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Fine Mapping of Zenith Derived Rice Stripe Virus Resistance Gene, *Stv-b*

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Rice stripe virus (RSV) disease is one of the major constraints in rice production, transmitted by the small brown planthopper (SBPH; *Laodelphax striatellus*). Upon RSV infection, plants develop typical symptoms, which include chlorosis and weakness of newly emerged leaves, white and yellow spots, stripe on leaves, and necrotic and wilting leaves, resulting in plant growth inhibition, oxidative damage that may culminate in programmed cell death (PCD) and plant death in severe epidemics. Although RSV-resistant quantitative trait loci (QTLs), *Stv-a*, *Stv-b*, and *Stv-bi*, were mapped using various resistant varieties, one RSV-resistant gene, *OsSOT1*, has been identified so far. In this study, we used the rice cultivar Zenith, known to carry *Stv-b*, to investigate novel RSV-genes through fine mapping. Therefore, we crossed Zenith (Donor parent, RSV resistant) with Ilpum (Recurrent parent, RSV susceptible) to fine-map using a BC_2F_2 population of 2100 plants. Chromosome segment introgression lines that were heterozygous at a different region were selected, two types of heterozygous lines showed an heterozygous genotype between Sid2 and Sid75 to Indel9 and RM6680. Interestingly, we identified *qSTV11*^{Z} region harboring *Stv-b*, covering about 171-kb region between the InDel markers Sid75 and Indel8. The localization of *qSTV11*^{Z} provides useful information that could be used for marker-assisted selection and determination of genetic resources in rice breeding.

Key words: Rice stripe virus, quantitative trait locus, *Stv-b*

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