OA-05

QTL analysis of different quantitative data to Bacterial Leaf Blight in rice

Xiao-Xuan Du¹, Hak Yoon Kim², Kyung-MinKim^{1*}

¹School of Applied Biosciences, College of Agriculture & Life Science, Kyungpook National University, Daegu, 41566, Korea ²Department of Global Environment, Keimyung University, Daegu, 42601, Korea

[Introduction]

In the world, Bacterial blight is one of the most serious stress of rice. The earlier the disease occurs, the higher the yield loss. Yield loss due to bacterial blight can be as much as 70% when susceptible varieties are grown, in environments favorable to the disease. When plants are infected at booting stage, bacterial blight does not affect yield but results in poor quality grains and a high proportion of broken kernels.

[Materials and Methods]

In this study, CNDH and SNDH two kinds of rice population were used as the materials. Plating and field trial were in spring and summer 2016, 2017 at trial station of Kyungpook National University at Gunwi in Korea. Cultivate k3 of bacterial leaf blight was cultured on PSA (Peptone Sucrose Agar). After 40 days field planting, make the K3 bacterial culture mix with sterile water and adjusted the culture suspension quantity to OD600= 1. Than used leaf clipping method (Kauffman, 1973) by inoculation on the plant materials.

[Results and Discussions]

In the world, Bacterial blight is one of the most serious stress of rice. The earlier the disease occurs, the higher the yield loss. Yield loss due to bacterial blight can be as much as 70% when susceptible varieties are grown, in environments favorable to the disease. When plants are infected at booting stage, bacterial blight does not affect yield but results in poor quality grains and a high proportion of broken kernels. Bacterial blight is caused by Xanthomonas oryzae pv. oryzae. the disease favors temperatures at 25—C, with relative humidity above 70%. In general, It is commonly observed when strong winds and continuous heavy rains occur, allowing the disease-causing bacteria to easily spread through ooze droplets on lesions of infected plants. In this study, through the 2016 and 2017 two years' field trials. I used QTL program found the defense genes in the CNDH rice population genetic map of chromosome 6, between RM20092 and RM20176. Also I used HPLC to analysis the compounds of the lesion length by BLB. The HPLC results for QTL analysis I get 9 regions in 6 chromosomes. And using plant molecular breeding techniques to make a new rice population can improve the resistance to BLB disease. Also these defense genes can be used for some other areas of molecular biology.

[Acknowledgements]

This work was supported by a grant from the Next-Generation BioGreen 21 Program (No. PJ013647032018), Rural Development Administration, Republic of Korea.

^{*}Corresponding author: Tel. +82-53-950-5711, E-mail. kkm@knu.ac.kr