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Extensive Genome, Transcriptome and eQTL Analysis of Xa39 Gene, OS11g0588600, Unraveling A Novel Gene through Haplotype and Evolutionary Analysis in KCore Rice

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[Introduction]

Bacterial leaf Blight (BLB) caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) is one of the major diseases in rice. BLB is a serious disease during the monsoon season and occurred in high yielding varieties under high nitrogenous fertilizers, especially in irrigated and rainfed lowland ecosystems. It attacks most rice cultivating areas such as Africa and Asia, causing 20-80% yield lost. Cultivating BLB resistance varieties is the most promising way to protect rice from BLB infection.

[Materials and Methods]

In this study, we used 475 core collection of Korean rice germplasms with 7 different ecotype groups. eQTLs analysis of specific *Xa39* gene was carried out and haplotype, haplotype diversity and *Fst* among ecotypes of *Xa39* gene were analyzed using genetic information.

[Results and Discussion]

In the Cis-regulatory element, 22,319,757 bp, the expression level was high with the high $-\log_{10} p$ value for eQTL analysis of *Xa39* gene. The genetic variance for the *Xa39* gene was observed 94.7% while that of residual variance was occurred 5.3%. As a result of haplotype analysis, a total of 171 haplotypes with 133 polymorphic sites (24 InDels, 109 SNPs) were identified in the coding region. For *Fst* analysis of *Xa39* gene, the highest mean weighted value was observed between Japonica and Aus and the lowest value was found between Indica and Admixture. In eQTL analysis of the Os11g0588600, *Xa39* gene, we found that SNP upstream 9kbp of *Xa39*, which T to C substitution, significantly reduced the expression of *Xa39* and our findings will provide important information to cultivate resistant rice varieties in the future.

Keywords: rice, Bacterial leaf Blight (BLB), haplotype diversity, eQTL, Xa39

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