

Selection of Germplasm Harboring Novel Sources of Rice Stripe Virus Resistance Gene

Sais-Beul Lee¹, Tae-Heon Kim¹, Joo-Won Kang¹, Su-Min Jo¹, Jun-Hyun Cho¹, Ji-Yoon Lee¹, Jong-Hee Lee¹, Yeong-Ho Kwon¹, You-Chun Song¹, Jong-Min Ko¹, Dong-Soo Park^{1*}

¹National Institute of Crop Science, Miryang 50424, Republic of Korea

[Introduction]

Rice stripe virus (RSV) is one of the major constraints which is transmitted by the small brown planthopper (SBPH; *Laodelphax striatellus*). Typical symptoms of RSV are chlorosis and weakness of newly emerged leaves, white and yellow spots, stripe and necrotic on leaves, necrotic and wilting leaves, as a consequence, plant growth decline and the contaminated plants are gradually die. (Takahashi et al. 1991). In our previous study, we screened 5 RSV resistant cultivar including ‘Padi Adongumarat’, ‘Tung Ting Wan Hien 1’, ‘02428’, ‘Erguailai’, and ‘Daw dam’, which harbors different resistance allele with *Stv-b*¹.

In this study, we further classified the resistant varieties by using MAS and sequence analysis on *Stv-b* (Lee et al., 2017) and *OsSOT1* (Zhang et al. 2014) to diversify resistance genes of rice stripe virus.

[Materials and Methods]

Five RSV resistance reported by Kwon et al. (2012) were used to identify novel source of resistance on rice stripe virus. Six Sid (Stripe virus Insertion and Deletion) markers (Lee et al., 2017) and Indel7 marker (Kwon et al., 2012) were used for analysing *Stv-b* and *Stv-bi*, respectively. Allele on *OsSOT1* (Zhang et al. 2014) were analyzed by sequence analysis on each varieties.

[Results and Discussions]

Sequence analysis revealed that Daw Dam and Erguailai harbor *OsSOT1*. Genotype analysis on *Stv-b* using six Sid markers in the *qSTV11²* region represent that Daw Dam and Erguailai expected to have *OsSOT1* gene as well as *Stv-b*. Finally, we identified three varieties, 02428, and Tung Ting Wan Hien 1 as the novel source of Rice Stripe Virus resistance. As a result of reaffirm bioassay, five cultivars including zenith were harbored the RSV resistance.

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*Corresponding author: Tel. +82-55-350-1184, E-mail. parkds9709@korea.kr