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# INHERITANCE AND ALLELIC RELATIONSHIPS OF GENE(S) FOR RESISTANCE TO RICE BACTERIAL BLIGHT (*XANTHOMONAS ORYZAE* PV. *ORYZAE*) IN SOME NEW DONORS

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## ABSTRACT

**Inheritance and allelic relationships of genes for resistance to rice bacterial blight present in 3 donor strains were studied. A single recessive gene in RP2151-33-2 and BG400-1 and two complementary dominant genes in S. 971 for resistance were detected. Allelic studies indicated that the genes for resistance present in these donors were different from the already reported genes Xa-1, Xa-2, Xa-3, Xa-4, xa-5, Xa-7, xa-8, Xa-10, Xa-11 and Xa-$1^h$.**

**Key words:** Bacterial blight, resistances, recessive, complementary genes.

The causal organism of bacterial blight in rice (*Xanthomonas oryzae* pv. *oryzae*) is highly variable and several races have been reported from Philippines, Japan, Indonesia and Thailand [1-3]. In India, Thrimurty et al. [4] reported six different races of this pathogen from eastern Madhya Pradesh alone. Sidhu et al. [5] and Kumar et al. [6] reported pathogenicity behaviour of the Punjab and eastern Madhya Pradesh isolates different from that of the Japanese and Philippine isolates.

Genetic studies aimed at identifying diverse sources of resistance at the International Rice Research Institute, Philippines, and in Japan led to the identification of as many as seventeen genes [7]. Busto et al. [8] reported presence of bacterial blight resistance gene(s) in Indian donors.

Regular screening of the Madhya Pradesh Rice Germplasm accessions has resulted in the identification of several highly resistant donors [9]. In the present study, one such

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resistant donor and two highly resistant breeding lines have been investigated for the mode of inheritance and allelic nature of resistance genes in them.

## MATERIALS AND METHODS

Ten isogenic lines (differentials), three new donors and two susceptible checks (MW-10, Madhuri) were inoculated with six isolates of *Xanthomonas oryzae* pv. *oryzae* prevalent in the Chhattisgarh region of Madhya Pradesh, as described by Thrimurty et al. [4] so as to confirm the reaction of individual isogenic lines and differentials against each isolate.

All the three donors were crossed with the susceptible check MW- 10 and the with isogenic lines and differentials resistant against the same specific isolate(s) for which a particular donor was resistant. Genetic studies were carried out by inoculating with the same specific isolate(s).

The parental strains were screened during kharif 1993, and $F_1$ and $F_2$ populations during kharif 1994. The test strains were inoculated at tillering stage with the bacterial inoculum ($10^9$ cells/ml) by the clipping method [10]. If necessary, different tillers of the same plant were inoculated with different isolates and marked with different colour tags. Host reactions were recorded 21 days after inoculation following the standard evaluation system of IRRI [11]. For genetic analysis, plants with disease scores 1–3 were classified as resistant and those with scores 5–9 as susceptible. The goodness of fit of segregation ratios was determined by $\chi^2$ test.

## RESULTS AND DISCUSSION

Screening of the isogenic lines and differentials against different isolates (Table 1) showed that among the known genes, Xa-3, Xa-4, xa-5 and xa-8 were resistant against isolate 6; Xa-1, Xa-2, Xa-3, Xa-4, Xa-7, Xa-11 and Xa-$1^h$ against 6R; and Xa-$1^h$ was resistant against 6-5R, 6-6R and 6-7R isolates. However, none of the isogenic lines and differentials was resistant against isolate 6-4R. The two breeding lines, BG400-1 and RP2151-33-2 were, however, resistant against isolates 6, 6R, 6-4R and 6-7R; and 6, 6R, 6-4R and 6-6R, respectively. S. 971, an accession in the Madhya Pradesh Rice Germplasm is resistant against isolates 6R, 6-5R and 6-7R.

The susceptible reaction of $F_1$ plants from crosses between the resistant donors and the susceptible check, MW-10 (Table 2) indicates recessive nature of the resistance genes of BG400-1 and RP2151-33-2; while the resistant reaction of $F_1$ plants of the cross S. 971 x MW-10 indicates dominant nature of genes for resistance in S. 971. The 1R: 3S segregation ratio in $F_2$ of the crosses BG400-1 and RP2151-33-2 with MW-10 (Table 2) revealed that resistance

**Table 1. Reaction of lines against different *X. o.* pv. *oryzae* isolates of Chhattisgarh**

| Line | Gene present | Reaction against different isolates | | | | | |
|---|---|---|---|---|---|---|---|
| | | 6 | 6R | 6-4R | 6-5R | 6-6R | 6-7R |
| **(A) Isogenic lines and differentials:** | | | | | | | |
| IRBB-1 | Xa-1 | S | R | S | S | S | S |
| IRBB-2 | Xa-2 | S | R | S | S | S | S |
| IRBB-3 | Xa-3 | R | R | S | S | MS | S |
| IRBB-4 | Xa-4 | R | R | S | S | MS | MS |
| IRBB-5 | xa-5 | R | MS | S | MS | MS | MS |
| IRBB-7 | Xa-7 | MS | R | S | S | MS | MS |
| IRBB-8 | xa-8 | R | MS | S | S | MS | MS |
| IRBB-10 | Xa-10 | MS | MS | S | S | MS | S |
| IRBB-$1^h$ | Xa-$1^h$ | MS | R | MS | R | R | R |
| IR8 | Xa-11 | S | R | S | S | S | S |
| **(B) Breeding lines and germplasm accessions** | | | | | | | |
| BG400-1 | — | R | R | R | MS | MS | R |
| RP2151-33-2 | — | R | R | R | MS | R | MS |
| S. 971 | — | MS | R | MS | R | MS | R |
| Madhuri | (S-check) | S | MS | S | S | S | S |
| MW-10 | (S-check) | S | S | S | S | S | MS |

R—resistant, MS—moderately susceptible, S—susceptible.

**Table 2. Inheritance of resistance against different isolates of *Xanthomonas oryzae* pv. *oryzae* (bacterial blight) of Chhattisgarh region**

| Cross | Isolate used | Reaction of $F_1$ | $F_2$ segregation (No. of plants) | | | $\chi^2$ |
|---|---|---|---|---|---|---|
| | | | R | S | ratio (R:S) | |
| BG400-1 x MW-10 | 6 | S | 84 | 306 | 1:3 | 2.492 |
| | 6R | S | 115 | 297 | 1:3 | 1.864 |
| | 6-4R | S | 88 | 307 | 1:3 | 1.560 |
| | 6-7R | S | 89 | 311 | 1:3 | 1.613 |
| RP2151-x MW-10 | 6 | S | 90 | 306 | 1:3 | 1.091 |
| | 6R | S | 89 | 309 | 1:3 | 1.477 |
| | 6-4R | S | 87 | 309 | 1:3 | 1.937 |
| | 6-6R | S | 92 | 301 | 1:3 | 0.530 |
| S. 971 x MW-10 | 6R | R | 345 | 257 | 9:7 | 0.895 |
| | 6-5R | R | 346 | 258 | 9:7 | 0.263 |
| | 6-7R | R | 342 | 262 | 9:7 | 0.034 |

R—resistant, S—susceptible.

against the respective isolate(s) was governed by a single recessive gene in BG400-1 and RP2151-33-2. The 9R : 7S segregation ratio in the $F_2$ population of the cross S. 971 x MW-10 indicates the presence of two complementary dominant resistant genes in S. 971.

Allelic tests with the isogenic lines and differentials (Table 3) showed that the gene(s) for resistance present in BG400-1 and RP2151-33-2 were different from the genes Xa-1, Xa-2,

**Table 3. Allelic relationships of gene(s) for resistance against rice bacterial blight (*X. o.* pv. *oryzae*)**

| Cross | Isolate used | Reaction of $F_1$ | $F_2$ segregation (No. of plants) | | | $\chi^2$ |
|---|---|---|---|---|---|---|
| | | | R | S | ratio (R:S) | |
| BG400-1 x IRBB-1 | 6R | R | 147 | 32 | 13:3 | 0.089 |
| BG400-1 x IRBB-2 | 6R | R | 163 | 31 | 13:3 | 0.977 |
| BG400-1 x IRBB-3 | 6 | R | 174 | 30 | 13:3 | 1.530 |
| | 6R | R | 176 | 29 | 13:3 | 2.852 |
| BG400-1 x IRBB-4 | 6 | R | 242 | 42 | 13:3 | 2.925 |
| | 6R | R | 240 | 41 | 13:3 | 3.191 |
| BG400-1 x IRBB-5 | 6 | S | 140 | 177 | 7:9 | 0.019 |
| BG400-1 x IRBB-7 | 6R | R | 159 | 32 | 13:3 | 0.499 |
| BG400-1 x IRBB-8 | 6 | S | 108 | 152 | 7:9 | 0.452 |
| BG400-1 x IRBB-1$^h$ | 6R | R | 307 | 64 | 13:3 | 0.547 |
| | 6-7R | R | 311 | 62 | 13:3 | 1.108 |
| BG400-1 x IR8 | 6R | R | 309 | 61 | 13:3 | 1.244 |
| RP2151-33-2 x IRBB-1 | 6R | R | 319 | 68 | 13:3 | 0.353 |
| RP2151-33-2 x IRBB-2 | 6R | R | 221 | 42 | 13:3 | 1.334 |
| RP2151-33-2 x IRBB-3 | 6 | R | 190 | 38 | 13:3 | 0.649 |
| | 6R | R | 193 | 36 | 13:3 | 1.379 |
| RP2151-33-2 x IRBB-4 | 6 | R | 304 | 70 | 13:3 | 0.003 |
| | 6R | R | 308 | 67 | 13:3 | 0.192 |
| RP3151-33-2 x IRBB-5 | 6 | S | 139 | 171 | 7:9 | 0.131 |
| RP2151-33-2 x IRBB-7 | 6R | R | 157 | 31 | 13:3 | 0.630 |
| RP2151-33-2 x IRBB-8 | 6 | S | 125 | 152 | 7:9 | 0.131 |
| RP1251-33-2 x IRBB-1$^h$ | 6R | R | 356 | 70 | 13:3 | 1.500 |
| | 6-6R | R | 361 | 69 | 13:3 | 2.062 |
| RP2151-33-2 x IR 8 | 6R | R | 231 | 38 | 13:3 | 3.770 |
| S. 971 x IRBB-1 | 6R | R | 234 | 25 | 57:7 | 0.439 |
| S.971 x IRBB-2 | 6R | R | 614 | 68 | 57:7 | 0.654 |
| S.971 x IRBB-3 | 6R | R | 501 | 54 | 57:7 | 0.831 |
| S.971 x IRBB-4 | 6R | R | 249 | 36 | 57:7 | 0.839 |
| S.971 x IRBB-7 | 6R | R | 400 | 58 | 57:7 | 1.401 |
| S-971 x IRBB-1$^h$ | 6R | R | 440 | 50 | 57:7 | 0.270 |
| | 6-5R | R | 321 | 42 | 57:7 | 0.149 |
| | 6-7R | R | 263 | 33 | 57:7 | 0.013 |
| S.971 x IR 8 | 6R | R | 448 | 50 | 57:7 | 0.412 |

R—resistant, S—susceptible.

Xa-3, Xa-4, xa-5, Xa-7, xa-8, Xa-11 and Xa-$1^h$. This was evident from the 13R : 3S segregation ratio in $F_2$ when BG400-1 and RP2151-33-2 were crossed with the parents carrying known dominant resistance gene (IRBB-1, IRBB-2, IRBB-3, IRBB-4, IRBB-7, IR 8 and IRBB-$1^h$); and 7R : 9S segregation in the crosses with the parents possessing the known recessive resistance gene (IRBB-5 and IRBB-8). Similarly, the gene for resistance present in S. 971 was different from Xa-1, Xa-2, Xa-3, Xa-4, Xa-7, Xa-11 and Xa-$1^h$ genes as was evident from the 57R : 7S segregation in the $F_2$ population of the crosses between S. 971 and IRBB-1, IRBB-2, IRRR-3, IRBB-4, IRBB-7, IR 8 and IRBB-$1^h$.

Screening and allelic tests with the isogenic lines and differentials clearly indicated that the gene(s) for resistance present in the three donors studied are different from the known genes Xa-1, Xa-2, Xa-3, Xa-4, xa-5, Xa-7, xa-8, Xa-10, Xa-11, and Xa-$1^h$ of blight resistance in rice.

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