

Short Research Article

SCREENING FOR BACTERIAL LEAF BLIGHT RESISTANT GENES IN RICE USING SSR MARKERS

ABSTRACT

Bacterial leaf blight disease plays a major detrimental effect in the yield and quality of Rice (*Oryza sativa*). To overcome the problem, finding bacterial leaf blight resistant gene is very crucial. In this study, identification of bacterial leaf blight resistant genes was attempted among 27 rice varieties including two control varieties using three Simple Sequence Repeats markers tagged with Bacterial leaf blight genes which are *Xa4*, *xa5* and *xa13*. As a result, six varieties naming, MTU1010, IR 68144-2B-2-2-3-1-127, ARC-10086, Mali 4, IR 64 and Kalinga-2 were classified as resistant to the disease due to the presence of bands of all of the three markers. 12 varieties were considered as susceptible and the other 7 varieties showed moderate resistance or susceptible results. The identified resistant genotypes can be utilized as a donor for developing Bacterial leaf blight tolerant rice varieties in future breeding programme.

Keywords: Bacterial leaf blight, Rice, Resistant, Simple Sequence Repeats.

1. INTRODUCTION

Rice is the most popular cereal crop because of its extensive consumption as a food crop for human needs. Approximately 60% of the World's population depends on rice for using as the basic food material [1]. Rice is also called as the "monocot model species" [2]. Though, around 21 viral and 6 bacterial diseases of rice were found, but among them Bacterial Leaf Blight (BLB) disease is very harmful in nature [3,4]. The causative agent of BLB disease is *Xanthomonas oryzae* pv. *oryzae* which is transmitted through seed. As the symptoms of BLB disease, "Seedling wilt-Kresek" and "bacterial ooze of the cut ends symptom" can be observed [5]. Approximately 50% yield loss happened in the world [6] and up to 81.3% yield loss happened in India as the effects of BLB [7,8].

Due to availability of the sequencing information of rice, the proper position of genes or Quantitative trait locus (QTL)s controlling resistant to abiotic stress like BLB disease can be identified. Screening of the genotype using the BLB resistant molecular markers which are gene based or tightly linked is more effective than the screening based on morphological parameters [9]. About 40 genes resistant to BLB disease have been recognized [10], among which *Xa4*, *xa5*, *xa7*, *xa13*, and *xa21* are considered as the major resistant genes [11]. Availability of Simple Sequence Repeats (SSR) markers for *Xa4*, *xa5*, *xa13*, and *xa21* were already reported [12]. The present study performed the screening of BLB resistant rice varieties among 27 rice varieties using three Simple Sequence Repeats (SSR) markers tagged with BLB resistant genes. These will help the breeders to select the BLB resistant varieties.

2. MATERIAL AND METHODS

The seeds of 27 rice varieties (Table 1) were collected from the Department of Genetic and Plant Breeding, RKMVERI, Narendrapur and the experiments were carried out at RKMVERI, Narendrapur in 2019. From the three leaves stage, the DNA was isolated using CTAB (Cetyl trimethyl ammonium bromide) method [13], separated in 0.8% agarose gel, visualized and quantified using Gel documentation system (BIO-RAD) and Nanodrop (Thermo Scientific) respectively. The DNA was amplified using a 25µl reaction mixture in a Polymerase chain reaction (PCR) tube containing 2.5µl 10X Taq buffer, 0.2 µl each Forward and Reverse primer, 2µl MgCl₂ (25mM), 2µl dNTPs, 0.2µl Taq pol (3U/ µl) and 200ng isolated rice genomic DNA on a Thermocycler machine (Eppendorf). The program of the thermocycler was- 5 minutes preheating at 95°C, 35 cycles of denaturation at 95°C for 30 seconds, 30 seconds primer annealing at specific temperature for particular primer pair, 1 minute primer extension at 72°C and 5 minutes final extension at 72°C. The used SSR primers are Primer-1: MP1 [Gene name- *Xa4*, Chromosome No: 11, (Forward primer sequence- ATCGATCGATCTTCACGAGG), (Reverse primer sequence- TCGTATAAAAGGCATTCGGG)], Primer-2: RM13 [Gene name- *xa5*, Chromosome No: 5, (Forward primer sequence- TCCAACATGGCAAGAGAGAG), (Reverse primer sequence- GGTGGCATTTCGATTCCAG)] and Primer-3: RM264 [Gene name- *xa13*, Chromosome No: 8, (Forward primer sequence- GTTGCGTCTCTACTGCTACTTC), (Reverse primer sequence- GATCCGTGTCGATGATTAGC)] [14]. After separating the amplified product on 2% agarose gel, it was observed on Gel documentation system (BIO-RAD) and the band size was estimated based on the size of 50bp DNA ladder.

3. RESULTS AND DISCUSSION

IRBB 59 was considered as the BLB resistant control variety whereas the susceptible variety control was IR 24 which were also described [15.16], these two varieties developed from IRR1 were used for identification. The MP1 primer is linked with *Xa4* gene, RM13 primer is linked with *xa5* gene and the primer named RM264 is linked with *xa13* gene. Bands of 150bp, 160bp and 190bp fragments exhibited for the resistant variety with MP1, RM13 and RM256 primers respectively (Fig. 1). For the susceptible variety, 140bp, 130bp and 170bp fragments were observed using MP1, RM13 and RM256 primers respectively. By observing the band sizes, the BLB resistant varieties among the 27 rice varieties were identified, which were MTU 1010, IR68144-2B-2-3-1-127, ARC-10086, Mali 4, IR 64 and Kalinga-2, these varieties were consisting all of the three resistant genes (*Xa4*, *xa5* and *xa13*) (Table. 1).

Tables should be explanatory enough to be understandable without any text reference. Double spacing should be maintained throughout the table, including table headings and footnotes. Table headings should be placed above the table. Footnotes should be placed below the table with superscript lowercase letters. Sample table format is given below.

Table 1. Genotypic screening for bacterial leaf blight resistance of 27 rice genotypes.*

| Sl, No. | Name of the | Origin | Genotyping of resistance genes using SSR Primer | Remarks |
|---------|-------------|--------|---|---------|
|---------|-------------|--------|---|---------|

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| Varieties | | | | MP1 | RM13 | RM264 | |
|-----------|-------------------------|-------------------------|--|-------|-------|-------|-------|
| 1 | IR 24 | IRRI | | 140bp | 130bp | 170bp | S |
| | (Susceptible Control) | | | | | | |
| 2 | IRBB 59 | IRRI | | 150bp | 160bp | 190bp | R |
| | (Resistant Control) | | | | | | |
| 3 | ARC 10086 | Assam | | + | + | + | R |
| 4 | Mali 4 | Mali | | + | + | + | R |
| | | Agritech, Ranaghat | | | | | |
| 5 | Kasalath | India | | + | + | - | MR/MS |
| 6 | MTU 1010 | ANGRAU, AP | | + | + | + | R |
| 7 | Swarna | IRRI collab CRR | | + | + | - | MR/MS |
| 8 | Dular | Landrace | | 0 | - | - | S |
| 9 | Azucena | Philippines | | 0 | - | 0 | S |
| 10 | Swarna Sub-1 | IRRI | | 0 | - | 0 | S |
| 11 | Samba Mahsuri | ANGRAU | | 0 | 0 | 0 | S |
| 12 | Lemont | Philippines | | 0 | 0 | 0 | S |
| 13 | Restorer Line-51 (R-51) | Mali Agritech, Ranaghat | | 0 | + | + | MR/MS |
| 14 | CN1646-2 | Chinsurah, West | | 0 | + | 0 | S |

| | | | | | | |
|----|--------------------|--------------------------------------|---|---|---|-------|
| | | Bengal | | | | |
| 15 | Sabita | Landrace | + | - | - | S |
| 16 | Ratna | India | + | 0 | 0 | S |
| 17 | Restorer | Mali | + | + | - | MR/MS |
| | Line (R-71) | Agritech, Ranaghat | | | | |
| 18 | Patharea | Thane, Maharashtra | + | - | - | S |
| 19 | <i>Indica</i> | Mali | + | + | - | MR/MS |
| | <i>Javanica</i> | Agritech, (TC-25-2-1) Ranaghat | | | | |
| 20 | <i>Indica</i> | Mali | 0 | - | - | S |
| | <i>Javanica</i> | Agritech, (TC-26-2-1) Ranaghat | | | | |
| 21 | Nippon bare | Japan | - | - | + | S |
| 22 | IR 64 | IRRI | + | + | + | R |
| 23 | IR 68144- | IRRI | + | + | + | R |
| | 2B-2-2-3-1- 127 | | | | | |
| 24 | Kalinga-2 | CRRI, Cuttack | + | + | + | R |
| 25 | Danaguri | Local landrace, West Bengal | - | - | - | S |
| 26 | Zheshan-2 | China | + | - | + | MR/MS |
| 27 | ARC | Assam | + | - | + | MR/MS |
| | 100372 | | | | | |

* R = resistant, S = susceptible, + = presence of resistant band, - = presence of susceptible bands, 0 = no bands, MR/MS = moderately resistant / moderately susceptible

The presence of Xa4, xa5, xa13 and xa21 BLB resistant genes were previously found for IR 64, IR68144-2B-2-3-1-127 and Kalinga-2 [14] which was also confirmed in this research work based on Xa4, xa5 and xa13 genes. In this study, Dular, Azucena, Swarna Sub-1, Samba Mahsuri, Lemont, Danaguri, CN1646-2, Sabita, Ratna, Patharea, Indica Javanica (TC-26-2-1) and Nippon bare are classified as susceptible varieties due to having susceptible reactions. The other varieties exhibited intermediate result.

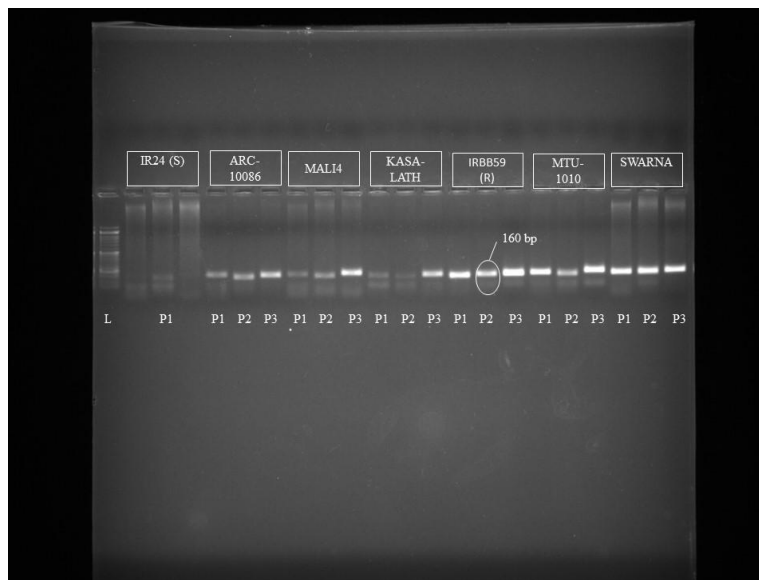


Fig. 1. Electrophoregram of different rice cultivars using three markers (where L= 50bp DNA ladder, P1= Primer-1: MP1, P2= Primer-2: RM13, P3= Primer-3: RM264)

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4. CONCLUSION

The appearance of the bands of all the three markers tagged with BLB resistance genes in the classified six rice varieties indicates that these varieties will be useful as donor of the BLB genes in developing BLB resistant rice varieties with the help of advance breeding programme.

CONSENT

Not applicable

ETHICAL APPROVAL (WHERE EVER APPLICABLE)

Not applicable

COMPETING INTERESTS DISCLAIMER:

Authors have declared that no competing interests exist. The products used for this research are commonly and predominantly use products in our area of research and country. There is absolutely no conflict of interest between the authors and producers of the products because we do not intend to use these products as an avenue for any litigation but for the advancement of knowledge. Also, the research was not funded by the producing company rather it was funded by personal efforts of the authors.

REFERENCES

1. Khush GS. What it will take to feed 5.0 billion rice consumers in 2030. Plant Mol. Biol. 2005;59(1):1-6.
2. Coudert Y, Périn C, Courtois B, Khong NG, Gantet P. Genetic control of root development in rice, the model cereal. Trends Plant Sci. 2010;15(4):219-26.
3. Shekhar S, Sinha D, Kumari A. An Overview of Bacterial Leaf Blight Disease of Rice and Different Strategies for its Management. Int. J. Curr. Microbiol. App. Sci. 2020;9(4):2250-65.
4. Khan MA., Naeem M, Iqbal M. Breeding approaches for bacterial leaf blight resistance in rice (*Oryza sativa* L.), current status and future directions. Eur J Plant Pathol. 2014;139:27–37.
5. Disease- and pest- resistant rice. Accessed on 10 January 2022.

134 <https://www.irri.org/disease-and-pest-resistant-rice>

135 6. Kulkarni S, Jahagirdar S. Evaluation of new molecules in the management of bacterial
136 blight of paddy in India. Internat J Plant Protec. 2011;4(2):289-91.

137 7. Prasad D, Singh R, Deep S. In-vitro and In-vivo Efficacy of Antibacterial Compounds
138 against *Xanthomonas oryzae* pv. *oryzae*, A Cause of Bacterial Leaf Blight of Rice. Int. J.
139 Curr. Microbiol. App. Sci. 2018;7(5):2960-69.

140 8. Swati, Kumar A, Roy SP, Kumari P. Studies on efficacy of different chemicals treatments
141 against Bacterial leaf blight of rice in Bihar. The Biobrio. 2015;2(1-2):56-61.

142 9. Sinha S, Kumar A, Satyendra, Kumar M, Singh SP, Singh PK. Screening of rice
143 genotypes for abiotic and biotic stresses using molecular markers. J. Pharmacogn.
144 Phytochem. 2018;7(2):2111-15.

145 10. Kim SM, Suh JP, Qin Y, Noh TH, Reinke RF, Jena KK. Identification and fine-mapping of
146 a new resistance gene, Xa40, conferring resistance to bacterial blight races in rice (*Oryza*
147 *sativa* L.). Theor Appl Genet. 2015;128:1933-43.

148 11. Singh AK, Dharmraj E, Nayak R, Singh PK, Singh NK. Identification of bacterial leaf
149 blight resistance genes in wild rice of eastern India. Turk. J. Bot. 2015;39(6):1060-66.

150 12. Shah BH, Xiaohua D, Liexian Z, Talukdar A, Zemin Z, Ruizhen Z, Guiquan Z. Pyramiding
151 four bacterial blight resistance genes into rice cultivars in south China. Mol Plant Breed,
152 2006;4(4):493-99.

153 13. Doyle JJ, Doyle JL. A rapid DNA isolation procedure for small quantities of fresh leaf
154 tissue. Phytochem. Bull. 1987;19:11-15.

155 14. Majumder K, Mondal SI, Mallick R, Dasgupta T. Identification of BLB resistant genes in
156 some rice varieties for development of high yielding bacterial leaf blight tolerant types. J.
157 Environ. Biol. 2020;41(1):85-91.

158 15. Salgotra RK, Gupta BB, Millwood RJ, Balasubramaniam M, Stewart CN Jr. Introgression
159 of bacterial leaf blight resistance and aroma genes using functional marker-assisted
160 selection in rice (*Oryza sativa* L.). Euphytica, 2012;187(3):313-23.

161 16. Singh PB, Ruchi T, Rallapalli R, Chet R, Subhash N. Molecular Marker-based Screening
162 for Bacterial Leaf Blight Resistance Genes in Landraces and Cultivars of Rice in Gujarat.
163 Indian Journal of Plant Genetic Resources, 2018;31(1):51-56.
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166 ABBREVIATIONS

167 BLB- Bacterial Leaf Blight

168 Bp- Base pair

169 CTAB- Cetyl trimethyl ammonium bromide

170 dNTPs- Deoxynucleotide triphosphates

171 MgCl₂- Magnesium chloride

172 SSR- Simple Sequence Repeat

173 QTL- Quantitative trait locus
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