

**25. Mapping of genetic locus associated with resistance to brown planthopper in a line derived from the cross *Oryza sativa* x *O. minuta***

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The brown planthopper (*Nilaparvata lugens* Stal) (BPH) is an important insect pest posing serious threat to rice production in India and other rice growing countries. Genetic resistance to BPH has been well documented in rice germplasm collection. Several major genes and quantitative trait loci (QTLs) have been reported for BPH resistance in varieties as well as wild species of rice (Khush and Brar, 1991 Soundararajan et al. 2004 Jena et al. 2005). In this study, an attempt was made to trace BPH resistance locus from IR71033-62-24, a derivative of *Oryza sativa*/*O. minuta* cross, using simple sequence repeat (SSR) markers.

A F<sub>3</sub> segregating population consisting of 284 families was produced from the cross Mahsuri (BF-selection)/IR71033-62-24. The parents and F<sub>3</sub> families were phenotyped for BPH resistance using standard seedbox screening test (SSST) as described by Heinrichs et al. (1985). BPH insects collected from the rice fields at Maruteru, Hyderabad and reared on the susceptible variety, TN1 were used for screening experiments. In greenhouse screening experiments, IR71033-62-24 showed moderate resistance (damage rating of 5) when Mahsuri (BF-selection) showed high level of susceptibility (damage rating of 9). The damage rating of F<sub>3</sub> families ranged from 1 to 9 with an average of 6. Phenotypic segregation in F<sub>3</sub> families did not conform to Mendelian segregation ratios indicating the quantitative nature of resistance in this population (Fig. 1). There was a strong indication of transgressive variation for BPH resistance in this population. Out of 284 F<sub>3</sub> families analyzed, 87 showed higher level of resistance (damage rating of less than 5) compared to the resistant parent IR71033-62-24.

An attempt was made to detect genetic locus or loci contributing to BPH resistance in IR71033-62-24 through bulked segregant analysis (BSA) using SSR markers. The results indicated that out of 125 polymorphic SSRs, six markers: RM585, RM225 and RM204 on chromosome 6, RM10 and RM346 on chromosome 7 and RM264 on chromosome 8 showed polymorphism between resistant and susceptible bulks as well as individuals constituting the bulks. A subset of 75 F<sub>2</sub> individuals was genotyped with the positive markers identified in BSA for marker-trait association. Single locus analysis through one-way ANOVA showed that SSR marker RM585 on chromosome 6 had significant association with BPH resistance (P=0.000) (Table 1). The mean phenotypic values of F<sub>3</sub> families carrying marker alleles (homozygous) of IR71033-62-24 was lower than F<sub>3</sub> families carrying marker alleles (homozygous) of Mahsuri (BF-selection) for the putative marker associated with BPH resistance. These results suggested the presence of a putative genetic locus for BPH resistance on chromosome 6 (near the marker RM585). The location of the putative BPH resistance locus detected in the mapping population is shown in the SSR linkage map published by Temnyk et al. (2000) (Fig. 2). The region on chromosome 6 carrying this putative locus is also reported to harbor a major gene *bph4* as well as a QTL (Alam and Cohen, 1998 Kawaguchi et al. 2001 Soundararajan et al. 2004) however, the allelic relationship remains to be established.

Table 1. Putative SSR markers identified for BPH resistance in one-way ANOVA

Marker	Chr.	Mahsuri (BF-selection) (homozygote)*	IR71033-62-24 (homozygote)*	Heterozygote*	LSD (5%)	P value**
RM225	6	5.62	3.74	4.81	1.430	0.057
<b>RM585</b>	6	<b>6.30</b>	<b>3.23</b>	<b>4.62</b>	<b>1.300</b>	<b>0.000</b>
RM204	6	6.02	3.75	4.62	1.380	0.018
RM346	7	4.53	4.07	5.32	1.420	0.160
RM10	7	4.54	3.64	5.50	1.380	0.021
RM264	8	4.69	5.04	4.68	1.450	0.862

\*mean phenotypic values of  $F_3$  families carrying marker alleles (homozygous) of Mahsuri (BF-selection), IR71033-62-24 and heterozygous of both the parents

\*\*marker showing  $P < 0.01$  was considered putative empirically

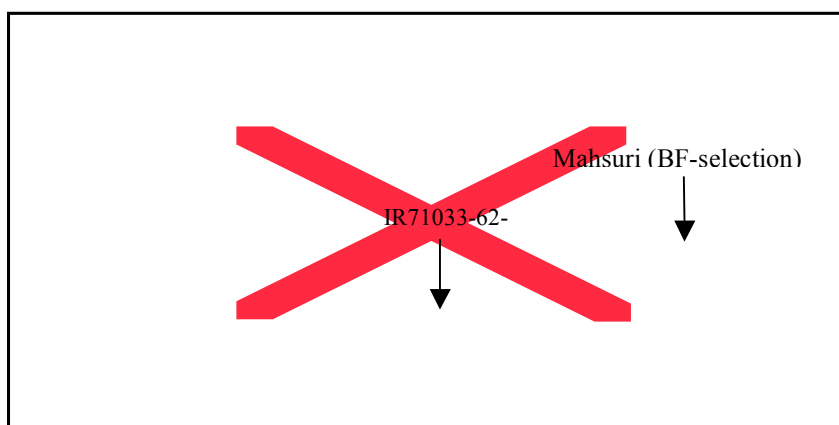


Fig.1 Frequency distribution of phenotypic values of  $F_3$  families for resistance to BPH

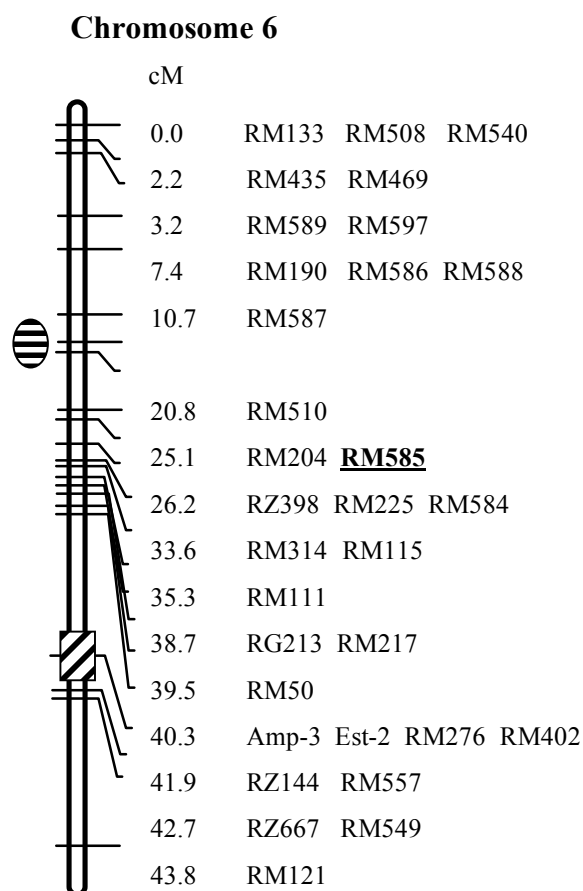


Fig. 2 Map position of putative SSR marker associated with BPH resistance in the SSR linkage map published by Temnyk et al. (2000). The distance between markers is given in centiMorgan (cM).

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