	0.23	2	24	0.23
Chuannong 17 (L98)	3	1, 2	11	0.11	2, 3	12	0.12	2, 3	11	0.14
Chuannong 21 (L99)	3	1, 2	5	0.09	2, 3	12	0.11	3, 4	15	0.14
Chuanyu 18 (L101)	4	1, 2	1	0.1	3	2	0.03	3+	2	0.02
Chuanyu 19 (L102)	4	3, 4	8	0.14	3, 4	5	0.06	4	4	0.11
LB 0288 (L106)	4	1, 2	15	0.07	2, 3	3	0.04	2, 3	14	0.11
LB 0458 (L108)	3	1, 2	7	0.05	1, 2	4	0.05	2	12	0.1
Mian 2000-13 (L111)	3	1, 2	9	0.18	3	12	0.08	3, 4	7	0.1
Mian 2000-18 (L112)	3	1	1	0.01	2	1	0.02	2, 3	2	0.06
Mian 2000-36 (L114)	4	1, 2	2	0.04	3, 4	9	0.09	3, 4	21	0.2
N1621-19-4 (L123)	3	1, 2	2	0.16	2	1	0.03	3, 4	5	0.11
N711 (L124)	4	0;	5	0.01	1, 2	1	0.03	2, 3	2	0.07
R88 (L130)	4	0;	1	0.01	3	2	0.02	3, 4	1	0.03
R97 (L131)	4	3	1	0.09	3	9	0.08	1, 2	2	0.06
SW 8588 (L132)	4	0;	1	0.01	2+	1	0.01	3	3	0.03
9021 (L139)	3	0;, 1	5	0.02	2, 3	22	0.19	2, 3	11	0.15
Jing 035-1 (L141)	4	0;, 1	11	0.19	0;, 2	21	0.21	2, 3	21	0.15
Yin 11-12 (L143)	4	3	3	0.04	2, 3	6	0.09	3	12	0.15
LSD (0.05)			13.01	0.21		10.73	0.12		9.40	0.10

^a Slow rusting check.

^b Susceptible check.

genetically unknown materials. Some gene combinations may be identified, but others cannot be postulated due to a lack of testers with confirmed single resistance genes. The near-isogenic lines developed in Avocet S may be a good option for reference lines (39), but the series including limited known genes needs to be extended to cover a wider range of genes. The differential lines used in this study are all with universally known genes (20). Most of them contain only one gene, assuring the postulation of resistance genes. In addition, the most frequent resistance gene, *Yr9*, identified in the seedling test was confirmed by a SCAR marker of 1B/IR (Table 1), and the pedigree information was also used in the postulation of seedling resistance genes.

In the seedling test for stripe rust, it very likely causes confusion with IT 0, confusing true immune response (low) and escape (missing data) with the other response that infection has occurred but variability between tests can still be a problem. In the present study, the seedling tests were conducted twice, and the results were consistent between two seedling tests with very few exceptions. In case disease scores with some pathotypes tested were not consistent between two repeats, the data with better disease development were used for the postulation of seedling resistance genes, because the low infection types might be due to inadequate inoculation.

Field resistance. Of 33 lines with slow rusting resistance to CYR32, 26 were tested on seedlings with 26 pathotypes; 15 lines carried *Yr9* and 6 lines gave high ITs to most of the pathotypes (Table 2). In these lines, the major seedling resistance genes were overcome by pathotype CYR32, and the slow rusting resistances probably resulted from minor genes. The resistance in 96-22-2-3 (L62) may be conferred by *Yr16* derived from Cappelle Desprez (Table 1) (41). Slow rusting in 94t-133 (L56) may be derived from Xiannong 4 with durable resistance to stripe rust (Table 1) (46). Slow rusting resistance in Chuanyu 18 (L101), Chuanyu 19 (L102), LB 0288 (L106), LB 0458 (L108), 9021 (L139), and Yin 11-12 (L143) may be derived from CIMMYT wheat germ plasm (Table 1). All lines except for Lankao 906-4 (L9) with slow rusting resistance identified in this study were from northwestern and southwestern China where stripe rust resistance is a major breeding objective, indicating that more attention was paid to wheat stripe rust resistance in western China than in other wheat growing regions.

Breeding for durable resistance with seedling and slow rusting genes. In China, urediospores of *P. striiformis* f. sp. *tritici* live over summer in southeastern Gansu and northeastern Sichuan, where climatic conditions, geographic characteristics, and cropping systems are favorable for stripe rust every year (11). The spores

spread from west to east in the autumn, winter, and early spring, and result in epidemics of stripe rust in the main wheat growing region of China. Therefore, reducing the amount of initial inoculum in the over-summer regions is a key strategy to achieving sustainable control of stripe rust in China (35). Several strategies, such as pyramiding of major resistance genes, deployment of different genes in mountainous regions (where urediospores can live in summer) and plains (over-winter region), and reducing wheat acreage by planting other crops, can largely reduce inoculum in the over-summer regions (35,42). In the present study, 26 lines with good agronomic performance were found to be highly resistant to stripe rust both in the seedling and adult plant stage with different resistance genes, which may be used as parents in the wheat breeding program for gene deployment and gene pyramiding in southeastern Gansu and northeastern Sichuan to reduce the amount of urediospores of *P. striiformis* f. sp. *tritici*. This will certainly help in the control of stripe rust in other wheat growing regions.

The eastern and northern epidemic region covers major wheat production areas with less frequent occurrence of favorable climatic conditions, especially in Hebei, Henan, Shandong, and Shanxi provinces (35). Strategies for controlling stripe rust in these regions are slightly different from those in the over-summer regions of western China. In addition to pyramiding and deploying major resistance genes, utilization of minor additive genes was strongly proposed for controlling stripe rust (21). During the past 5 years, a shuttle-breeding program was conducted between CIMMYT and China for developing slow rusting cultivars with a limited backcrossing method (31). CIMMYT wheat cultivars Chapio, Tukur, Kukuna, and Vivitsi, with four to five minor additive genes, were used as parents in wheat breeding. In this study, six lines, including Chuanyu 18 (L101), Chuanyu 19 (L102), LB 0288 (L106), LB 0458 (L108), 9021 (L139), and Yin 11-12 (L143), were identified as having slow rusting resistance, which was derived from the CIMMYT wheat germ plasm, indicating that it is possible to combine slow rusting resistance with good agronomic performance through shuttle breeding between Mexico and China. Because multiple genes may confer durable resistance (27,31), the use of slow rusting resistance should be a more sustainable strategy for developing wheat cultivars in eastern and northern China.

In the evaluation of adult-plant resistance (APR) to wheat rusts, AUDPC is certainly a more reliable indicator than FDS. However, in the wheat breeding program, breeders need to evaluate the disease severity for hundreds of thousands of individuals and thousands of lines. They may have no time to score the disease several

times to calculate AUDPC. A simple method is therefore needed for evaluating such a great number of materials. In the present study, a high correlation was found between AUDPC and FDS, which is consistent with our previous studies in the characterization of APR to powdery mildew in wheat (12,38). Hence, we suggested using FDS as an indicator for the evaluation of APR to stripe rust in wheat breeding with a single scoring at an appropriate time. The high correlations of FDS and AUDPC between Beijing and Tianshui environment with low temperature and much more rain is very favorable to the development of stripe rust and for selection of slow rusting resistance in wheat breeding populations.

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