

QTL Analysis with HPLC Data to Bacterial Leaf Blight in Rice (*Oryza sativa* L.)

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[Introduction]

Agriculture is the most primitive civilized Activities of mankind but also the propellant of civilization development. Because it is the most basic material goods source of mankind. Among these materials rice is one of the most important part of these, we call them the substance of survival. From the beginning of the agricultural activities to the present we have experienced three industrial revolutions and are experiencing the Fourth Industrial Revolution. With the development of science and technology makes the efficiency of agricultural production is higher and higher, but compared with the original we are facing the same problem: natural disasters; pests and diseases; now also face the depletion of resources, environmental degradation and other issues. Therefore, improve and cultivate new crop varieties to make it better resistance and more production for better develop modern agriculture. It's very helpful for human social development. And also it is the responsibility and task of modern molecular breeding.

[Materials and Methods]

In this study, through the 2016 and 2017 two years' field trials. I used QTL program to analysis HPLC data to find the defense genes in the CNDH rice population genetic map and select the target gene to cloning for molecular breeding.

[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 25–34°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. 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.

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