Candidate Gene Analysis to Rice Bacterial Leaf Blight Resistance of Korean Races of Xoo (*Xanthomonas oryzae*) in Rice Genetic Resources by GWAS Analysis

Myung Chul Lee*, Yu-Mi Choi, Myoung-Jae Shin, Hyemyeong Yoon, Sukyeung Lee and Kebede Taye Desta

National Agrobiodiversity Center, National Institute of Agricultural Sciences, RDA, Jeonju 54874, Republic of Korea

Bacterial leaf blight (BLB), caused by *X. oryzae* pv. *oryzae*(Xoo), is one of the most destructive diseases of rice due to its high epidemic potential. Understanding BLB resistance at a genetic level is important to further improve the rice breeding that provides one of the best approaches to control BLB disease. In the present investigation, a total of 10,000 accessions of rice germplasm were tested to resistance degree of four Korean isolated races (K1, K2, K3 and K3a) of Xoo by bioassay and a diverse 268 accessions was selected to the genome-wide association study (GWAS) using high quality 34,724 SNPs to identify the associated with resistance loci. LOC_Os04g53160 of chromosome 4 was significantly associated with K1 race resistant. LOC_Os11g46230 and LOC_Os11g47150 of chromosome 11 were highly associated with K2 and K3 races as 23.7 and 27.4 of *-log*(P) value, but K3a resistant loci was weakly associated at LOC_Os03g55270 of chromosome 3. The results of the GWAS validate known gene of BLB resistant and identified novel loci of R genes that provide useful targets for further investigation to help the breeding system and identified gene and QTL provide valuable sources for further functional characterization.

Key words: Rice, Genome-wide association analysis (GWAS), Rice bacterial leaf blight (BLB)

[This work was supported by a grant (No. PJ013539012020) from the National Institute of Agricultural Sciences, Rural Development Administration, Republic of Korea.]

*(Corresponding author) E-mail: mcleekor@korea.kr, Tel: +82-63-238-4900