

Le Quang Tuyen. 2011. "Genetic analysis for the resistance to small brown planthopper (*Laodelphax striatellus* Fallén) in two rice varieties". PhD Thesis Abstract (e-mail: lequangtuyen71@yahoo.com). Sugarcane Research and Development Centre.

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Rice (*Oryza sativa* L.) is the staple food for more than 50% of the world's population, although insect pests are the major biotic constraints to production of this crop. The Small brown planthopper, *Laodelphax striatellus* Fallén (Homoptera: Delphacidae), is one of the most destructive and wide spread insect pests found throughout the temperate rice-growing regions such as China, Japan and Korea. The population of *Laodelphax striatellus* Fallén has increased steadily due to alteration of the cropping system and infested South East China. The adults and nymphs of *Laodelphax striatellus* Fallén suck rice sap causing yellowing of leaves, wilting and eventually death resulting in yield loss. The pest also transmits viral diseases such as *Rice stripe virus*, and *rice black streaked dwarf virus* causing further yield loss. Chemicals have mostly been used to control *Laodelphax striatellus* Fallén, although it has developed resistance to most of them. Use of these chemicals has also resulted into death of natural enemies and pollution of the environment leading to the resurgence of the pest. Development of resistant varieties is the most effective and economical way in controlling this pest. The feeding behaviour of the pest was evaluated on two rice varieties bearing resistance genes derived from three basic resistance mechanisms: antibiosis, antixenosis and tolerance by identifying the resistance genes in rice varieties with the help of the QTL.

1. A set of F₂ and BC₁ population derived from the cross between 02428 and Rathu Heenati were used to investigate the small brown planthopper resistance loci. Using the F₂ population, three QTLs for antixenosis resistance were located on chromosome 2, 5 and 6, respectively accounting for 30.75% of the phenotypic variance. The QTL on chromosome 2 was also identified in BC₁ population. Three QTLs for antibiosis against the pest were detected on chromosome 8, 9 and 12, respectively in F₂ population. *qSBPH5-c* explaining 7.21% of phenotypic variance for antibiosis against the insect was identified on chromosome 5 using BC₁ population. A major QTL *qSBPH12-a1* explained about 40% of phenotypic variance and a minor QTL (*qSBPH4-a*) were detected by SSST method using both the F₂ and BC₁ population. The QTLs identified in present study will be useful for mark assisted selection for SBPH resistance in rice.

2. The *Japonica* rice 02428 and the *indica* rice Changhui891, was used to detect quantitative trait loci (QTLs) for the resistance to SBPH. Modified seedling screening test (MSST), along with antixenosis test and antibiosis test were applied to evaluate the resistance response of the two parents and 149 plant F₂ to the insect and composite interval mapping (CIM) was used for QTL analysis. When the resistance was measured by MSST method, two QTLs conferring resistance to Small brown planthopper were mapped on chromosome 6 and chromosome 7 namely *qSBPH6-a* and *qSBPH7-a*, with log of odds (LOD) scores 2.61 and 2.91, respectively; and two QTLs explained 8.75% and 13.1% of the phenotypic variance in this population, respectively. Two QTLs, namely *qSBPH1-c* and *qSBPH2-c*, expressing antibiosis to SBPH were mapped on chromosomes 1 and 2, respectively, explaining 30.16% of the total phenotypic variance.

Keywords: Rice; SBPH (*Laodelphax striatellus* Fallén); Resistance; Quantitative trait loci(QTL).