

Tibet Development and Breeding Application of the Fluorescence Molecular Marker of Rice Bacterial Blight Resistance Gene *Xa7*

Wu Hao¹, Deng Guofu¹, Gao Lijun¹, Dai Gaoxing², Huang Juan¹, Gao Ju¹, Qing Dongjin¹, Chen Weiwei², Yan Shuangyong³, Liang Haifu²✉

¹ Guangxi Crop Genetic Improvement and Biotechnology Laboratory, Guangxi Academy of Agricultural Sciences, Nanning, 530007, China

² Rice Research Institute, Guangxi Academy of Agricultural Sciences, Nanning, 530007, China

³ Tianjin Key Laboratory of Crop Genetics and Breeding, Tianjin Crop Research Institute, Tianjin, 300384, China

✉ Corresponding author email: lianghaifu7711@xaas.net

Molecular Plant Breeding, 2021, Vol.12, No.23 doi: [10.5376/mpb.2021.12.0023](https://doi.org/10.5376/mpb.2021.12.0023)

Received: 16 Jul., 2021

Accepted: 19 Jul., 2021

Published: 25 Jul., 2021

Copyright © 2021 Wu et al., This article was first published in Molecular Plant Breeding in Chinese, and here was authorized to translate and publish the paper in English under the terms of Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Preferred citation for this article:

Wu H., Deng G.F., Gao L.J., Dai G.X., Huang J., Gao J., Qing D.J., Chen W.W., Yan S.Y., and Liang H.F., 2021, Development and breeding application of the fluorescence molecular marker of rice bacterial blight resistance gene *Xa7*, Molecular Plant Breeding, 12(23): 1-8 (doi: [10.5376/mpb.2021.12.0023](https://doi.org/10.5376/mpb.2021.12.0023))

Abstract In this study, the closely linked fluorescence molecular marker PM-*Xa7* of *Xa7* gene was developed on the basis of sequence difference between the resistant variety 'IRBB7' containing *Xa7* and other nine bacterial blight susceptible rice varieties, and combine with PARMS technology (Penta-primer amplification refractory mutation system). Genotypes of *Xa7* were identified in 72 rice germplasm and the bacterial blight resistance level of 'Mei B' was improved by backcross and screening with this marker. The results showed that two rice germplasms containing *Xa7* were screened out from 72 rice germplasm; By introducing the resistant *Xa7* gene from 'IRBB7' into 'Mei B' with PM-*Xa7*, a stable new maintainer with resistance to bacterial blight was successfully obtained. The bacterial blight resistant fluorescence signal was detected in 289 plants and the bacterial blight susceptible fluorescence signal was detected in 93 plants of BC₂F₂ population generated from 'IRBB7' and 'Mei B', and the genotypes were consistent with the phenotypes of *Xoo* inoculation. These research results indicated that PM-*Xa7* can be effectively used for the marker-assisted breeding of bacterial blight resistant rice variety with the resistant *Xa7* gene.

Keywords Rice; Bacterial blight; *Xa7*; Fluorescence molecular marker

Rice bacterial blight is a bacterial disease caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*). The disease was first detected in Fukuoka, Japan in 1884 (Li et al., 2017). Subsequently, the disease was found in every major rice-growing area in the world. In China, rice bacterial blight was first discovered in the suburbs of Nanjing in 1950 (Shen, 2001). At present, the disease has occurred in all rice areas in China, especially in the southern coastal rice areas (Yu et al., 2012). The outbreak of bacterial blight not only resulted in severe rice yield, but also reduced rice quality. Practice shows that breeding resistant varieties is the most economical and effective way to control bacterial blight. However, many resistant varieties in production lose their resistance after 3~5 years (Shi et al., 2008). Therefore, it is of great significance to breed rice varieties with long-lasting and broad-spectrum resistance to bacterial blight.

In order to develop rice varieties with long-lasting and broad-spectrum resistance to bacterial blight, the key lies in the discovery and utilization of genes with long-lasting, broad spectrum and high resistance to bacterial blight. Among the resistance genes to bacterial blight, *Xa7* gene from the rice variety 'DV85' from Bangladesh is a gene with high resistance, broad-spectrum and persistent resistance to bacterial blight (Ma et al., 2013), which has not been cloned so far. Studies have shown that *Xa7* gene shows high resistance to 52 different bacterial blight strains from China and Japan (Liu et al., 2016), and *Xa7* is relatively stronger in high temperature environment (Webb et al., 2009), which makes it suitable for utilization in rice areas of South China. At present, some scholars have carried out molecular marker-assisted breeding for *Xa7* gene. The 'DV85' *Xa7* genes were incorporated into the 'Minghui63' and selected by markers STSP3 and M5 to improve the resistance of 'Minghui63' to bacterial blight (http://www.cropscience.org.au/icsc2004/poster/3/4/4/1041_heyuqing.htm). Lan et al. (2011) improved the resistance of 'Hua 201S' to bacterial blight by selecting the linkage marker STSP3 of *Xa7* and combining with

conventional breeding methods. Yan et al. (2013) used linkage markers to polymerize the anti-bacterial blight genes *Xa7* and *Xa21* and anti-borer gene *cry1C** into 'Xianhui 207', and improved the resistance of 'Xianhui 207' to the blight and the borers. In the above studies, the markers selected for *Xa7* gene were all linkage markers that were detected by electrophoresis after PCR amplification, and the detection process was relatively complicated, which was not conducive to the detection of large-scale samples. However, the fluorescent molecular markers developed by PARMS technology do not need electrophoresis detection, but can read the genotype signal directly by fluorescence scanning, and then the genotype can be obtained by combining with software data analysis, which can perform *Xa7* genotyping on a large number of rice samples at the same time.

1 Results and Analysis

1.1 A fluorescent molecular marker for *Xa7* gene selection

Referring to the locus of co-dominant marker M5 of *Xa7* gene developed by Porter et al. (2003), the sequence was compared with that of 9 susceptible cultivars (Ce253, Gui582, Guanghui998, R128, Ce138, Guanghui308, Shen08S, 186B, II-32B). It was found that there were differences in A/C and T/A between 'IRBB7' and the 9 susceptible cultivars at the location of marker M5 (Figure 1). Based on this, primers *Xa7*-FaT and *Xa7*-FCA were designed to match the fluorescence primers of FAM and HEX in PARMS master mix, respectively. Primers *Xa7*-FaT, *Xa7*-FCA and general primers *Xa7*-R jointly constituted the fluorescent molecular marker PM-*Xa7* of *Xa7* gene (Table 1). The genotype of the *Xa7* gene in the sample can be determined by analyzing the different signals obtained from the PCR amplification product scan of the marker PM-*Xa7*, so the marker can be used for selection of the *Xa7* gene.

| | | | | | |
|-------------|------------------------|----------|---------------------|----------|--------------------|
| Ce253 | gaaatctaatacaatttcagag | c | attactgtattcatctttc | a | gtgtatattcgtctgggt |
| Gui582 | gaaatctaatacaatttcagag | c | attactgtattcatctttc | a | gtgtatattcgtctgggt |
| GuangHui998 | gaaatctaatacaatttcagag | c | attactgtattcatctttc | a | gtgtatattcgtctgggt |
| R128 | gaaatctaatacaatttcagag | c | attactgtattcatctttc | a | gtgtatattcgtctgggt |
| Ce138 | gaaatctaatacaatttcagag | c | attactgtattcatctttc | a | gtgtatattcgtctgggt |
| GuangHui308 | gaaatctaatacaatttcagag | c | attactgtattcatctttc | a | gtgtatattcgtctgggt |
| Shen08S | gaaatctaatacaatttcagag | c | attactgtattcatctttc | a | gtgtatattcgtctgggt |
| 186B | gaaatctaatacaatttcagag | c | attactgtattcatctttc | a | gtgtatattcgtctgggt |
| II-32B | gaaatctaatacaatttcagag | c | attactgtattcatctttc | a | gtgtatattcgtctgggt |
| IRBB7 | gaaatctaatacaatttcagag | a | attactgtattcatctttc | t | gtgtatattcgtctgggt |

Figure 1 Allelic analysis of *Xa7* gene

Table 1 Information of developed primers

| Marker name | Primer name | Primer sequence (5'-3') | Fluorescence signal | Allelic genotype |
|----------------|-----------------|--|---------------------|------------------|
| PM- <i>Xa7</i> | <i>Xa7</i> -FaT | GAAGGTGACCAAGTTCATGCTTTTCAGAG A ATTACTGTATTTCATCTTTCT | FAM | AT |
| | <i>Xa7</i> -FCA | GAAGGTCGGAGTCAACGGATTTCAGAGCA TTACTGTATTTCATCTTTCA | HEX | CA |
| | <i>Xa7</i> -R | ATCAGCACTACCCAGACGAATATAC | ___ | ___ |

1.2 Two germplasms containing *Xa7* gene were identified by PM-XA7 marker from 72 rice germplasms

72 rice germplasms were inoculated with the predominant species IV of Blight from Guangxi, and many of them showed resistance to bacterial blight. Furthermore, the *Xa7* gene in 72 rice germplasm was identified by fluorescence molecular marker PM-*Xa7*. The results showed that two rice cultivars, 'IRBB7' and '82B', contained *Xa7* allele. Other rice varieties, such as 'IRBB5' containing resistance gene *Xa5* and 'CBB23' containing resistance gene *Xa23*, were all susceptible to *Xa7* alleles (Figure 2). The results of inoculation identification and marker detection indicated that the fluorescent molecular marker PM-*Xa7* could specifically and effectively detect *Xa7* gene in the 72 rice germplasm resources, which would be helpful to explore new germplasm carrying *Xa7* gene and improve the utilization rate of *Xa7* gene in breeding work.

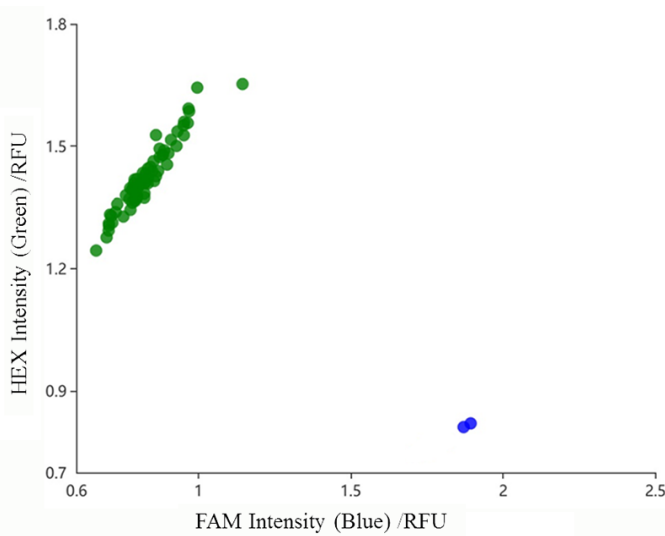


Figure 2 Genotyping of 72 rice germplasm using PM-Xa7

1.3 A new maintainer material against bacterial blight was created by labeling PM-Xa7

By using the marker PM-Xa7 for selection and phenotypic identification, a new mainstay material resistant to bacterial blight was created (Figure 3). In this process, the hybrid rice breeding parent 'MeiB' was cross-bred with the resistant parent 'IRBB7' and backcrossed in succession. 382 single plants of its BC₂F₂ generation were detected by using the marker PM-Xa7. The detection results showed (Figure 4) that the blue dots were 92 homozygous single plants of *Xa7* gene with FAM fluorescence signal detected. Green dots represent 93 *Xa7* homozygous plants with HEX fluorescence signals detected, red dots represent 197 heterozygous plants with both FAM and HEX fluorescence signals detected, and gray dots represent negative controls. Field inoculation and identification (Figure 5) showed that 289 single plants were resistant, while the remaining 93 were all susceptible, which was consistent with the results of marker detection genotype. The separation ratio of resistant and susceptible single plants was close to 3:1 (chi-square 0.09). These results indicate that PM-Xa7 can accurately track *Xa7* gene and can be used for molecular marker-assisted breeding of *Xa7* gene.

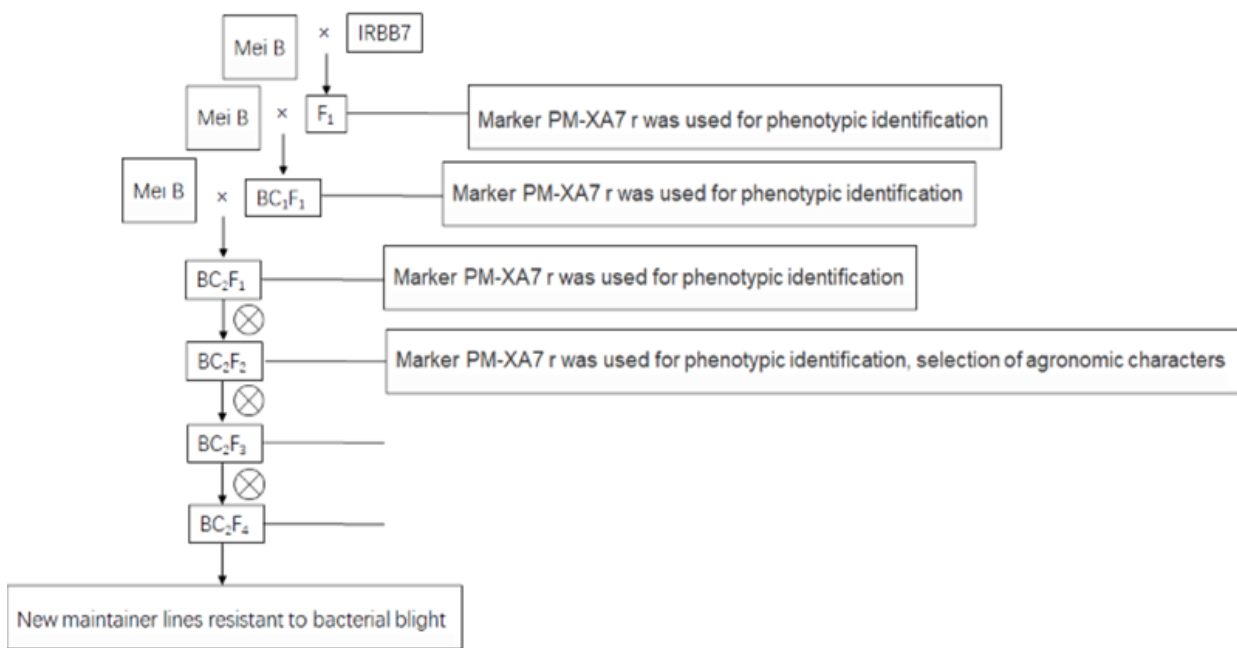


Figure 3 A new line of resistance to bacterial blight created by PM-Xa7 was identified

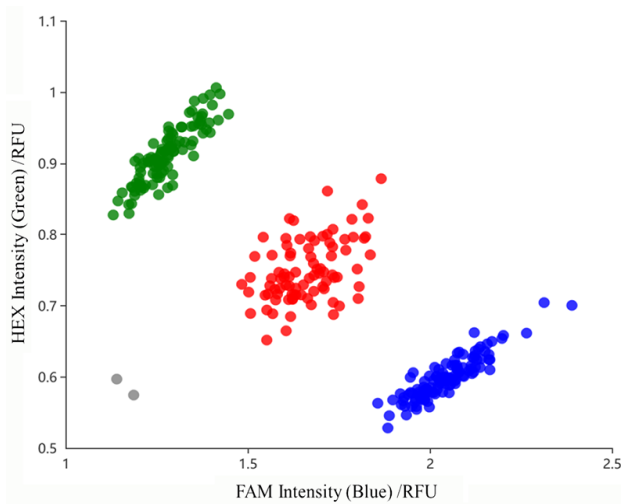


Figure 4 Genotype identification of 382 F₂ generation plants by PM-Xa7



Figure 5 Inoculation identified 382 plants of BC₂F₂ generation of 'Mei B' and resistant parent 'IRBB7'

2 Discussion

Molecular marker-assisted selection is not limited by environmental conditions or affected by physiological species of pathogenic bacteria, and can accelerate the selection of rice varieties resistant to bacterial blight (Li et al., 2011). At present, most of the molecular markers used in molecular marker-assisted breeding are those detected by polyacrylamide gel or agarose gel electrophoresis after PCR amplification. However, with the development of molecular marker technology, a fluorescent molecular marker technology based on PARMs established by PCR amplification of blocked mutation system has been applied in rice molecular marker-assisted breeding (Qing et al., 2018). The molecular markers developed by this technology do not need electrophoresis detection, and the genotype signal can be read directly by fluorescence scanning. Combined with software analysis, the genotype can be quickly realized. Compared with the traditional molecular markers, it has the advantages of convenience, fast, pollution-free, high detection efficiency and low detection cost, and is more suitable for large-scale genotyping. Therefore, the development of fluorescent molecular markers of rice resistance genes and their application in production practice will further promote the effective utilization of rice resistance genes and accelerate the breeding of resistant varieties.

Porter et al. (2003) developed a linkage marker of *Xa7* gene, M5, which was used to screen bacterial blight resistant varieties. The marker was only 0.5 cM away from *Xa7* gene, and AFLP31-10 (3 cM) was closer to *Xa7* gene than the marker G1091 (6.0 cM). In this study, a fluorescent marker PM-Xa7 was designed based on the sequence contrast between the resistant variety 'IRBB7' and 9 susceptible varieties by referring to the locus of marker M5. This marker is closely linked to *Xa7* gene and has good stability. Compared with previous M5

markers, it does not need to detect PCR products by electrophoresis. The operation is simpler and faster, which is more suitable for the detection of large-scale samples. In this study, the PM-Xa7 marker was further used to identify the *Xa7* gene in the rice germplasm resources, and the *Xa7* gene was selected from the hybrid offspring of 'IRBB7' and the susceptible variety 'Mei B', and the combination inoculation identification confirmed the effectiveness and stability of the marker. It is believed that the further utilization of PM-Xa7 will improve the utilization of *Xa7* gene in rice breeding against bacterial blight.

Xa7 is a highly resistant, broad-spectrum and persistent bacterial blight resistant gene. Many researchers have used different linkage markers to identify this gene in rice germplasm resources and carry out molecular marker breeding application. Wu et al. (2019) identified one disease-resistant material containing *Xa7* gene from 148 weedy rice samples using RM20582 marker. Liu et al. (2016) analyzed some rice germplasm resources in Guangdong Province with linkage markers and identified two germplasm containing *Xa7* gene. He (2012) detected *Xa7* gene in 72 rice parental materials through inoculation identification and M5 labeling, and found several rice parents containing *Xa7* gene. In this study, fluorescence marker PM-Xa7 was used to detect 72 rice germplasm resources and inoculation identification. Only two varieties 'IRBB7' and '82B' were found to contain *Xa7* gene, which indicated that *Xa7* gene had low utilization rate in rice breeding for resistance to bacterial blight, which may be related to the easier expression of resistance under high temperature conditions and the expression of non-whole growth period. In order to take advantage of the stronger resistance of *Xa7* gene under high temperature conditions, this study used 'IRBB7' to improve the resistance of susceptible parent 'Mei B' to bacterial blight, and combined with the marker PM-Xa7 for selection, a new mainstay material with stable resistance was obtained. Predecessors' (http://www.cropsscience.org.au/icsc2004/poster/3/4/4/1041_heyuqing.htm) using *Xa7* gene to rice bacterial leaf blight resistant effect of improvement is consistent. It was confirmed that this gene is an excellent disease resistance gene which can play a role in production. In this study, only *Xa7* resistance genes were polymerized into the varieties to be improved, but studies have shown that rice varieties with multiple resistance genes to bacterial blight can show more durable, stronger and broader resistance (Huang et al., 2012). The next step is to combine other resistance genes with existing materials to develop rice varieties with long duration, broad-spectrum and high resistance to bacterial blight.

3 Materials and Methods

3.1 Experimental materials

The experimental materials were 72 rice parents including 'IRBB7' containing *Xa7* gene, 'IRBB5' containing *Xa5* and 'CBB23' containing *Xa23* collected by Guangxi Crop Genetic Improvement and Biotechnology Laboratory (Table 2), and 382 single plants of BC₂F₂ generation of 'IRBB7' and susceptible maintainer line 'Mei B'.

3.2 Development of fluorescent molecular marker for *Xa7* gene

According to the locus of co-dominant marker M5 of *Xa7* gene in rice variety 'IRBB7', the 200 kb sequence near was selected. According to the difference between 'IRBB7' and 9 susceptible cultivars, the sequence was compared with 9 susceptible cultivars (Ce253, Gui582, Guanghui998, R128, R138, Guanghui308, Shen08S, 186B, II-32B). Primers Xa7-FaT and Xa7-FCA, which can match with the fluorescence primers of FAM and HEX in PARMS Master Mix, were designed and combined with the universal primer Xa7-R to form the fluorescence molecular marker PM-Xa7 of *Xa7* gene.

3.3 DNA extraction and PCR amplification

Rice genomic DNA was extracted from individual leaves two weeks after transplanting according to the CTAB method used by Murray and Thompson (1980). The *Xa7* gene of the test material was amplified by PCR amplification system of 10 μ L. The system composition was as follows: 2 \times PARMS master mix 5 μ L, 10 mmol/L forward labeled primer (Xa7-FaT) 0.15 μ L, 10 mmol/L forward labeled primer (Xa7-FCA) 0.15 μ L, 10 mmol/L general reverse marker primer (Xa7-R) 0.4 μ L, template DNA 1.0 μ L, ddH₂O 3.55 μ L. PCR amplification procedure: 95°C for 4 min, 94°C for 20 s, 65°C (decrease 0.8°C per cycle) for 1 min, 10 cycles. Then 94°C for 20 s, 56°C for 1 min, 32 cycles.

Table 2 72 rice variety and genotypes of marker PM-Xa7

| No. | Variety name | Fluorescent type | Genotype | No. | Variety name | Fluorescent type | Genotype |
|-----|--------------|------------------|----------|-----|----------------|------------------|----------|
| 1 | IRBB7 | FAM | AT | 37 | 9802S | HEX | CA |
| 2 | IRBB5 | HEX | CA | 38 | Jing S | HEX | CA |
| 3 | 112B | HEX | CA | 39 | Long S | HEX | CA |
| 4 | 186B | HEX | CA | 40 | 838R(luo) | HEX | CA |
| 5 | 9311B | HEX | CA | 41 | Fuhui 838 | HEX | CA |
| 6 | II-32B | HEX | CA | 42 | GR076 | HEX | CA |
| 7 | 82B | FAM | AT | 43 | GS2 | HEX | CA |
| 8 | Bo B | HEX | CA | 44 | CBB23 | HEX | CA |
| 9 | Bo IIB | HEX | CA | 45 | Mei B | HEX | CA |
| 10 | Bo IIIB | HEX | CA | 46 | R128 | HEX | CA |
| 11 | | HEX | CA | 47 | R138 | HEX | CA |
| 12 | Gang 46B | HEX | CA | 48 | R1439 | HEX | CA |
| 13 | Gufeng B | HEX | CA | 49 | R273 | HEX | CA |
| 14 | Guang 8B | HEX | CA | 50 | Molixiang No.2 | HEX | CA |
| 15 | Hengfeng B | HEX | CA | 51 | Guanghui 308 | HEX | CA |
| 16 | Hua 2048B | HEX | CA | 52 | R318 | HEX | CA |
| 17 | Jing 23B | HEX | CA | 53 | R319 | HEX | CA |
| 18 | Liangfeng B | HEX | CA | 54 | R402 | HEX | CA |
| 19 | Shan B | HEX | CA | 55 | R463 | HEX | CA |
| 20 | Shen 95B | HEX | CA | 56 | R8 | HEX | CA |
| 21 | Taifeng B | HEX | CA | 57 | R527 | HEX | CA |
| 22 | Te B | HEX | CA | 58 | Gui 582 | HEX | CA |
| 23 | Tianfeng B | HEX | CA | 59 | R5867 | HEX | CA |
| 24 | Wufeng B | HEX | CA | 60 | Gui 7571 | HEX | CA |
| 25 | Xifei B | HEX | CA | 61 | R774 | HEX | CA |
| 26 | Yexiang B | HEX | CA | 62 | R789 | HEX | CA |
| 27 | Yixiang B | HEX | CA | 63 | R795 | HEX | CA |
| 28 | Yu 19B | HEX | CA | 64 | R9516 | HEX | CA |
| 29 | Yu 4B | HEX | CA | 65 | R087 | HEX | CA |
| 30 | Zhenfeng B | HEX | CA | 66 | R07-1 | HEX | CA |
| 31 | Zhongjiu B | HEX | CA | 67 | Bing 4114 | HEX | CA |
| 32 | Zhongzhe B | HEX | CA | 68 | Ce 253 | HEX | CA |
| 33 | Zhun S | HEX | CA | 69 | Duoxi No.1 | HEX | CA |
| 34 | H068S | HEX | CA | 70 | Guanghui 998 | HEX | CA |
| 35 | 151S | HEX | CA | 71 | 696B | HEX | CA |
| 36 | 342S | HEX | CA | 72 | Sheng B | HEX | CA |

3.2 Development of fluorescent molecular marker for *Xa7* gene

According to the locus of co-dominant marker M5 of *Xa7* gene in rice variety 'IRBB7', the 200 kb sequence near was selected. According to the difference between 'IRBB7' and 9 susceptible cultivars, the sequence was compared with 9 susceptible cultivars (Ce253, Gui582, Guanghui998, R128, R138, Guanghui308, Shen08S, 186B, II-32B). Primers Xa7-FaT and Xa7-FCA, which can match with the fluorescence primers of FAM and HEX in PARMS Master Mix, were designed and combined with the universal primer Xa7-R to form the fluorescence molecular marker PM-Xa7 of *Xa7* gene.

3.3 DNA extraction and PCR amplification

Rice genomic DNA was extracted from individual leaves two weeks after transplanting according to the CTAB method used by Murray and Thompson (1980). The *Xa7* gene of the test material was amplified by PCR amplification system of 10 μ L. The system composition was as follows: 2 \times PARMS master mix 5 μ L, 10 mmol/L forward labeled primer (Xa7-FaT) 0.15 μ L, 10 mmol/L forward labeled primer (Xa7-FCA) 0.15 μ L, 10 mmol/L general reverse marker primer (Xa7-R) 0.4 μ L, template DNA 1.0 μ L, ddH₂O 3.55 μ L. PCR amplification procedure: 95°C for 4 min, 94°C for 20 s, 65°C (decrease 0.8°C per cycle) for 1 min, 10 cycles. Then 94°C for 20 s, 56°C for 1 min, 32 cycles.

3.4 Phenotypic identification of the tested material

The tested pathogen was the bacterial blight (IV) strain of rice in Guangxi, which had the highest occurrence frequency and the most extensive damage distribution in Guangxi, and was considered as the dominant pathogenic bacteria in Guangxi (Sun et al., 1993). According to the bacterial culture and inoculation methods of Wu et al. (2019), the disease was investigated about 20 days after inoculation. The disease was graded according to the percentage (%) of disordered spots in the total leaf length (Qin et al., 2014): 0~3.0% of high resistance (HR), 4%~12.0% of resistance (R) and 13%~25.0% of moderate resistance (MR), 26%~50.0% of moderate susceptible (MS), 51%~85.0% of susceptible (S), 86%~100.0% of high susceptible (HS).

3.5 *Xa7* allele type

The fluorescence signal intensity of PCR amplification products was detected by using the enzyme label analyzer of FAM, HEX and ROX fluorescence detection channels. By SNP decoder (<http://www.snpway.com/snpdecoder01/>) software analysis each sample PCR amplification of FAM and HEX fluorescent signal values, and the corresponding scatter plot format output, genotyping of amplification products. If the fluorescence signal of FAM is obtained by scanning, it is the *Xa7* allele containing A and T bases, which is divided into green dots on the scatter map. If the HEX fluorescence signal is obtained by scanning, it is the *Xa7* allele containing C and A bases, which is the blue dot on the typing map. If the fluorescence signals of both FAM and HEX are obtained by scanning, the genotype contains heterozygous A/C and T/A base alleles, which are represented by red dots on the typing map.

3.6 Breeding application

Using *Xa7* gene 'IRBB7' as the donor, cross with Guangxi high quality hybrid rice susceptible parent 'Mei B' and backcross to BC₂F₁ generation. After three successive self-crossing generations, each generation was selected by using the marker PM-*Xa7* and combined with phenotypic identification to create a new maintenance line material resistant to bacterial blight. In this process, in order to verify the accuracy of *Xa7* gene selection by marker PM-*Xa7*, 382 BC₂F₂ generation single strains were detected by marker PM-*Xa7*, and 2 negative controls were added.

Authors' contributions

WH is the experimental designer and the executor of this study. DGF, GLJ, DXX and HJ completed the data analysis and the writing of the first draft of the paper. GH, QDJ, CWW and YSY participated in the experimental design and analysis of the experimental results. LHF was the architect and the person in charge of the project, guiding the experimental design, data analysis, paper writing and revision. All authors read and approved the final manuscript.

Acknowledgments

This research was supported by the Basic Scientific Research Business Special Project of Guangxi Academy of Agricultural Sciences (Guinongke2020YM102 and Guinongke2018YT24), Guangxi Rice Quality Breeding Research Talent Cultivation Fund for Young Talents (QN-6), Guangxi Natural Science Foundation Project (2018GXNSFBA050058) and Tianjin Support Plan Project (18YFZCNC01210).

Reference

- He L., 2012, Marker assisted selection of bacterial blight resistance genes *xa5*, *Xa7*, *Xa23*, Thesis for M.S., College of Agriculture, Guangxi University, Supervisor: Wang Z.W., pp.31
- Huang B., Xu J.Y., Hou M.S., Ali J., and Mou T.M., 2012, Introgression of bacterial blight resistance genes *Xa7*, *Xa21*, *Xa22* and *Xa23* into hybrid rice restorer lines by molecular marker assisted selection, *Euphytica*, 187(3): 449-459
<https://doi.org/10.1007/s10681-012-0758-1>
- Lan Y.R., Wang J.Y., Wang G., and Mou T.M., 2011, Improvement of rice bacterial blight resistance of Hua 201S, an elite photo-thermo-sensitive genic male sterile line, by molecular marker-assisted selection, *Zhongguo Shuidao Kexue (Chinese Journal of Rice Science)*, 25(2): 169-174
- Li D.Q., Zhong Q.F., Zeng M., Chen Y., Wang B., and Cheng Z.Q., 2017, Progress in mapping, cloning and application of resistance genes to bacterial blight disease in rice, *Zhongguo Daomi (China Rice)*, 23(5): 19-27
- Liu F., Liang Q., Chen W.X., Chen Y.Y., Liang J.S., and Chen X.Y., 2019, Analysis of molecular marker on rice germplasm of bacterial blight resistant gene *Xa7* and *Xa23*, *Fenzi Zhiwu Yuzhong (Molecular Plant Breeding)*, 14(4): 935-940
- Li Y., Nie Y.Y., Cai Y.H., Yan M.L., Mao L.H., Li Y.H., Lu M., and Li M.D., 2011, Research progress in resistant genes to bacterial blight of rice and its molecular marker assisted selection, *Jiangxi Nongye Xuebao (Acta Agriculturae Jiangxi)*, 23(9): 115-117
- Ma B.J., Zheng X.X., Zhang P.H., Hu N.N., and Chen X.F., 2013, Metabolism of reactive oxygen species in resistant response of rice *Xa7* gene to bacterial blight, *Zhejiang Shifan Daxue Xuebao (Journal of Zhejiang Normal University (Natural Science))*, 36(1): 7-11
- Murray M.G., and Thompson W.F., 1980, Rapid isolation of high molecular weight plant DNA, *Nucleic Acids Research*, 8(19): 4321-4326
<https://doi.org/10.1093/nar/8.19.4321>
- Porter B.W., Chittoor J.M., Yano M., Sasaki T., and White F.F., 2003, Development and mapping of markers linked to the rice bacterial blight resistance gene *Xa7*, *Crop Sci*, 43(4): 1484-1492
<https://doi.org/10.2135/cropsci2003.1484>
- Qin B.X., Liu C., Jiao X.Z., Huang D.H., Zhang Y.X., Ma Z.F., Feng J.X., Chen Z.L., and Liu F., 2014, Identification and evaluation of Guangxi wild rice (*Oryza rufipogon* Griff) resources with wide spectrum resistance to bacterial blight, *Nanfeng Nongye Xuebao (Journal of Southern Agriculture)*, 45(9): 1527-1531
- Qing D.J., Liu K.Q., Yang Y.Y., Gao L.L., Huang J., Gao J., Dai G.X., Zhou W.Y., Liang H.F., and Deng G.F., 2018, Development of molecular marker of rice blast resistance gene *Pigm* on basis of PARMS technology, *Xinan Nongye Xuebao (Southwest China Journal of Agricultural Science)*, 31(8): 70-74
- Shen G.B., 2001, Fundament study on monitoring and management of resistance of *Xanthomonas oryzae* to saikuzuo bactericide, Thesis for M.S., Nanjing Agricultural University, Supervisor: Zhou G.M., pp.3
- Sun H.H., Li Q.B., and Huang L.J., 1993, Restudy on the pathogenicity of *Xanthomonas oryzae* in Guangxi, *Guangxi Nongye Kexue (Guangxi Agricultural Sciences)*, (3): 128-130
- Shi Y.M., Xie L.P., Wei S.F., Wang W.H., Song Z.P., Zhou H., and Mao C.X., 2008, Current situation of disease resistance and improvement of rice in Guangxi province, *Zhongzi (Seed)*, (27): 82-84
- Webb K.M., Oña I., Bai J., Garrett K.A., Mew T., Vera Cruz C.M., and Leach J.E., 2010, A benefit of high temperature: increased effectiveness of a rice bacterial blight disease resistance gene, *New Phytologist*, 185(2): 568-576
<https://doi.org/10.1111/j.1469-8137.2009.03076.x>
- Wu H., Wang W.H., Liu B.L., Zhou H., Shi Y.M., and Wei S.F., 2019, Screening and identification of bacterial blight resistance gene in weedy rice, *Guizhou Nongye Kexue (Guizhou Agricultural Sciences)*, 47(4): 1-4
- Yan C.Y., Liu Y., and Mou T.M., 2013, Pyramiding *Xa7*, *Xa21* and *cry1C** for the improvement of bacterial blight and borer resistance of hybrid rice Jinyou 207 by molecular marker-assisted selection, *Zajiao Shuidao (Hybrid Rice)*, 28(5): 52-59
- Yu L.J., Zhang G.L., Ding X.W., Gao Y., and Xie Y.F., 2012, Progress in identification and application of resistance genes to bacterial blight, *Zhiwu Shengli Xuebao (Plant Physiology Journal)*, 48(3): 223-231