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Postulation of Seedling Stem Rust Resistance Genes of Yunnan Wheat Cultivars in China

Tian-ya LI, Xian-xin WU, Xiao-feng XU, Wan-lin WANG and Yuan-yin CAO

College of Plant Protection, Shenyang Agricultural University, Shenyang, P.R. China

Abstract

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To determine stem rust resistance genes of wheat varieties in Yunnan province, 11 Chinese strains of *Puccinia graminis* f.sp. *tritici* with different virulence and 1 artificial mutant strain were used in 110 wheat varieties. The results indicated that among the 45 *Sr* genes, *Sr*31, *Sr*5, *SrTmp*, *Sr*30, *Sr*36, *Sr*8a, *Sr*11, *Sr*24, *Sr*29, *Sr*34, *Sr*9e, *Sr*26, *Sr*38, *Sr*47, and *Sr*Tt3 were characterised in 55 wheat varieties singly or in combination. *Sr*5, *Sr*31, *Sr*Tmp, *Sr*36, and *Sr*30 were contained in 17, 16, 5, 5, and 3 cultivars, respectively. Six cultivars contained *Sr24* and/or *Sr34*. Three plant materials likely contained one or more of *Sr*8a, *Sr*11, *Sr*34, and *Sr*23 genes as well as other unknown genes. The 16 immune or highly resistant varieties contained one or more of *Sr*9e, *Sr*26, *Sr*38, *Sr*47, *Sr*Tt3, and other unknown resistance genes. The reaction types on 22 of the tested cultivars were different from those on *Sr* genes tested, and their resistance genes could not be analysed. Additionally, 17 varieties were susceptible to all the tested strains, having no postulation value. Our study provides a basis for improved breeding of stem rust resistant wheat in China.

Keywords: *Triticum aestivum* L.; *Puccinia graminis*; *Sr* gene; gene postulation

Understanding resistance genes to *Puccinia graminis* f.sp. *tritici* and their characteristics in wheat cultivars is one of the most important premises for reasonable, effective application and distribution of the resistance source in the comprehensive control of wheat stem rust (Cao *et al*. 2007). Resistance genes of wheat stem rust have been officially named *Sr58* (Liu *et al*. 2009), and there are many unnamed ones. Moreover, some of them have been applied in wheat cultivation (Da & Yan 2011). According to the gene-for-gene hypothesis, every virulence gene has a corresponding resistance gene (Flor 1971). When breeders and researchers are aware of the existence of stem rust-resistance genes in wheat cultivars, the resistance source is used and distributed in the comprehensive control of wheat stem rust, timely and effectively. On the other hand, virulence of pathogenic populations can be monitored.

Wheat stem rust is one of the most devastating diseases of wheat production in the world (Ravi *et al*. 2011). Yunnan province, located at the southwest border of China, owns the common cultivation pattern of wheat stereoscopic plantation year-round, and a distinct environment of diverse microclimate, where *P. graminis* f.sp. *tritici* is able to complete its life cycle with urediospores or through sexual reproduction (Cao *et al*. 2001; Wu *et al*. 2014). Under certain conditions, Yunnan province can still provide initial pathogens for wheat stem rust in China (Cao *et al*. 2001; Wu *et al*. 2014), playing a key role in the regional spread and epidemic of wheat stem rust. Moreover, the resistance level of production cultivars to *P. graminis* f.sp. *tritici* in Yunnan province has a direct relationship to wheat stem rust epidemic and the accumulation of initial pathogens. Planting resist-

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ant cultivars is the most economical, reasonable, and environmental measure for controlling this disease (Bai *et al*. 2010). Therefore, analysing the genetic background of disease-resistant cultivars as well as resistance genes contained in the main production cultivars, reserve lines, and new cultivated varieties can provide a theoretical basis for exploring resistance source and planning disease-resistant plant breeding in the future (Han 2009). Gene postulation is an effective and fast method to assess resistance of multiple cultivars macroscopically, and widely used in the identification of resistance genes in wheat (Niu *et al*. 2000; Yuan *et al*. 2007; Cao *et al*. 2010). Postulation of resistance genes to *P. graminis* f.sp. *tritici* for some important cultivars and resistant sources has been carried out in China and other countries (Qiu *et al*. 1999; Singh *et al*. 2001; Li *et al*. 2011).

In this study, 11 national epidemic strains of *P. graminis* f.sp. *tritici* and one mutant strain obtained by artificial ultraviolet with '2' infection type (IT) to *Sr31* were applied for the postulation of resistance genes of wheat cultivars (lines) in Yunnan province.

MATERIAL AND METHODS

Wheat cultivars tested and near-isogenic lines of the known genes. A total of 110 wheat cultivars tested were provided by Li Mingju, Yunnan Provincial Institute of Agricultural Environment and Resources, including the main productive cultivars and reserve lines in Yunnan province.

Forty five *Sr* single genes tested: *Sr*5, *Sr*6, *Sr*7b, *Sr*8a, *Sr*9a, *Sr*9b, *Sr*9d, *Sr*9e, *Sr*9f, *Sr*9g, *Sr*10, *Sr*11, *Sr*12, *Sr*13, *Sr*14, *Sr*15, *Sr*16, *Sr*17, *Sr*18, *Sr*19, *Sr*20, *Sr*21, *Sr*22, *Sr*23, *Sr*24, *Sr*25, *Sr*26, *Sr*27, *Sr*28, *Sr*29, *Sr*30, *Sr*31, *Sr*32, *Sr*33, *Sr*34, *Sr*35, *Sr*37, *Sr*36, *Sr*38, *Sr*47, *Sr*Tt3, *Sr*Tmp, *Sr*GT, *Sr*dp-2, and *Sr*McN were offered by the Institute of Plant Immunology of Shenyang Agricultural University.

***P. graminis* f.sp. *tritici* races**. A total of 12 *P. graminis* f.sp. *tritici* races were used as strains tested, namely 21C3CTHTM, 21C3CTQSM, 21C3 CTTSC, 21C3HTTTM, 34MKGQM, 34MRGQM, 34MTGSM, 34OroIIMRGQM, 34C3RKGQM, 34C3RKGSM, 34C3RTGQM, and a mutant strain by artificial ultraviolet.

Postulation of resistance genes. Forty-five *Sr* standard lines and wheat cultivars tested were sown in pots of 10 cm caliber. Meanwhile, cv. Little Club was used as control. Races with various pathogenic types were inoculated to wheat seedlings with primary leaves fully expanded and second leaves sprouting (7 days), separately. The inoculated seedlings were moisturised for 14~16 h, and cultured at 21 ± 1°C and light intensity of 5.8~6.0 klx. Infection types were assessed after the interaction of 45 *Sr* differential lines and 12 tested races with full incidence; they were recorded according to 6 class standards, including 0, ;, 1, 2, 3, 4, and mixed types (X, Y, Z) (0 – no uredia or other macroscopic sign of infection; ; – no uredia, but hypersensitive necrotic or chlorotic flecks of varying size present; 1 – small uredia often surrounded by a necrosis; 2– small to medium uredia often surrounded by chlorosis or necrosis; 3 – medium-sized uredia that may be associated with chlorosis or rarely necrosis; 4– large uredia without chlorosis or nectosis; X – random distribution of variable-sized uredia on single leaf with a pure culture; Y– ordered distribution of variable-sized uredia, with larger uredia at leaf tip; Z– ordered distribution of variable-sized uredia, with larger uredia at leaf base) (Roelfs & William 1988; Roelfs *et al*. 1995). If necessary, the symbols '+' or '–' are added to indicate minor differences of infection severity; the letter C was used for cases with significant chlorosis. Postulation of resistance genes was carried out as proposed by Statler (1984): based on the low infection types after gene interaction, the genes resistant to *P. graminis* f.sp. *tritici* contained by the tested cultivars were postulated.

RESULTS

Interactions of 45 differential lines (Host A) and 12 P. graminis f.sp. tritici strains with different pathogenic types. From the infection types of the 12 *P. graminis* f.sp. *tritici* strains to the *Sr* standard lines, *Sr*6, *Sr*7b, *Sr*9a, *Sr*9b, *Sr*9d, *Sr*9f, *Sr*9g, and *Sr*16 were highly susceptible to all the tested strains, and whether the tested cultivars contained these genes could not be determined; *Sr*9e, *Sr*26, *Sr*38, *Sr*47, and *Sr*Tt3 showed low reactions to all tested strains; interaction types of the remaining lines and the tested strains varied (Table 1); the susceptible control McN701 (winter wheat) and Little Club (spring wheat) without resistance genes were highly susceptible to all the 12 *P. graminis* f.sp. *tritici* strains tested, indicating that inoculation was successful.

Interactions of 110 cultivars tested (Host B) and 12 P. graminis f.sp. tritici strains with different

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Table 1. Infection types produced by interactions between 12 strains of *P. graminis* f.sp. *tritici* and *Sr* genes

Sr gene	Tested races											
	21C3				34			34OroII	34C3			mutant strain
	CTHTM	CTQSM	CTTSC	HTTTM	MKGQM	MRGQM	MTGSM	MRGQM	RKGQM	RKGSM	RTGQM	
5	1	0	1	0	4	4	4	4	4	3	4	4
8a	4	3	4	4	4	1	4	2	4	4	4	4
10	4	4	4	4	1	1+	4	1+	;	4	;	3
11	3	4	3	4	0	4	4	4	1	;	4	4
12	4	4	4	4	3	0	1	4	4	4	0	4
13	4	4	4	4	1+	1	1	3	0	1+	1+	0
14	4	4	0	1+	0	1+	0	3	1	3	3	0
15	4	4	4	3	3	4	3	4	1	4	0	3
17	4	2	3	4	0	1+	;	0	0	;	;	;1–
18	4	3	1+	4	0	3	4	4	;	0	3	0
19	0	0	0	0	0	0	3-	1	3–	0	0	0
20	0	4	3	4	4	3	4	4	1	3	0	0
21	2	1+	1–	3	1	1	2	2	4	3	3	4
22	0	1+	3	0	1	0	0	4	1	0	3	1
23	1	3-	3	0	0	1	0	1	3	0	0	1
24	3	3	;1–	3	4	3-	4	4	3	3	3	4
25	0	0	0	3	1	0	4	4	0	0	4	0
27	1	4	4	4	4	0	4	4	4	4	0	1
28	4	4	4	4	4	0	4	4	4	4	4	1
29	3	4	4	4	4	0	4	4	3	4	4	1
30	1	2	4	4	1	;	1	2	;	0	1	3
31	1	;1-	1–	1	1	1	;	;1–	1	0	;	2
32	3	3	1	3+	3	0	4	1	4	4	4	1+
33	0	0	0	3+	1	0	0	1-	0	0	0	0
34	4	3-	4	4	1	0	3	4	0	0	4	3
35	4	0	4	0	0	1	1	1	0	1	1	3
36	0	4	4	4	;	1	0	;1	0	;1	1	0
37	0	1++	4	1+	1	1	1	3	;	0	1	0
Tmp	4	;	;1	4	;1	;	;	;1	;	0	0	4
GT	0	4	3	3	3	0	1	3	2	0	2	4
dp-2	4	4	4	4	0	0	1	3	1	1	1+	4
Little Club	4	4	4	4	4	4	4	4	4	4	4	4
McN	4	4	4	4	4	4	4	4	4	4	4	4

The infection types are often refined by modifying characters as follows: =, uredia at the lower size limit for the infection type; –, uredia somewhat smaller than normal for the infection type; +, uredia somewhat larger than normal for the infection type; ++, uredia at the upper size limit for the infection type; C, more chlorosis than normal for the infection type; for other symbols see Material and Methods

pathogenic types. The infection types after the interaction of cultivars and the 12 strains are shown in Table 2, in which cultivars susceptible or immune to all the strains tested are not listed. Based on infection types, the 110 cultivars were classified into several groups according to their putative resistance genes. The following results were obtained:

Group 1: cultivars immune to all tested strains – nearly immune (IT = 0–1). A total of 16 cultivars were included in this group: Linmai 6, Demai 4, I18, Fengmai 36, Wenmai 8, R101, Linmai 17, Demai 7, 08-11 (Germany), Feng 0483, Feng 615, 4-8, Kunmai 4, E33, Feng 0230, and Kunming spring wheat. Their reaction types were similar to the tested standard lines *Sr*9e, *Sr*26, *Sr*38, and *Sr*47, with resistance spectrum of immune–nearly immune (IT 0–1) to all the strains tested. Therefore, these cultivars might contain one or more of these four genes, as well as unknown resistance genes.

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Table 2. The infection types of tested cultivars (lines) to 12 *P. graminis* f.sp. *tritici*

Cultivars (lines)	Tested races											
	21C3				34			34OroII	34C3			mutant strain
	CTHTM	CTQSM	CTTSC	HTTTM	MKGQM	MRGQM	MTGSM	MRGQM	RKGQM	RKGSM	RTGQM	
Yunxuan 2	1	0	0	1	0	0	0	0	0	0	0	2
Yunxuan 3	0	;	0	1	0	0	0	0	0	0	0	2
Yunxuan 11-12	0	1	0	1+	1	1+	0	0	1+	0	1	2
Yunmai 101	0	1	0	1	0	;1	0	0	0	0	;1	2
Kunmai 5	0	1+	0	1+	0	0	0	0	0	0	;1	2
Jingmai 11	0	1	0	0	1	;1=	1	;	;	;	1	2
Jingmai 14	0	0	0	1++	0	1	1	1	1	0	1	2
Jing 0202	0	0	1	1+	1	;1	;	;	;	;	;	2
Jing 06-4	1	1+	0	;	1	;	0	0	;1=	0	1	2
De 05-81	0	1	1	;	0	1+	1	0	1	0	1	2
Linmai 15	0	1	1	;	1	;1	1+	0	0	0	1;	2
Feng 1124	0	0	0	0	0	1	1	1	0	1+	1+	2
Wenmai 12	1	1+	1+	2	0	;	1	1	1+	1+	1+	2
Liangmai 4	1	0	0	0	0	;	0	0	0	0	1	2
R57	0	1	0	1+	1	;1=	1	0	1+	1+	1	2
Yumai 3	1+	0	0	; 1	0	0	0	0	0	0	;	2
Yimai 10	0	1	1	2	4	3	4	4	4	4	4	4
Yimai 1	0	1	1	1+	4	4	4	4	4	4	4	4
K07-295	0	1	0	2	3	3	3	3	3+	3+	3	3
Yixi 96-6	0	0	1	1+	4	4	4	4	4	4	4	4
08-3 (De)	0	0	0	1+	0	3+	3	4	3	4	3	4
098-10	0	0	0	0	3	3	4	3-	4	4	3+	3
Yimai lines 2003-27	0	0	0	0	4	4	3	4	4	4	4	4
Chu 2008 Jian-4	1+	1	1+	0	0	2	1	3	3	3	3	3+
06D6-6	0	0	0	0	0	0	0	4	3	3	4	4
088-16	0	0	0	0	0	1+	3	3	3	3	1+	3
K042-39	1+	1+	;	2	4	2	0	4	4	3	3	4
Linmai 17	1+	1+	1+	1+	0	;1	3	0	0	3	1	0
Chumai 12	0	0	0	2	1	3	1	3	4	3	3	3
05-1	0	0	1	0	0	2	0	1	3	3	3	3
Fengmai 37	0	0	0	0	0	4	4	4	3	4	1+	3
08 yu F-5	0	1	1	1–	4	3	0	0	0	0	3	1+
Guoji 13	1	1+	1+	3	0	;	0	0	;	;1	0	3-
Wen 06-3	3	1	1+	3	0	;	;	0	0	;	;	3-
07-20(De)	0	1	3	3	0	0	0	0	0	0	;	4
098-4	3	1+	1	3-	0	0	0	0	0	0	;	;
098-2	3	1+	1+	3-	0	0	0	0	0	0	;	3
91E001	0	1+	4	4	0	0	0	0	0	0	0	3
4-8	0	1	4	3	0	;	0	0	0	0	;	4
07-19(De)	0	1+	3	3	0	1	0	0	0	0	1	4
Jingmai 8	1	4	3	3	;1=	1+	0	0	0	0	0	0
066-3	0	4	3	3	0	2	1+	0	1+	1	;1	0
De 0716	0	3	3	3+	0	0	0	0	0	0	;	;
07-21(De)	0	3	3	3	0	;	0	0	0	0	;	;
Jingxuan 9	0	3	4	4	0	;	;1	0	0	;1	;1	1+
Wenmai 5	4	4	4	4	0	4	0	0	0	;	3	0
Jingmai 9	1	1+	3	1+	0	1	1	0	3	3	1	1

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Table 2 to be continued

Cultivars (lines)	Tested races											
	21C3				34			34OroII	34C3			mutant strain
	CTHTM	CTQSM	CTTSC	HTTTM	MKGQM	MRGQM	MTGSM	MRGQM	RKGQM	RKGSM	RTGQM	
Jingmai 10	1	3	3	1	0	1	0	0	0	0	1	4
Yunmai 47	4	4	1	4	4	4	0	0	;	4	0	4
Yunmai 48	0	1	1	1	4	2	1	0	3–	3–	0	4
Yunmai 51	3+	1+	4	1	0	1	0	3	0	0	3	0
Yunmai 53	3+	1	3	4	0	4	;	0	3	;	4	4
Yunmai 54	4	3	0	3+	0	3+	3	0	3	;	4	3
Yunmai 56	3	1	1	3	3	3	0	1+	1	0	3	3
Fengmai 34	1+	4	4	1	0	;	4	1	0	3	0	0
098-12	1	;	4	1	;	3	3	1	3	3	;1	3
098-13	0	1	1+	3	1	3	3	1	3	3	;1	4
Jingmai 7	;	4	3-	3	4	4	4	4	0	1	3	3
Fengmai 39	0	4	4	2	0	0	0	0	0	;	;	0
Yumai 2	3	3	3	4	0	3	0	0	3	0	1	4
Fengmai 35	4	4	4	4	0	3	0	4	4	4	0	4
Fengmai 38	0	3	4	3	0	3	4	3	3	4	4	4
Yixi 2003-64	0	3	4	1	3	3	4	4	4	1+	1+	3
Yixuan A03-2	1	3	3	4	1+	3	1	3+	4	1	0	4
HX-06-1	0	3	1	2	0	3–	4	1++	4	4	3	1
Jingmai 12	3	3	4	3	0	4	0	3+	0	0	3	3
Fengyin 03-2	0	4	3	1	1	;1	0	1+	3	1	0	;
Fengmai 31	0	3	3	1	0	;	0	0	3–C	0	0	1
09D4-6	4	4	4	1	4	3	;1=	4	1+	4	1	4
Yumai 1	3	3	4	3+	0	0	0	0	0	0	0	1+
Fengmai 24	0	4	4	0	0	4	1+	4	0	4	3	4
Kun 022-222-1	1	0	0	2	0	3	0	0	3	3	2	4
05-1(Wen)	0	0	4	0	0	1+	3	1	1+	3	0	0
Yunmai 52	4	4	0	4	;	3	4	0	4	0	4	4
Yunmai 39	1	;1	1	3+	;	1+	3	4	1+	;1–	4	1++
Dianmai 34	1+	0	0	3	0	1+	1	4	3	3	4	3

The infection types are often refined by modifying characters as follows: =, uredia at the lower size limit for the infection type; –, uredia somewhat smaller than normal for the infection type; +, uredia somewhat larger than normal for the infection type; ++, uredia at the upper size limit for the infection type; C, more chlorosis than normal for the infection type; for other symbols see Material and Methods

Group 2: cultivars highly susceptible to all tested strains. This group comprised 17 cultivars (lines) in total, including Mianyang 19, I1, 4-12, 084-12, Yunmai 43, Yu 095, Chu 06-9, Yunmai 29 Fengmai 13, Nanyuan 1, SH710 (miscellaneous), Jing 05-1, Yunza 7, Yunza 6, Yunza 5, Yunmai 42, and Mianyang 20. These cultivars were highly susceptible to all strains tested. They likely contained none of the 45 *Sr* genes used in this study, but could still harbour *Sr*6, *Sr*7b, *Sr*9a, *Sr*9b, *Sr*9d, *Sr*9f, *Sr*9g or *Sr*16 without independent resistance to all strains tested.

Group 3: cultivars likely harbouring the resistance gene *Sr31*. A total of 16 cultivars (lines) tested, including Yunmai 101 Yunxuan 2, Jingmai 14, Jingmai 06-4, Yunxuan 11-12, Jingmai 11, Yumai 3, Yunxuan 3, Kunmai 5, Liangmai 4, R57, Wenmai 12, Feng 1124, Linmai 15, De 05-81, and Jing 0202 showed infection type (IT) '2' to the mutant strain, with infection type (IT) '0–1' to all other strains tested. This resistance spectrum was identical to that of *Sr*31, and these cultivars were likely to contain *Sr*31.

Group 4: cultivars likely to carry the resistance gene *Sr5* or *Sr5*+. The resistance spectra of Yimai 10, Yimai 1, K07-295, Yixi 96-6, Demai 3 and Yimai lines 2003-27 were the same as that of the standard cultivar *Sr*5; therefore, these six cultivars were likely to

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contain *Sr5*. Additionally, 9 cultivars, namely Chu 2008 Jian-4, 06D6-6, 088-16, K042-39, Linmai 17, Chumai 12, 05-1, Fengmai 37, and 08yu F_5, showed high resistance to different group 21 strains and also to one or more additional strains; their resistance spectra were wider than that of *Sr*5. Therefore, besides *Sr5*, these cultivars were considered to contain other resistance genes. For instance, Linmai 17, 088-16, and K042-39 might contain *Sr*5 in addition to one or more of the resistance genes *Sr*24, *Sr*29, *Sr*8a, and *Sr*32.

Group 5: cultivars likely to contain *Sr*Tmp. Guoji13, Wen 06-3, De 07-20, 098-2, and 098-4 were susceptible to 21C3CTHTM, 21C3HTTTM and the mutant strain, and immune to most of the remaining races, identical to *Sr*Tmp spectrum. Therefore, these five cultivars likely contained *Sr*Tmp.

Group 6: 91E001, 4-8 and De07-19, with similar resistance spectrum to *Sr*30, were immune to most of strains with low infection types to *Sr*30. The three cultivars were speculated to contain *Sr*30 and other resistance genes.

Group 7: resistance spectra of Jingmai 8, 066-3, De 0716, De 07-21, and Jingxuan 9 were close to that of *Sr*36. However, their resistance was stronger than that of single or multiple genes of *Sr*36, *Sr*8a, *Sr*29, and *Sr*dp-2. Therefore, in addition to *Sr36*, these five cultivars were postulated to likely contain one or more of the other three resistance genes.

According to their resistance spectra, cvs Wenmai 5, Jingmai 9, and Jingmai 10 were postulated to likely contain one or more genes of *Sr*8a, *Sr*11, *Sr*34, and *Sr*23. Moreover, they might also contain other yet unknown genes. Resistance spectra of cvs Yunmai 47, Yunmai 48, Yunmai 51, Yunmai 53, Yunmai 54, and Yunmai 56 were analysed, and it was suggested that they may contain *Sr*24 and/or *Sr*34 resistance genes.

Resistance spectra of 22 tested cultivars, namely Fengmai 34, 098-12, Jingmai 7, Fengmai 39, Yumai 2, Fengmai 35, Fengmai 38, Yixi 2003-64, YixuanA 032, HX-06-1, Jingmai 12, Fengyin 03-2, Fengmai 31, 09D4-6,Yumai 1, Fengmai 24, Kun 022-222-1, 05-1(Wen), Yunmai 52, Yunmai 39, and Dianmai 34, differed considerably from those of any known single genes. Therefore, the resistance genes contained in these 22 cultivars could not be postulated.

DISCUSSION

From gene postulation results, Yunnan wheat varieties mainly contained the resistance genes *Sr*31, *Sr*5, *Sr*Tmp, *Sr*30, and *Sr*36, and may also contain one or more of *Sr*8a, *Sr*11, *Sr*24, *Sr*29, *Sr*34, and *Sr*39. The immune/highly resistant cultivars are also likely to contain one or more resistance genes *Sr*9e, *Sr*26, *Sr*38, *Sr*47, and *Sr*Tt3, effective to all strains tested, and may contain unknown resistance genes. In the 110 cultivars tested, 16 were postulated to contain *Sr*31, and accounted for the largest proportion; 17 cultivars were deduced to likely contain *Sr*5 or *Sr*5+. Additionally, five cultivars were postulated to contain the resistance gene *Sr*Tmp; five cultivars were considered to contain *Sr*36 and three cultivars to harbour *Sr*30.

*Sr*31 mainly originates from rye (*Secale cereale*) (Roelfs & William 1985; Das *et al*. 2007), distributed in worldwide wheat cultivars, and is resistant to all pathotypes of stem rust (*P. graminis* f.sp. *tritici*) in China. Luofulin lines, introduced from the Soviet Union and Romania in the 1960s (Jiang *et al*. 2007), and the recently introduced cultivars Alondra "S", Aftab LeEr, Kavkaz, and Cattle Jutes, also contain 1BL/1RS translocation chromosome fragment carrying *Sr31*, widely distributed in the wheat cultivars of China (Li *et al*. 2012). This study showed that the occurrence frequency of *Sr*31 in wheat cvs from Yunnan province was as high as 13.6%. Indeed, 16 cultivars, including Yunmai 101 Yunxuan 2, Jingmai 14, Jingmai 06-4, Yunxuan 11-12, Jingmai 11, Yumai 3, Yunxuan 3, Kunmai 5, Liangmai 4, R57, Wenmai 12, Feng 1124, Linmai 15, De 05-81, and Jing 0202, were found to likely carry this gene. Kavkaz 78-385, Jingmai 11 parent, was found to contain *Sr31* by traceable pedigree analysis, while no helpful information regarding the other cultivars was obtained. However, according to postulations on resistance genes to powdery mildew and stripe rust of wheat cultivars in Yunnan province by Li Mingju and co-workers (Li *et al*. 2011), Wenmai 11, Linmai 6, and Jingmai 11 are likely to contain the resistance gene *Pm8*; Kunmai 5, Jing 0202, Linmai 6, Jingmai 11, Liangmai 4, De 05-81, and Jingmai 06-4 may contain the resistance gene *Yr*9. Moreover, *Sr*31, *Lr*26, *Yr*9, and *Pm*8 are known to be closely genetically linked (Dyck 1992, 1993); therefore, cultivars containing *Pm*8 or *Yr9* may also contain *Sr*31; thus the above cultivars are likely to contain *Sr*31.

Sr5 is a major gene carried in Reliance, a standard differential of *P. graminis* f.sp. *tritici* in China, almost having distinguished effects on *P. graminis* f.sp. *tritici* from various regions and countries (Zhang *et al*. 1987). This gene distinguishes race group 21 from race group 34 in China (Zhang *et al*. 1992). A total of 15 cultivars were found to possibly contain this gene in this study.

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By analysing the history of wheat resistance breeding in Yunnan, it is speculated that these genes might originate from Momai (Mocha, Moba 65, and Moba 66), Funo or Orofen. Interestingly, some Fengmai, Linmai, Yunmai, Feng, and Dian lines are found to carry *Sr*5 consanguinity, by analysing the genetic relationship of wheat cultivars in Yunnan province (Wu *et al*. 1998).

Gen *Sr30*, located on 5DL in wheat cultivars, is harboured by the Chinese assistant differential Rulofen (McIntosh *et al*. 1976; Zhang *et al*. 1992). This gene has further distinct effects on strain group 34 of *P. graminis* f.sp. *tritici*: it is susceptible to strain groups 34C4 and 34C5, while resistant to groups 34, 34C1, 34C2, and 34C3. Therefore, the *Sr*30 gene may separate strains of groups 34C4 and 34C5 from the other group of 34 strains. It is worth mentioning that *Sr30* has good resistance against 34C3. 34C3 was first discovered in 1976, severely threatening the safety of wheat production in China, and did not appear after 1987 (Cao *et al*. 1996). However, 34C3 was once more identified in 2013 in our research (unpublished). Therefore, the three cultivars 91E001, 4-8, and 07-19 (De), postulated to possibly contain *Sr30* in this study, can be used as resistance source.

*Sr*Tmp has had good resistance in China for a long time, e.g. to Ug99 and its variants. In this study, Guoji 13, Wen 06-3, De 07-20, 098-4, and 098-2 were postulated to likely contain this gene, and can be used as valuable materials resistant to Ug99 in future resistance breeding.

The number of *P. graminis* f.sp. *tritici* strains applied in this study was relatively small; therefore, the resistance genes contained in cultivars with entire low, high or relatively complex infection types could not be postulated, especially the excellent resistance genes (*Sr*9e, *Sr*26, *Sr*38, *Sr*47, and *Sr*Tt3) harboured by cultivars with entire low infection types to all strains could not be identified.

Determining resistance gene construction of wheat cultivars (lines) has a great significance in the prevention and management of wheat stem rust; clarifying the origin and background of excellent resistance materials can help increase their use. Resistance gene postulation is one of the most important methods to gather information regarding resistance genes, but further improvement and perfection are needed. For example in the postulation process, the limited number of known single differential lines resistant to stem rust and strains with different virulence spectra used contribute to decrease the accuracy of this method. However, compared with molecular markers and genetic analysis, this technique can achieve postulation of resistance genes harboured by large-scale cultivars (lines) in a short term, greatly reducing the workload. Meanwhile, results of resistance gene postulation can render molecular markers and genetic analysis more targeted; conversely, additional validation by molecular and genetic methods can improve the accuracy of resistance gene postulation. Therefore, resistance gene postulation combined with traceable pedigree, molecular markers, and genetic analysis are effective methods to define the resistance of cultivars (lines) for application.

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Corresponding author:

Dr Yuanyin Cao, Shenyang Agricultural University, College of Plant Protection, Shenyang 110866, P.R. China; E-mail: caoyy66@aliyun.com