

Identification of SNP Related to Leaf-angle Traits Using a Genome-Wide Association Study in Rice (*Oryza sativa* L.)

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[Introduction]

Leaf traits are always key issue to investigate in plant research.

[Materials and Methods]

In this study, we conducted to investigate a morphological trait in 294 rice accessions including Korean breeding lines. We also carried out a genome-wide association study (GWAS) to detect significant single nucleotide polymorphism markers and candidate genes affecting major agronomic traits. A Manhattan plot analysis of GWAS using morphological traits showed that phenotypic and statistical significance was associated with a chromosome in each group. The significance of SNPs that were detected in this study was investigated by comparing them with those found previously studied QTL regions related to agronomic traits. As a result, SNP (S8-19815442), which is significant with regard to leaf angle, was located in the known QTL regions. To observe gene mutations related to leaf angle in a candidate gene, Os08g31950, its sequences were compared with sequences in previously selected rice varieties.

[Results and Discussions]

In Os08g31950, a single nucleotide mutation occurred in one region. To compare relative RNA expression levels of candidate gene Os08g31950, obtained from GWAS analysis of 294 rice accessions and related to lateral leaf angle, we investigated relative levels by selecting 10 erect leaf-angle varieties and 10 horizontal leaf-angle varieties and examining real-time PCR. In Os08g31950, a high level of expression and various expression patterns were observed in all tissues. Also, Os08g31950 showed higher expression levels in the erect leaf-angle variety group and higher expression rates in the leaf than in the root. The candidate gene detected through GWAS would be useful in the development of new rice varieties with improved yield potential through future molecular breeding.

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