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Development of the *OsWRKYq6* Gene Breeding Line related to *Xanthomonas oryzae pv. Oryzae* Resistance based on QTL Mapping

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[Introduction]

Rice is cultivated in almost all over the world due to its adaptable nature under various environmental conditions due to which it is regarded as a strategic crop for food security throughout the world. However, susceptibility of rice variety to different diseases and insect is a major problem which may lead to reduce the rice yield in the near future. Previous reports show that, 25% annually yield loss causes by diseases and insects, such as stem borers insects are most destructive, while rice blast caused by the fungus *Pyricularia oryzae*, and bacterial blight caused by *Xanthomonas oryzae pv. oryzae* (*Xoo*) are the two of the most dangerous and common diseases in rice production.

[Materials and Methods]

Bacterial leaf blight (BLB) is an important and devastating rice disease caused by pathogenic *Xanthomonas oryzae pv. oryzae* (*Xoo*). Quantitative trait locus (QTL) analysis was conducted for genetic mapping and target region identification using WinQTLcart software version 2.5 at threshold of 3.0 LOD. In this study, 140 line of Cheongcheong-Nagdong double haploid (CNDH). And using NCBI, RAPDB, RICEPRO and JUSTBIO data bases.

[Results and Discussions]

In the current study, we have confirmed the location of new QTLs related to BLB resistance on chromosomes 6, 8 and 11, which have not been fully evaluated. At the same time, the research on the resistance target gene *OsWRKYq6* screened on chromosome 6 gives us full confidence in the research of candidate genes in other target regions. In the future, we will identify other QTL characteristics for the desired traits on chromosomes 8 and 11 in this study, which will also improve the efficiency of the marker-assisted breeding program. This research has opened up a new field for molecular breeders to overexpress the identified genes of *Xoo* and other pathogenic bacteria.

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