



Inheritance of resistance to bacterial blight (*Xanthomonas oryzae* pv. *oryzae*) in rice (*Oryza sativa* L.)

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Abstract

The mode of inheritance and allelic relationship among genes for resistance to bacterial blight (*Xanthomonas oryzae* pv. *oryzae*, iso-6R) in eight rice (*Oryza sativa* L.) cultivars was studied. The reaction of F₁ and segregation pattern in F₂ and F₃ generations from the crosses of the test cultivars with MW-10, revealed the presence of single recessive gene in IR-54, R732-2-49-2-2, R744-1-107-2-2 and RP2151-33-2 and two independent recessive genes in R712-1-65-2-2, R731-1-73-2-1, R738-1-64-2- and R741-1-55-2-2. The resistant gene(s) present in these cultivars, segregated independently to Xa-1 gene of IRBB-1.

Key words : Rice, bacterial blight, inheritance, resistance.

Introduction

Among sixty odd diseases attacking the rice (*Oryza sativa* L.) crop, bacterial blight caused by *Xanthomonas oryzae* pv. *oryzae* is one of the most destructive disease in almost all rice growing regions [1-2]. The disease has attained greater prevalence with the spread of high yielding varieties cultivated under improved agronomic practices. Since effective chemical control of this disease is not available, use of resistant cultivars has been suggested by several workers to combat the disease. Few cultivars resistant to bacterial leaf blight have been identified and are being extensively grown in different parts of the world, however, evolution of new pathotypes have rendered these cultivars susceptible. Six strains have been identified in Chhattisgarh State and isolate-6R is one of them. Twenty one resistant genes have been identified by now, however there is need to identify the resistant donors against local strains and to investigate their mode of inheritance. Keeping this in view the present study was carried out.

Materials and methods

Eight cultivars (IR-54, R712-1-65-2-2, R731-1-73-2-1, R732-2-49-2-2, R738-1-64-2-2, R741-1-55-2-2, R744-1-107-2-2 and RP2151-33-2) of rice resistant to

bacterial blight were crossed with susceptible variety MW-10 and with resistant donor IRBB-1, an IRR1 differential, to obtain F₁, F₂ and F₃ generations. The experiment was conducted under field conditions. All standard agronomic practices were followed during the cultivation of crop. The progenies of different crosses were tested at maximum tillering stage for their reaction to isolate-6R of bacterial blight pathogen, following clipping method of inoculation suggested by Kauffman *et al.* [3]. Isolate-6R was cultured on potato semisynthetic agar medium for 3 days at 28°C, suspended in sterilized water with concentration adjusted to about 10⁹ cells/ml and was used for inoculation. Disease reaction was scored visually 21 days after inoculation and the disease score on the host was noted as per the standard evaluation system (SES) developed by International Rice Research Institute, Philippines. According to this system a plant with a score of 0-3 was considered as resistant and the plants with score between 5-9 were considered as susceptible.

F₁'s on row basis and F₂'s on individual plant basis were scored as resistant or susceptible whereas, the F₃'s (coming from randomly selected F₂ plants) were classified as breeding true for either resistance or susceptible or segregating. Simple chi-square (χ^2) test was applied to test the goodness of fit of different genetic ratios.

Results and discussion

Inheritance of resistance : The disease reaction of F₁ of all the crosses between resistant cultivars with MW-10 (susceptible) were susceptible to local isolate - 6R of bacterial leaf blight pathogen, indicating that the resistance is due to recessive gene(s).

The F₂ and F₃ populations of the crosses MW-10 with IR-54, R732-2-49-2-2, R744-1-107-2-2 and RP2151-33-2 segregated in 1R:3S and 1HR:2seg:1HS ratios respectively suggesting monogenic recessive nature of resistance in these cultivars. Similarly F₂ and

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Table 1. Reaction of F₁, F₂ and F₃ population to *Xanthomonas oryzae* pv. *oryzae* isolate-6R, in eight crosses

| S. No. | Crosses | F ₁ reaction | *F ₂ segregation | | Ratio R:S | χ ² Value | **F ₃ segregation | | | Ratio | χ ² Value |
|--------|---------------------|-------------------------|-----------------------------|-----|-----------|----------------------|------------------------------|------|----|-------|----------------------|
| | | | R | S | | | HR | Seg. | HS | | |
| 1. | MW10/IR 54 | S | 94 | 329 | 1:3 | 1.740 | 21 | 54 | 18 | 1:2:1 | 3.264 |
| 2. | MW10/R712-1-65-2-2 | S | 210 | 300 | 7:9 | 1.372 | 38 | 49 | 7 | 7:8:1 | 0.537 |
| 3. | MW10/R731-1-73-2-1 | S | 215 | 295 | 7:9 | 0.525 | 33 | 43 | 8 | 7:8:1 | 1.846 |
| 4. | MW10/R732-2-49-2-2 | S | 139 | 366 | 1:3 | 1.716 | 21 | 49 | 33 | 1:2:1 | 3.038 |
| 5. | MW10/R738-1-64-2-2 | S | 170 | 231 | 7:9 | 0.299 | 41 | 57 | 9 | 7:8:1 | 1.750 |
| 6. | MW10/R741-1-55-2-2 | S | 180 | 239 | 7:9 | 0.106 | 38 | 48 | 5 | 7:8:1 | 0.303 |
| 7. | MW10/R744-1-107-2-2 | S | 89 | 289 | 1:3 | 0.426 | 21 | 58 | 19 | 1:2:1 | 3.589 |
| 8. | MW10/RP2151-33-2 | S | 110 | 317 | 1:3 | 0.132 | 18 | 41 | 25 | 1:2:1 | 1.218 |

* R - Resistant; S - Susceptible; **HR - Homozygous resistant; Seg - Segregating; HS - Homozygous Susceptible

Table 2. Allelic relationship of Xa-1 gene with the gene(s) from eight resistant cultivars

| S. No. | Crosses | F ₁ reaction | *F ₂ segregation | | | Ratio R:S | χ ² Value |
|--------|-----------------------|-------------------------|-----------------------------|----|-------|-----------|----------------------|
| | | | R | S | Total | | |
| 1. | IRBB-1/IR54 | R | 340 | 70 | 410 | 13:3 | 0.756 |
| 2. | IRBB-1/R712-1-65-2-2 | R | 379 | 58 | 437 | 55:9 | 0.226 |
| 3. | IRBB-1/R731-1-73-2-1 | R | 370 | 63 | 433 | 55:9 | 0.085 |
| 4. | IRBB-1/R732-2-49-2-2 | R | 285 | 51 | 336 | 13:3 | 2.813 |
| 5. | IRBB-1/R738-1-64-2-2 | R | 361 | 51 | 412 | 55:9 | 0.966 |
| 6. | IRBB-1/R741-1-55-2-2 | R | 355 | 66 | 421 | 55:9 | 0.907 |
| 7. | IRBB-1/R744-1-107-2-2 | R | 321 | 79 | 400 | 13:3 | 0.262 |
| 8. | IRBB-1/RP2151-33-2 | R | 330 | 85 | 415 | 13:3 | 0.817 |

* R - Resistant; S - Susceptible

F₃ populations of the crosses MW10 with R712-1-65-2-2, R731-1-73-2-1, R738-1-64-2-2 and R741-1-55-2-2 segregated in 7R:9S and 7HR:8 Seg:1HS ratios respectively indicating the presence of two independent recessive genes in these cultivars (Table 1).

Allelic test : IRBB-1 was found resistant against isolate 6R. Therefore, selected test entries possessing recessive gene(s) for resistance were crossed with IRBB-1 possessing Xa-1, dominant resistant gene to test the allelic relationship. The F₁ plants of all the crosses were resistant, assumed to be due to dominant gene Xa-1 of IRBB-1.

The F₂ population from the crosses of IRBB-1 with IR54, R732-2-49-2-2, R744-1-107-2-2, RP 2151-33-2 segregated in a ratio of 13R:3S and from the crosses of IRBB-1 with R712-1-65-2-2, R731-1-73-2-1, R738-1-64-2-2, R741-1-55-2-2 segregated in a ratio of 55R:9S. This indicates the independent segregation of Xa-1 dominant gene with the single recessive gene present in IR-54, R732-2-49-2-2, R744-1-107-2-2, RP 2151-33-2 and two recessive genes present in R712-1-65-2-2, R731-1-73-2-1, R738-1-64-2-2 R741-1-55-2-2. Thus none of the cultivars are allelic to Xa-1 (Table 2). Similar nature of resistance has also been reported earlier (4-6).

In the present case these cultivars were studied against the prevalent isolate for the first time and can be claimed that the gene present in these test entries

could be other than Xa-1, Xa-3, Xa-4, xa-5, Xa-7, xa-8, Xa-10, Xa-11 and/or Xa-12 because Xa-1, Xa-3, Xa-4, Xa-7, Xa-10, Xa-11 and Xa-12 are dominant in nature and recessive gene xa-5 and xa-8 are susceptible at Raipur. Only after testing for allelism with Xa-13, it will be clear whether it is allelic to xa-13 or some new recessive gene(s) in the cultivars under study.

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