

Mapping the stripe rust resistance gene in Chinese wheat Guinong 775

Luhua Li^{a,b}, Mingjian Ren^{a,b}, Fang He^{a,b}, Ruhong Xu^{a,b,*}

^a College of Agriculture, Guizhou University, Guiyang 550025, China

^b Guizhou Subcentre of National Wheat Improvement Centre, Guiyang 550025, China

*Corresponding author, e-mail: xrhgz@163.com

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ABSTRACT: Wheat stripe rust, caused by *Puccinia striiformis* Eriks. f. sp. *tritici*, is a destructive wheat disease worldwide. To find new sources of resistance, Guinong 775 wheat was previously bred and identified as having a strong resistance against stripe rust, powdery mild and leaf rust. Guinong 775 showed a strong resistance against mixed fungi (CYR32 and CH42) associated with stripe rust that are common in Guiyang and Qianxinan. It was crossed with the susceptible wheat line Huixianhong to develop F1, F2 and F3 hybrids. In this study, 173 simple sequence repeat markers were used to map the stripe rust resistance gene in Guinong 775, and the resistance phenotype of Guinong 775 was regulated by a single dominant gene named *YrGn775*. *YrGn775* was mapped to chromosome 1BS with the marker *Xgwm413* flanking the gene at a distance of 12.0 cM. Genetic and molecular marker analyses demonstrated that this dominant gene may have originated in *Aegilops ventricosa*. Thus *YrGn775* may be a novel gene in wheat.

KEYWORDS: stripe rust, simple sequence repeat, single dominant gene, *Xgwm413*

INTRODUCTION

Stripe or yellow rust (YR), caused by *Puccinia striiformis* Eriks. f. sp. *tritici*, is a destructive disease of common wheat and is a constant threat to wheat production (5–25% yield losses)¹. The development of resistant commercial cultivars with effective YR resistance (*Yr*) genes is the most effective, economical and environmentally friendly strategy to control stripe rust². At present, 130 *Yr* resistance genes have been documented, among which 83 have been formally designated and 47 have been temporarily designated³. Although the number of documented *Yr* resistance genes is increasing, new variants can be generated in *P. striiformis*⁴, resulting in most stripe rust resistant wheat varieties losing their resistance. Hence identifying new durable resistance genes to stripe rust has been emphasized in international wheat breeding.

Molecular markers, such as sequence-characterized amplified regions⁵, restriction fragment length polymorphisms⁶ and simple sequence repeats (SSRs)⁷, have been widely used for mapping stripe rust resistance genes in wheat. However, owing to the large allohexaploid genome (17 Gb) of wheat, the fine mapping of resistance genes is difficult and time-consuming⁸. Currently, quantitative trait locus (QTL) mapping

is the preferred method of mapping wheat resistance genes. QTL mapping requires that entire populations be analysed, and the lack of high-density polymorphic markers limits the application of QTL mapping⁹. Bulk segregant analyses (BSAs) involving selected and pooled DNA samples from two contrasting groups, such as biparental populations of individuals, have been modified by using large populations, high-density markers and increased tail sizes to map the target genes. Compared with QTL mapping, a BSA significantly reduces the scale and cost by simplifying the mapping procedure¹⁰.

Aegilops species are important genetic sources for improving the variability of cultivated wheat, and formally designated resistance genes for stripe rust, such as *Yr28*, *Yr17* and *YrCH42*, have been transferred to wheat from various *Aegilops* species¹¹. Martynov et al demonstrated that the percentage of wheat varieties containing *Aegilops* genetic materials has gradually increased and that they have retained their effectiveness. From 1962–2011, wheat varieties created with the involvement of *Aegilops tauschii* increased from 0% to 14–18%, while those with *Aegilops ventricosa* increased from 1% to 34–37%¹². Meanwhile, others powdery mildew and leaf rust resistant genes have also trans-

ferred to wheat from various *Aegilops* species.

Wheat germplasm Guinong 775 is a cultivar obtained in 1995¹³. Because Guinong 775 was identified as being resistant to stripe rust and powdery mildew by the Chinese Academy of Sciences of Beijing and Northwest A&F University of Shanxi in China, it has been widely used as a parent in wheat breeding in the Guizhou Province of China. In addition, Guinong 775 has provided strong resistance against stripe rust and powdery mildew according to several years of field observations. However, the genetic basis of cultivar Guinong 775's stripe rust resistance is not clear. Here, we explore the genomic locations of the potential stripe rust resistance genes of Guinong 775.

MATERIALS AND METHODS

Plant materials

Guinong 775, as a wheat material immune to stripe rust and powdery mildew, is cultivated from complex wide-crossing hybrids of *A. tauschii* Coss/*Avena fatua* Linn/*A. ventricosa* Tausch/Sauwne20. Guinong 775 has been stored in the Wheat Research Center at the College of Agriculture in Guizhou University since 1995¹³. Wheat line Huixianhong, with a high susceptible to stripe rust and powdery mildew was provided by Northwest A&F University.

Resistance test for stripe rust in the field

Guinong 775, Huixianhong, and the F_{2:3} populations from Guinong 775 × Huixianhong were tested for the presence of stripe rust resistance genes, in the field in Huaxi, Guiyang and at the Institute of Agricultural Science of Qianxinan. Equal amounts of *P. striiformis* pathotypes CYR32 and CH42, which are common in Guiyang and Qianxinan, respectively, were mixed and sprayed onto rows at tilling. When the disease severity reached 90–100%, then the infection types (ITs) were investigated. The ITs were scored on a 0–4 scale according to Roelfs¹⁵: 0 indicated immune, no lesion in plant; 0: indicated nearly immune, hypersensitive reaction and dead spots in leaf; 1 indicated highly resistant, the diameter of lesion is less than 1 mm, sparse mycelium, occasionally larger lesions but still green and rare sporulation; 2 indicated mildly resistant, the diameter of lesion is less than 1 mm, thicker mycelium, green-proof and can produce a certain amount of spores; 3 indicated mildly susceptible, leaf lesions are numerous, the diameter of lesion is greater than 1 mm, thick mycelium, larger spores

but the lesion is not patchy; and 4 indicated highly susceptible, the diameter of lesion is greater than 1 mm, thick mycelium, larger spores and form lesion patches.

DNA extraction

Fresh leaf tissues of five-leaf stage plants were cut and stored at –80 °C. Then the CTAB method was used to carry out DNA extraction¹⁴.

PCR analysis

PCR amplification was performed in 20 µl reaction volumes containing 10 mM Tris-HCl (pH 8.8), 50 mM KCl, 2.0 mM MgCl₂, 0.08% Nonidet P40, 0.2 mM dNTPs, 1 unit *Taq* DNA polymerase, 0.4 µM of each primer (Sangon Biotech, China) and 35–50 ng of genomic DNA. Specific primer amplification was performed with following program: 5 min at 94 °C (pre-denaturation), followed by 35 cycles of 45 s at 94 °C, 45 s at 50–61 °C (according to the specific primer) and 1 min at 72 °C, then by a final extension of 10 min at 72 °C. The PCR products were detected on a 5% non-denatured PAGE combined with silver staining¹⁴. Gels were then visualized.

Inheritance analysis and linkage map construction of resistance genes

The segregation of the resistance genes in the F_{2:3} populations were detected by χ^2 -tests. Specific primers were used to amplify and classify the genotypes of the populations. A and B indicated that the band type of the molecular marker was the same as in Guinong 775 and Huixianhong, respectively. H indicated the heterozygous lines and – indicated a missing or not detected sample. MAPMAKER 3.0 was used to carry out molecular marker and resistance linkage analyses, and the linkage map was constructed using MAP DRAW V2.1.

RESULTS

Parental ITs and the inheritance analysis

Wheat seedlings were infected with mixed fungi, isolates CYR32 and CH42, associated with stripe rust that are common in Guiyang and Qianxinan, respectively. Guinong 775 had durable immune resistance (IT = 0) to stripe rust for over 20 years of field testing, and the wheat line Huixianhong was susceptible (IT = 4) to stripe rust. An F₁ population of the cross Guinong 775 × Huixianhong exhibited immune resistance (IT = 0) to stripe rust, whereas the F_{2:3} population of 131 lines in Guiyang and 63 lines in Qianxinan exhibited segregated stripe

Table 1 Stripe rust infection levels of parents, and an inheritance analysis of the F_{2:3} population of the Guinong 775 × Huixianhong cross.[†]

Population	Progeny	Number of seedlings						Expected ratio	χ^2
		0	0:	1	2	3	4		
Guinong 775	P1	50							
Huixianhong	P2						50		
Guinong 775 × Huixianhong	F ₁	12							
Guinong 775 × Huixianhong	F _{2:3}	68	37	27	15	16	31	3:1	0.0275

[†] Plants belong to ITs 0–2 scale were grouped into resistant and 3–4 scale were grouped into susceptible for testing the 3:1 ratio. χ^2 represents the chi squared value of 3:1, $\chi_{0.05}^2 = 3.841$. The calculated $\chi^2 < \chi_{0.05}^2$ demonstrated a significant difference of the value.

rust resistance. Among the 194 lines in Guiyang and Qianxinan, 68 lines were immune resistant (IT = 0), 37 lines were nearly immune resistant (IT = 0:), 27 lines were highly resistant (IT = 1), 15 lines were mildly resistant (IT = 2), 16 lines were mildly susceptible (IT = 3), and 31 lines were susceptible (IT = 4) (Table 1). The χ^2 results of the combined F_{2:3} population lines ($\chi_{3:1}^2 = 0.028 < \chi_{0.05}^2 = 3.841$) demonstrated that one independent dominant complementary gene participated in the stripe rust resistance of Guinong 775 (Table 1). The gene was named *YrGn775*.

Molecular markers screening

In total, 173 pairs of SSR primers, including those specifically linked to stripe rust resistance genes, were used for screening the resistance gene of Guinong 775. We found 52 pairs of SSR primers displayed polymorphisms in the parents. Additionally, highly resistant and susceptible pools were constructed according to the BSA using genomic DNA mixtures of 10 homozygous F_{2:3} lines each. Further, among the 52 pairs of SSR primers we found *Xgwm413*, *Xbarc187*, *Xgwm131*, *Xgwm169* and *Xbarc3* displayed polymorphisms in the resistant and susceptible pools, and the primer sequence are listed (Table 2). These five dominant markers were then used to analyse two different collection sites, the 131 lines in Guiyang and the 63 lines in Qianxinan that constituted the F_{2:3} population. Only *Xgwm413* was determined to be linked with *YrGn775* (Fig. 1, Table 3).

Genomic location of *YrGn775*

Based on the GrainGenes2.0 database, *Xgwm413* was located in chromosome 1BS. Among the 147 stripe rust resistant F_{2:3} lines identified with the *Xgwm413* primer, 52 lines amplified the same band as Guinong 775, 14 lines amplified the same band

as Huixianhong, and 81 lines were heterozygous (Fig. 1a, Table 3). Meanwhile, among the 47 stripe rust susceptible F_{2:3} lines, 3 lines amplified the same band as Guinong 775, 39 lines amplified the same band as Huixianhong and 5 lines were heterozygous (Fig. 1b). The F_{2:3} population results (Fig. 1, Table 3) demonstrated that the dominant *YrGn775* gene was located in chromosome 1BS, which was 12.0 cM from marker *Xgwm413* (Fig. 2).

Source of *YrGn775*

The *Xgwm413* marker was used to identify the pedigree parents of *YrGn775*. The *Xgwm413* primer could amplify a specific band in Guinong 775 and *A. ventricosa* Tausch. However, there was no specific band present in *A. tauschii* Coss, *A. fatua* Linn, Sauwne20 or *Haynaldia villosa* (Fig. 3a). Hence *YrGn775* may originate from *A. ventricosa* Tausch. The *Xgwm413* and *Xgwm11* markers were linked to the stripe rust resistant gene *YrH52* in *Triticum dicoccoides* at distances of 1.3 cM and 2.3 cM, respectively¹⁶. Then these two markers were used to detect Guinong 775, *A. ventricosa* and *T. dicoccoides* to verify if *YrGn775* is *YrH52*. We found the *Xgwm413* and *Xgwm11* markers could amplify a specific band in Guinong 775 and *A. ventricosa* Tausch (Fig. 3b), which differed from the band in *T. dicoccoides*. The results indicated that *YrGn775* was not *YrH52* and further confirmed that *YrGn775* originated from *A. ventricosa* Tausch.

DISCUSSION

Most wheat cultivars have gradually lost their resistance to the fungi isolates CYR32 and especially CH42 in China. Han et al¹⁷ demonstrated that the resistance of Guinong 775 was conferred by two different single dominant genes to CYR32 and CH42. An allelic analysis indicated that the gene providing resistance to CYR32 was linked to the

Table 2 Sequences of five specific markers for the bulked segregant analysis.

Marker	Primer sequence (5'–3')	Location	T _m
<i>Xgwm413</i>	TGCTTGCTAGATTGCTTGGG GATCGTCTCGTCCTTGGCA	1B	58 °C
<i>Xbarc187</i>	GTGGTATTTACAGGTGGAGTTGTTTTC CGGAGGAGCAGTAAGGAAGG	1B	58 °C
<i>Xgwm131</i>	AATCCCCACCGATTCTTCTC AGTTCGTGGGTCTCTGATGG	1B	60 °C
<i>Xgwm169</i>	ACCACTGCAGAGAACACATACG GTGCTCTGCTCTAAGTGTGGG	6A	60 °C
<i>Xbarc3</i>	TTCCCTGTGTCTTTCTAATTTTTTTT GCGAACTCCCGAACATTTTTTAT	6A	52 °C

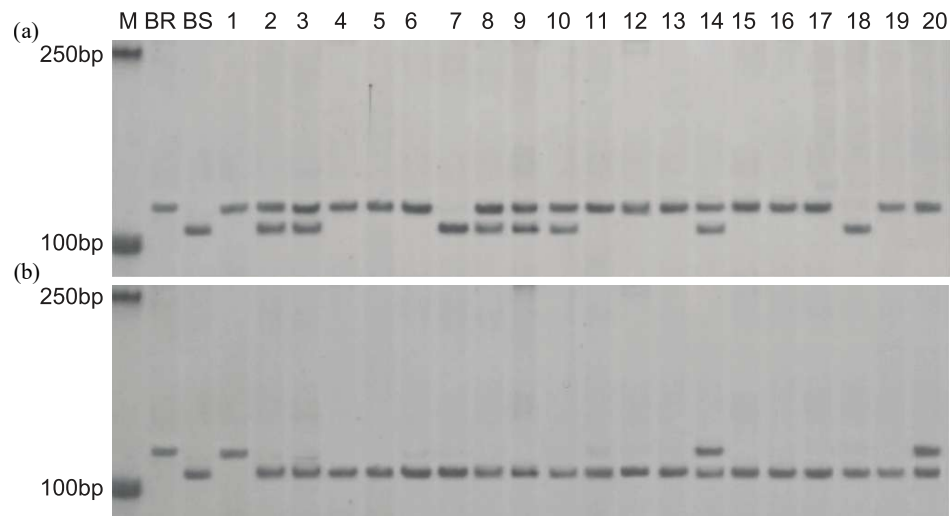


Fig. 1 Marker analysis of the F_{2.3} population. (a) Detection results of *Xgwm413* primers in the resistant lines. (b) Detection results of *Xgwm413* primers in the susceptible lines. M: 100-bp marker; BR: stripe rust resistant pool; BS: stripe rust susceptible pool; 1–20: F_{2.3} lines.

Table 3 Band types of *Xgwm413* marker in F_{2.3} lines[†]

Marker	1			4			$\chi^2_{1:2:1}$
	A	H	B	A	H	B	
<i>Xgwm413</i>	52	81	14	3	5	39	0.440

[†] 1, the 147 stripe rust resistant F_{2.3} lines (IT = 0–2); 4, the 47 stripe rust susceptible F_{2.3} lines (IT = 3–4); A, the band type of the molecular marker was the same as that of Guinong 775; B, the band type of the molecular marker was the same as that of Huixianhong; H, the heterozygous lines.

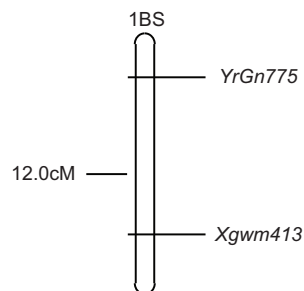


Fig. 2 Genetic map of *YrGn775*.

formally designated stripe rust resistant genes *Yr24* and *Yr26*, and that the gene providing resistance to CH42 may be a novel gene¹⁷. However, the CH42-associated resistance gene of Guinong 775 has not been mapped. In this study, we identified a single dominant gene from the Chinese wheat line Guinong 775 that shows a high resistance to mixed fungi (isolates CYR32 and CH42) associated with stripe rust that are common in Guiyang and Qianxinan, Guizhou Province, China (Table 1).

Here, we mapped the dominant gene from a cross between Guinong 775 and Huixianhong. Only one specific marker, *Xgwm413*, was selected from 173 SSR primer pairs to map the resistance gene, named *YrGn775*.

The *Xgwm413* marker is located in chromosome 1BS according to the GrainGenes2.0 database. At present, there are nine stripe rust resistance genes documented in chromosome 1BS, among which six (*Yr10*, *Yr15*, *Yr24*, *Yr26*, *Yr64* and

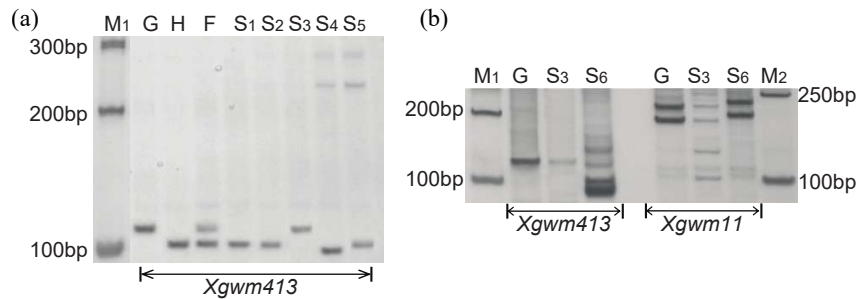


Fig. 3 The source detection of *YrGn775*. (a) The *Xgwm413* primer amplification results in the pedigree parents. (b) The *Xgwm413* and *Xgwm11* primer amplification results in S3 and S6. M₁: 100-bp marker; G: Guinong 775; H: Huixianhong; F: the F₁ line of Guinong 775 × Huixianhong cross; S1: *A. tauschii* Coss; S2: *A. fatua* Linn; S3: *A. ventricosa* Tausch; S4: Sauwne20; S5: *H. villosa*; S6: *T. dicoccoides*; M2: DL2000 marker.

Yr65) have been formally designated and three (*YrAlp*, *YrC142* and *YrH52*) have been temporarily designated³. SSR markers *Xpsp3000*, *Xgwm33*, *Xbarc187*, *Xgwm11/Xgwm18*, *Xgdm33*, *Xgwm18*, *Xgwm18*, *Xgwm273* and *Xgwm413* are closely linked to *Yr10*, *Yr15*, *Yr24*, *Yr26*, *Yr64*, *Yr65*, *YrAlp*, *YrC142* and *YrH52*, respectively. All of these SSR markers were used to screen for the resistance gene of Guinong 775. The *Xbarc187* and *Xgwm413* markers displayed polymorphisms in the parents (Table 2). The F_{2:3} population analysis indicated that only *Xgwm413* was linked to *YrGn775* (Fig. 1, Table 3). The specific markers *Xbarc187* and *Xgwm11/Xgwm18* that are closely linked to *Yr24* and *Yr26*, respectively, were not linked to *YrGn775*, which indicated that *YrGn775* may be the stripe rust resistance gene to isolates of CH42 in Guinong 775.

The *Xgwm413* marker detection results indicated that *YrGn775* was in chromosome 1BS (Fig. 1) and 12.0 cM from the *YrGn775* gene (Fig. 2). *Aegilops* species are sources of stripe rust resistance genes, and partly resistant *Aegilops* genes have been introgressed into common wheat for the cultivation of cultivars with resistance to stripe rust¹¹. The wheat Guinong 775 was obtained from complex wide-crossing hybrids of *A. tauschii* Coss/*A. fatua* Linn/*A. ventricosa* Tausch/Sauwne20. Also, Guinong775 had been proved possess 6VS/6AL translocation chromosome and the powdery mildew resistance is correlative to the alien chromosome arm, original from *H. villosa*¹⁸. The pedigree parents of *YrGn775* were identified using the *Xgwm413* marker (Fig. 3a), and the result indicated that the specific resistance gene may have originated from *A. ventricosa* Tausch. Peng et al reported that the *Xgwm413* marker is linked with *YrH52* in *T. dicoccoides* at 1.3 cM¹⁹. Hence

the resistance gene *YrGn775* could be *YrH52* or may be a new stripe rust resistance gene. Further, we detected the *Xgwm413* and *Xgwm11* markers which were linked to *YrH52* in *T. dicoccoides*. The detection result of *Xgwm413* marker showed that Guinong 775 and *A. ventricosa* Tausch amplified the same specific band, however *T. dicoccoides* did not, which demonstrated that *YrGn775* may originate from *A. ventricosa* Tausch and was not *YrH52* (Fig. 3b left). In addition, the *Xgwm11* marker test coincided with the result of *Xgwm413* marker (Fig. 3b right) further indicated that *YrGn775* originated from *A. ventricosa* Tausch and that it may be a novel resistant gene of stripe rust in wheat.

Stripe rust has a long history, wide distribution and rapid ability to spread, making it a devastating wheat disease. Because *P. striiformis* is highly variable and evolves new virulent races, resistance genes gradually lose their effectiveness and the corresponding wheat cultivars lose their resistance²⁰. Hence wheat breeders need to identify new resistance genes to improve the spectrum and persistence of stripe rust resistance. We observed that the wheat line Guinong 775 exhibited a persistent resistance for over 20 years to stripe rust, which is common in Guizhou Province. Our results confirmed that the resistance of Guinong 775 was controlled by a single dominant gene, consistent with the results of Han et al¹⁵. Here, the resistance gene *YrGn775* was mapped to chromosome 1BS. The genetic distance of 12.0 cM from *Xgwm413* to *YrGn775* is still large; hence the genetic populations studied will be increased and more molecular markers will be explored to confirm the specific location of *YrGn775*.

In summary, this study confirmed that the persistent stripe rust resistance to *P. striiformis* in

Guinong 775 wheat is controlled by a single dominant gene. The genomic location analysis demonstrated that *YrGr775* localized in chromosome 1BS and may be a novel stripe rust resistance gene.

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