

Category	: 8th Rice Genetics Symposium
Select Theme	: Genetics of Biotic interactions: Stress tolerance, Mitigation and Microbiome
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Title of Entry	: Natural allelic variations among 3000 rice genomes associated with tungro virus resistance
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Select only one type of presentation	: 15 minute oral presentation
Abstract	: Candidates for stress resistance genes in rice can be selected by association mapping. Analyses of natural alleles for a target trait can substantiate the functional relevance of candidate genes. We attempted to identify genes controlling resistance to rice tungro viruses by combining analyses of association mapping and natural allelic variations of candidate genes. Tungro is caused by Rice tungro bacilliform virus (RTBV) and Rice tungro spherical virus (RTSV). Cultivar Utri Merah (UM) is resistant to RTBV and RTSV. An association mapping analysis suggested that RTSV resistance in UM was controlled by a recessive gene within a 200-kb region of chromosome 7. A gene for translation initiation factor 4 gamma (EIF4G) involved in virus replication found in the 200-kb region was selected as the candidate gene for RTSV resistance. EIF4G sequences from a set of RTSV-resistant rice plants indicated the association of RTSV resistance with non-synonymous SNPs within a 30-nt region of EIF4G. Examination for the 30-nt region among 3,000 rice genotypes revealed that 10% of the genotypes carry a tentative resistance EIF4G allele containing SNPs in the 30-nt region. Phenotyping for RTSV confirmed that about 90% of rice genotypes homozygous for a tentative resistance EIF4G allele were RTSV-resistant and those heterozygous for a resistance EIF4G allele segregated for RTSV resistance. Another association mapping analysis showed that RTBV resistance in UM was controlled by at least two dominant genes, one of which

was mapped to a 200-kb region in chromosome 4. The 200-kb region contains tandem Argonaute genes (AGO2-AGO3). Both genes are involved in RNA interference-mediated virus resistance, and thus were selected as the candidate genes for RTBV resistance. Examination for AGO2-AGO3 alleles among the 3,000 genotypes identified 59 genotypes carrying AGO2-AGO3 alleles containing at least one UM-specific SNP. Phenotyping for RTBV showed that average RTBV accumulation in 44 genotypes carrying two UM-specific AGO2 SNPs was significantly lower than that in 34 genotypes lacking UM-specific AGO2 SNPs, indicating strong association of AGO2 with RTBV resistance. Overall, these results demonstrate that analyses of natural allelic variations among the 3000 rice genotypes can facilitate identification of genes associated with specific traits.

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