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Molecular mapping of stripe rust resistance gene *YrCH42* in Chinese wheat cultivar Chuanmai 42 and its allelism with *Yr24* and *Yr26*

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Abstract Stripe rust, caused by *Puccinia striiformis* f. sp. *tritici* (PST), is one of the most devastating diseases in common wheat (*Triticum aestivum* L.) worldwide. The objectives of this study were to map a stripe rust resistance gene in Chinese wheat cultivar Chuanmai 42 using molecular markers and to investigate its allelism with *Yr24* and *Yr26*. A total of 787 F_2 plants and 186 F_3 lines derived from a cross between resistant cultivar Chuanmai 42 and susceptible line Taichung 29 were used for resistance gene tagging. Also 197 F_2 plants from the cross Chuanmai 42×*Yr24*/3*Avocet S and 726 F_2 plants from Chuanmai 42×*Yr26*/3*Avocet S were employed for allelic test of the resistance genes. In all, 819 pairs of wheat SSR primers were used to test the two parents, as well as resistant and susceptible bulks. Subsequently, nine polymorphic markers were employed for genotyping the F_2 and F_3 populations. Results indicated that the stripe rust resistance in Chuanmai 42 was conferred by a single dominant gene, temporarily designated *YrCH42*, located close to the centromere of chromosome 1B and flanked by nine SSR markers *Xwmc626*, *Xgwm273*, *Xgwm11*, *Xgwm18*, *Xbarc137*, *Xbarc187*, *Xgwm498*, *Xbarc240* and *Xwmc216*. The resistance gene was closely linked to *Xgwm498* and *Xbarc187* with genetic distances of 1.6 and 2.3 cM, respectively. The seedling tests with 26 PST isolates and allelic tests indicated that *YrCH42*, *Yr24* and *Yr26* are likely to be the same gene.

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Introduction

Stripe rust, caused by *Puccinia striiformis* f. sp. *tritici*, is one of the most important diseases in common wheat production worldwide, especially in the cooler and wetter environments (Roelfs et al. 1992). It is the most destructive disease in autumn-sown wheat in northwestern and southwestern China, where stripe rust resistance is a major breeding objective. Fifteen countrywide stripe rust epidemics have been recorded since 1950, and losses of 6.0, 3.2, 1.8 and 1.3 million metric tons of wheat occurred during 1950, 1964, 1990 and 2002, respectively (Wan et al. 2004). Since the appearance of PST race CYR32 in China, wheat cultivars with resistance gene *Yr9* and derivatives of Fan 6 have become susceptible, resulting in the 2002 epidemic (Wan et al. 2004). It is, therefore, urgent to identify new stripe rust resistance genes and to use more effective genes in wheat breeding programs. Molecular markers are appropriate tools to speed up the development of

resistant wheat cultivars in the pyramiding of resistance genes.

Forty genes at 37 loci (*Yr1* to *Yr37*) for resistance to stripe rust have been designated and located in different chromosomes in wheat (McIntosh et al. 1998, 2003, 2004, 2005). Molecular markers have been widely used for tagging resistance genes to stripe rust in wheat. Using SSR and RFLP markers, Peng et al. (2000a) located *Yr15* near *Nor1* and *Xgwm413-1B* loci with genetic distances of 2.6 and 4.3 cM, respectively. Zakari et al. (2003) reported close genetic association of *Yr15* and *Yr24* with *Xgwm11-1B*. Ma et al. (2001) mapped *Yr26*, originally from a Chinese landrace γ80-1 (*Triticum turgidum*), on chromosome 1BS of R55, closely linked to *Xgwm11*/*Xgwm18* and *Xgwm413* with genetic distances of 1.9 and 5.1 cM, respectively. Peng et al. (1999, 2000a, b) reported that *YrH52*, derived from wild emmer wheat (*T. dicoccoides*), was flanked by *Xgwm413-1B* and *Xgwm273a-1B* with genetic distances of 1.3 and 2.7 cM, respectively.

Among the officially named stripe rust resistance genes, only *Yr5*, *Yr10*, *Yr15*, *Yr24* and *Yr26* confer resistance to the race CYR32 (Yang et al. 2003; Wan and Wu 2003; Wan et al. 2004). Hence, it is essential to identify new stripe rust resistance genes, preferably with closely associated molecular markers for marker-assisted selection. The objectives of the present study were to map a stripe rust resistance gene in Chinese wheat cultivar Chuanmai 42 and to investigate its allelism with *Yr24* and *Yr26*.

Materials and methods

Plant materials

An F_2 population with 787 plants and 186 F_3 lines with 30–40 plants each, derived from the cross between a resistant cultivar, Chuanmai 42, and a susceptible line, Taichung 29, were used for the mapping of stripe rust resistance gene. Chuanmai 42, a popular cultivar in Sichuan province and highly resistant to all predominant Chinese PST races at both the seedling and adult stages, was developed from the cross Syn 769/Sw 3243//Chuan 6415 by the Crop Research Institute, Sichuan Academy of Agricultural Sciences. Seven cultivars and lines with different stripe rust resistance genes (McIntosh et al. 2003) were used for comparing the responses conferred by *YrCH42* and other resistance genes (Table 1). A total of 197 F_2 plants from the cross Chuanmai 42×*Yr24*/3*Avocet S and 726 F_2 plants from Chuanmai 42×*Yr26*/3*Avocet S were employed to test the allelism of *YrCH42*, *Yr24* and *Yr26*.

Isolates of *Puccinia striiformis* f. sp. *tritici* (PST) and seedling test

The predominant Chinese PST race CYR32 was used to test the F_2 and F_3 populations and their parents. A total of 26 PST isolates, collected in different countries and maintained by the Institute of Plant Protection, CAAS (Niu et al. 2000, Table 1), were used for seedling tests to investigate the relationship of *YrCH42*, *Yr24*, *Yr26* and other resistance genes.

Seeds were planted in small pots with seven plants each, and three plants of susceptible cultivar Mingxian 169 were used as check in each pot. Seedlings were inoculated with PST isolates when the first leaf was fully expanded. After inoculation, the seedlings were placed in a dew chamber at 9°C and 100% of relative humidity for 24 h and then transferred to a greenhouse maintained with 14 h light/10 h dark photoperiod at 12–17°C. Infection types (IT) were scored 14–15 days after inoculation when rust was fully developed on the susceptible check, Mingxian 169.

Infection types were based on a 0–4 scale (Bariana and McIntosh 1993), with 0 for no visible uredia, 0; for small chlorotic flecks without sporulation, $0;^{+}$ for large chlorotic areas without sporulation, 1 for chlorosis and necrosis associated with extremely limited uredial development, 1^{+} for chlorosis and necrosis associated with limited uredial development, 2 for chlorosis and necrosis with little intermediate sporulation, 2^{+} for chlorosis and necrosis among abundant intermediate sporulation, 3^{-} for chlorosis and necrosis among increased uredial development, 3 for chlorosis with increased uredial development, 3^{+} for occasional necrosis with abundant sporulation and 4 for abundant sporulation without chlorosis. Rating of the seedling reactions was simplified to two classes (resistant and susceptible) as there was a clear distinction between these two categories. Based on the reactions of the heterozygous F_2 plants and F_3 lines to the isolate CYR32, the F_2 plants with IT 0 to 2^{+} were considered to be resistant and those with IT of 3^{-} to 4 susceptible.

SSR analysis

Genomic DNA was extracted using the CTAB protocol (Sharp et al. 1988). Resistant and susceptible bulks comprising equal amounts of DNA from 20 resistant and 20 susceptible F_2 plants, respectively, were used for bulked segregant analysis (Michelmore et al. 1991).

In all, 819 pairs of wheat SSR primers were screened on the two parents and the resistant and susceptible bulks. The primers included 240 gwm (Gatersleben wheat microsatellite) primer sequences (Röder et al. 1998; Pestsova et al. 2000), 560 wmc primer sequences developed by the Wheat Microsatellite Consortium (WMC), a private effort coordinated by Dr. P. Isaac (IDnagenetics, Norwich, UK), ten BARC markers on chromosome 1B were from Song et al. (2002), and nine CFA and CFD markers on chromosome 1B came from Dr. P. Sourdille (INRA). These SSR primers are listed at http://www.graingenes.org.

The PCR reaction was performed in a PTC200 Peltier Thermal Cycler in a volume of 20 μl containing 1.0 U

Table 1 Infection types of seven wheat genotypes to 26 international isolates and Chinese races of *Puccinia striiformis* f. sp. *tritici*

Isolate	Origin[a]	Clement *Yr9* + *YrCle*	Moro *Yr10* + *YrMor*	*Yr15*/6* Avocet S *Yr15*	*Yr24*/3* Avocet S *Yr24*	*Yr26*/3* Avocet S *Yr26*	Chuanmai 42 *YrCH42*	Avocet S
58893	Netherlands	0	0, 0;	0	0;	0;$^{+}$	0;	4
59791	Netherlands	0;	0	0	0;, 1	0, 1	0	4
60105	Germany	0	0	0	0;$^{+}$	0;$^{+}$	0;	4
61009	Netherlands	0, 0;	0	0;	0;	0;	0, 0;	4
68009	Netherlands	0	0	0;	0;	0;	0;	4
72107	–	0	4	0	0;$^{+}$, 1^{+}	0;$^{+}$, 1	0;$^{+}$, 1	4
74187	Ecuador	0	0	0	0;	0;	0;	4
75078	Egypt	0	3^{+}, 4	0	2^{+}	2^{+}, 3	2^{+}, 3	4
76088	Afghanistan	0	0	0	0	0;	0;	4
76093	Pakistan	0	0	0	0;, 1^{+}	0;	0;	4
78028	Israel	0	0	0	0;	0;	0, 0;	4
78080	Mexico	0	0	0	0;	0;	0;	4
80551	Netherlands	4	0	0	0;	0;	0;	4
82061	Chile	4	0	0;	0;	0;	0;	4
82517	France	0;	0	0	0;$^{+}$	0;$^{+}$	0;$^{+}$	4
85019	Chile	0;	0	0	0;	0, 1	0; 1	4
86036	Bolivia	0	0, 0;	0	0;$^{+}$	0;$^{+}$	0;	4
86094	Kenya	3	0;	0	0;, 1	0;	0;	4
86106	Ethiopia	0	0	0	0;$^{+}$	0;$^{+}$	0;$^{+}$	4
86107	Ethiopia	4	0, 0;	0	0;	0;	0;	4
PE92	Italy	0	0;	0	0;$^{+}$	0;	0;$^{+}$	4
CYR26	China	0	0	0	0	0;	0	4
CYR27	China	0	0;	0;	0;	0;	0, 0;	4
CYR29	China	4	0	0	0;$^{+}$	0;$^{+}$	0;$^{+}$	4
CYR32	China	4	0	0, 0;	0;$^{+}$	0;$^{+}$	0;$^{+}$	4
CYR-Su-1	China	0;	0	0	0	0, 0;	0;	4

[a]Information obtained from Niu et al. (2000)

Taq DNA polymerase, 2 µl of 10× buffer (50 mmol KCl, 10 mmol Tris–HCl, 1.5 mmol $MgCl_2$, pH 8.3), 200 µmol of each dNTP, 6 pmol of each primer and 50–100 ng of template DNA. The PCR conditions were as follows: denaturation at 94°C for 4 min, followed by 35 cycles of 94°C for 1 min, 50–61°C (depending on primers) for 1 min, 72°C for 1 min and a final extension for 10 min at 72°C. PCR products were mixed with 4 µl of the formamide loading buffer (98% formamide, 10 mM EDTA, 0.25% bromophenol blue, 0.25% xylene cynol, pH 8.0) and heated at 94°C for 5 min. Each sample of 5–7 µl was loaded on 6% denaturing polyacrylamide gels and run at 80 W for approximately 1.5 h and then resolved by the silver staining method as described by Bassam et al. (1991).

Statistical analysis and genetic mapping

Chi-squared (χ^2) tests were used to evaluate the goodness of fit of observed and expected segregation ratios. Linkage analysis was conducted with Mapmaker 3.0b (Lincoln et al. 1992). The Kosambi (Kosambi 1944) function was employed to calculate the map distance in Mapmaker 3.0b, and an LOD score of 3.0 was used as a threshold for the declaration of linkage. The genetic map was drawn with the software Mapdraw V2.1 (Liu and Meng 2003).

Results

Stripe rust resistance gene in Chuanmai 42

In seedling tests with CYR32, Chuanmai 42 was highly resistant (IT 0;) and Taichung 29 was highly susceptible (IT 3^{+} to 4) (Table 2). Among the three parents of Chuanmai 42, Syn 769 was highly resistant (0;) to CYR32, whereas Sw 3243 and Chuan 6415 were highly susceptible (IT 3^{+} to 4). In the F_2 population, 602 plants were resistant (IT 0 to 2^{+}) and 185 were susceptible to CYR32 (ITs 3^{-} to 4) ($\chi^2_{3:1} = 0.94$, $df = 1$, $P > 0.30$, Table 2). The distribution of F_3 lines conformed to a ratio of one homozygous parental type resistant to two segregating to one homozygous parental type susceptible ($\chi^2_{1:2:1} = 1.04$, $df = 2$, $P > 0.50$, Table 3). Results obtained from the F_2 and F_3 populations indicated that the stripe rust resistance of Chuanmai 42 was controlled by a single dominant gene, temporarily designated *YrCH42*.

Linkage analysis and genetic map

Of the 819 SSR primers, 9 (namely, *Xwmc626*, *Xgwm273*, *Xgwm11*, *Xgwm18*, *Xbarc137*, *Xbarc187*, *Xgwm498*, *Xbarc240* and *Xwmc216*) in chromosome 1B showed clear polymorphisms between the resistant and susceptible DNA bulks as well as their parents. The

Table 2 Segregation for seedling reaction to race CYR32 of *Puccinia striiformis* f. sp. *tritici* in the F_2 population of Chuanmai 42/Taichung 29

Material	Frequency of plants with infection type[a]									
	0	0;	1	1^+	2	2^+	3^-	3	3^+	4
Chuanmai 42		30								
Taichung 29									7	23
F_2	3	324	98	97	67	13	3	23	15	144

[a]Plants with ITs 0; to 2^+ were classified as resistant and those with ITs 3^- to 4 susceptible

Table 3 F_2 genotypes inferred from seedling reactions of F_3 lines and the corresponding alleles at SSR loci *Xgwm498-1B* and *Xbarc187-1B*

Genotype[a]	Total	*Xgwm498-1B*[b]			*Xbarc187-1B*[b]		
		A	H	B	A	H	B
RR	50	49	1	0	48	2	0
Rr	95	4	89	2	4	89	2
rr	41	0	1	40	0	1	40
Total	186	53	91	42	52	92	42

[a]*RR* all plants of the F_3 lines were resistant with ITs 0; to 2, *Rr* segregating, ITs of seedlings in a family range from 0; to 4, *rr* all plants in the F_3 lines were susceptible, with ITs from 3^- to 4
[b]*A* homozygous for the allele from Chuanmai 42, *B* homozygous for the allele from Taichung 29, *H* heterozygous

entire F_2 population was then genotyped with the nine polymorphic markers (e.g., Fig. 1).

By means of two-point tests using Mapmaker 3.0b, close linkages were detected between *YrCH42* and the nine SSR loci, with genetic distances ranging from 1.5 to 14.8 cM and LOD scores from 15.7 to 35.7 (Table 4). All nine SSR loci exhibited co-dominant inheritance and a 1:2:1 segregation ratio in the F_2 population. Using the multipoint analysis of Mapmaker 3.0b, a highly reliable linkage group consisting of nine SSR loci and *YrCH42* was established in a threshold of LOD score 3.0 and a maximum recombination frequency of 0.5. As shown in Fig. 2, *YrCH42* was flanked by the nine markers, and the two closest flanking loci were *Xgwm498-1B* and *Xbarc187-1B* with genetic distances of 1.6 and 2.3 cM, respectively. *Xgwm498-1B* and *Xbarc187-1B* were screened on 186 F_3 lines, revealing that *YrCH42* was linked to them with genetic distances of 2.2 and 2.4 cM (Table 3). The results indicated that the resistance gene *YrCH42* is close to the centromere of chromosome 1B (Röder et al. 1998).

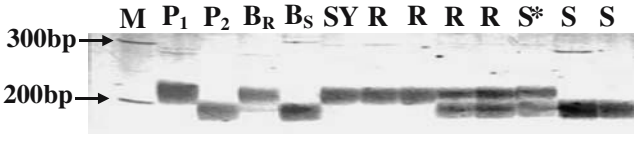

Fig. 1 Gel scan showing *Xgwm11-1B* amplification products when DNA from parents, resistant bulk, susceptible bulk, two resistant plants (IT 0;), two susceptible plants (IT 4), two plants with intermediate response (IT 2) and recombinants were used. *M* 100 bp DNA ladder, P_1 Chuanmai 42, P_2 Taichung 29, B_R resistant bulk, B_S susceptible bulk, *SY* Syn 769, *R* resistant plants, *S* susceptible plants, *S** susceptible plant with recombinant genotype. *Arrow* on the *left side* indicates the fragment sizes of 100 bp DNA ladder

Reaction patterns of *YrCH42*, *Yr24* and *Yr26* to 26 PST isolates tested

Seedling tests with 26 PST isolates (Table 1) showed an identical reaction pattern for Chuanmai 42 (*YrCH42*), *Yr24*/3*Avocet S (*Yr24*) and *Yr26*/3*Avocet S (*Yr26*). They were highly resistant to 25 isolates but gave significantly higher responses to culture 75078 from Egypt. The 197 F_2 plants from Chuanmai 42×*Yr24*/3*Avocet S and the 726 F_2 plants from Chuanmai 42×*Yr26*/3*Avocet S showed high resistance to CYR32 (0;), indicating that *YrCH42*, *Yr24* and *Yr26* were likely to be the same gene. The reaction patterns of these three lines were clearly different from those of lines with *Yr9*, *Yr10* and *Yr15*.

Discussion

Classification of resistant and susceptible groups in F_2 population

In the F_2 population, around three-fourths of plants have ITs 0; to 2 and one-fourth with ITs from 3 to 4, and the plants with ITs 2^+ and 3^- were only 13 and 3, respectively (Table 2). Almost all of the F_2 plants with IT 2^+ were heterozygous based on the genotypic data with two closest linked SSR markers *Xgwm498-1B* and *Xbarc187-1B* (Table 5) and, therefore, should be classified into the resistant group. In the F_3 lines, the ITs of homozygous resistant lines ranged from 0; to 2^+, and those of homozygous susceptible lines are from 3^- to 4 (Table 3), which also indicated that the F_2 plants with IT 0 to 2^+ should be considered to be resistant and those with IT of 3^- to 4 susceptible. Because heterozygous F_2 plants had variable infection types higher than that of the resistant parent but lower than that of the susceptible parent and more F_2 plants had the resistant parent infection types, the resistance in Chuanmai 42 is partially dominant.

Origin of the stripe rust resistance gene *YrCH42*

With the objective of exploiting new genetic resources for resistance to biotic and abiotic stresses, many synthetic hexaploid wheats were derived from AB-genomes

Table 4 Linkage analysis of stripe rust resistance gene *YrCH42* with nine polymorphic SSR markers in F_2 population of 787 plants

Marker	Resistant plant			Susceptible plant			Missing data[b]	Expected ratio	χ^2 [c]	Linkage to *YrCH42*	
	A[a]	H[a]	B[a]	A[a]	H[a]	B[a]				Distance (cM)	LOD[d]
Xwmc626	207	375	10	2	10	172	11	A:H:B = 1:2:1	1.84	3.3	30.7
Xgwm273	205	381	8	0	10	173	10	A:H:B = 1:2:1	1.48	2.5	32.5
Xgwm11	207	386	8	0	9	174	3	A:H:B = 1:2:1	1.61	2.3	33.0
Xgwm18	204	388	8	0	8	175	4	A:H:B = 1:2:1	1.22	2.2	33.4
Xbarc137	205	388	7	0	9	175	3	A:H:B = 1:2:1	1.46	2.2	33.4
Xbarc187	204	379	7	0	9	174	14	A:H:B = 1:2:1	1.35	2.2	33.0
Xgwm498	200	382	7	0	4	181	13	A:H:B = 1:2:1	0.38	1.5	35.7
Xbarc240	191	388	13	0	15	169	11	A:H:B = 1:2:1	1.37	3.8	29.6
Xwmc216	176	376	45	3	45	136	6	A:H:B = 1:2:1	4.90	14.8	15.7

[a] *A* homozygous for the allele from Chuanmai 42, *B* homozygous for the allele from Taichung 29, *H* heterozygous
[b] No PCR products were obtained
[c] Value for significance at $P = 0.05$ is 5.99
[d] The threshold of LOD is 3.0

of durum wheat and D-genome of *Ae. tauschii* in CIMMYT (Mujeeb-Kazi et al. 1996). More than 600 synthetics were reported to have resistances to diseases such as Karnal bunt [caused by *Tilletia indica* Mitra (Multani et al. 1988; Mujeeb-Kazi et al. 2001)], leaf rust [*P. recondita* Eriks. (Singh et al. 1998; Honrao et al. 2003)] and stripe rust [*P. striiformis* Westend. (Ma et al. 1995, 1997)].

Chuanmai 42 was developed from the cross Syn 769/Sw 3243//Chuan 6415. Seedling tests of the parents, Syn 769, Sw 3243 and Chuan 6415, with CYR32 showed that Syn 769 was highly resistant to the isolate CYR32 (IT 0;), whereas Sw 3243 and Chuan 6415 were susceptible (IT 3^+ to 4). Syn 769 (AABBDD) was synthesized from Decoy 1, a *T. turgidum* accession (AABB), and *Ae. tauschii* 188, an *Ae. tauschii* accession (DD) in the International Maize and Wheat Improvement Center (CIMMYT). Ma et al. (1995, 1997) reported that the synthetic (Decoy 1/*Ae. tauschii* 188) was resistant (IT 2 to 3 based on 0–9 scales) to Mexican PST isolate 14E14 at the seedling stage and the relative AUDPC (the area under the disease progress curve) was 0 in the field. Decoy 1 was resistant to 14E14 (IT 0 to 3) at seedling stage and the relative AUDPC was less than 1, whereas *Ae. tauschii* 188 was highly susceptible. These results suggested that the resistance gene *YrCH42* was derived from Decoy 1.

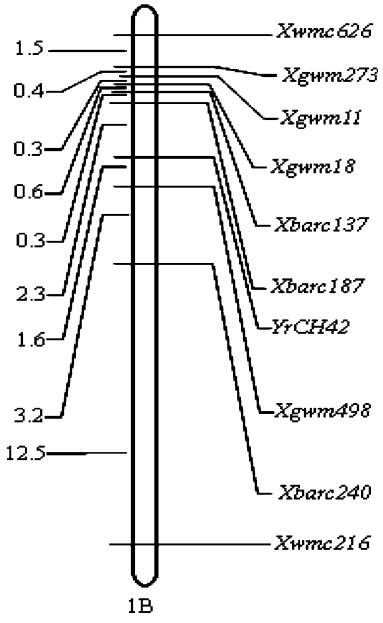

Fig. 2 Linkage map involving the resistance gene *YrCH42* constructed with nine SSR markers on chromosome 1B. Locus names are indicated on the *right side* of the map. Kosambi map distances (cM) are shown on the *left side*

Allelism of *YrCH42*, *Yr24* and *Yr26*

The 6VS/6AL translocation line R64 (92R-149), with stripe rust resistance gene *Yr26*, was derived from the cross Yangmai 5/4/γ80-1/*Haynaldia villosa*//Ningmai6/3/Yangmai 2 (Ma et al. 2001). Originally, *Yr26* was assumed to be located in the short arm of chromosome 6 V (Yildirim et al. 2000). However, Ma et al. (2001) mapped *Yr26* on chromosome 1BS with molecular markers, which was later confirmed by Yildirim et al. (2004). Presumably *Yr26* originated from Chinese landrace, γ80-1 (*T. turgidum*), and was closely linked to *Xgwm11*/*Xgwm18* with a genetic distance of 1.9 cM (Ma et al. 2001). On the other hand, *Yr24* derived from *T. turgidum var. durum* accession K733 was located on chromosome 1BS by monosomic analysis (McIntosh and Lagudah 2000). Zakari et al. (2003) reported close association of *Yr24* with *Xgwm11-1B*. The resistance gene *YrCH42* was also derived from a *T. turgidum* accession and was closely linked to *Xgwm11-1B*. The similar pathogenic specificity displayed by *Yr24*/3*Avocet S, *Yr26*/3*Avocet S and Chuanmai 42 against 26 PST isolates (Table 1) suggested that *Yr24*, *Yr26* and *YrCH42* represent the same locus. Absence of segregation among intercrosses of these genotypes confirmed this observation.

Table 5 Distribution of F_2 individuals with different ITs and their relationship with genotypic status of two closely linked marker loci *Xgwm498-1B* and *Xbarc187-1B*

Marker	Allele[a]	Frequency of F_2 population with different infection type										
		0	0;	1	1^+	2	2^+	3^-	3	3^+	4	Total
Xgwm498-1B	A	3	185	9	2	1	0	0	0	0	0	200
	H	0	131	81	94	63	13	1	0	0	3	386
	B	0	1	3	1	2	0	2	23	15	141	188
	–	0	7	5	0	1	0	0	0	0	0	13
	Total	3	324	98	97	67	13	3	23	15	144	787
Xbarc187-1B	A	3	189	9	1	1	1	0	0	0	0	204
	H	0	126	84	95	62	12	2	1	1	5	388
	B	0	0	3	1	3	0	1	22	14	137	181
	–	0	9	2	0	1	0	0	0	0	2	14
	Total	3	324	98	97	67	13	3	23	15	144	787

[a] *A* Homozygous for the allele from Chuanmai 42, *B* homozygous for the allele from Taichung 29, *H* heterozygous, – no PCR products

Comparison of *YrCH42* with other stripe rust resistance genes located on chromosome 1B

In addition to *YrCH42*, *Yr24* and *Yr26*, stripe rust resistance genes *Yr10*, *Yr15* and *YrH52* were also located on the chromosome arm 1BS by different workers (McIntosh et al. 2003). The resistance gene *Yr10* originated from common wheat (*T. aestivum* L.). Wang et al. (2002) located *Yr10* at the end of the chromosome 1BS with SSR markers *Xpsp3000* with a genetic distance of 1.2 ± 1.1 cM. In addition, *Yr10* was highly susceptible (ITs 3^+ to 4) to the isolate 72107, whereas *YrCH42* was highly resistant. Based on the origin, chromosomal location and seedling reactions to the 26 isolates tested, it can be concluded that *YrCH42* is different from *Yr10*. Both *Yr15* and *YrH52* were derived from Israeli wild emmer wheat (*T. dicoccoides*). Peng et al. (2000a) reported that *Yr15* was linked to *Xgwm498* with a genetic distance of 10.3 cM, while *YrCH42* was closely linked to *Xgwm498* with a distance of 1.6 cM. In addition, *Yr15* was resistant to all of the 26 PST isolates, while *YrCH42* displayed an intermediate reaction to the isolate 75078 with ITs 2^+ to 3 (Table 1). Hence, *YrCH42* is a different gene from *Yr15*. The resistance gene *YrH52*, derived from Hermon 52 (*T. dicoccoides*), was linked to *Xgwm18* and *Xgwm498* with mapping distances of 3.3 and 4.3 cM, respectively (Peng et al. 2000b), while *YrCH42* was bracketed by *Xgwm18* and *Xgwm498* with genetic distances of 3.2 and 1.6 cM, respectively (Fig. 2). Seeds of Hermon H52 with *YrH52* were not available for comparative studies. Considering their origins, *YrCH42* may not be the same as *YrH52*.

Plant breeders and pathologists are much interested in the utilization of durable resistance for disease control. Pyramiding of resistance genes has been considered as a strategy to provide durable resistance to pathogens, and molecular marker technology was one of the important tools for pyramiding genes (Michelmore 1995). Hittalmani et al. (2000) used DNA marker-assisted selection to pyramid resistance genes to both fungal blast and bacterial leaf blight infection into new rice cultivars. Molecular markers can certainly contribute to the selection of the lines with different resistance genes. In particular, DNA markers would be essential for combining major and minor resistance genes in wheat breeding programs targeting durable resistance (William et al. 2003).

YrCH42 is highly resistant to many PST isolates, but intermediately resistant or susceptible (ITs 2^+ to 3) to the isolate 75078 (Table 1), thus it is a race-specific resistance gene at seedling stage. In wheat breeding programs, it should be used in combination with other major or minor resistance genes. Currently, many stripe rust resistance genes have already been mapped with PCR-based markers, such as *Yr5*, *Yr10*, *Yr15*, *Yr18*, *Yr26* and *YrH52*. In the present study, eight of the nine SSR markers (*Xgwm11*, *Xgwm18*, *Xgwm273*, *Xgwm498*, *Xbarc137*, *Xbarc187* and *Xbarc240*) were very closely linked to the resistance gene *YrCH42* with genetic distances ranging from 1.5 to 3.8 cM (Table 4). Such close linkages should be useful for marker-assisted selection. In wheat breeding program, use of molecular markers may greatly facilitate resistance gene pyramiding and deployment and improve breeding efforts in achieving durable stripe rust resistance.

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