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Title of Entry	: Mapping brown planthopper (<i>Nilaparvata lugens</i>) resistance gene (bph 5) in rice (<i>Oryza sativa</i> L.)
Presenting author	: Dr. G. Padmavathi
Presenting author email	: padmaguntupalli6@gmail.com
Co author 1	: (1) Ramdeen, (2) K. Ramesh, (3) B.C. Viraktamath and (4) T.Ram
Co author 2	:
Affiliation presenting author	: Principal Scientist, Plant Breeding dept, ICAR-Indian Institute of Rice Research, Hyderabad, India.
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Abstract	: Mapping brown planthopper (<i>Nilaparvata lugens</i>) resistance gene (bph 5) in rice (<i>Oryza sativa</i> L.) G. Padmavathi, Ramdeen, K. Ramesh, B.C. Viraktamath and T.Ram Plant Breeding dept, ICAR-Indian Institute of Rice Research, Hyderabad, India. Brown planthopper (BPH) is the most dreaded pest of rice threatening rice production worldwide. Under severe infestation popularly known as “Hopper-burn” 100% yield loss occurs in susceptible cultivars. In spite of chemical control measures, the crop damage is intensifying day by day. Therefore it is imperative to identify BPH resistance gene(s) in donors for utilization in breeding resistant rice cultivars. Since the conventional strategies involving phenotype-based selection is time consuming, the strategy of molecular marker-assisted selection enables accelerated development of broad spectrum resistant varieties. ARC 10550, an Indian land race possesses a major recessive gene ie., bph 5 effective against biotype 4 of BPH existing in India, Bangladesh and Sri Lanka. ARC 10550 showed broad spectrum resistance over the years which may be due to the presence of QTLs along with major gene, bph 5. In the present study, we analysed the QTLs associated with resistance in ARC10550 for having durable resistance. A population of 255 F2:3 families from the cross Taichung Native 1/ARC10550 was used to map BPH resistance with 106 polymorphic simple sequence repeat markers. The inheritance pattern of nine phenotypic traits governing non-preference, antibiosis and antixenosis mechanisms of resistance suggested the polygenic control of resistance. QTL analysis revealed that five major loci were associated with resistance, one for damage score (qBphDS6) on chromosome 6, two for nymphal preference at 48 and 72 h (qBphNp(48h)-1 and qBphNp(72h)-12) on chromosome 1 and 12 and two for days

to wilt (qBphDw(30)-3 and qBphDw(30)- 8) on chromosome 3 and 8 explaining the phenotypic variance of 24.23%, 8.69%, 7.66%, 4.55% and 10.48% respectively. These QTLs jointly explained 55.6% of the phenotypic variance for BPH resistance. The QTLs indicated the negative additive effects suggesting that the resistant alleles identified were from ARC10550 donor parent. The two major QTLs identified namely qBphDS-6 and qBphDW(30)-8 are presently in the processes of validation and fine mapping for use in marker aided breeding programme.

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