

## D11 Detection of Resistance Gene to Brown Planthopper(*Nilaparvata lugens* Stal.) Using RFLP and Isozyme Markers in Rice

Kyungpook National Univ. : Won Ho Ha\*, Kyung Min Kim, Jea KeunSohn  
National Yeongnam Agriculture Experiment Station : Un Sang Yeo

### Objectives

This study was to identify the DNA markers tightly linked to brown planthopper (BPH) resistance and to utilize the markers in the breeding of rice cultivars with BPH resistance.

### Materials and Methods

- o Plant material : Parents, F<sub>1</sub> and F<sub>2</sub> derived from 'Samgangbyeo/Nagdongbyeo' and 'Suweon 397/Nagdongbyeo'
- o Inoculation stage of BPH biotype-1 : Seedlings regrown for 7 days after cutting stem at 4~5 leaf stage
- o *Sdh* isozyme analysis : Glazmann's method(1988)
- o DNA extraction : Modified CTAB method(Rogers & Bendich, 1994)
- o Southern hybridization : ECL kit(Amersham) method
- o Linkage map of resistance gene to BPH : MAPL program(Ukai, Y. et al. 1995)

### Results and Discussion

The resistances of 'Samgangbyeo' and 'Suweon 397' to BPH biotype-1 were governed by a single dominant gene(Table 1). The relationship between DNA markers and BPH resistance were analyzed in the hybrid population from a cross of 'Samgangbyeo/Nagdongbyeo'. Linkage analysis showed that BPH resistance of 'Samgangbyeo' was linked to 8 RFLP markers and *Sdh* on chromosome 12. Based on the linkage map which constructed by the 9 markers associated with BPH resistance of 'Samgangbyeo', the resistance gene of 'Samgangbyeo' was *Bph I* which originated from 'Mudgo' closely linked with *G258* at a distance of 4.1cM(Fig. 1,2). This study showed that RFLP marker '*G258*' could be used for marker-assisted selection of resistance gene against biotype-1 of BPH for rice improvement.

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연락처 전화 : 053-950-5711, E-mail : jhsohn@bh.kyungpook.ac.kr

Table 1. Linkage between BPH resistance and *Sdh* isozyme in F<sub>2</sub> populations derived from 'Samgangbyeo/Nagdongbyeo' and 'Suweon 397/Nagdongbyeo'

Crosses	Segregation mode in F <sub>2</sub> population				Expected ratio	$\chi^2$	P	R.V
	AB	Ab	aB	ab				
Samgangbyeo/ Nagdongbyeo	85	5	7	24	9:3:3:1	68.975	-	9.9%
	90A			31a	3 : 1	0.025	0.50~0.90	-
	92B			29b	3 : 1	0.069	0.50~0.90	-
Suweon 397/ Nagdongbyeo	75	5	8	21	9:3:3:1	51.834	-	11.9%
	79A			30a	3 : 1	0.303	0.05~0.10	
	84B			25b	3 : 1	0.109	0.50~0.90	

AB: number of plants showed resistant reaction to BPH and *Sdh* type of 'Samgangbyeo' and 'Suweon 397',  
 Ab: number of plants showed resistant reaction to BPH and *Sdh* type of 'Nagdongbyeo',  
 aB: number of plants showed susceptible reaction to BPH and *Sdh* type of 'Samgangbyeo' and 'Suweon 397',  
 ab: number of plants showed susceptible reaction to BPH and *Sdh* type of 'Nagdongbyeo'.

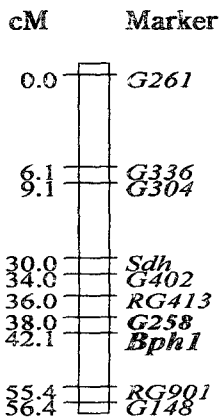


Fig 1. Linkage map of *Bph 1* genomic region on Chromosome 12. The map was constructed using F<sub>2</sub> population derived from 'Samgangbyeo/Nagdongbyeo'.

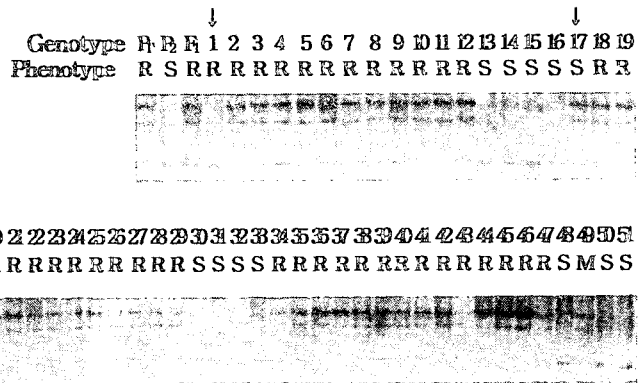


Fig 2. Relationship between BPH resistance and RFLP pattern in 51 individuals 'Samgangbyeo(P<sub>1</sub>)/Nagdongbyeo(P<sub>2</sub>)' with a labeled probe G258. Total DNA was digested with *Pst I*. Arrows(↓) designates recombinants produced by crossing over in the DNA region. 1~51: F<sub>2</sub> individuals. R: resistance, S: susceptibility, M: moderate resistance.