Abstract Book

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Identifying a candidate gene for the broad-spectrum resistance qtl to phytophthora root rot and blight in pepper

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Root rot and blight caused by Phytophthora capsici is one of the most damaging diseases of pepper. While no R gene has been reported, all studied resistant accessions display a major effect QTL on chromosome P5. The clustering of 14 QTLs from independent studies resulted in 3 linked metaQTLs. We showed that the QTL Pc5.1 confers a broad-spectrum resistance to the 12 tested isolates collected worldwide and genetically divergent. A fine mapping delimited Pc5.1 to <0.4 cM. The physical map based on two BAC libraries delivered a reference sequence covering ~1.1 Mb. Automatic and manual gene annotation identified a huge proportion of transposable elements and a few ORFs. One ORF shows homology with a transcript differentially expressed in P. capsici-infected peppers, and exhibits SNPs between resistant and susceptible lines. We are now validating the candidate gene by Agrobacterium rhizogenes transformation, and achieving an association study to confirm the causal SNP. Identifying the responsible gene should facilitate marker-assisted selection, and the study of the molecular crosstalk between plant and pathogen.

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