

APPROACHES TO BROAD-SPECTRUM DURABLE RESISTANCE IN RICE

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Quantitative trait loci (QTL) that control disease resistance are predicted to confer broad-spectrum and durable resistance (BSDR). Practical application of disease resistance QTL in crop improvement programs is hindered because we lack several levels of knowledge, including an understanding of (1) the genes contributing to the QTL-governed phenotype, (2) why certain alleles of those genes are more effective than others in conferring resistance, and (3) how the genes function in BSDR. We are using two approaches to address these knowledge gaps. In a candidate gene approach, rice genes that are candidates for contributing to BSDR were identified by co-localization with resistance QTL in mapping studies. Subsequently, rice lines that exhibited high levels of resistance in multilocation trials were constructed by using marker assisted selection to accumulate chromosomal segments associated with different candidate genes. Targeted gene expression and functional analyses of candidate gene family members allowed us to focus on gene members involved in BSDR. In a second approach, we asked if transcriptome analysis can be selectively used to reveal genes/genetic regions under selection for BSDR in breeding programs. The relationships between expression patterns and genotypes were investigated under biotic and abiotic stresses using the 22K oligo chips (Agilent). The results suggest that transcript maps of parental and advanced backcross lines can be used to reveal genes of interest in regions contributing to QTL in the absence of a large recombinant population, a common situation in breeding programs. Identification of genomic regions with correlated expression enables us to identify discrete chromosomal regions (10-20 genes) that may underlie QTL. We are evaluating the possibility that coordinated expression of multiple adjacent genes could be contributing to a single QTL, a hypothesis with practical implications for selecting genotypes with the desired phenotypes.