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Inheritance of Resistance to Bacterial Blight in Tongil Type Rice Cultivar 'Changseongbyeo'

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ABSTRACT

The inheritance of resistance to bacterial blight in a Tongil-type rice cultivar 'Changseongbyeo' was studied using a Korean isolate HB9101, which belongs to race K_1. The resistance of Changseongbyeo to the HB9101 was controlled by a single dominant gene. This gene was allelic with *Xa-1* gene and linked to *lg* gene on chromosome 4 with the recombination value of 7.5%.

Key words: rice, inheritance, resistance, bacterial blight, *Xa-1*.

Bacterial blight (BB) disease due to *Xanthomonas oryzae* pv. oryzae commonly is observed in the southern plain area of Korea. In susceptible rice cultivars, the disease causes yield loss of about 8-14%, increases the number of unfilled grains, reduces 1000-grain weight, and lowers grain quality (Shin et al., 1992).

Therefore, the use of resistant cultivars is generally considered the most effective and economical means for controlling this disease. For improving the breeding efficiency of resistance to BB, genetic evaluation of rice germplasms is very important.

Twenty genes for resistance to BB have so far been identified (Kinoshita, 1995; Shin et al., 1995). *Xa-1, Xa-2, Xa-12, xa-14,* and *Xa-22* (*t*) are located on chromosome 4. *Xa-5* and *Xa-13* are located on chromosome 5. *Xa-7* is located on chromosome 6. *Xa-3, Xa-4, Xa-10,* and *Xa-21* are located on chromosome 11. Shin et al. (1990a & 1991) revealed that several japonica rice cultivars developed in Korea had *Xa-1* gene and HP744-2-1 line with Tongil background had multiple allele at the *Xa-1* locus. This study was carried to investigate the mode of inheritance, allelic relationships and linkage relation of gene for resistance in Changseongbyeo.

MATERIALS AND METHODS

The reactions of parental genotypes or lines to race K_1 of BB are shown in Table 1. 'LK_1A-2-4-12-1-1' carrying morphological marker gene (lg) and 'Milyang 23' showed susceptible reaction. Changseongbyeo, 'HR11395-19-1' and 'HR11397-28-1' showed resistant reaction. 'HR11395-19-1' and 'HR11397-28-1' are near-isogenic lines having different resistant gene with Milyang 23 genetic background (Shin et al., 1994).

Table 1. Reaction of parents to race K_1 of bacterial blight.

Parent	Chromosome number	Marker gene	Reaction†
Milyang 23			S
Changseongbyeo			R
HR11395-19-1	4	*Xa-1*	R
HR11397-28-1	11	*Xa-3*	R
LK_1A-2-4-12-1-1	4	*lg*	S

† R=Resistant, S=Susceptible

For the mode of inheritance, allelic and linkage relationships of the resistant gene to BB, Changseongbyeo (indica/japonica) was crossed with each tester line as shown in Table 2 and 3. Parents, F_1 and F_2 plants were grown under field conditions and inoculated with a race K_1 (HB9101 isolate) of BB pathogens at maximum tillering stage. The plants were inoculated by the clipping method with bacterial suspension of about 10^8-10^9 cells /ml. The bacterial pathogen was cultured in the peptone sucrose liquid medium except agar for 72 hours.

Disease reaction was examined at 21 days after inoculation visually and classified into two categories, resistant and susceptible. Marker character, liguleless, was investigated at the flowering stage.

RESULTS AND DISCUSSION

The F_1 individuals from the cross of Milyang 23 and Changseongbyeo showed resistant and the F_2 populations segregated in the ratio of three resistant to one susceptible, indicating that Changseongbyeo has a single dominant gene for resistance (Table 2). The allelic relationships between the dominant gene of Changseongbyeo and *Xa-1* or *Xa-3* gene were determined from the reaction of F_1 and F_2 progenies (Table 2). The F_1 progenies from the cross of Changseongbyeo and HR11395-19-1 (*Xa-1*) were resistant and the F_2 populations did not segregate for susceptibility. This result indicates that Changseongbyeo has *Xa-1* for resistance. On the other hand, the F_1 progenies from the cross of Changseongbyeo and HR 11397-28-1 (*Xa-3*) were resistant and the F_2 populations segregated in a ratio of fifteen resistant to one susceptible, indicating that the dominant gene of Changseong-

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Table 2. Segregation mode of resistance to race K_1 of BB in three crosses.

Cross combination	F_1	F_2			Expected ratio	X^2	P
		R	S	Total			
Milyang23 /Changseongbyeo	R	119	45	164	3:1	0.520	0.50-0.30
Changseongbyeo /HR11395-19-1	R	190	0	190			
Changseongbyeo /HR11397-28-1	R	180	15	195	15:1	0.692	0.50-0.30

Table 3. Linkage relation between resistant gene of bacterial blight and *lg* gene on chromosome 4.

Cross combination	Linkage relation				Total
LK_1A-2-4-12-1-1 /	Resistant		Susceptible		
Changseongbyeo	Normal	Liguleless	Normal	Liguleless	
	132	8	7	50	197
	$\chi^2(9:3:3:1) = 166.34$				
	$P < 0.005$				
	Linkage phase = coupling				
	Recombination value(%) = 7.5 ± 0.0004				

byeo is non-allelic to and independent of *Xa-3*. Kim et al. (1981) & Park et al. (1984) reported that some Tongil-type varieties had a single dominant gene for resistance to race K_1 of BB, but they did not reveal allelic relationships for already known dominant genes.

Linkage relation between a dominant gene of Changseongbyeo and the marker gene, lg located on chromosome 4 was examined in the cross of LK_1A-2-4-12-1-1 and Changseongbyeo (Table 3). Segregation of F_2 plants with combined characters for two genes did not fit to the ratio of independent segregation with 9:3:3:1, indicating that these two genes are linked with each other. The recombination value calculated by the maximum likelihood method was 7.5%. This result agreed with the findings of previous papers (Heu et al., 1976; Shin et al., 1990b; 1995). Therefore, the resistant gene of Changseongbyeo will henceforth be designated as *Xa-1*.

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