

Allele Mining for Rice Sheath Blight Resistance by Whole-Genome Association Mapping in a Tail-End Population

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Abstract : Rice sheath blight is one of the destructive fungal diseases in rice. We have thought that rice sheath blight resistance is a polygenic trait. Host-pathogen interactions and secondary metabolites such as lignin and phytoalexins are likely to be involved in defense against *R. solani*. However, to our knowledge, it is still unknown how sheath blight resistance can be enhanced in rice breeding. To seek for an alternative genetic factor that contribute to sheath blight resistance, we mined relevant allelic variations from rice core collections created in Japan. Based on disease lesion length on detached leaf sheath, we selected 30 varieties of the top tail-end and the bottom tail-end, respectively, from the core collections to perform genome-wide association mapping. Re-sequencing reads for these varieties were used for calling single nucleotide polymorphisms among the 60 varieties to create a SNP panel, which contained 1,137,131 homozygous variant sites after filtering. Association mapping highlighted a locus on the long arm of chromosome 11, which is co-localized with three sheath blight QTLs, qShB11-2-TX, qShB11, and qSBR-11-2. Based on the localization of the trait-associated alleles, we identified an ankyrin repeat-containing protein gene (ANK-M) as an uncharacterized candidate factor for rice sheath blight resistance. Allelic distributions for ANK-M in the whole rice population supported the reliability of trait-allele associations. Gene expression characteristics were checked to evaluate the functionality of ANK-M. Since an ANK-M homolog (OsPIANK1) in rice seems a basal defense regulator against rice blast and bacterial leaf blight, ANK-M may also play a role in the rice immune system.

Keywords : allele mining, GWAS, QTL, rice sheath blight

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