



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

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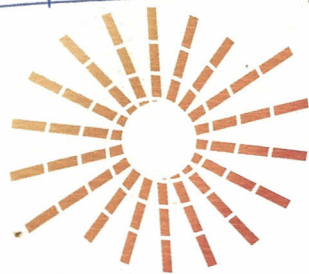
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Veronique Lefebvre

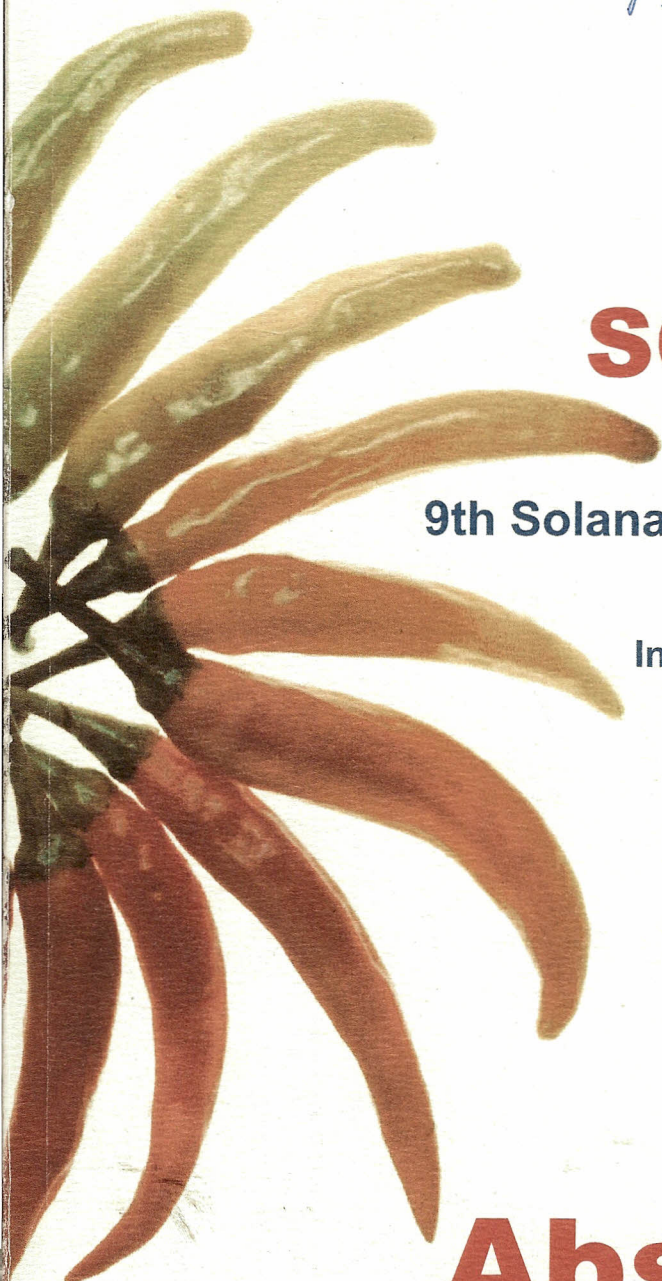


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Identifying a candidate gene for the broad-spectrum resistance qtl to phytophthora root rot and blight in pepper

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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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