

**PB-73**

## Fine Mapping of *Stv-b* derived Rice Stripe Virus Resistance Gene

Sais-Beul Lee<sup>1</sup>, Hyunggon Mang<sup>1</sup>, Nkulu Rolly Kabange<sup>1</sup>, Ju-Won Kang<sup>1</sup>, Ji-Yun Lee<sup>1</sup>, Youngho Kwon<sup>1</sup>, Gi-Un Seong<sup>1</sup>, So-Myeong Lee<sup>1</sup>, Dongjin Shin<sup>1</sup>, Jong-Hee Lee<sup>1</sup>, Ki-Won Oh<sup>1</sup>, Dong-Soo Park<sup>1\*</sup>

<sup>1</sup>National Institute of Crop Science, Miryang 50424, Republic of Korea

### [Introduction]

Rice Stripe Virus (RSV) disease, transmitted by the leafhopper (SBPH; *Laodelphax striatellus*), is one of the major biotic constraints in rice production. Plants infected with RSV develop typical symptoms such as chlorosis, weak newly emerged leaves, white and yellow spots, streaks on the leaves, and necrotic and wilted leaves, and stunted plant growth. In the process, plants experience oxidative stress, which may lead to oxidative damage and culminate to programmed cell death (PCD), and eventually plant necrosis in severe epidemics. In this study, we used the rice variety Zenith that carries *Stv-b*, to examine novel RSV genes by fine mapping. For fine mapping, we employed a BC<sub>3</sub>F<sub>2</sub> NILs population (n=659) derived from a cross between Zenith (donor parent, RSV resistant) and Ilpum (recurrent parent, RSV susceptible). The localization of *qSTV11<sup>Z</sup>* provides useful information that could be used for marker-assisted selection and developing genetic resources for rice breeding.

### [Materials and Methods]

The population was developed in the experimental fields of the National Institute of Crop Science of the Rural Development Administration in Miryang, Korea. The BC<sub>3</sub>F<sub>2</sub> NILs population (n=659) was used for fine mapping. The bioassay was performed using the method described by Kwon et al. (2012)

### [Results and Discussions]

Mapping RSV-resistant quantitative trait loci (QTLs), *Stv-a*, *Stv-b*, and *Stv-bi* using various resistant varieties has so far revealed one RSV-resistant gene, *OsSOT1*. We narrowed down the position of *qSTV11<sup>Z</sup>* region that harbors *Stv-b* and covers a region of approximately 129kb between the InDel markers Indel9 and Indel8 using newly selected two separate lines (61005-1-78 and 61005-2-69). From this results, we could not conclusively determine whether *Stv-b* and *Stv-bi* are allelic or independent genes,

### [Acknowledgement]

This work was conducted with support from the Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ014774012022 ), Rural Development Administration, Republic of Korea.

\*Corresponding author: E-mail parkds9709@korea.kr Tel. +82-55-350-1165N